



รายงานวิจัยฉบับสมบูรณ์

โครงการ: อนุชีววิทยาและวิทยาภูมิคุ้มกันของเชื้อไวรัสไข้หวัดนก H5N1

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มหาวิทยาลัยมหิดล

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รายงานວิจัยฉบับสมบูรณ์

ໂຄງການ: ອຸນໜີວິທີການແລະວິທີກາງຸມືຄຸມກັນຂອງເຊື້ອໄວຣສໄໝ້ວັດນກ H5N1

¹ພິໄລພັນນີ້ ພຸນວັດນະ, ¹ປະເສົຣີຈູ ເອົວຮາກຸລ, ¹ສຸດາ ລູຍຄີຣີໂຈນກຸລ,

²ວິທີວັນ ວິຣີຍະຮັດນີ້, ²ກອ່ານຸ້າ ໄຈ້ນ, ²ປານເທັນ ຮັດນາກ,

³ໂສກຄນ ເອີມຄີຣິຄາວ, ³ຄໍານວານ ອຶ່ງໜູ້ສັກດີ, ³ຈັກຮັ້ງ ພິທີຍາວງຄ້ອານໜໍ,

³ຮູ້ງເຮືອງ ກິຈພາຕີ

¹ ການວິຊາຈຸລຊີວິທີການ ດະແຫຼາຍຄາສົກສົງ ມະຫາວິທະຍາລັບມິດລ

² ດະແຫຼາຍຄາສົກສົງ ມະຫາວິທະຍາລັບມິດລ

³ ສຳນັກະບາດວິທີການ ກຽມຄວບຄຸມໂຮດ ກະທຽວງສາຫະການສຸຂ

ສັບສນຸນໂດຍສໍານັກງານກອງທຸນສັບສນຸນກາງວິຈີ

(ຄວາມເຫັນໃນรายงานນີ້ເປັນຂອງຜູ້ວິຈີ ສກວ.ໄມ່ຈໍາເປັນຕ້ອງເຫັນດ້ວຍເສມອໄປ)

กิตติกรรมประกาศ

งานวิจัยครั้งนี้ได้ตั้งเป็นที่จะศึกษาเรื่องราวเกี่ยวกับเรื่องของไข้หวัดนก แต่เนื่องจากผู้ป่วยไข้หวัดนกได้หมดไปจากประเทศไทยตั้งแต่กลางปี พ.ศ. 2549 และในปี พ.ศ. 2552 ได้มีการระบาดทั่วโลกของเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ A (H1N1) ลุก浪มาถึงประเทศไทย ขณะผู้วิจัยจึงได้ขยายขอบเขตของการศึกษาวิจัยครอบคลุมทั้งไวรัส H5N1 และไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ A(H1N1) ดังปรากฏอยู่ในผลงานเล่มนี้

ขณะผู้วิจัยขอขอบพระคุณ สำนักงานกองทุนสนับสนุนการวิจัย (สกว.) เป็นอย่างสูง ที่ให้ทุนสนับสนุนโครงการวิจัยนี้ นอกจากผลงานตีพิมพ์ดังที่ปรากฏอยู่ในรายงานฉบับนี้แล้ว ทุนวิจัย สกว. ยังมีส่วนทำให้คณะผู้วิจัยได้มีส่วนช่วยเหลือหน่วยงานสาธารณสุขของประเทศไทย ใน การเป็นทีมงานคุ้นเคยช่วยนิจัยผู้ป่วยไข้หวัดนกในรายที่เป็นปัญหา และสืบสานการระบาดของโรคไข้หวัดใหญ่สายพันธุ์ใหม่ จนนำไปสู่การค้นพบผู้ป่วยสองรายแรกของประเทศไทย และช่วยทำการตรวจสอบความคุ้มกันให้แก่บุคลากรทางการแพทย์ของหลายหน่วยงาน ขณะผู้วิจัยขอขอบพระคุณ US Centers for Disease Control and Prevention ที่ให้การสนับสนุนงานวิจัย “ไข้หวัดนกภาคสนาม; Professor Robert Webster ที่ปรึกษาการวิจัยและให้ความอนุเคราะห์ low pathogenic influenza 16 subtypes; Dr Adrian Farmer ที่ปรึกษาด้าน satellite telemetry technique; Dr. Bernard Moss, US. National Institute of Health ที่ให้ความอนุเคราะห์ plasmid สำหรับการสร้าง recombinant vaccinia virus; Southeast Asia Infectious Clinical Research Network ที่อนุเคราะห์ archival samples; ขอบคุณ บริษัท Roche, Belgium สำหรับ oseltamivir carboxylate และบริษัท GlaxoSmithKline สาธารณนาจักร สำหรับ zanamivir ขอบพระคุณสำนักงำนbadวิทยา กรมควบคุมโรค และกรมวิทยาศาสตร์การแพทย์ กระทรวงสาธารณสุข กรมอุทยานแห่งชาติ สัตว์ป่าและพันธุ์พืช ที่ได้ร่วมโครงการวิจัยนี้ ขอบพระคุณสำนักงานพัฒนาวิทยาศาสตร์และเทคโนโลยีแห่งชาติ ที่ร่วมให้การสนับสนุนค่าใช้จ่ายในการวิจัยบางโครงการ ขอขอบพระคุณผู้ร่วมวิจัยและอาสาสมัครในโครงการ ขอขอบคุณนักศึกษา บัณฑิตในความดูแลทุกคน นางสาวสตีริกซ์ ไสงาน ผู้ประสานงานโครงการวิจัย นางสาวพิชณุ ภู่รักษ์ นางสาวกรรณิการ์ นทีรัตน์ และ นางสาวรำพร กุหลาบ นักวิทยาศาสตร์ผู้ปฏิบัติงานซึ่งมีความรับผิดชอบ ทำงานหนัก และทุ่มเทเพื่อให้งานวิจัยนี้สำเร็จลงได้ ขอกราบขอบพระคุณผู้บริหาร สกว. และขอบคุณ คุณพรพิมล กิตติมศักดิ์ เจ้าหน้าที่บริหารโครงการ สำนักงานกองทุนสนับสนุนการวิจัย ที่ได้ช่วยบริหารจัดการและประสานงานตลอดโครงการด้วยน้ำใจและอัชฌาสัย อันดีเยี่ยม สุดท้ายนี้คณะผู้วิจัยขอขอบพระคุณคณะแพทยศาสตร์ศิริราชพยาบาล และมหาวิทยาลัยมหิดล ที่ได้ให้การสนับสนุนการวิจัยในสถาบันเป็นอย่างดีเยี่ยมตลอดมา

บทคัดย่อ

รหัสโครงการ:

ชื่อโครงการ : อนุชีววิทยาและวิทยาภูมิคุ้มกันของเชื้อไวรัสไข้หวัดนก H5N1

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ระยะเวลาโครงการ : 3 ปี

งานวิจัยนี้ได้ทำการศึกษาคุณสมบัติทางอนุชีววิทยาระดับโมเลกุลของเชื้อไวรัสไข้หวัดนก H5N1 ที่มีความสามารถในการก่อโรครุนแรง และเชื้อไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ A(H1N1) 2009 รวมทั้งศึกษาการตอบสนองทางภูมิคุ้มกันต่อการติดเชื้อไวรัสทั้งสองด้วย การศึกษาด้วยกล้องจุลทรรศน์อิเล็กตรอนแสดงให้เห็นว่าอนุภาคไวรัสมากกว่า 80% มีรูปร่างเป็นทรงกลม และส่วนน้อยที่เหลือ มีรูปร่างแบบสายยาว หรือรูปร่างไม่แน่นอน กลไกในการก่อโรคของไวรัส H5N1 ประการหนึ่ง คือความสามารถในการเพิ่มจำนวนและกระตุ้นให้เกิดการสร้าง cytokine ในเซลล์เยื่อบุหลอดเลือดดำของมนุษย์ได้ดี นอกจากนี้ยังได้ค้นพบกลไกใหม่อีกประการหนึ่ง ที่ทำให้ไข้หวัดนกมีความรุนแรงในการก่อโรค คือ ชีแมกกลูตินของเชื้อไวรัส H5N1 ช่วยให้ไวรัสสามารถทบทานต่อสารบัญที่มีอยู่ในเชื้อริมได้ งานวิจัยนี้ได้ทำการเฝ้าระวังและสำรวจหาไวรัสไข้หวัดนกสูกผสมที่อาจมีอยู่ของไวรัสไข้หวัดใหญ่ของมนุษย์รวมอยู่ในอนุภาคด้วย ได้ตรวจไวรัสไข้หวัดนกทั้งหมดจำนวน 109 สายพันธุ์ ในระหว่างปี พ.ศ. 2546-2549 โดยวิธี multiplex RT-PCR แต่ก็ไม่พบว่ามีไวรัสสูกผสมเกิดขึ้น การวิเคราะห์ทาง phylogenetic แสดงให้เห็นว่า การกลับมาของการระบาดของเชื้อ H5N1 มักเกิดจากไวรัสที่รอดเหลือจากการระบาดครั้งก่อน ไม่ใช่เป็นการนำสายพันธุ์ใหม่เข้ามายากประเทศอื่น การวิจัยยังได้พบไวรัสสูกผสม 2 เชื้อ อุบัติขึ้นในปี พ.ศ. 2550 จากการรวมตัวระหว่างไวรัสไข้หวัดนก H5N1 ด้วยกันเอง ในปี พ.ศ. 2550 ได้ทำการวินิจฉัยการติดเชื้อไข้หวัดนก clade 2.3.4, genotype V ในผู้ป่วยชาวลาวซึ่งเข้ามารับการรักษาในประเทศไทยและเสียชีวิตในโรงพยาบาลที่จังหวัดหนองคาย

เทคนิค hemagglutination-inhibition (HI) assay โดยการใช้เม็ดเลือดแดงห่านร่วมกับ เทคนิค microneutralization (microNT) assay ซึ่งทำการทดสอบในเซลล์ MDCK ได้ถูกพัฒนาขึ้นเพื่อใช้ตรวจหาแอนติบอดีต่อเชื้อ H5N1 ระดับของแอนติบอดีที่เพิ่มขึ้นในเชื้อริมคู่จะสามารถตรวจพบได้ที่ประมาณ 15 วัน หลังเริ่มมีอาการป่วย ทั้ง HI และ NT antibody ที่ระดับ titer ≥ 40 (ไม่คิดรวมปริมาตรในหลุมทดสอบ) สามารถคงอยู่ได้เป็นเวลาระยะถึง 5 ปี หลังจากการป่วย นอกจากนี้ยังพบว่า ผู้สูงอายุที่ได้รับวัคซีนไข้หวัดใหญ่จำนวน 5.2% มีการเพิ่มขึ้นของระดับ

แอนติบอดีที่สามารถทำปฏิกิริยาข้าม (cross-neutralizing antibody) กับเชื้อ H5N1 ได้ งานวิจัยนี้ ได้ทำการสร้าง vaccinia recombinant viruses ทั้งหมด 6 แบบ ที่มีการสอดแทรกยีนต่างๆ ของ ไวรัส H5N1 ได้แก่ HA, NA, NP, M, และ NS รวมทั้ง vaccinia recombinant virus ที่มีการใส่ เนพะ pSC11 plasmid vector เข้าไปเท่านั้นเพื่อใช้เป็น control จากการวิเคราะห์ด้วยวิธี Western blot พบว่าผู้รอดชีวิตจากการติดเชื้อ H5N1 ทั้ง 4 ราย มีแอนติบอดีต่อชีวิตนิโน 3 แบบ คือ HA0, HA1 และ HA2 domains ในขณะที่ผู้ไม่ติดเชื้อ H5N1 จะมีแอนติบอดีต่อ HA2 domain เท่านั้น และเมื่อนำเชลล์ที่ติดเชื้อ vaccinia recombinant viruses ที่มีการแสดงออกของ โปรตีนต่างๆ ของเชื้อไปหัวดันกมาใช้เป็นแอนติเจนในการทดสอบหาแอนติบอดีต่อเชื้อ H5N1 ด้วยวิธี indirect immunofluorescence ได้ผลว่าชีรั่มของผู้รอดชีวิตจากการติดเชื้อ H5N1 ทั้ง 4 ราย และชีรั่มจากกลุ่มที่ไม่มีการติดเชื้อ H5N1 เกือบทั้งหมดสามารถมีแอนติบอดีต่อโปรตีน ทดสอบทุกชนิด แต่กลุ่มผู้รอดชีวิตจากการติดเชื้อ H5N1 จะมีระดับของแอนติบอดีที่สูงกว่า นอกจานี้การทดสอบด้วยวิธี ELISpot โดยใช้ overlapping peptide pools ที่ครอบคลุมโปรตีน NP และ M ทั้งสาย ยังทำให้ทราบว่าผู้รอดชีวิตจาก H5N1 มีการสร้างภูมิคุ้มกันด้านเชลล์ซึ่ง สามารถคงอยู่ได้นานเท่ากับภูมิคุ้มกันแบบสารน้ำ และเมื่อทำการวิเคราะห์ต่อไปด้วยเทคนิค flow cytometry ก็พบว่า cytotoxic T cells ที่มีอยู่นั้นส่วนมากเป็นชนิด CD4+ T lymphocyte ในขณะที่พบ CD8+ T lymphocytes เป็นส่วนน้อย และ NP peptides ทำให้เกิดการกระตุ้นได้ สูงกว่า M peptides

จากการใช้เทคนิคการสื่อสารผ่านสัญญาณดาวเทียม (satellite telemetry) ในการติดตามนก นางนวลที่บางปู แสดงให้เห็นว่าเส้นทางบินของนกนางนวลครอบคลุมถึง 7 ประเทศที่มีรายงาน การระบาดของเชื้อไข้หวัดนก ได้แก่ ไทย กัมพูชา เวียดนาม จีน อินเดีย บังคลาเทศ และ เมียนมาร์ โดยมี 3 ประเทศเป็นถิ่นที่อยู่อาศัย ได้แก่บริเวณทะเลสาบในธิเบต และซินเจียงเป็นที่ ผสมพันธุ์และวางไข่ บริเวณอ่าวไทยตอนใน และทะเลสาบกัมพูชา เป็นที่ที่นกอพยพมาอาศัยใน ฤดูหนาว ส่วนอีก 4 ประเทศที่เหลือเป็นจุดหยุดพักในระหว่างอพยพ เนื่องจากลักษณะ พันธุกรรมของไวรัสในประเทศไทยและจีนมีความแตกต่างกัน โดยไวรัสในประเทศไทยจดอยู่ใน clade 1 แต่ไวรัสในประเทศจีนจดอยู่ใน clade 2 จึงไม่พบความเชื่อมโยงระหว่างเชื้อที่ก่อการ ระบาดในสองประเทศนี้ ในขณะที่เชื้อไข้หวัดนกที่พบในไทย กัมพูชา และเวียดนาม เป็นไวรัส clade 1 เหมือนกัน นอกจากนั้นการระบาดของโรคไข้หวัดนกครั้งแรกๆ ในประเทศไทยทั้งสามนี้ยัง เกิดขึ้นในเวลาใกล้เคียงกันแสดงว่าเชื้อไวรัสจะมีที่มาจากการแพร่กระจายจากข้อมูลที่ได้จาก การติดตามเส้นทางการบินของนกประกอบกับผลการทดสอบเกี่ยวกับความทันท่วงของนกที่มีดีเชื้อ ไวรัสเข้าไป ทำให้สันนิษฐานได้ว่านกอพยพอาจมีบทบาทในการแพร่กระจายของเชื้อไข้หวัดนก

หลังจากสิ้นสุดการระบาดของเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ H1N1 2009 ระลอกแรก พบอัตรา การติดเชื้อในกลุ่มผู้บริจากโลหิตจำนวน 7% และ ในกลุ่มบุคลากรทางการแพทย์จำนวน 12.8% การศึกษาในระดับชุมชนพบอัตราการติดเชื้อในเด็กจำนวน 58% ในขณะที่พบการติดเชื้อใน

ผู้ใหญ่เพียง 3.1% เท่านั้น นอกงานนี้งานศึกษาวิจัยนี้ยังแสดงให้เห็นว่า nasopharyngeal aspirate เป็นสิ่งส่งตรวจที่ให้ผลໄວต่อการวินิจฉัยการติดเชื้อตี่สุด รองลงมาคือ nasal swab และ throat swab ตามลำดับ การวิเคราะห์ตัวอย่างจากทางเดินหายใจที่เก็บอย่างต่อเนื่องพบว่าปริมาณไวรัสที่ถูกปล่อยออกมายังจากผู้ป่วยจะอยู่ในช่วง 2.6×10^2 - 8.1×10^9 copies/ml และช่วงเวลาที่ผู้ป่วยสามารถแพร่เชื้อจะอยู่ระหว่าง 1 ถึง 11 วัน (เฉลี่ย 5 วัน) การประเมินความสามารถของวัคซีนซึ่งใช้ไข้หวัดใหญ่สายพันธุ์ใหม่ H1N1 ชนิด monovalent inactivated ในการกระตุ้นภูมิคุ้มกันในผู้ติดเชื้อ HIV เปรียบเทียบกับกลุ่มผู้ไม่ติดเชื้อ พบว่าในกลุ่มผู้ติดเชื้อ HIV ที่ได้รับวัคซีน มีอัตรา seroconversion เท่ากับ 32% และ seroprotection เท่ากับ 33.3% ขณะที่ในกลุ่มผู้ไม่ติดเชื้อ HIV พบอัตรา seroconversion และ seroprotection เท่ากันคือ 35%

งานวิจัยนี้ได้นำเทคนิค 4 อย่าง ได้แก่ การหาลำดับนิวคลิโอล่าด้วย NA, การลดลงของจำนวน plaque (plaque reduction assay), การยับยั้งเอนไซม์นิวราไมนิดาส (neuraminidase inhibition- NAI assay) และ วิธีวัดปริมาณนิวคลิโอล่าโปรตีนที่ลดลง (ELISA-based viral nucleoprotein reduction assay) มาใช้ในการศึกษาและเฝ้าระวังการเกิดเชื้อไข้หวัดใหญ่ต่อตัวยา โดยข้อดีของเทคนิค ELISA based viral nucleoprotein reduction assay คือ สามารถใช้ใน การทดสอบกับยาหรือสารที่ออกฤทธิ์ยับยั้งต่อเชื้อไวรัสได้ ดังนั้นวิธีนี้จึงดีกว่าวิธี NAI ที่ใช้ทดสอบกับยาที่ออกฤทธิ์ต้านเฉพาะนิวราไมนิดาสของไวรัสเท่านั้น นอกจากนี้วิธีนี้ใช้เวลาไม่นานและใช้สารเคมีทดสอบในปริมาณน้อยเมื่อเทียบกับวิธีมาตรฐานคือ plaque reduction assay แต่ข้อเสียของวิธี ELISA based viral nucleoprotein reduction assay คือ ไม่สามารถใช้ทดสอบกับไวรัสซึ่งมีอัตราการเพิ่มจำนวนที่ช้าผิดปกติได้

คำหลัก : ไข้หวัดนก H5N1, ไข้หวัดใหญ่สายพันธุ์ใหม่ 2009, การตอบสนองทางภูมิคุ้มกัน, ระบบวิทยาทางชีรร์ม, นกอพยพ, ระบบสื่อสารผ่านดาวเทียม

Abstract

Project Code:

Project Title: Molecular biology and immunology of avian influenza H5N1 viruses

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The present study investigated the molecular biological properties of the highly pathogenic avian influenza (HPAI) H5N1 viruses and the 2009 pandemic A(H1N1) viruses (H1N1pdm virus) as well as the immunological responses against those viral infections. Electron microscopy demonstrated that more than 80% of the viral particles in a population of an influenza isolate were spherical type, while filamentous and pleomorphic forms were the minor populations. Based on M protein, morphological type of influenza viruses was unlikely under control of genetic control. A pathogenic mechanism of HPAI H5N1 viruses involved the active replication and cytokine induction in human vein endothelial cells. Additionally, a novel pathogenic mechanism that made HPAI H5N1 virus virulent involved the viral hemagglutinin mediated resistance to the serum inhibitors. Surveillance for the reassortant H5N1 virus carrying human genomic segment had been conducted in 109 HPAI H5N1 viruses collected between 2003 and 2006 by using multiplex reverse transcription-polymerase chain reaction (RT-PCR), and no reassortant was found. Our genetic analysis showed that the resurgence of the HPAI H5N1 outbreak usually occurred from the indigenous viruses surviving after subsidence of the previous outbreaks, not from the re-introducing of the new strain from the other country. Two reassortants emerged from the reassortment between two H5N1 parental viruses were discovered in 2007. An infection caused by the clade 2.3.4, genotype V virus was diagnosed in a Lao patient who came into Thailand for receiving medical care and died in the Nongkhai hospital in 2007.

Goose erythrocyte-hemagglutination inhibition (HI) assay together with microneutralization (microNT) assay in MDCK cells were used for the detection of antibody to H5N1 viruses. The increasing antibody titer in paired blood was shown

approximately 15 days after disease onset. Both HI and NT antibodies at the titer of \geq 40 (regardless of total volume in the reaction) persisted for almost 5 years after the disease onset in cases that could be followed-up that far. An increase in level of cross neutralizing antibody against HPAI H5N1 could be seen in 5.2% of the old-age vaccinees who received seasonal influenza vaccine. Six recombinant vaccinia viruses carrying individual gene of HPAI H5N1 virus, i.e., HA, NA, NP, M and NS and the pSC11 plasmid vector control were constructed. Western blot analysis showed that all 3 form of HA: HA0 and its cleavage products, HA1 and HA2 domains were expressed in the HA recombinant vaccinia virus-infected TK⁻ cells. H5N1 survivors contained the antibodies that directed against all 3 forms of HA; while all non-H5N1 subjects contained cross reactive antibody against the HA2 domain only. The viral proteins expressed in cells infected with these constructs were used as the test antigen in the indirect immunofluorescence assay for detection of the H5N1 antibodies. The result demonstrated that sera from all 4 survivors and almost of the non-H5N1 subjects were reactive against all kinds of these viral proteins; but the antibody titers were higher in the survivors. H5N1 survivors also developed cell-mediated immunity which lasted as long as the humoral immunity as determined by ELISpot assay using overlapping peptide pools spanning the entire NP and M proteins. Flow cytometry assay demonstrated that majority of the reactive cytotoxic T cells from H5N1 survivors were CD4+T lymphocytes whereas CD8+T lymphocytes were the minor population; and NP peptides yielded stronger reactivity than M peptides.

Satellite telemetry tracking of the Brown headed gulls from the Bang Poo study site demonstrated their flyways that spanned 7 countries (Thailand, Cambodia, Vietnam, China, India, Bangladesh and Myanmar) which were affected by H5N1 AI. This gull species inhabits 3 countries; Tibet lake area and Xinjiang in west China as the breeding grounds, and the inner gulf of Thailand as well as the TonLe Sap lake area in Cambodia as the places for overwintering. The other 4 countries were the places for stopover during migration. The difference in the viral genetic clades between H5N1 viruses in Thailand (clade 1 virus) and China (clade 2 virus) suggested that there was no linkage between AI spread between the two countries. On the other hand, the HPAI H5N1 virus found in Thailand, Cambodia and Vietnam belonged to clade 1; and the firstly AI outbreaks in these countries occurred at about the same time, suggestive of the same virus origin. The data from satellite telemetry together with the result on virus

inoculation in gulls kept in captivity suggested the possible role of AI spread by migratory birds.

At the end of the first epidemic wave of the 2009 pandemic influenza the infection rates of 7% were found in blood donors and 12.8% in health care workers. The community based study reported the higher infection rates in children (58%) than adults (3.1%). Our study also showed that nasopharyngeal aspirate was the best sample which yielded the most sensitive result in the disease diagnosis, and followed in order by nasal swab and throat swab specimens. Using sequential respiratory samples, the viral load at the amount of 2.6×10^2 - 8.1×10^9 copies/ml were shed from the patients and duration of viral shedding lasted between 1 and 11 days (mean = 5 days). The immunogenicity of monovalent, inactivated H1N1pdm vaccine was evaluated in HIV infected individuals and the uninfected controls after single injection by HI assay. The seroconversion rate of 32% and the seroprotection rate of 33.3% were found in the HIV infected vaccinees; while the seroconversion rate as well as the seroprotection rate of 35% was found in the uninfected control group.

Our group has established 4 techniques: direct nucleotide sequencing, plaque reduction assay, neuraminidase inhibition (NAI) assay and ELISA based viral nucleoprotein (NP) reduction assay for using in the surveillance for anti-viral drug resistant influenza viruses. The advantage of ELISA based viral NP reduction assay is its ability to investigate the drug or compounds targeting any viral gene; therefore, it has an advantage over the NAI assay which can investigate only the compounds targeting NA protein. Moreover, it has an advantage over the gold standard plaque reduction assay such that it consumes less reagents and time. The pitfall of ELISA based viral NP reduction assay is its inability to test the viruses with unusually slow rate of replication.

Keywords : Highly pathogenic influenza H5N1 virus, 2009 pandemic A(H1N1) virus, satellite telemetry

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เนื้อเรื่องย่อ

งานวิจัยนี้ทำการศึกษาเกี่ยวกับคุณสมบัติทางชีววิทยาระดับโมเลกุลของเชื้อไวรัสไข้หวัดนก H5N1 และเชื้อไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ (2009 pandemic A(H1N1) virus, H1N1pdm) รวมทั้งการตอบสนองทางภูมิคุ้มกันต่อการติดเชื้อด้วย ภาพถ่ายจากกล้องจุลทรรศน์อิเล็กตรอน ของเชื้อไข้หวัดนก H5N1 ซึ่งมีความรุนแรงในการก่อโรคสูงไม่มีความแตกต่างจากไวรัสไข้หวัดนกที่มีความรุนแรงในการก่อโรคต่ำ และไม่แตกต่างจากไวรัสไข้หวัดใหญ่ของคน การย้อมสี negative stain แสดงให้เห็นรูปร่างของอนุภาคไวรัส 3 แบบ คือ ทรงกลมขนาด 80-120 nm สายยาวขนาด >300 nm และอนุภาคที่มีรูปร่างไม่แน่นอนขนาด 120-300 nm โดยอนุภาคทรงกลมมีจำนวนมากกว่า 80% ของอนุภาคทั้งหมด การศึกษาเปรียบเทียบลำดับนิวคลิโอลิทิดของ M gene กับข้อมูลที่เคยมีผู้รายงานไว้ก่อนซึ่งแนะนำว่าลักษณะรูปร่างของไวรัสไม่ได้ถูกกำหนดด้วยลักษณะทางพันธุกรรมซึ่งแบ่งกับที่เคยมีผู้รายงานไว้ ลักษณะเด่นของโรคไข้หวัดนก H5N1 คือความล้มเหลวในการทำงานของอวัยวะหลายชนิดและการสร้าง cytokine มากเกินไป มีปัจจัยหลายอย่างซึ่งทำให้ไวรัสไข้หวัดนก H5N1 มีความรุนแรงในการก่อโรคในมนุษย์ ได้แก่ การที่ cleavage site ของ ชีแมกกลูติน มี basic amino acids หลายตัวติดต่อกัน ซึ่งไวรัสทุกตัวที่แยกได้ในประเทศไทยมีลักษณะนี้ นักวิจัยแต่ก่อนซึ่งแนะนำว่า นี้เป็นคุณสมบัติสำคัญที่ทำให้ไวรัสไข้หวัดนกแพร่กระจายออกจากระบบทางเดินหายใจไปสู่ระบบอื่นๆ ได้ ซึ่งคุณสมบัตินี้พบได้น้อยมากในไวรัสไข้หวัดใหญ่ของมนุษย์ และงานวิจัยนี้ยังพบว่า กลไกในการก่อโรคของไวรัส H5N1 ประการหนึ่งคือ ความสามารถในการเพิ่มจำนวนในเซลล์เยื่อบุหลอดเลือด และมี proinflammatory cytokine หลายชนิดถูกสร้างขึ้นด้วย ในขณะที่ไวรัสไข้หวัดใหญ่ของคนจะเพิ่มจำนวนในเซลล์เยื่อบุหลอดเลือดได้ไม่ดี นอกจากนี้ยังได้พบกลไกใหม่ที่ทำให้ไข้หวัดนกมีความรุนแรงในการก่อโรค คือเชื้อไวรัสไข้หวัดนกไม่ถูกยับยั้งโดย serum innate inhibitor ในขณะที่ไวรัสไข้หวัดใหญ่ของคนจะถูกยับยั้งได้เกือบหมดและการศึกษานี้ยังแสดงให้เห็นว่า ความทันทันนี้ขึ้นอยู่กับชีแมกกลูตินของเชื้อไข้หวัดนก

เชื้อไวรัสไข้หวัดนก H5N1 มีความรุนแรงมาก แต่โศคดีที่ไวรัสชนิดนี้ไม่มีการติดต่อระหว่างประชากรมนุษย์เนื่องจากเชื้อไวรัสไข้หวัดนกสามารถติดกับที่รับนผิวเซลล์ (receptor site) ของคนได้ไม่ดี แต่เนื่องจากการผสมกันระหว่างยีนของไวรัสสองชนิดเกิดขึ้นบ่อย ดังนั้นจึงอาจเป็นไปได้ที่จะเกิดไวรัสลูกผสม (reassortant) ซึ่งได้รับคุณสมบัติความรุนแรงในการก่อโรคจากไวรัส H5N1 และความสามารถในการแพร่กระจายเชื้อในประชากรมนุษย์จากไข้หวัดใหญ่ของมนุษย์ งานวิจัยนี้จึงได้ทำการสำรวจไวรัสลูกผสมที่อาจปะปนอยู่กับไวรัสไข้หวัดนก ทั้งหมดจำนวน 109 สายพันธุ์ ในระหว่างปี พ.ศ. 2546-2549 โดยใช้วิธี multiplex RT-PCR ซึ่งสามารถขยายยีนทั้ง 8 ชิ้นของไวรัสไข้หวัดนกได้ แต่ก็ไม่พบว่ามีไวรัสลูกผสมเกิดขึ้น

ประเทศไทยได้ผ่านการระบาดของไวรัสไข้หวัดนก H5N1 มาแล้วหลายระลอกนับตั้งแต่ปีพ.ศ. 2547 การวิเคราะห์ทาง phylogenetic แสดงให้เห็นว่าเชื้อไวรัส H5N1 ในช่วงการระบาดแรกๆ มีลักษณะทางพันธุกรรมที่แตกต่างกันมาก แต่เมื่อมีการควบคุมการระบาดในสัตว์ปีกก์เหลือไวรัสไข้หวัดนกเพียง 2-3 lineages เท่านั้น ภายหลังจากที่การระบาดแต่ละปีส่งบ่งประวัติการณ์นี้สังเกตเห็นได้ในฤดูร้อนของปีพ.ศ. 2549-2550 การกลับมาของการระบาดมักจะเกิดขึ้นในบริเวณลุ่มแม่น้ำยม และแม่น้ำน่าน และเกิดจากไวรัสที่รอดเหลือจากการระบาดครั้งก่อนมิใช่เกิดจากการนำเชื้อสายพันธุ์ใหม่เข้ามายังประเทศไทย นอกจากนี้การวิจัยยังได้พบไวรัสลูกผสม 2 เชื้อ อุบัติขึ้นในปี พ.ศ. 2550 จากการรวมตัวระหว่างไวรัสไข้หวัดนก H5N1 ด้วยกันเอง ไวรัสไข้หวัดนก H5N1 ที่ก่อการระบาดในประเทศไทยตั้งแต่ปี พ.ศ. 2547 จัดอยู่ใน clade 1 genotype Z และได้ระบาดอยู่ในประเทศไทยตั้งแต่นั้นมา เป็นไวรัส clade เดียวที่อยู่ในภาคกลางและภาคเหนือของประเทศไทยทั้งปี พ.ศ. 2551 และในปี พ.ศ. 2549 นักวิจัยกลุ่มอื่นในประเทศไทยได้พบร่องรอยของไวรัส clade 2.3.4 ในภาคอีสานของประเทศไทย โครงการวิจัยนี้ได้ทำหน้าที่เป็นห้องปฏิบัติการคุ้นเคยของสถาบันสุขภาพแห่งชาติ (National Institute of Health, NIH) ในการวินิจฉัยโรคไข้หวัดนกในผู้ป่วยชาวลาวที่มารับการรักษาตัวในโรงพยาบาลหนองคายในปีพ.ศ. 2550 และได้พบว่าเป็นการติดเชื้อไวรัส H5N1 clade 2.3.4 เช่นกัน ในการประเมิน selective pressure ที่เกิดกับชีวภาพกลุ่มนี้ เกี่ยวกับ synonymous codon usage ซึ่งหมายความว่า ไวรัส subclade 2.1 จากอินโดนีเซีย มี codon volatility ต่ำสุด เมื่อเทียบกับไวรัสใน clade และ subclade อื่นๆ

จากการที่ไวรัสไข้หวัดนก H5N1 มีความจำเพาะกับ receptor ชนิด α2,3 galactose-linked sialic acid ซึ่งเป็น avian type receptor กลุ่มผู้วิจัยที่ทำการศึกษาเชื้อ H5N1 ที่ระบาดในช่องกงในปี พ.ศ. 2540 จึงได้แนะนำให้ใช้เม็ดเลือดแดงของม้าในการทดสอบหาแอนติบอดีต่อเชื้อ H5N1 ด้วยวิธี hemagglutination inhibition (HI) assay รวมไปถึง WHO ที่ได้มีการแนะนำให้ใช้เม็ดเลือดแดงของม้าในการทดสอบด้วยวิธีนี้ เช่นกัน แต่อย่างไรก็ตาม การแนะนำนี้เกิดจาก การทดสอบเบรียบเทียบโดยใช้เลือดเพียง 2 ชนิด คือ เม็ดเลือดแดงจากม้าและจากหนูตะเภา เท่านั้น สำหรับประเทศไทย เม็ดเลือดแดงม้าเป็นเลือดที่หาได้ไม่ง่ายนัก งานวิจัยนี้จึงทำการทดสอบโดยเบรียบเทียบเม็ดเลือดแดง 5 ชนิด คือ คนหมูเลือดโว ไก่ ห่าน หนูตะเภา และม้า จากการทดสอบ พบว่าเชื้อ H5N1 ที่ทดสอบสามารถจับกับ receptor บนผิวเม็ดเลือดแดงของห่านได้ดี และจากการวิเคราะห์ receptor binding site ที่อยู่บนชีวภาพกลุ่มนี้ พบร่องรอยที่ใช้ในการทดสอบมี receptor binding site ที่ไม่ต่างจากเชื้อ H5N1 ที่ก่อการระบาดในช่องกงเมื่อปี พ.ศ. 2540 เม็ดเลือดแดงห่านให้ความไวสูงในการทดสอบ hemagglutination assay ซึ่งใช้ในขั้นตอนของการแยกเชื้อไวรัส และการทดสอบหาแอนติบอดีด้วยวิธี HI assay พบว่าผลการทดสอบที่ใช้เม็ดเลือดแดงห่านกับผลการทดสอบที่ใช้เม็ดเลือดแดงม้าให้ผลไม่ต่างกัน ในขณะนี้ เม็ดเลือดแดงห่านจึงเป็นที่ยอมรับสำหรับการทำ HI assay และถูกนำไปใช้ในห้องปฏิบัติการหลายแห่งของประเทศไทย และเม็ดเลือดแดงชนิดนี้ถูกนำไปใช้ในการทดสอบเพื่อศึกษาเชิงระบาด

วิทยาทางชีรั่มต่อไปด้วย นอกจากเชื้อ HPAI H5N1 และ คณะผู้วิจัยยังพบว่าเม็ดเลือดแดงห่าน มีความไวสูงในการทดสอบเชื้อ LPAI ทั้ง 16 subtypes รวมทั้งเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ด้วย งานวิจัยนี้ได้ทำการศึกษาจนศาสตร์และความคงอยู่ของระดับแอนติบอดีที่ตอบสนองต่อการติด เชื้อ HPAI H5N1 ในชีรั่มของผู้ป่วยที่เสียชีวิตจากการติดเชื้อ H5N1 จำนวน 4 ราย และจากผู้รอดชีวิต จำนวน 4 ราย โดยใช้วิธี microNT, HI และ Western blot ผลการศึกษาพบว่า HI antibody ถูกตรวจพบได้เร็วกว่า NT antibody โดยส่วนใหญ่แล้วการเพิ่มขึ้นของระดับ แอนติบอดีในชีรั่มคุ้มครองที่ประมาณ 15 วัน หลังเริ่มมีอาการป่วย กลุ่มตัวอย่างผู้รอดชีวิตจากการติดเชื้อ H5N1 จะถูกเก็บตัวอย่างเลือดทุกๆ 6 เดือน เป็นเวลา 3 ปีหลังจากเข้าร่วมโครงการ ผลการวิจัยพบว่าทั้ง HI และ NT antibody ที่ระดับ titer ≥ 40 (ไม่คิดรวมปริมาตรในหลุมทดสอบ) สามารถคงอยู่ได้เป็นเวลานานประมาณ 5 ปีหลังจากการป่วย ดังนั้นค่า titer 40 สามารถใช้เป็นค่า cut-off ในการวินิจฉัยเพื่อจำแนกรหัสว่าผู้ติดเชื้อและไม่ติดเชื้อ H5N1 และสามารถใช้ประโยชน์ในการติดตามเฝ้าระวังกลุ่มเสี่ยงที่อาจติดเชื้อแต่ไม่แสดงอาการได้ เช่น กลุ่มผู้เลี้ยงสัตว์ปีก กลุ่มผู้ทำหน้าที่ทำลายสัตว์ป่วย และชาวชนบท เป็นต้น นอกจากนี้ยังพบว่าประมาณ 6.7-10.3% ของกลุ่มผู้สูงอายุมี cross-neutralizing antibody ต่อเชื้อ H5N1 ที่ titer 10 และพบ seroconversion 5.2% ในกลุ่มผู้สูงอายุที่ได้รับวัคซีนไข้หวัดใหญ่ งานวิจัยนี้ได้ทำการสร้าง vaccinia recombinant viruses ทั้งหมด 6 ชนิด โดยมีการสอดแทรกยีนต่างๆ ของไวรัส HPAI H5N1 ได้แก่ HA, NA, NP, M หรือ NS ลงในยีโนมของ vaccinia virus และชนิดที่ 6 คือ vaccinia recombinant virus ที่มีการใส่เฉพาะ pSC11 plasmid vector เข้าไปเท่านั้นเพื่อใช้เป็น control หลังจากสร้าง vaccinia recombinant viruses ขึ้นมาแล้วก็นำไปเลี้ยงในเซลล์ TK⁻ เพื่อให้มีการแสดงออกของโปรตีนจากไวรัสซึ่งสามารถตรวจสอบการแสดงออกของโปรตีนนั้นๆ ได้ด้วยวิธี immunofluorescence และ Western blot ในการศึกษา vaccinia recombinant virus ที่มีการแสดงออกของ H5N1 HA protein ซึ่งเป็น immunodominant epitope ที่สำคัญในการกระตุนให้เกิด protective antibody พบว่าเซลล์ที่ติดเชื้อมีการแสดงออกของ HA ทั้ง 3 รูปแบบ คือ HA0, HA1 และ HA2 ผู้รอดชีวิตจากการติดเชื้อ H5N1 จะมีแอนติบอดีต่อ HA ทั้ง 3 รูปแบบนั้น ในขณะที่ผู้ไม่ติดเชื้อ H5N1 จะมีเพียงแอนติบอดีที่ทำปฏิกิริยาข้าม (cross-reactive antibody) กับส่วน HA2 เท่านั้น การกระตุนภูมิคุ้มกันในหนู BALB/c ด้วย HA recombinant vaccinia virus สามารถกระตุนให้เกิดทั้ง HI และ NT antibody ต่อเชื้อ H5N1 ได้ซึ่งได้ทำการทดสอบกับทั้ง reverse genetic virus ที่มีการแสดงออกของ H5 HA protein และ parental HPAI H5N1 virus แอนติบอดีที่ถูกสร้างขึ้นจากการกระตุนด้วยโปรตีนเขี้มแกกถูตินินจะเป็น protective antibody สามารถป้องกันการติดเชื้อได้แต่กว่าโปรตีนส่วนอื่นๆ ของเชื้อไวรัสก็สามารถกระตุนให้เกิดแอนติบอดีที่มีหน้าที่ต่างๆ กัน เช่น opsonization, antibody dependent cell cytotoxicity หรือขัดขวางการทำงานของโปรตีนของไวรัส งานวิจัยนี้ได้ใช้เซลล์ TK⁻ ที่ติดเชื้อ recombinant vaccinia virus และมีการแสดงออกของโปรตีน HA, NA, NP, M หรือ NS มาใช้เป็นแอนติเจนเพื่อตรวจหาแอนติบอดีโดยวิธี indirect

immunofluorescence ผลการทดสอบแสดงให้เห็นว่า ซีรัมของผู้อุดชีวิตจากการติดเชื้อ H5N1 ทั้ง 4 ราย และซีรัมเกือบทั้งหมดจากผู้ที่ไม่มีการติดเชื้อ H5N1 มีแอนติบอดีต่อโปรตีนต่างๆ ที่ใช้ในการทดสอบ แต่ผู้อุดชีวิตจากการติดเชื้อ H5N1 จะมีระดับของแอนติบอดีที่สูงกว่า

ในการทดสอบด้วยวิธี ELISpot assay โดยใช้ overlapping peptide pools ที่ครอบคลุมโปรตีน NP และ M ทั้งส่าย พบว่าผู้อุดชีวิตจากการติดเชื้อ H5N1 มีการสร้างภูมิคุ้มกันด้านเซลล์ซึ่งสามารถอยู่ได้ในช่วงระยะเวลาใกล้เคียงกับภูมิคุ้มกันแบบสารน้ำ และผลจากการวิเคราะห์ด้วยเทคนิค flow cytometry โดยใช้ immunophenotype marker (CD4+ หรือ CD8+) ร่วมกับ γ -interferon, TNF- α , และ T cell-related cytotoxic marker CD107a พบว่า cytotoxic T cells ที่ถูกกระตุ้นนั้นส่วนใหญ่เป็นชนิด CD4+ T lymphocyte ในขณะที่พบ CD8+ T lymphocytes เป็นส่วนน้อย และ NP peptides มีความสามารถในการกระตุ้นได้สูงกว่า M peptides การศึกษานี้ยังแสดงให้เห็นว่า ผู้ที่ไม่เคยได้รับเชื้อ H5N1 มีการแสดงออกของ cross-reactive cellular immunity ต่อ NP peptides ได้เช่นกัน

มหาวิทยาลัยทิดอลได้รับความร่วมมือจากการมอุทัยานแห่งชาติ สัตตว์ป่า และพันธุ์พืชในการศึกษาวิจัยถึงบทบาทของนกอพยพในการแพร่กระจายของเชื้อไข้หวัดนก โดยใช้ transmitter ติดไว้กับตัวนกในการส่งข้อมูลทางไกลผ่านระบบดาวเทียม (satellite telemetry) ทำให้สามารถทราบถึงเส้นทางการบิน และถี่นที่อยู่ของนกได้ การศึกษาครั้งนี้ใช้เครื่องส่งสัญญาณจำนวน 20 เครื่องติดกับตัวนก 4 ชนิด ได้แก่ นกนางนวลธรรมชาติ (Brown headed gulls), นกปากห่าง (Open-billed storks), นกยางโทนใหญ่ (Great egrets) และ นกเป็ดแดง (Lesser whistling ducks) ซึ่งการศึกษานี้ไม่สามารถติดตามเส้นทางบินของนกเป็ดแดงได้ เนื่องจากสัญญาณจากเครื่องส่งที่ติดกับตัวนกมีการขาดหายไปหลังจากเริ่มการติดตามเพียงไม่กี่สัปดาห์ โดยในขณะนี้การศึกษาถือว่าอยู่ในช่วงต้น นกนางนวลธรรมชาติ 8 ตัวที่ได้ทำการติดตามนั้น มีเพียง 5 ตัว ที่สามารถทำการบันทึกเส้นทางอพยพระหว่างประเทศไทยและจีนได้อย่างสมบูรณ์ 1-2 รอบ เส้นทางบินของนกนางนวลครอบคลุม 7 ประเทศที่มีรายงานการระบาดของเชื้อไข้หวัดนก ได้แก่ ไทย, กัมพูชา, เวียดนาม, จีน, อินเดีย, บังกลาเทศ และพม่า แต่มีเพียงประเทศไทย กัมพูชา และจีนเท่านั้นที่เป็นถิ่นที่อยู่ของนกนางนวล ขณะที่ประเทศไทยเป็นเพียงที่หยุดพักระหว่างการอพยพเท่านั้น ดังนั้นด้วยข้อมูลของระยะทางและช่วงเวลาของการอพยพ ประกอบกับข้อมูลจากการศึกษาทดลองเกี่ยวกับระยะเวลาที่นกนางนวลที่ถูกจัดเชื้อ H5N1 จะขับเชื้อออกจากร่างกายจนกว่าจะตายหรือหายจากโรค ซึ่งให้เห็นว่ามีความเป็นไปได้ที่นกนางนวลที่ติดเชื้อจะสามารถแพร่เชื้อไวรัสไปตามเส้นทางบินอพยพในเดือนมีนาคม ปีพ.ศ. 2552 พบรการอุบัติขึ้นของเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 ที่ประเทศไทยโดยผู้ป่วย 2 รายแรกของไทยนั้นเดินทางกลับมาจากประเทศไทยเม็กซิโกเช่นกัน ที่มีวิจัยได้ให้ความร่วมมือกับสถาบันสุขภาพแห่งชาติ (Thai NIH) ในการวินิจฉัยและรายงานผู้ติดเชื้อทั้งสองราย เมื่อวันที่ 4 พฤษภาคม พ.ศ. 2552 และสามารถแยกเชื้อจากผู้ป่วยสองรายนี้

ได้ และให้ชื่อว่า A/Nonthaburi/102/2009 (H1N1) และ A/Thailand/104/2009 (H1N1) ที่มีวิจัยได้ทำการศึกษาลำดับพันธุกรรมของเชื้อทั้งสองนี้และได้เผยแพร่ไว้ใน GenBank database เชื้อไวรัส A/Thailand/104 นั้นสามารถเพิ่มจำนวนได้ง่ายกว่า ดังนั้นเชื้อนี้จึงถูกนำไปใช้เป็นแอนติเจนในการทดสอบหาภูมิคุ้มกันตอบสนองต่อการติดเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ การทดสอบชี้รัมที่ได้มีการเก็บไว้ก่อนปีพ.ศ. 2552 พบว่าแอนติบอดีที่มีอยู่ในชี้รัมก่อนการระบาดนั้นสามารถเกิด cross-neutralize ต่อเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ได้ โดยมีระดับ titer ที่ต่างกันไป แสดงให้เห็นว่าในกลุ่มประชากรไทยนั้นมีภูมิคุ้มกันบางส่วนต่อเชื้อชนิดนี้อยู่แล้ว และยังสามารถอธิบายถึงเหตุผลที่ว่าทำไมเชื้อชนิดนี้จึงก่อให้เกิดความรุนแรงของโรคไม่มากนัก ในการทำ HI assay โดยใช้เม็ดเลือดแดงของห่าน ร่วมกับการใช้ microNT assay ในการศึกษาชี้รัมคู่ของผู้ป่วย ทำให้ได้ค่า cut-off antibody titer ที่สามารถจำแนกระหว่างผู้ติดเชื้อกับผู้ที่ไม่ติดเชื้อ กล่าวคือ ผู้ติดเชื้อซึ่งเป็นผู้ใหญ่จะมี HI titer สูงกว่าหรือเท่ากับ 40 และเด็กที่ติดเชื้อจะมี HI titer สูงกว่าหรือเท่ากับ 20 ค่า cut-off titer นี้ได้ถูกนำมาใช้ในการศึกษาขนาดของการระบาดระลอกแรกในกลุ่มประชากรไทย โดยพบอัตราการติดเชื้อ 7% ในกลุ่มผู้บริจาคโลหิต และ 12.8% ในกลุ่มนบุคคลการทางการแพทย์ ซึ่งอัตราการติดเชื้อระหว่างสองกลุ่มนี้ไม่มีความแตกต่างกันในเชิงสถิติ และจากการตอบแบบสอบถามของเจ้าหน้าที่พยาบาลเกี่ยวกับวิธีการและอุปกรณ์ป้องกันตนเองจากการติดเชื้อ (เช่น การล้างมือ การใส่หน้ากากอนามัย และการสวมถุงมือ) พบว่าการไม่สวมหน้ากากอนามัยระหว่างสัมผัสถกับบุคคลการทางการแพทย์ด้วยกันที่ติดเชื้อ เป็นปัจจัยเสี่ยงสำคัญที่ทำให้เจ้าหน้าที่ติดเชื้อได้ อย่างไรก็ตามการศึกษาได้แสดงให้เห็นว่าประชากรส่วนใหญ่ยังไม่มีภูมิคุ้มกันต่อเชื้อไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ และผลการวิจัยนี้คาดการณ์ว่าจะมีการระบาดระลอกถัดไปเกิดขึ้นภายในหลังการระบาดในระลอกแรก ซึ่งต่อมาได้พบว่ามีการระบาดเกิดขึ้นแล้วถึง 4 ระลอก และเชื้อ H1N1 ตามถูกากลที่เป็นเชื้อที่มีอยู่เดิมได้ถูกแทนที่โดยเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ตั้งแต่ปี พ.ศ. 2552 เป็นต้นมา จากการศึกษาในระดับชุมชน ร่วมกับสำนักงานสาธารณสุขทั่วไปในพื้นที่ชนบท (จังหวัดเชียงใหม่ และนครศรีธรรมราช) ภายในหลังจากการระบาดระลอกแรกพบว่ามีอัตราการติดเชื้อในเด็กสูงถึง 58% และพบในผู้ใหญ่เพียง 3.1% งานวิจัยนี้ได้มีการศึกษาระดับแอนติบอดีในกลุ่มผู้ติดเชื้อ HIV เปรียบเทียบกับกลุ่มผู้ไม่ติดเชื้อ ที่ได้รับวัคซีนไข้หวัดใหญ่ ชนิด monovalent inactivated pandemic influenza vaccine โดยใช้วิธี HI assay ผลการศึกษาพบว่า ในกลุ่มผู้ติดเชื้อ HIV ที่ได้รับวัคซีน มีอัตรา seroconversion เท่ากับ 32% และ seroprotection เท่ากับ 33.3% ขณะที่ในกลุ่มผู้ไม่ติดเชื้อ HIV ที่ได้รับวัคซีนพบอัตรา seroconversion และ seroprotection เท่ากันคือ 35%

ในการวินิจฉัยการติดเชื้อไข้หวัดใหญ่โดยการตรวจหาภูมิโนมของเชื้อด้วยวิธี real time RT-PCR สามารถใช้สิ่งส่งตรวจจากระบบทางเดินหายใจของผู้ป่วยได้หลายชนิด เช่น nasopharyngeal aspirate (NPA), nasal swab (NS) และ throat swab (TS) งานวิจัยนี้ได้ทำการทดสอบเก็บสิ่ง

ส่งตรวจเหล่านี้จากผู้ป่วยคนเดียวกันก่อนการให้ยาต้านไวรัส ผลการทดสอบพบว่า NPA เป็นสิ่งส่งตรวจที่สามารถตรวจพบยีโนมของเชื้อได้มากที่สุด รองลงมาคือ NS และ TS ตามลำดับ

เมื่อมีการระบาดเกิดขึ้นในชุมชนปิด เช่น ในค่ายทหาร พบว่าการคัดแยกผู้ป่วยออกมานั้นเป็นวิธีการหนึ่งที่สามารถจะยับยั้งการแพร่กระจายของเชื้อได้ แต่จะต้องพิจารณาถึงระยะเวลาที่จะต้องแยกผู้ป่วยออกมานั้น ที่มีวิจัยได้ให้ความร่วมมือกับสำนักงาน疾控ที่ทำการศึกษาปริมาณไวรัสและช่วงเวลาที่ผู้ป่วยจะแพร่เชื้อ โดยใช้ real time RT-PCR ในการวิเคราะห์ตัวอย่างตรวจที่เก็บอย่างต่อเนื่องจากทางเดินหายใจของผู้ติดเชื้อ พบว่าปริมาณไวรัส $2.6 \times 10^2 - 8.1 \times 10^9$ copies/ml จะถูกปล่อยออกมานานจากผู้ป่วย และช่วงเวลาที่ผู้ป่วยจะสามารถแพร่เชื้อจะอยู่ระหว่าง 1 ถึง 11 วัน (เฉลี่ย 5 วัน)

ปัจจุบันยานิกกลุ่มที่ออกฤทธิ์ยับยั้งเอนไซม์นิวราไมนิเดสของไวรัสที่ใช้กันทั่วไปมีอยู่ 2 ชนิด คือ oseltamivir และ zanamivir งานวิจัยนี้ได้นำวิธีการ 4 อย่าง ได้แก่ การหาลำดับนิวคลิโอลีท์ของยีน NA, การลดลงของจำนวน plaque (plaque reduction assay), การยับยั้งเอนไซม์นิวราไมนิเดส (neuraminidase inhibition- NAI assay) และ วิธีวัดปริมาณนิวคลิโอลีโพรตีนที่ลดลง (ELISA-based viral nucleoprotein reduction assay) มาใช้ในการศึกษาและเฝ้าระวังการเกิดเชื้อไข้หวัดใหญ่ดื้อต่อยา โดยก่อนหน้านี้ทีมวิจัยได้พบว่า 90-100% ของเชื้อไข้หวัดใหญ่ตามฤดูกาล H1N1 ที่ศึกษาในช่วงปี พ.ศ.2551 และ พ.ศ. 2552 ดื้อต่อยา oseltamivir ซึ่งเป็นผลจากการที่ histidine ที่ตำแหน่ง 274 ในโปรตีนนิวราไมนิเดสเกิด mutation เป็น tyrosine แต่พบว่าโซคดีที่ไวรัสสายพันธุ์นี้ได้ลดน้อยและหายไปหลังจากปี พ.ศ. 2553 คงจะผู้วิจัยได้ใช้วิธี ELISA-based viral nucleoprotein reduction assay ในการทดสอบคัดกรองหาสารเคมี หรือสารสกัดจากสมุนไพรที่มีฤทธิ์ต้านเชื้อไวรัสให้กับสถาบันหลายแห่ง ข้อดีของวิธีนี้คือ สามารถใช้ในการทดสอบกับยาหรือสารที่ออกฤทธิ์ยับยั้งต่อยีนใดของไวรัสก็ได้ ดังนั้นวิธีนี้จึงดีกว่าวิธี NAI ที่ใช้ทดสอบกับยาที่ออกฤทธิ์ต้านเฉพาะนิวราไมนิเดสของไวรัสได้เพียงอย่างเดียว นอกจากนั้น วิธีนี้ยังใช้เวลาไม่นานและใช้สารเคมีทดสอบในปริมาณน้อยเมื่อเทียบกับวิธีมาตรฐานคือ plaque reduction assay แต่ข้อเสียของวิธี ELISA based viral nucleoprotein reduction assay คือ ไม่สามารถใช้ทดสอบกับไวรัสซึ่งมีอัตราการเพิ่มจำนวนที่ช้าผิดปกติได้

Executive Summary

The present study investigated the molecular biological properties of the highly pathogenic avian influenza (HPAI) H5N1 viruses and the 2009 pandemic A (H1N1) virus (H1N1pdm virus) together with the immunological responses against these two viral infections. Electron micrographs of HPAI H5N1 viruses were not different from those of the low pathogenic avian influenza (LPAI) viruses and human influenza viruses. With negative staining, 3 morphological forms of the virus particles, i.e., spherical form at size of 80-120 nm, filamentous form at size of >300 nm and the pleomorphous particles at size of 120-300 nm were visualized under a transmission electron microscope. However, the spherical form took account of greater than 80% of the entire viral population. Based on an alignment of the M genomic sequences, our study also suggested that viral morphology was not under control of the viral genetics as had been previously reported. The hallmarks of H5N1 avian influenza are multi-organ failure and cytokine storm. There are several factors that contribute to the highly virulent property of this virus subtype. Presence of multiple basic amino acids at the hemagglutinin (HA) cleavage site is present in the entire virus isolates ever reported in Thailand. Previous investigators suggested that this is an important property that facilitated the virus spreading beyond the respiratory tract to the other distal end organs, the property that is extremely rare for human viruses. Moreover, we have found that a pathogenic mechanism of HPAI H5N1 viruses involved the active replication in human endothelial cells, while human viruses poorly replicated. Production of certain pro-inflammatory cytokines/ chemokines was induced in the infected human vein endothelial cells. Additionally, we discovered a new pathogenic mechanism that made HPAI H5N1 viruses virulent, that was the ability to resist the serum inhibitors. Using guinea pig sera as the model, we demonstrated that the serum innate inhibitors could not block the infectivity of HPAI H5N1 viruses; while the infectivity of human viruses was almost completely inhibited. We also showed that this resistance was mediated through the H5 HA gene. Collectively, our findings add up the information on what made the HPAI H5N1 viruses become virulent.

HPAI H5N1 viruses are highly virulent; fortunately, the viruses are rarely transmitted among human population according to the difference in receptor site binding preference between human and avian viruses. As gene reassortment is common among influenza

viruses, an emergence of a reassortant virus which might gain the virulence property from the HPAI H5N1 virus and the ability to transmit among human population from the human viruses is possible. Surveillance for the reassortant virus had been conducted by our group when the occurrence of HPAI outbreaks was at its peak. A total of 109 HPAI H5N1 viruses collected between 2003 and 2006 were analyzed by multiplex reverse transcription-polymerase chain reaction (RT-PCR) using 8 primer pairs specific for each viral genomic segment. No reassortant had been found.

Thailand had suffered from many epidemic waves of H5N1 avian influenza outbreaks since 2004. Our phylogenetic analysis showed that the H5N1 virus isolates at the firstly outbreaks were genetically diverse. By various strategic control plan of avian influenza (AI) in poultry, our genetic analysis showed that only few virus lineages did exist after subsiding of the outbreaks each year as shown by the bottle neck effect in summer of 2006 and 2007. Resurgence of the outbreak usually occurred in the areas around the Yom-Nan river basin from the indigenous viruses surviving the control after previous outbreak, not the re-introducing of the virus from other countries. Additionally, we had discovered 2 reassortants emerged in 2007 from the reassortment of two H5N1 parental viruses. HPAI H5N1 viruses causing the outbreak in Thailand since 2004 belonged to clade 1, genotype Z and had been circulating throughout Thailand since then. The clade 1 virus was the only clade remained in Central and Northern Thailand upto 2008. On the other hand, the clade 2.3.4 was reported by the other group of Thai investigators in Northeast of the country in 2006. As the parallel laboratory of the National Institute of Health, we had diagnosed an infection caused by the clade 2.3.4, genotype V virus in a Lao patient who came into Thailand for receiving medical care and died in the Nongkhai hospital in 2007. An estimation for the selective pressure on HA proteins regarding synonymous codon usage suggested that the subclade 2.1 virus from Indonesia had lowest codon volatility as compared among different clades and subclades of HPAI H5N1 viruses.

Regarding the binding preference to α 2, 3 galactose linked-sialic acid (α 2, 3 gal-linked SA) avian type receptor, the other group of investigators studied the HPAI H5N1 viruses from the 1997 outbreak in Hong Kong and suggested the usage of horse erythrocytes in hemagglutination-inhibition (HI) assay for detection of the viral specific antibody. This suggestion has lead to an issue of a WHO recommendation on using horse erythrocytes in HI assay. It is to be notified that this recommendation is relied on the comparison on 2 erythrocyte species (horse and guinea pig) only. Nevertheless, it is not convenient to

obtain the horse erythrocytes in Thailand. We then compared 5 erythrocyte species from human O blood group, chicken, goose, guinea pig and horse, and found that the current HPAI H5N1 viruses preferentially bound the goose erythrocytes, even though the analysis of receptor binding sites on *HA* genes of our study viruses and those of the 1997 Hong Kong viruses are not different. Goose erythrocytes yielded the most sensitive result in hemagglutination assay for recognition of the virus isolates; and the HI antibody titers obtained as using horse or goose erythrocytes were comparable. At present, goose erythrocytes are accepted for HI assay in general laboratories in Thailand; and this erythrocyte species had been employed in our subsequent seroepidemiological studies. Additionally, we also found that goose erythrocyte is also the most sensitive to detect all 16 subtypes of low pathogenic avian influenza (LPAI) viruses and the H1N1pdm virus as compared among the 5 erythrocyte species mentioned above.

Kinetics and longevity of antibody response to the HPAI H5N1 viral infection was explored in 4 fatal cases and 4 survivors by microNT, HI and Western blot assays. HI antibody was detected slightly earlier than NT antibody. In general, the increasing antibody titer in paired blood was shown approximately 15 days after disease onset. The H5N1 survivors were bled at an interval of 6 months during 3 years of the follow-up study. We found that both HI and NT antibodies at the titer of ≥ 40 (regardless of total volume in the reaction) persisted for almost 5 years after the disease onset in cases that we could follow-up that far. As a result, the titer of 40 has been established as the cut-off titer for differentiating the H5N1 cases from the non-H5N1 cases; and then applied in the surveillance for asymptomatic H5N1 infection in populations at risk such as poultry farmers, poultry cullers and villagers. We also found that cross neutralizing antibody against HPAI H5N1 at the titer of 10 were found in 6.7-10.3% of the elderly; and seroconversion could be seen in 5.2% of the old-age vaccinees who received seasonal influenza vaccine. We had constructed 6 recombinant vaccinia viruses carrying individual gene of HPAI H5N1 virus, i.e., HA, NA, NP, M, NS and the 6th construct carries only the pSC11 plasmid vector. These constructs infected TK⁻ cells and expressed the viral protein which could be detected by immunofluorescence and Western blot assays. The recombinant H5 HA was extensively characterized as it is the most important immunodominant epitope that induces the protective immunity. Western blot analysis showed that all 3 forms of HA were expressed in the infected cells: HA0 and its cleavage products, HA1 and HA2 domains. H5N1 survivors contained the

antibodies that directed against all 3 forms of HA; while all non-H5N1 subjects contained cross reactive antibody against the HA2 domain only. BALB/c mice immunized with the recombinant HA developed both HI and NT antibody against the reverse genetic virus carrying H5 HA gene and also with the wild type HPAI H5N1 parental virus. NT antibody mostly directs against HA protein and functions as the protective antibody. However, the other viral proteins might induce the antibody that serve other roles such as opsonization, antibody dependent cell cytotoxicity and antagonize with the action of certain viral protein. The infected TK⁻ cells expressing HA, NA, NP, M, or NS protein together with the pSC11 carrying cells were used as the antigen in the indirect immunofluorescence assay for detection of the antibodies in H5N1 survivors and non-H5N1 subjects including the patients infected with the 2009 pandemic virus, H3N2 virus and healthy controls. The result demonstrated that sera from all 4 survivors and almost of the non-H5N1 subjects were reactive against all kinds of these viral proteins; but the antibody titers were higher in the survivors.

H5N1 survivors also developed cell-mediated immunity which lasted as long as the humoral immunity as determined by ELISpot assay using overlapping peptide pools spanning the entire NP and M proteins. Flow cytometry assay using immunophenotype markers (CD4+ or CD8+) together with γ -interferon, TNF- α and T cell-related cytotoxic marker CD107a demonstrated that majority of the reactive cytotoxic T cells from H5N1 survivors were CD4+T lymphocytes whereas CD8+T lymphocytes were the minor population; and NP peptides yielded stronger reactivity than M peptides. The study also demonstrated that the non-H5N1 subjects also contained the cross reactive cellular immunity against the NP peptide pools, the only peptides used in this group of subjects.

Mahidol University in collaboration with the Department of National Parks, Wildlife and Plant Conservation had conducted the satellite telemetry study to explore the role of migratory birds in AI spread. An analysis in adjunct with GPS program, the birds' flyways and their habitats could be positioned. A total of 20 transmitter platforms were tagged in 4 bird species: Brown headed gulls (*Larus brunnicephalus*), Open-billed storks (*Anastomus oscitans*), Gret egrets (*Egretta alba*) and Lesser whistling ducks (*Dendrocygna javanica*). We did not success to monitor the flyway of Lessler whistling ducks because the transmitter signals were lost within few weeks after tracking. At present, the study on the habitats of the Open-billed storks and Gret egrets are ongoing. Of 8 gulls tracked, only 5 gulls could complete 1-2 migratory cycles between Thailand and China. The flyways of gulls spanned 7 countries that were affected by

avian influenza: Thailand, Cambodia, Vietnam, China, India, Bangladesh and Myanmar. Based on duration of staying for longer than one month, only Thailand, Cambodia and China were considered to be the gulls' habitats; while the other countries were the places of stopover during migration. With the distance and duration of migration together with the experiment on duration of virus shedding till death or survival in the gulls inoculated with H5N1 virus, our study suggested that it is possible for the infected gulls to spread the virus along their migratory flyways.

The emergence of the 2009 pandemic influenza began in Mexico in March 2009. The first 2 cases of Thailand were also imported from Mexico. As the companion laboratory of the National Institute of Health, Thailand, these 2 cases were diagnosed and reported on May 4, 2009. The causative viruses were isolated and named A/Nonthaburi/102/2009 (H1N1) and A/Thailand/104/2009(H1N1). Their entire genomes were sequenced and deposited in the GenBank database. A/Thailand/104 is easier to be propagated; therefore, it has been used by our group as the test antigen in many serological studies. The investigation in archival serum samples collected before 2009 showed the presence of pre-existing antibody that could cross neutralize the H1N1pdm virus to various extents of titers. This finding implied that the Thai population had been partially protected; and explained why the disease caused by the pandemic virus was not severe. Goose erythrocyte HI assay together with microNT assay were employed to investigate paired blood samples from the patients. The result led to the establishment of the cut-off antibody titer that can differentiate between the cases and non-cases, i.e., the HI titer of ≥ 40 for adults and ≥ 20 for children. These cut-off titers were applied to investigate the magnitude of the pandemic in Thai people at the end of the first epidemic wave. The infection rates of 7% were found in blood donors and 12.8% in health care workers which were statistically non-significant different. Questionnaires regarding self-reported adherence of nurses to the infection control practices (hand hygiene, masks and gloves) revealed that the exposure to health care professionals with influenza-like illness without wearing a mask was the only identified risk factor for the infection. Eventually, our study showed that most of the Thai people were lack of immunity. So, we predicted that subsequent epidemic waves would occur following the first one. Our estimation has been confirmed by the occurrence of at least 4 subsequent outbreaks thereafter. The H1N1pdm virus has completely replaced the original seasonal H1N1 virus since 2009. The community based study conducted in collaboration with the Bureau of Epidemiology (BoE) after the first epidemic wave in

rural areas (Chiang Mai and Nakhon Si Thammarat) showed that the infection rates were much higher in children (58%) than adults (3.1%). HI assay had been used to evaluate the antibody response in HIV infected vaccinees and the uninfected controls who received single injection of the monovalent inactivated pandemic influenza vaccine. The seroconversion rate of 32% and the seroprotection of 33.3% were found in the HIV infected vaccinees; while the seroconversion rate as well as the seroprotection rate of 35% were found in the uninfected control group.

Various kinds of respiratory specimens: nasopharyngeal aspirates (NPA), nasal swabs (NS) and throat swabs (TS) can be used for the viral genome detection by real time RT-PCR to diagnose the influenza disease. Our study investigated those specimens collected from the same infected individual prior to drug treatment and showed that NPA was the best sample that yielded the most sensitive result in the disease diagnosis, and followed in order by NS and TS specimens. During an outbreak in a closed community such as a military camp, the isolation of the infected case is one approach to stop the virus spread; but how long is the isolation period needed to be determined. BoE in collaboration with our group had investigated the viral loads and duration of viral shedding from the infected cases by real time RT-PCR using sequential respiratory samples. We found that the viral load at the amount of 2.6×10^2 - 8.1×10^9 copies/ml were shed from the patients and duration of viral shedding lasted between 1 and 11 days (mean = 5 days).

At present, 2 kinds of neuraminidase inhibitors: oseltamivir and zanamivir have been licensed for general use. Our group has established 4 techniques: direct nucleotide sequencing, plaque reduction assay, neuraminidase inhibition (NAI) assay employing 2'2'-(4-methylumbelliferyl)- α -D-N-acetylneuraminic acid (MUNANA) and ELISA based viral nucleoprotein (NP) reduction assay to conduct the surveillance for anti-viral drug resistant influenza viruses. We previously showed that 90-100% of the seasonal influenza A(H1N1) viruses investigated in 2008 and 2009 were oseltamivir resistant according to H274Y substitution in NA gene. Fortunately, this virus has been extinct after 2010. We have successfully applied the newly developed ELISA based viral NP reduction assay to investigate the anti-viral activity of the compounds or plant extracts prepared by other institutes. The advantage of this technique is its ability to investigate the drug or compounds targeting any viral gene, while NAI assay can be used for the drugs that target the NA protein only. ELISA based viral NP reduction assay also has

an advantage over the gold standard plaque reduction assay such that it consumes less reagents and time.

บทนำ

คุณสมบัติทั่วไปของเชื้อไวรัสไข้หวัดใหญ่

ไวรัสไข้หวัดใหญ่ (influenza virus) จัดอยู่ใน Family *Orthomyxoviridae* แบ่งออกเป็น 3 immunological types คือ A B และ C โดย type A มีการติดเชื้อในคนและสัตว์หลายชนิด เช่น สัตว์ปีก หมู ม้า เสือ เป็นต้น type B มีการติดเชื้อก่อโรคในคนเท่านั้น สำหรับ type C มีรายงานการติดเชื้อในคนโดยไม่แสดงอาการ ไวรัสไข้หวัดใหญ่เป็นไวรัสที่มียีโนมเป็น RNA ซึ่งมีลักษณะเป็นท่อนจำนวน 7-8 ท่อน แต่ละท่อนล้อมรอบด้วยโปรตีน capsid เกิดเป็นแกนกลาง หรือ ribonucleoprotein ซึ่งอยู่ภายในเยื่อหุ้ม (envelope) เดียวกัน บน envelope มี glycoprotein spikes 2 ชนิด ได้แก่ hemagglutinin (HA) และ neuraminidase (NA) อนุภาคของไวรัสไข้หวัดใหญ่มีรูปร่างได้หลายแบบ คือ กลม เป็นสายยาว หรือมีรูปร่างไม่แน่นอน ไวรัสไข้หวัดใหญ่เป็นไวรัสที่มีการกลายพันธุ์สูงมาก ทั้งแบบ point mutation หรือ reassortment ซึ่งเป็นการแลกเปลี่ยน genomic segment ของไวรัสไข้หวัดใหญ่ type A สองสายพันธุ์ ที่มีการติดเชื้อภายในเซลล์เดียวกัน ทำให้มีไวรัสลูกผสมสายพันธุ์ใหม่ หรือ subtype ใหม่เกิดขึ้นอยู่เรื่อยๆ

ไวรัสไข้หวัดใหญ่ type A สามารถแบ่งตามความแตกต่างของ H และ N ออกเป็น 17 H และ 9 N subtypes ทุก H และ N subtypes พบรดีในนกน้ำ จึงเชื่อว่านกน้ำเป็นรังโรค (reservoir host) ของไข้หวัดใหญ่ type A

ระบาดวิทยาของเชื้อไวรัสไข้หวัดนก H5N1 ในประเทศไทย

เชื้อไข้หวัดนก (avian influenza virus) ที่มีรายงานการระบาดมาสู่คนมีอยู่หลาย subtype ที่สำคัญได้แก่ H5N1, H9N2, H7N1 และ H7N3 viruses แต่เชื้อ H5N1 เป็น subtype ที่ก่อโรครุนแรงมากที่สุด การแพร่กระจายมาสู่คน มีรายงานครั้งแรกที่อ่องกง ในปี 2540 ประเทศไทยรายงานการเกิดขึ้นของโรคไข้หวัดนก H5N1 virus เป็นครั้งแรกและรายงานผู้ป่วยรายแรกของประเทศไทย เมื่อวันที่ 23 มกราคม 2547 ผู้ป่วยรายสุดท้ายของประเทศไทยเกิดขึ้นในเดือนกรกฎาคม 2549 รวมมีผู้ป่วยทั้งสิ้น 25 ราย ถึงแก่ชีวิต 17 ราย คิดเป็นอัตราตาย 68% ส่วนการระบาดในสัตว์ปีกมีรายงานครั้งสุดท้ายในประเทศไทยในปี 2551 ในปัจจุบัน โรคไข้หวัดนก H5N1 ก็ยังไม่หมดไป ในปี 2555 ยังพบการระบาดมีผู้ติดเชื้อและผู้เสียชีวิตใน 6 ประเทศทั่วโลก คือ จีน เวียดนาม กัมพูชา อินโดนีเซีย บังคลาเทศ และ อียิปต์

เชื้อ H5N1 virus ของอ่องกง และ H5N1 virus ในปัจจุบันเป็นไวรัสลูกผสม (reassortant) เกิดจาก avian viruses หลาย serotype ผสมกัน โดยมียีน HA เป็นบรรพบุรุษ ร่วม แม้ทางอ่องกงได้ทำลายสัตว์ปีกไปจนหมดสิ้นในการระบาดครั้งแรก แต่บรรพบุรุษของไวรัส ซึ่งอยู่ทางตอนใต้ของจีนยังคงอยู่ การศึกษาทางวิวัฒนาการของไวรัส ชี้แนะนำไวรัสเหล่านั้นได้มีการ reassort กันอีกหลายครั้ง ได้ไวรัสลูกผสมที่มีคุณสมบัติทางชีววิทยาเปลี่ยนไปโดยลำดับ และจนกระทั่งเกิดเป็นไวรัส H5N1 ในปัจจุบันซึ่งมีความรุนแรงมากขึ้น การระบาดเป็นวงกว้าง

ขึ้น อัตราตายในผู้ป่วย 60-70% ทั้งนกบกและนกนำตายจากการติดเชื้อ ในขณะที่ไวรัสของอ่องกง ปี พ.ศ. 2540 มีอัตราตายในผู้ป่วยเพียง 33% และมีเพียงนกบกเท่านั้นที่ติดเชื้อแล้วตายแต่นกนำจะไม่ตาย

ในขณะที่มีไวรัสไข้หวัดนกเกิดขึ้นในประเทศไทยนั้น มีคนติดเชื้อไม่มากนัก และการติดต่อจากคนสู่คนไม่ได้เกิดขึ้นง่าย เนื่องจาก receptor บนผิวเซลล์ สำหรับเชื้อไข้หวัดนกนั้น เป็น SAα2,3Gal ในขณะที่ receptor บนผิวเซลล์สำหรับเชื้อไข้หวัดใหญ่เป็น SAα2,6Gal เนื่องจากข้อจำกัดในด้านความจำเพาะต่อ receptor ทำให้เชื้อไข้หวัดนก ยังไม่สามารถติดเชื้อกับเซลล์ของคนได้ดีนัก แต่ถ้าเชื้อยังมีการระบาดอยู่โดยควบคุมไม่ได้ อาจเป็นไปได้ว่า เชื้อมีโอกาสสามารถขึ้นในการปรับตัวให้เข้ากับเซลล์มนุษย์ หรือเกิด reassortment กับ human virus เกิดเป็นไวรัสสูกผสมที่มีทั้งความรุนแรง ติดเชื้อและเพิ่มจำนวนในเซลล์คนได้

เชื้อไวรัสไข้หวัดนกในประเทศไทยจากไหน

การระบาดของโรคไข้หวัดนกในโลกอาจมีสาเหตุเกิดจากนกอพยพ การค้าตามชายแดน และการค้าข้ามประเทศระยะไกล ในประเทศไทยการระบาดครั้งแรกๆ เกิดขึ้นในภาคกลางของประเทศไทยและจังหวัดนครสวรรค์ ทำให้มีข้อสันนิษฐานว่า นกอพยพน่าจะเป็นตัวการนำเชื้อมาสู่ประเทศไทย เนื่องจากจังหวัดนครสวรรค์มีบึงบอระเพ็ดเป็นแหล่งน้ำขนาดใหญ่ซึ่งเป็นที่ชุมนุมของนกอพยพชนิดต่างๆ เป็นจำนวนมาก จึงอาจเป็นไปได้ว่านกอพยพเหล่านี้อาจนำพาเชื้อไข้หวัดนกจากประเทศอื่นมาสู่ประเทศไทย

พยาธิวิทยาของการติดเชื้อไข้หวัดใหญ่/ไข้หวัดนก

ลักษณะพยาธิสภาพที่เด่นที่สุดของเชื้อไวรัสไข้หวัดนกที่ต่างจากไวรัสไข้หวัดใหญ่ (human influenza viruses) ทั่วไป คือ การแพร่กระจายของเชื้อไวรัสออกนอกระบบทางเดินหายใจ และภาวะการสร้าง proinflamatory cytokines มากเกินไป (cytokine storm) การติดเชื้อ human influenza จะจำกัดตัวอยู่ในทางเดินหายใจเท่านั้น และมักจะเป็นทางเดินหายใจส่วนต้นแต่เชื้อไข้หวัดนกชอบติดเชื้อในทางเดินหายใจส่วนล่าง คือ ปอดใน pneumocyte type 2 และยังสามารถแพร่กระจายไปสู่อวัยวะอื่นโดยทางกระแสเลือด เป็น free virus particle viremia หรือ cell associated viremia การตรวจพบ anti-sense RNA ของไวรัสในลำไส้ ทำให้คาดว่าไวรัสน่าจะเพิ่มจำนวนได้ในลำไส้ ผู้วิจัยได้พยายามที่จะแยกเชื้อไวรัสจากอวัยวะต่างๆ ของ autopsy แต่ไม่ประสบผลสำเร็จ อย่างไรก็ตามการตรวจทางพยาธิวิทยา ได้พบพยาธิสภาพที่เกี่ยวเนื่องจากการติดเชื้อในหลายอวัยวะ และภาวะเลือดออกในอวัยวะต่างๆ จึงเชื่อว่าไข้หวัดนกน่าจะก่อการติดเชื้อได้ในหลายอวัยวะและในเซลล์หลายชนิด แต่ก็ยังไม่ทราบว่าเป็นเซลล์ใด มีเพียงรายงานใน macrophage เท่านั้น เซลล์เหล่านั้นอาจยอมให้ไวรัสเพิ่มจำนวนได้ หรือมีเพียงการติดเชื้อ แต่ไม่มีการเพิ่มจำนวนก็เป็นได้ การตรวจหาการเพิ่มจำนวนของไวรัสในเซลล์ ซึ่งไม่ใช่ respiratory epithelial cells อาจทำให้ทราบถึงความสามารถของเชื้อในการแพร่กระจายออก

นอก respiratory system ซึ่งถือเป็นกลไกสำคัญอย่างหนึ่งที่ทำให้การติดเชื้อไข้หวัดใหญ่มีความรุนแรงเพิ่มมากขึ้น ในสัตว์ปีกได้พบว่า endothelial cell สามารถติดเชื้อไวรัสไข้หวัดนกได้ดี

ระบบวิทยาของเชื้อไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 pandemic influenza A (H1N1) ในประเทศไทย

โรคไข้หวัดใหญ่สายพันธุ์ใหม่เดิมเคยเรียกว่า swine-origin influenza A (H1N1) หรือเรียกชื่อใหม่ในปัจจุบันว่า 2009 pandemic influenza A (H1N1) เริ่มพบการระบาดครั้งแรกในประเทศไทยเม็กซิโก เมื่อเดือนมีนาคม พ.ศ. 2552 และองค์การอนามัยโลก (World Health Organization, WHO) ได้ประกาศการระบาดอย่างเป็นทางการในวันที่ 24 เมษายน พ.ศ. 2552 การติดเชื้อมีการแพร่กระจายออกไปยังสหรัฐอเมริกา และอีกหลายประเทศในหลายทวีปทั่วโลก องค์การอนามัยโลกจึงประกาศภาวะการระบาดทั่วโลก (pandemic phase 6) ในวันที่ 11 มิถุนายน พ.ศ. 2552 และประกาศการเข้าสู่ภาวะการระบาดตามถูกต้อง (post-pandemic phase) ในวันที่ 10 สิงหาคม พ.ศ. 2553 ประเทศไทยรายงานผู้ป่วยรายแรกเมื่อ วันที่ 4 พฤษภาคม 2552 การระบาดระลอกแรกในประเทศไทยเริ่มขึ้นในปลายเดือนพฤษภาคม 2552 พบผู้ป่วยสูงสุดในเดือนกรกฎาคม และสิ้นสุดลงในเดือนพฤษจิกายน 2552 ตามมาด้วยการระบาดเล็กๆ เป็นระลอกที่ 2 ระหว่างเดือนธันวาคม 2552 ถึงเดือนเมษายน 2553 โดยผู้ป่วยสูงสุดในเดือนกุมภาพันธ์ 2553 และการระบาดระลอกที่ 3 ซึ่งเกิดขึ้นในเดือนมิถุนายน 2553 พบผู้ป่วยสูงสุดในเดือนสิงหาคม และสิ้นสุดลงในเดือนตุลาคม 2553 ซึ่งเป็นการระบาดขนาดใหญ่มีผู้ติดเชื้อจำนวนมาก และระลอกที่ 4 เกิดขึ้นในเดือนกันยายน 2554 ในปี พ.ศ. 2555 ยังคงมีการระบาดเล็กๆ และพบผู้ป่วยอยู่เป็นระยะ กลยุยเป็นเชื้อประจำ ในขณะที่ไข้หวัดใหญ่ A(H1N1) สายพันธุ์เดิมได้สูญหายไปจากโลก ความรุนแรงจากการติดเชื้อไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ไม่ได้สูงไปกว่าไข้หวัดใหญ่ทั่วไป อาการของโรคก็คล้ายกับไข้หวัดใหญ่ตามถูกต้องแต่เดิม และมีอัตราการเสียชีวิตไม่ต่างกันคือน้อยกว่า 1% แต่การแพร่กระจายโรคจะเกิดรวดเร็วมากเนื่องจากคนส่วนใหญ่ยังไม่มีภูมิคุ้มกัน จึงทำให้มีจำนวนผู้ติดเชื้อจำนวนมาก และโดยเฉพาะเมื่อโรคเกิดขึ้นในผู้ที่มี underlying conditions อาการมักจะรุนแรงจนถึงแก่ชีวิต

ไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่มียืนทั้ง 8 ชี้นเกิดขึ้นจากการผสมผสานของยืนจากไวรัสสายพันธุ์ของคน สุกรและนก (quadruple reassortment) ดังนี้

- 1) ยืน hemagglutinin (HA), nucleoprotein (NP) และ non-structural (NS) มาจากสุกรในอเมริกาเหนือ (North America swine influenza virus lineage)
- 2) ยืน neuraminidase (NA) และ matrix (M) มาจากสุกรในยุโรป (Eurasian swine influenza virus lineage)
- 3) ยืน polymerase basic protein 2 (PB2) และ polymerase acidic protein (PA) มาจากนกในอเมริกาเหนือ (North America avian influenza virus lineage)
- 4) ยืน polymerase basic protein 1 (PB1) มาจากไวรัสไข้หวัดใหญ่ของคน (human seasonal H3N2 virus)

เมื่อการระบาดแพร่กระจายไปทั่วโลก นักวิจัยจากประเทศต่างๆ ได้นำวิธีการทางระบบวิทยา และ วิธีการทาง serology ซึ่งมีความแม่นยำ มาใช้เพื่อประเมินสถานการณ์และแนวโน้มว่าจะเกิดการระบาดครั้งต่อๆไปอีกหรือไม่ จากการประเมินอัตราการติดเชื้อหรือภาวะภูมิคุ้มกันโรคของประชากรภายหลังการระบาดแต่ละครั้ง งานวิจัยนี้จึงใช้เทคนิคทาง serology คือ hemagglutination inhibition assay และ microneutralization assay มาใช้ในการประเมินอัตราการติดเชื้อและตรวจหาภาวะภูมิคุ้มกัน และวินิจฉัยการเกิด asymptomatic infection ในประชากรทั่วไป ได้พบว่าวิธี microNT มีปฏิกิริยาข้ามค่อนข้างมากไม่เหมาะสมกับการนำมาใช้ในการประเมินอัตราการติดเชื้อ ในขณะที่สามารถใช้ HI assay ในการประเมินได้ดีกว่า นอกจากนี้ คณะผู้วิจัยได้ทำการศึกษาเกี่ยวกับลักษณะทาง genotype และ phenotype ของเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 A(H1N1) เปรียบเทียบกับเชื้อไข้หวัดนก H5N1 และเชื้อไข้หวัดใหญ่ตามฤดูกาล seasonal H1N1 และ H3N2 ควบคู่กันไปด้วย โดยตีพิมพ์ข้อมูลทางพันธุกรรมเหล่านี้ใน GenBank database

ภาวะภูมิคุ้มกันต่อเชื้อไข้หวัดใหญ่

ภูมิคุ้มกันโรคไข้รัสท์ไวรัสไข้หวัดใหญ่ เกิดจากการทำงานร่วมกัน ทั้ง humoral immunity (ได้แก่ แอนติบอดีและสารน้ำ) และ cell-mediated immunity (CMI) โดย neutralizing (NT) antibody จะจับกับตำแหน่งที่ไวรัสใช้ในการเกาะติดกับเซลล์ (attachment site) ทำให้ไวรัสเข้าเซลล์ไม่ได้ หรือเข้าสู่เซลล์ได้แต่จะไม่เกิด uncoating และ replication การติดเชื้อจึงไม่เกิดขึ้น นอกจากนี้ mucosal antibody ที่อยู่ในเมือกนุททางเดินหายใจยังดักจับไวรัสไว ทำให้การแพร่กระจายของเชื้อไวรัสถูกยับยั้ง ส่วน CMI นั้นจะทำงานต่อเมื่อเซลล์มีการติดเชื้อไปแล้ว โดย cytotoxic T lymphocytes (CTL) จะ recognize antigenic epitopes ของไวรัสร่วมกับ HLA class I antigen ของเซลล์ แล้วทำลายเซลล์ติดเชื้อนั้น

ความรุนแรงของ H5N1 virus ทำให้องค์กรต่างๆ ตื่นตัวในการพัฒนาวัคซีนเพื่อป้องกัน H5N1 virus ความพยายามทั้งหมดมุ่งไปที่การผลิตวัคซีนเชื้อตาย ซึ่งเป็นที่ยอมรับกันโดยทั่วไปว่าวัคซีนเชื้อตายนั้นกระตุ้นการสร้างแอนติบอดี และจะมีความจำเพาะต่อ antigen ค่อนข้างแคบ และจะต้องเปลี่ยน HA gene ในไวรัสที่ใช้เตรียมวัคซีนไปเรื่อยๆ ทีมผู้วิจัยได้ใช้แนวทางของการพัฒนาวัคซีนเอ็ดส์มาเป็นสมมุติฐานของหัวข้อวิจัย คือ เชื้อเอชไอวี คล้ายกับเชื้อไข้หวัดใหญ่ในเชิงของการมี หลาย serotype การพัฒนาวัคซีนเอ็ดส์มุ่งไปที่การผลิต live recombinant vector vaccine โดยมียีนสำคัญคือ gag gene (group specific gene ซึ่งเป็นรหัสสำหรับสร้าง capsid protein) ซึ่งเป็น conserve gene สามารถกระตุ้นให้เกิด cytotoxic T lymphocyte activity ที่มีผลในการทำลายเซลล์ติดเชื้อเอชไอวีที่ต่าง subtype กันได้ งานวิจัยเกี่ยวกับภูมิคุ้มกันของเชื้อไข้หวัดใหญ่เมื่อค่อนข้างจำกัด แต่ก็มีนักวิจัยหลายกลุ่มเชื่อว่าการกระตุ้นให้เกิดภูมิคุ้มกันขึ้น subtype หรือข้ามสายพันธุ์ มีความเป็นไปได้ ในการใช้ low pathogenic AI virus หรือ live virus เป็น immunogen งานวิจัยจึงเป็นการนำเสนอแนวทางใหม่ในการพัฒนาวัคซีนป้องกันไข้หวัดนก

อัตราการเสียชีวิตของผู้ป่วยไข้หวัดนกในประเทศไทย 25 ราย ถึงแก่กรรม 17 ราย หรือคิดเป็น 68% ซึ่งถือว่ามีความรุนแรงมาก นอกเหนือจากนี้คุณผู้วิจัยยังได้พบ neutralizing antibody ต่อเชื้อไข้หวัดนกในระดับต่ำๆ ในซีรัมที่ได้จากการเจาะเลือดผู้สัมผัสกับสัตว์ที่เป็นโรค ได้แก่ เกษตรกรผู้เลี้ยง และผู้ทำหน้าที่ทำลายสัตว์ รวมทั้ง ญาติผู้ดูแลผู้ป่วย แต่ก็ไม่ทราบว่า แอนติบอดีนี้เกิดขึ้นจากปฏิกริยาข้ามกับไวรัส subtype อื่น หรือจากการติดเชื้อไวรัสไข้หวัดนกเอง การศึกษาระดับแอนติบอดีในผู้ป่วยและผู้อุดชีวิต และระยะเวลาที่อาจตรวจพบแอนติบอดี จะเป็นประโยชน์ในการศึกษาทางระบบวิทยาต่อไป

มีผู้ศึกษาในกลุ่มตัวอย่างจากผู้บริจากเลือด โดยใช้วิธี CTL assay และ ELISpot พบ การตอบสนองต่อไวรัสไข้หวัดใหญ่ในหลาย epitopes ได้แก่ PB1, PB2, NP, NA, HA, M1, NS1, และ M2 ซึ่ง epitope ที่น่าจะ common ในผู้โดยติดเชื้อ คือ NP และยังได้พบ CTL activity ที่ข้าม subtype กันได้ด้วย

ในขณะที่ NP gene จะมีความ conserve ภายในไวรัสไข้หวัดใหญ่ type เดียวกันยืน HA จะเป็นยืนที่มี diversity สูง การใช้วิธี ELISpot เพื่อศึกษา T cell epitopes (ทั้ง CD4⁺ และ CD8⁺ T cells) ของผู้ติดเชื้อไข้หวัดนก โดยใช้ overlapping peptides ของ NP ของ H5N1 virus ในการทดสอบในผู้อุดชีวิตจากโรคไข้หวัดนกและโรคไข้หวัดใหญ่ ก็จะทำให้ทราบได้ว่า epitopes ใด เป็น common epitopes และ epitopes ใด เป็น NP specific epitopes ประโยชน์ที่จะได้จากการศึกษา คือ ทำให้ทราบ immunogenicity ของ regions ต่างๆ ของ NP molecules นอกจากนี้ยังสามารถนำ peptides ที่มี immunogenic epitopes ไปศึกษา T cell และ B cell functions ต่อไปได้ ซึ่งจะนำไปสู่ความเข้าใจในเรื่องของภูมิคุ้มกันในโรคไข้หวัดนก และเป็นแนวทางในการพัฒนาวัคซีนต่อไป

การวินิจฉัยผู้ติดเชื้อไวรัสไข้หวัดใหญ่/ไข้หวัดนก

การวินิจฉัยผู้ติดเชื้อไข้หวัดนก/ไข้หวัดใหญ่ สามารถทำได้หลายวิธี ได้แก่

1. การตรวจหาเชื้อในตัวอย่างโดยวิธี conventional reverse transcription-polymerase chain reaction (RT-PCR) และ real time RT-PCR ซึ่งสามารถให้การวินิจฉัยได้ถึงระดับของเชื้อตันเหตุ วิธีการตรวจเป็นวิธีมาตรฐานที่ใช้กันทั่วไปตามข้อแนะนำขององค์กรอนามัยโลก และศูนย์ควบคุมและป้องกันโรค สหรัฐอเมริกา ซึ่งจะต้องลงนามในข้อตกลง Material transfer agreement

การติดตามการขับเชื้อไวรัสออกจากระบบทางเดินหายใจของผู้ป่วย ทั้งในเชิงปริมาณ และเชิงคุณภาพ มักใช้การตรวจหาเชื้อในแมวน้ำและการแยกเชื้อ แม้ว่าในที่ตรวจพบนั้นจะไม่ได้มามาก เชื้อไวรัสที่มีชีวิตก็ตาม แต่ก็เป็นวิธีการที่ทั่วโลกนิยมใช้

2. การแยกเชื้อไวรัสในเซลล์เพาะเลี้ยงและในไข่ไก่ฟัก การตรวจกรองว่าแยกเชื้อได้จะนำน้ำเซลล์เพาะเลี้ยงหรือ allantoic fluid ของไข่มาทดสอบเม็ดเลือดแดงของสัตว์บางชนิด ก็

จะเห็นปฏิกิริยาการเกาะกลุ่มของเม็ดเลือดแดง (hemagglutination) ถ้าเม็ดเลือดแดงมาจากสัตว์ที่เหมาะสมก็จะมีความไวในการตรวจไวรัสที่มีจำนวนน้อยได้ วิธีการแยกเชื้อ ก็จะมีความไวมากขึ้น เชื้อไวรัสที่แยกได้นี้จะถูกนำไปใช้ในการทดสอบยาและพัฒนาวัคซีน เชื้อจากทั่วโลกจะถูกส่งไปยังห้องปฏิบัติการอ้างอิงเพื่อนำไปพิจารณาเป็นองค์ประกอบของวัคซีนที่ใช้ในปีต่างๆ

ตัวอย่างตรวจที่ดีที่สุดสำหรับการตรวจหาไวรัสในมือและการแยกเชื้อ คือ nasopharyngeal aspirate ซึ่งเป็นตัวอย่างตรวจที่ต้องอาศัยความชำนาญของผู้เก็บ และไม่เหมาะสมสำหรับการออกภาคสนาม ดังนั้นตัวอย่างตรวจที่ถูกส่งมายังห้องปฏิบัติการจะได้แก่ nasal swab, nasopharyngeal swab และ throat swab เป็นส่วนใหญ่ ยังไม่มีข้อสรุปว่า swab ชนิดใดที่มีปริมาณไวรัสมากกว่ากัน ซึ่งจะมีผลต่อความไวของวิธีทดสอบด้วย

3. การตรวจหาแอนติเจน อาจทำโดยการตรวจหาแอนติเจนใน epithelial cells ที่ติดเชื้อซึ่งหลุดลอกปนออกมากับ respiratory secretion ต่างๆ โดยใช้แอนติบอดีจำเพาะในการทดสอบด้วยวิธีอิมมูนเรืองแสง (immunofluorescent assay) วิธีการนี้ต้องการผู้อ่านสไลด์ที่มีประสบการณ์สูง มีความสามารถจะเกิดผลลบปลอมหรือผลบวกปลอมได้ง่าย ในปัจจุบันมีวิธีทดสอบรวดเร็ว (rapid test) เช่นวิธี immunochromatography ทดสอบหาแอนติเจนของไวรัสไข้หวัดใหญ่ไทย A และ B ซึ่งได้ผลภายในเวลาไม่กี่นาที แต่ความไวในการทดสอบต่ำเพียง 50-60% เท่านั้น

4. การตรวจหาแอนติบอดี เพื่อการวินิจฉัยโรคไข้หวัดใหญ่ นิยมทำด้วยการตรวจหาแอนติบอดีต่อเชื้อไวรัสในชีรั่มคู่ (paired blood samples) ซึ่งจะห่างกันประมาณ 2 สัปดาห์ ถ้าเป็นโรคจริงระดับแอนติบอดีในเลือดครั้งที่สอง (convalescent blood) จะสูงกว่าเลือดครั้งแรก (acute blood) อย่างน้อย 4 เท่า วิธีการที่นิยมใช้ได้แก่วิธี hemagglutination inhibition assay อย่างไรก็ได้ในการวินิจฉัยผู้ป่วยไข้หวัดนก องค์การอนามัยโลกแนะนำให้ใช้วิธี microneutralization (microNT) assay และ Western blot assay เป็นวิธีตรวจยืนยันร่วมด้วยโดยในผู้ป่วยไข้หวัดนกจะต้องพบ neutralizing (NT) antibody titer มากกว่าหรือเท่ากับ 80 (หรือ titer 40 ถ้าไม่คิดปริมาตรใน reaction well) ถ้าทราบว่าแอนติบอดีในระดับนี้สามารถถอยได้ นานก็จะเป็นประโยชน์ในการสำรวจหาผู้ที่ติดเชื้อไข้หวัดนกที่มีอาการอย่างอ่อนหรือไม่มีอาการได้ ซึ่งจะทำให้ทราบถึงความชุกของผู้ติดเชื้อไข้หวัดนกในประชากรกลุ่มเสี่ยง เช่น เกษตรกรผู้เลี้ยงสัตว์ปีกและผู้ทำงานในโรงงานสัตว์ปีก เป็นต้น

วิธี microNT ใช้สำหรับตรวจ NT antibody ซึ่งเป็น protective antibody ในกรณีคุ้มกันโรค แต่วิธีนี้ทำได้ไม่ง่ายนัก และผู้ปฏิบัติงานมีความเสี่ยงต่อการติดเชื้อ เนื่องจากต้องใช้เซลล์เพาะเลี้ยง และใช้ไวรัสที่มีชีวิต นอกจากนี้ถ้าเป็นไวรัสไข้หวัดนก ยังต้องปฏิบัติงานในห้องชีวนิรภัยระดับ BSL 3 หรือ BSL 2 enhanced ด้วย ส่วนวิธี HI ทำได้ง่ายกว่า และใช้เชื้อที่ตายแล้ว หรือใช้เชื้อที่ยังมีชีวิตเป็นแอนติเจนทดสอบก็ได้ เพียงแต่ต้องเลือกใช้ fresh erythrocyte species ที่เหมาะสม และ HI antibody ไม่สามารถบ่งถึงการมี protective antibody ได้โดยตรง แต่เนื่องจากผู้ที่มี HI antibody ก็มักจะมี NT antibody รวมอยู่ด้วย องค์การอนามัยโลกจึงอนุโลมให้ใช้วิธี HI ในการประเมินประสิทธิภาพของ seasonal vaccine แต่ละ lot ก่อนนำออกจำหน่ายในห้องตลาด วัคซีนที่ใช้ได้จะต้องกระตุ้นให้เกิดการสร้าง HI antibody ที่ titer 40

เป็นอย่างน้อย และค่านี้อาจสามารถนำมาใช้ในการป้องกันภัยการมีภูมิคุ้มกันต่อเชื้อไข้หวัดใหญ่ได้

โดยทั่วไปแล้วเชื้อไข้หวัดใหญ่สามารถ agglutinate เม็ดเลือดแดงจากหลาย species เช่น คนหมูเลือดโอ หนูตะเภา ไก่ ห่าน แมว และ ไก่งวง แต่งานวิจัยที่ผ่านมาชี้แนะนำว่า เม็ดเลือดแดงจากม้าอาจมีความไวมากที่สุดในการทำ HI assay สำหรับเชื้อไข้หวัดนก H5N1 แต่เนื่องจากเม็ดเลือดแดงม้าหาได้ยากในประเทศไทยและหลายประเทศในเอเชียอาคเนย์ และยังไม่มีผู้ใดทดสอบว่าเม็ดเลือดแดงม้าบังคับต้องในการเป็น detector ที่ดีที่สุดสำหรับเชื้อ H5N1 ในปัจจุบัน นอกจาคนี้เชื้อที่มีการระบาดขึ้นใหม่ก็จำเป็นต้องมีการเลือกชนิดของเม็ดเลือดแดงที่เหมาะสมสำหรับใช้ในการทดสอบ hemagglutination เพื่อตรวจหาเชื้อไวรัส และตรวจหาแอนติบอดีโดยวิธี HI ดังนั้นชนิดของเม็ดเลือดแดงที่เหมาะสมจึงมีความสำคัญต่อการวินิจฉัยและการทดสอบระดับภูมิคุ้มกันต่อการติดเชื้อไข้หวัดใหญ่

การดื้อยาของเชื้อไวรัสไข้หวัดใหญ่

ยาที่ใช้ในการรักษาไข้หวัดใหญ่ในมนุษย์ แต่เดิมมานั้นได้แก่ amantadine rimantadine ซึ่งออกฤทธิ์เป็น M2 ion channel blocker ยานี้ออกฤทธิ์ยับยั้งได้เฉพาะไวรัสไข้หวัดใหญ่ type A เท่านั้น ต่อมาได้พบว่าเชื้อไวรัสไข้หวัดใหญ่ของมนุษย์เริ่มดื้อต่อ yan นี้ การเปลี่ยนแปลง amino acid เพียง 1 ใน 5 ตำแหน่ง ซึ่งอยู่ใน transmembrane portion (residues 26, 27, 30, 31 และ 34) จะทำให้ไวรัสไข้หวัดใหญ่ดื้อต่อยาตัวนี้อย่างสมบูรณ์ จากการศึกษาโดยคณะผู้วิจัยได้พบว่า เชื้อไวรัสไข้หวัดนก clade 1 ดื้อต่อ yan นี้ ในขณะที่ไวรัส clade 2 ยังไม่ดื้อต่อ yan นี้ สำหรับเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 A(H1N1) ก็ดื้อต่อ yan นี้ด้วย amino acid substitution ที่ตำแหน่งนี้เช่นกัน

ปัจจุบันยาที่นิยมใช้ในการรักษาโรคไข้หวัดใหญ่รวมถึงไข้หวัดนกด้วยคือ neuraminidase inhibitor (NI) ยานี้ออกฤทธิ์ยับยั้งไวรัสไข้หวัดใหญ่ทั้ง A และ B ในขั้นตอนปลดปล่อยไวรัสรุนลุกออกจากเซลล์ติดเชื้อ ยาที่เป็น NI ได้แก่ zanamivir ซึ่งใช้พ่นทางปาก (oral inhalation) และยา oseltamivir ซึ่งให้โดยการกิน ดังนั้น oseltamivir จึงมีความสะดวกในการใช้งานมากกว่า NI และถูกนำไปใช้ทั้งเพื่อป้องกัน (prophylaxis) และการรักษา (treatment) แต่อาจไม่ปลอดภัยสำหรับการนำไปใช้ในทารกอายุน้อยกว่า 1 ปี การเกิด mutation ใน NA protein ที่ amino acid substitution H274Y เป็นตำแหน่งสำคัญที่ทำให้ทั้งไวรัสไข้หวัดนกและไวรัสไข้หวัดใหญ่ดื้อต่อยา oseltamivir ในขณะที่ยัง sensitive ต่อ zanamivir และนอกจากนี้ยังพบว่า mutation ในตำแหน่งอื่นๆ ก็อาจทำให้ไวรัสดื้อต่อยาทั้งสองชนิดนี้ได้ อย่างไรก็ได้ mutation ที่ receptor binding site ของ HA molecule มีผลร่วมต่อการดื้อ NI ด้วย ในปี 2008-2009 เชื้อไวรัส seasonal influenza A H1N1 ดังเดิมจากทั่วโลกรวมทั้งประเทศไทยดื้อต่อยา oseltamivir

ในประเทศไทยได้มีการนำยา oseltamivir เข้ามาใช้ในการรักษาผู้ป่วยไข้หวัดนก
นอกจากนี้ยังมีการกินยาเพื่อป้องกันในนักวิจัยบางกลุ่มด้วย การเฝ้าระวังการดื้อยาของเชื้อ

วัตถุประสงค์

ประเทศไทยมีการรายงานผู้ป่วยไข้หวัดนก H5N1 รายสุดท้ายของประเทศไทยเมื่อเดือนกรกฎาคม 2549 แต่ต่อมามีในช่วงเดือนพฤษภาคม 2552 ได้มีการระบาดของเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 A(H1N1) เกิดขึ้น ขณะผู้วิจัยจึงได้ทำการศึกษาวิจัยเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ร่วมด้วย เพื่อเป็นประโยชน์ในการป้องกันและควบคุมการระบาดของโรคเป็นการเร่งด่วนในขณะนั้น ดังนั้นโครงการวิจัยจึงมีวัตถุประสงค์ ดังนี้

1. เพื่อเฝ้าระวังไวรัสไข้หวัดนกกลุ่มผสมตัวใหม่ ที่อาจมีความรุนแรงในการก่อโรคและแพร่กระจายระหว่างคนได้ดี
2. ศึกษาลักษณะทางพันธุกรรมของเชื้อไวรัสไข้หวัดนกที่พบในประเทศไทยในช่วงการระบาดระลอกต่างๆ เพื่อทราบว่าเชื้อตันเหตุนั้นเป็นเชื้อที่ถูกนำเข้ามาใหม่ หรือเป็นเชื้อที่รอดเหลือจากการระบาดครั้งก่อน
3. ศึกษาลักษณะทั่วไปทางชีววิทยาของไวรัสไข้หวัดนก ได้แก่ ความสามารถในการจับกับเม็ดเลือดแดง species ต่างๆ ลักษณะรูปร่างเมื่อส่องดูด้วยกล้องจุลทรรศน์อิเล็กตรอน
4. เพื่อศึกษาความสามารถของเชื้อไวรัสไข้หวัดนกในการติดเชื้อและเพิ่มจำนวนในเซลล์ที่ไม่ใช่ respiratory epithelial cells โดยเฉพาะเซลล์เยื่อบุหลอดเลือดดำ ซึ่งจะทำให้เข้าใจถึงสาเหตุที่ทำให้เชื้อไวรัสไข้หวัดนกสามารถก่อพยาธิสภาพนอกรอบทางเดินหายใจได้ รวมทั้งความสามารถในการหลัง cytokines/mediators ในเซลล์เยื่อบุหลอดเลือดดำ โดยศึกษาเปรียบเทียบกับไข้หวัดใหญ่ของคน
5. ศึกษา innate immunity ที่มีอยู่ในซีรั่ม (serum inhibitors) ที่มีฤทธิ์ยับยั้งความสามารถในการติดเชื้อไข้หวัดนก โดยเปรียบเทียบกับเชื้อไข้หวัดใหญ่ของมนุษย์สายพันธุ์ต่างๆ
6. ศึกษาการตอบสนองทางด้าน humoral immunity ต่อเชื้อไข้หวัดนก
 - 6.1 ศึกษา kinetics การสร้างแอนติบอดีในผู้ติดเชื้อไข้หวัดนกและติดตามการคงอยู่ของระดับแอนติบอดีโดยการเจาะเลือดเป็นระยะๆ 6 เดือน เป็นเวลา 3 ปี เพื่อใช้เป็นค่า cut-off ในการสำรวจประชากรกลุ่มเสี่ยงที่อาจติดเชื้อไข้หวัดนกด้วยไม่แสดงอาการ
 - 6.2 ศึกษา cross-neutralizing antibody ต่อเชื้อไข้หวัดนกที่เกิดขึ้นในกลุ่มผู้รับวัคซีน seasonal influenza
 - 6.3 ศึกษาแอนติบอดีต่อโปรตีนแต่ละชนิดของไวรัสไข้หวัดนก ซึ่งสามารถทำได้โดยการสร้าง vaccinia recombinant viruses ซึ่งมีการสอดแทรกยีน HA NA NP M หรือ NS ของไวรัสไข้หวัดนก รวมทั้งหมวด 5 constructs และใช้ recombinant viruses เหล่านี้ในการ infect TK cell เพื่อเตรียมแอนติเจนสำหรับทดสอบหาแอนติบอดีโดยวิธีอิมมูนเรืองแสง

7. ศึกษา cellular immunity ต่อ epitopes ของ NP protein ของเชื้อไข้หวัดนกในผู้อุดชีวิตโดยการวัด function ของ cytotoxic T lymphocytes ด้วยวิธี ELISpot และเนื่องจาก NP เป็น conserved gene จึงควรพบได้ในกลุ่มคนที่เป็น non-H5N1 exposure ด้วย เป็นการสร้างแนวความคิดใหม่ในการพัฒนาวัคซีนที่กระตุ้นให้เกิดภูมิคุ้มกันข้าม subtype หรือ cross immunity

8. เพื่อศึกษาความสัมพันธ์ระหว่างเส้นทางของนกอพยพในประเทศไทย กับพื้นที่ระบาดของโรค โดยใช้เทคนิคการสื่อสารผ่านดาวเทียม satellite telemetry

9. เพื่อศึกษาการตอบสนองทางภูมิคุ้มกันต่อเชื้อไข้หวัดใหญ่/ไข้หวัดนก รวมทั้งหาค่า cut-off ในการประเมินอัตราการติดเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ A/H1N1 2009 ภายหลังจากการระบาดในระลอกแรกเพื่อประเมินความเสี่ยงที่จะเกิดการระบาดของโรคในระลอกถัดไป

10. ศึกษา viral load และ viral shedding จากสิ่งส่งตรวจนิดต่างๆ จากผู้ที่ติดเชื้อ seasonal influenza virus A/H1N1, A/H3N2 และ A/H1N1 2009 เพื่อวิเคราะห์หาสิ่งส่งตรวจที่เหมาะสมในการวินิจฉัยการติดเชื้อและเป็นประโยชน์ในการควบคุมการแพร่กระจายของโรค

11. เพื่อเฝ้าระวังเชื้อไข้หวัดใหญ่/ไข้หวัดนก และ ไข้หวัดใหญ่สายพันธุ์ใหม่ A/H1N1 2009 ด้วยต่อยา neuraminidase inhibitors: oseltamivir และ zanamivir

วิธีการทดลอง

1. จริยธรรมการวิจัย

การดำเนินงานวิจัยในมนุษย์ได้ผ่านการอนุมัติ จากคณะกรรมการจริยธรรมวิจัยในคน (Ethic committee) คณะแพทยศาสตร์ศิริราชพยาบาล มหาวิทยาลัยมหิดล และจากกระทรวงสาธารณสุข

การวิจัยในสัตว์ได้รับอนุมัติการทำวิจัยจากคณะกรรมการกำกับดูแลการเลี้ยงและการใช้สัตว์ คณะสัตวแพทยศาสตร์ มหาวิทยาลัยมหิดล และได้รับการรับรองจาก Standards for Humane Care and Use of Laboratory Animals of the Office of Laboratory Animal Welfare (OLAW No. A5731-01), U.S. และได้รับอนุญาตและความร่วมมือจากเจ้าหน้าที่กรมอุทิยานแห่งชาติ สัตว์ป่า และพันธุ์พืช

2. เทคนิควิธีการที่ใช้ในการศึกษาวิจัย

- 2.1 การแยกเชื้อและเพาะเลี้ยงเพิ่มจำนวนไวรัส ในไข่ไก่ฟักและเซลล์เพาะเลี้ยง
- 2.2 ทดสอบหาปริมาณไวรัสโดย TCID50 virus titration, plaque assay
- 2.3 การวินิจฉัยการติดเชื้อไวรัสไข้หวัดใหญ่ โดยใช้เทคนิค RT-PCR, realtime RT-PCR, immunofluorescence และ serology diagnosis โดยวิธี microNT และ HI assays
- 2.4 การศึกษาลักษณะทางพันธุกรรมของไวรัสโดยการหาลำดับนิวคลิโอลีด์ และการทำ phylogenetic analysis
- 2.5 ศึกษา viral load และ viral shedding จาก clinical samples ชนิดต่างๆ โดยใช้เทคนิค quantitative real time RT-PCR ในการตรวจหา M gene ของเชื้อไวรัส
- 2.6 การศึกษาการตอบสนองทางภูมิคุ้มกันของเชื้อไวรัสไข้หวัดใหญ่/ไข้หวัดนกด้วยวิธี microNT และ HI
- 2.7 ศึกษาสารในเชื้อรึ่ม ซึ่งมีผลต่อการยับยั้งการติดเชื้อและเพิ่มจำนวนของเชื้อไวรัส ไข้หวัดนกและไข้หวัดใหญ่สายพันธุ์ต่างๆ ด้วยวิธี infectivity reduction assay
- 2.8 ศึกษาภูมิคุ้มกันชนิด cross-subtype cellular immunity ระหว่างเชื้อไข้หวัดใหญ่ และไข้หวัดนก (H5N1) ด้วยวิธี ELISpot assay และ Flow cytometry
- 2.9 การตรวจระดับ cytokine/chemokine ที่หลังจาก mononuclear cell และเซลล์บุหลอดเลือดโดยวิธี ELISA
- 2.10 ศึกษาความสัมพันธ์ระหว่างเส้นทางของนกอพยพในประเทศไทยกับพื้นที่ระบาดของโรคโดยใช้เทคนิคการสื่อสารผ่านดาวเทียม (satellite telemetry)
- 2.11 การทดสอบหาความไวของไวรัสต่อยาต้านไวรัส neuraminidase inhibitor

2.11.1 วิธี genotypic-based assay โดยวิเคราะห์ลำดับนิวคลิโอลิโด้ร์ของยีน NA ของไวรัส เพื่อหาตำแหน่ง mutation ที่ทำให้ไวรัสดื้อต่อยาต้านไวรัส วิธีนี้ทำได้รวดเร็วแต่มีข้อเสีย คือ สามารถใช้กับการเกิด mutation ที่เคยมีการศึกษาไว้ก่อนแล้ว แต่ไม่สามารถใช้ในการตรวจหาเชื้อดื้อยาที่เกิดจากการ mutation ในตำแหน่งที่เกิดขึ้นใหม่ได้

2.11.2 วิธี phenotypic-based assay โดย MUNANA-based neuraminidase inhibition assay (NAI), ELISA-based viral nucleoprotein (NP) reduction assay และ plaque reduction assay

ในการศึกษานี้จะทดสอบความไวของเชื้อต่อยาที่มีฤทธิ์ยับยั้ง neuraminidase ของไวรัส 2 ชนิด คือ oseltamivir และ zanamivir ซึ่ง oseltamivir carboxylate จากบริษัท Roche, Belgium ได้รับการสนับสนุนจาก Southeast Asia Infectious Clinical Research Network และ zanamivir จาก บริษัท GlaxoSmithKline, UK ได้รับการสนับสนุนจาก US. Centre for Disease Control and Prevention ในปัจจุบันยังไม่มีเทคนิคมาตรฐานเพื่อใช้ในการทดสอบความไวต่อยาต้านไวรัสด้วยวิธีที่พิจารณาจากการติดเชื้อในเซลล์เพาะเลี้ยง (cell culture-based infectivity) ที่ยอมรับใช้ทั่วไปในห้องปฏิบัติการต่างๆ โครงการวิจัยนี้จึงได้พัฒนาเทคนิค ELISA-based viral nucleoprotein reduction assay ขึ้นเป็นครั้งแรกเพื่อใช้เป็น alternative test โดยเปรียบเทียบกับ plaque reduction assay และ neuraminidase inhibition assay (NAI)

MUNANA-based NAI assay เป็นการทดสอบการทำงานของเอนไซม์ neuraminidase ของเชื้อไวรัสโดยตรง ซึ่งใช้ 2-(4-methylumbelliferyl)- α -D-N-acetylneurameric acid (MUNANA) เป็น substrate

Plaque reduction assay เป็นเทคนิคหลักที่ใช้กันทั่วโลก แต่ยังไม่มีการกำหนดวิธีมาตรฐานอย่างกว้าง ควรใช้ไวรัสปริมาณเท่าๆ นอกจากนี้วิธีนี้ใช้เวลานาน และมี variation สูง นอกจากนี้ plaque ของไวรัสยังมีขนาดไม่เท่ากัน ขณะผู้วิจัยจึงกำหนดว่า หากศึกษาไวรัส H5N1 ซึ่งมีขนาดใหญ่จะกำหนดไว้ที่ 50 plaque forming unit (PFU) ส่วน H1N1/ H3N2 จะกำหนดไว้ที่ 50-100 PFU แต่ทั้งนี้วิธีนี้ก็มีข้อเสีย คือ ไวรัสบางสายพันธุ์มีลักษณะการเกิด plaque ที่มีขนาดเล็กและไม่ชัดเจน จึงทำให้ไม่สามารถทดสอบการดื้อยาด้วยวิธีนี้ได้

ELISA-based NP reduction assay เป็นเทคนิคที่พัฒนาและดัดแปลงมาจากวิธี microneutralization assay ที่ใช้ในการตรวจหาเอนติบอดีต่อเชื้อไวรัส โดยใช้การตรวจหาปริมาณการสร้าง nucleoprotein ของไวรัสภายในเซลล์ที่มีการติดเชื้อโดยวิธี ELISA สามารถทดสอบกับไวรัสได้คราวละมากๆ และใช้ยาปริมาณน้อย และเมื่อนำมาผลลัพธ์ศึกษาความสัมพันธ์กับเทคนิค plaque reduction assay พบร่วมกับความสัมพันธ์กัน นอกจากนี้เทคนิคนี้ได้ถูกนำไปใช้ตรวจคัดกรองหาสารสกัดสมุนไพรซึ่งมีฤทธิ์ต้านเชื้อไว้หวัดใหญ่และไข้หวัดนก

ผลการศึกษาวิจัย

1. Electron micrographs of highly and low pathogenic avian influenza viruses

Background: The outbreak of highly pathogenic avian influenza (HPAI) H5N1 virus was first reported in Thailand in 2004. Up to present, electron micrographs demonstrating the morphology of HPAI H5N1 virus particle are quite limited. *Objective:* To demonstrate the morphology of free particles of human influenza viruses, HPAI H5N1 viruses and low pathogenic avian influenza (LPAI) viruses as well as the H5N1 structural components in the infected cells. In addition, the amino acid substitutions affecting the virus morphology was also investigated. *Methods:* Electron micrographs of the negative stained virus particles and the positive stained thin sections of the HPAI H5N1 virus infected cells were visualized under a transmission electron microscope (TEM). The M1 and M2 amino acid sequences were retrieved from GenBank. *Results:* Morphologically, the free influenza virus particles appeared in 3 forms: spherical, regular and irregular rods, and long filamentous particles, were demonstrated. However, spherical form was the most predominant morphological type and took account of more than 80% of the virus populations examined. In addition, the step of viral entry and exit including incomplete particles in the infected MDCK cells were found. *Conclusion:* Of all virus isolates studied, we demonstrated that the spherical particles were the major population observed regardless of virus subtypes, host of origin, virus virulence, passage history and amino acid substitutions in M1and M2 proteins.

2. A novel pathogenic mechanism of highly pathogenic avian influenza H5N1 viruses involves hemagglutinin mediated resistance to serum innate inhibitors

In this study, the effect of innate serum inhibitors on influenza virus infection was addressed. Seasonal influenza A(H1N1) and A(H3N2), 2009 pandemic A(H1N1) (H1N1pdm) and highly pathogenic avian influenza (HPAI) A(H5N1) viruses were tested with guinea pig sera negative for antibodies against all of these viruses as evaluated by hemagglutination-inhibition and microneutralization assays. In the presence of serum inhibitors, the infection by each virus was inhibited differently as measured by the amount of viral nucleoprotein produced in Madin-Darby canine kidney cells. The serum

inhibitors inhibited seasonal influenza A (H3N2) virus the most, while the effect was less in seasonal influenza A(H1N1) and H1N1pdm viruses. The suppression by serum inhibitors could be reduced by heat inactivation or treatment with receptor destroying enzyme. In contrast, all H5N1 strains tested were resistant to serum inhibitors. To determine which structure (hemagglutinin (HA) and/or neuraminidase (NA)) on the virus particles that provided the resistance, reverse genetics (rg) was applied to construct chimeric recombinant viruses from A/Puerto Rico/8/1934(H1N1) (PR8) plasmid vectors. rgPR8-H5 HA and rgPR8-H5 HANA were resistant to serum inhibitors while rgPR8-H5 NA and PR8 A(H1N1) parental viruses were sensitive, suggesting that HA of HPAI H5N1 viruses bestowed viral resistance to serum inhibition. These results suggested that the ability to resist serum inhibition might enable the viremic H5N1 viruses to disseminate to distal end organs. The present study also analyzed for correlation between susceptibility to serum inhibitors and number of glycosylation sites present on the globular heads of HA and NA. H3N2 viruses, the subtype with highest susceptibility to serum inhibitors, harbored the highest number of glycosylation sites on the HA globular head. However, this positive correlation cannot be drawn for the other influenza subtypes.

3. Surveillance for reassortant virus by multiplex reverse transcription-PCR specific for eight genomic segments of avian influenza A H5N1 viruses

Avian influenza H5N1 virus is a global threat. An emergence of a reassortant virus with a pandemic potential is a major concern. Here we describe a multiplex reverse transcription-PCR assay that is specific for the eight genomic segments of the currently circulating H5N1 viruses to facilitate surveillance for a virus resulting from reassortment between human influenza virus and the H5N1 virus.

4. Indigenous sources of 2007–2008 H5N1 avian influenza outbreaks in Thailand

Outbreaks of H5N1 avian influenza show strong seasonality. It is not clear where the source of virus originates from in each new outbreak season. This study sought to understand the nature of viral resurgence in recent outbreak seasons in Thailand, where the epidemic is relatively well controlled. In such a situation, indigenous viruses surviving the inter-outbreak season would have to pass through a bottleneck. In order to look for evidence of the bottleneck effect, viral genome sequences from recent outbreaks in the country were analysed. H5N1 avian influenza

viruses were isolated from six outbreaks in the rainy season and winter of 2007 through to early 2008. Most of the outbreaks were in the Yom–Nan River basin in the southern part of the northern region of the country. Sequences of these viral isolates were identified as clade 1, genotype Z, similar to viruses from previous years in the central region of the country. The sequences clustered into two groups, one of which was closely related to viruses isolated from the same area in July 2006. These analyses indicated that there was a strong bottleneck effect on the virus population and that only a few lineages remained in the area. In addition, evidence of reassortment among these viruses was found. These indicated re-emergence of viruses from a small pool of indigenous sources that had been silently perpetuated over the dry summer months. Therefore, an approach to eradicate H5N1 avian influenza from the area by eliminating these local reservoirs may be feasible and should be seriously considered.

5. Avian influenza virus (H5N1) in human, Laos

The first avian influenza (H5N1) outbreak in poultry in Laos occurred in 2003 and subsided in March 2004 after massive killing of poultry to contain the disease. Extensive surveillance from July 2005 through January 2006 did not detect any influenza virus subtypes in chicken, ducks, quails, and pigs in live bird markets in the Vientiane, Champasak, and Savannakhet Provinces. Avian influenza virus (H5N1) was reintroduced into Laos in February 2006 but showed a lower incidence. Viruses isolated in this country in 2004 belonged to genotype Z, clade 1, and 2006 isolates belonged to clade 2.3.4

6. Codon volatility of hemagglutinin genes of H5N1 avian influenza viruses from different clades

Codon volatility is a method recently developed to estimate selective pressures on proteins on the basis of their synonymous codon usage. Volatility of a codon was defined as the fraction of single nucleotide substitutions that would be nonsynonymous. Higher volatility may indicate that the gene has been under more positive selection in the recent past. We analyzed volatility of hemagglutinin genes of H5N1 viruses in the recent outbreaks and observed differences in the volatility among viruses of different clades. The codon volatility of subclade 2.1 viruses from Indonesia was the lowest among all H5N1 clades and subclades. Time series analyses since the beginning of the epidemic in 2004 showed that codon volatility of subclade 2.1 has gradually decreased, while those of other major clades have been increasing. This may reflect differences in the recent evolution of these viruses.

7. Erythrocyte binding preference of avian influenza H5N1 viruses

Five erythrocyte species (horse, goose, chicken, guinea pig, and human) were used to agglutinate avian influenza H5N1 viruses by hemagglutination assay and to detect specific antibody by hemagglutination inhibition test. We found that goose erythrocytes confer a greater advantage over other erythrocyte species in both assays.

8. Erythrocyte binding preference of 16 subtypes of low pathogenic avian influenza and 2009 pandemic influenza A (H1N1) viruses

All 16 subtypes of avian influenza viruses of low pathogenicity (LPAIV) as well as their hemagglutinin (H) antigens, and four 2009 pandemic influenza A (H1N1) virus isolates were assayed for hemagglutinating activity against 5 erythrocyte species: goose, guinea pig, human group O, chicken and horse. Of all viruses and antigens assayed, the highest hemagglutination (HA) titers were obtained with goose and guinea pig erythrocytes. Hemagglutinating activity of replicating LPAIV and LPAIV antigens decreased, in order, with chicken and human group O; meanwhile, horse erythrocytes yielded lowest or no HA titer. Moreover, the 2009 pandemic viruses did not agglutinate both horse and chicken erythrocytes. Our study concluded that goose and guinea pig erythrocytes are the best in HA assay for all subtypes of influenza viruses.

9. Kinetics and longevity of antibody response to influenza A H5N1 virus infection in humans

Anti-H5N1 antibody was determined by microneutralization, hemagglutination inhibition, and Western blotting assays in serial blood samples collected from eight Thai patients, including four fatal cases and four survivors. The antibody was detected as early as 5 days and, typically, with an increase in titer in paired blood at about 15 days after disease onset. The anti-H5 antibody response was long-lasting, for almost 5 years in cases which can be followed that far. In addition, cross-neutralizing activity to related clade 1 viruses was observed.

10. Induction of cross-neutralizing antibody against H5N1 virus after vaccination with seasonal influenza vaccine in COPD patients

Archival serum samples from elderly individuals with underlying chronic obstructive pulmonary disease (COPD) who were enrolled in a double-blind case-control study of seasonal influenza vaccine efficacy were assayed for cross-neutralizing antibody formation to avian influenza A (H5N1) virus. Of 118 serum samples, 58 were collected from influenza vaccinees (mean age 68.5 y), and 60 from placebo controls (mean age 68.4 y) who received vitamin B injections. Blood samples were collected before and at 1mo after seasonal influenza vaccination from all subjects; in addition, for a longitudinal follow-up period of 1 y paired-blood samples were collected again from subjects who developed acute respiratory illness. Hemagglutination inhibition assay for antibodies to influenza A (H1N1), influenza A (H3N2), and influenza B viruses was carried out to determine the serological response to vaccination, and to diagnose influenza viral infection, while microneutralization assays were performed to detect cross-reactive antibody to H5N1 virus. Pre-existing cross-reactive H5N1 antibody at reciprocal titer 10 was found in 6 (10.3%) vaccinees and 4 (6.7%) placebo controls. There was no change in H5N1 antibody titer in these subjects after vaccination. On the other hand, 3 (5.2%) vaccinees developed seroconversion to H5N1 virus at 1mo after vaccination, even though they had no pre-existing H5N1 antibody in their first blood samples. No cross-neutralizing antibody to H5N1 virus was detected in the placebo controls or in the 22 influenza patients, suggesting that influenza vaccination, but not influenza virus infection, induces cross-neutralizing antibody against avian influenza H5N1 virus.

11. Biological properties of H5 hemagglutinin expressed by vaccinia virus vector and its immunological reactivity with human sera

A recombinant vaccinia virus harboring the full length hemagglutinin (*HA*) gene derived from a highly pathogenic avian influenza A/Thailand/1(KAN-1)/2004 (H5N1) virus (rVac-H5 HA virus) was constructed. The immunogenicity of the expressed HA protein was characterized using goat antiserum, mouse monoclonal antibody and human sera. Expressed HA protein localized both in the cytoplasm and on the cytoplasmic membrane of the thymidine kinase negative cells infected with the rVac-H5 HA virus, as determined by immunofluorescence assay. Moreover, Western blot analysis demonstrated that the rVac-H5 HA protein was post-translationally processed by proteolytic cleavage of the HA0 precursor into HA1 and HA2 domains; and all of these HA forms were immunogenic in BALB/c mice. The molecular weight (MW) of each

HA domain was the same as the wild-type H5 HA produced in Madin-Darby canine kidney cells infected with the H5N1 virus, but was higher than that expressed by a baculovirus-insect cell system. Sera from all H5N1 survivors reacted to HA0, HA1 and HA2 domains; whereas sera from H5N1-uninfected subjects reacted to the rVac-H5 HA2 domain only, but not to HA0 or HA1, indicating that some cross-subtypic immunity exists in the general population. There was a lot-to-lot variation of the recombinant HA produced in the baculovirus-insect cell system that might affect the detection rate of antibody directed against certain HA domain.

12. The difference in IL-1 β , MIP-1 α , IL-8 and IL-18 production between the infection of PMA activated U937 cells with recombinant vaccinia viruses inserted 2004 H5N1 influenza HA genes and NS genes

Summary Background: The severity of avian influenza H5N1 disease is correlated with the ability of the virus to induce an over production of pro-inflammatory cytokines from innate immune cells. However, the role of each virus gene is unknown. To elaborate the function of each virus gene, the recombinant vaccinia virus inserted HA and NS gene from the 2004 H5N1 virus were used in the study. *Methods:* U937 cells and PMA activated U937 cells were infected with recombinant vaccinia virus inserted with HA or NS gene. The expressions of HA and NS proteins in cells were detected on immunofluorescence stained slides using a confocal microscope. The cytokine productions in the cell supernatant were quantitated by ELISA. *Results:* The recombinant vaccinia virus inserted with HA genes induces the production of IL-1 β , MIP-1 α , IL-8 and IL-18 cytokines from PMA activated U937 cells significantly more than cells infected with wild type vaccinia, whereas the recombinant vaccinia virus inserted with NS genes it was similar to that with the wild type vaccinia virus. However, there was no synergistic nor antagonistic effect of HA genes and NS genes in relation to cytokines production. *Conclusion:* Only the HA gene from the 2004 H5N1 virus induces IL-1 β , MIP-1 α , IL-8 and IL-18 cytokine productions from activated U937 cells. The same HA gene effect may or may not be the same in respiratory epithelial cells and this needs to be explored.

13. Satellite tracking on the flyways of Brown-headed gulls and their potential role in the spread of highly pathogenic avian influenza H5N1 virus

Brown-headed gulls (*Larus brunnicephalus*), winter visitors of Thailand, were tracked by satellite telemetry during 2008-2011 for investigating their roles in the highly pathogenic avian influenza (HPAI) H5N1 virus spread. Eight gulls negative for influenza virus infection were marked with solar-powered satellite platform transmitters, their movements were monitored by the Argos satellite tracking system, and locations were mapped. Five gulls completed their migratory cycles, which spanned 7 countries (China, Bangladesh, India, Myanmar, Thailand, Cambodia, and Vietnam) affected by the HPAI H5N1 virus. Gulls migrated from their breeding grounds in China to stay overwinter in Thailand and Cambodia; while Bangladesh, India, Myanmar, and Vietnam were the places of stopovers during migration. Gulls traveled an average distance of about 2400 km between Thailand and China and spent 1-2 weeks on migration. Although AI surveillance among gulls was conducted at the study site, no AI virus was isolated and no H5N1 viral genome or specific antibody was detected in the 75 gulls tested, but 6.6% of blood samples were positive for pan-influenza A antibody. No AI outbreaks were reported in areas along flyways of gulls in Thailand during the study period. Distance and duration of migration, tolerability of the captive gulls to survive the HPAI H5N1 virus challenge and days at viral shedding after the virus challenging suggested that the Brown-headed gull could be a potential species for AI spread, especially among neighboring countries. This is the only study that demonstrated flyways which links between China and Southeast Asia, the epicenter of H5N1 AI outbreak.

14. Serological response to the 2009 pandemic influenza A (H1N1) virus for disease diagnosis and estimating the infection rate in Thai population

Background: Individuals infected with the 2009 pandemic virus A(H1N1) developed serological response which can be measured by hemagglutination-inhibition (HI) and microneutralization (microNT) assays. Methodology/Principal Findings: MicroNT and HI assays for specific antibody to the 2009 pandemic virus were conducted in serum samples collected at the end of the first epidemic wave from various groups of Thai people: laboratory confirmed cases, blood donors and health care workers (HCW) in Bangkok and neighboring province, general population in the North and the South, as well as archival sera collected at pre- and post-vaccination from vaccinees who received influenza vaccine of the 2006 season. This study demonstrated that goose erythrocytes yielded comparable HI antibody titer as compared to turkey erythrocytes. In contrast to the standard protocol, our investigation found out the necessity to eliminate nonspecific

inhibitor present in the test sera by receptor destroying enzyme (RDE) prior to performing microNT assay. The investigation in pre-pandemic serum samples showed that HI antibody was more specific to the 2009 pandemic virus than NT antibody. Based on data from pre-pandemic sera together with those from the laboratory confirmed cases, HI antibody titers ≥ 40 for adults and ≥ 20 for children could be used as the cut-off level to differentiate between the individuals with or without past infection by the 2009 pandemic virus. Conclusions/Significance: Based on the cut-off criteria, the infection rates of 7 and 12.8% were estimated in blood donors and HCW, respectively after the first wave of the 2009 influenza pandemic. Among general population, the infection rate of 58.6% was found in children versus 3.1% in adults.

15. Seroprevalence of 2009 H1N1 virus infection and self-reported infection control practices among healthcare professionals following the first outbreak in Bangkok, Thailand

A serologic study with simultaneous self-administered questionnaire regarding infection control (IC) practices and other risks of influenza A (H1N1) pdm09 (2009 H1N1) infection was performed approximately 1 month after the first outbreak among frontline health care professionals (HCPs). Of 256 HCPs, 33 (13%) were infected. Self-reported adherence to IC practices in $>90\%$ of exposure events was 82.1%, 73.8%, and 53.5% for use of hand hygiene, masks, and gloves, respectively. Visiting crowded public places during the outbreak was associated with acquiring infection (OR 3.1, $P=0.019$). Amongst nurses, exposure to HCPs with influenza-like illness during the outbreak without wearing a mask was the only identified risk factor for infection (OR = 2.3, $P=0.039$).

16. Monitoring the influenza pandemic of 2009 in Thailand by a community-based survey

As an international traveling hub of South-East Asia, Thailand was one of the countries hardest and earliest hit by the influenza A (H1N1) 2009 pandemic. In order to understand the epidemic spread in the country, we conducted community-based surveys in metropolitan, urban, and rural areas using questionnaire interviews. We also determined sero-positive rates from randomly selected samples within the surveyed population. Recalled incidences of fever and acute respiratory symptoms in the survey correlated well with systematic reports of 2009 pandemic influenza cases from hospitals

in the same areas, giving a ratio of total cases extrapolated from the surveyed data for persons who sought medical attention reported in the hospital-based surveillance system at 275:1. Conducting a large scale survey of the influenza outbreak is time consuming and also can be difficult to complete in a short time. Therefore, we used the survey for monitoring the outbreak of respiratory disease in the early pandemic phase. The seroprevalence rate was 8 to 10%, with higher rate for younger age groups, and suggests that sufficient herd immunity may have been reached in Thailand, especially in urban areas, while others may still be vulnerable to the second wave of the pandemic.

17. Immune response to 2009 H1N1 vaccine in HIV-infected adults in Northern Thailand

Background: In late 2009, the Thai Ministry of Public Health provided two million doses of the monovalent pandemic influenza H1N1 2009 vaccine (Panenza (®) Sanofi Pasteur), which was the only vaccine formulation available in Thailand, to persons at risk of more severe manifestations of the disease including HIV infection. Several studies have shown poorer immune responses to the 2009 H1N1 vaccines in HIV-infected individuals. There are limited data in this population in resource-limited countries. **Results:** At day 28 post-vaccination, seroconversion was found in 32.0% (95%CI 24.5 - 40.2) of the HIV-infected group and 35.0% (95%CI 15.4- 59.2) of the healthy controls ($p = 0.79$). Seroprotection rate was observed in 33.3% (95%CI 25.8- 41.6) and 35.0% (95%CI 15.4-59.2) of the HIV-infected group and the control group, respectively ($p = 0.88$). Among HIV-infected participants, the strongest factor associated with vaccine response was age 42 y or younger ($p = 0.05$). **Methods:** We evaluated the immunogenicity of a single, 15 μ g/0.5ml dose of a monovalent, non-adjuvanted 2009 H1N1 vaccine in 150 HIV-infected Thai adults and 20 healthy controls. Immunogenicity was measured by hemagglutination inhibition assay (HI) at baseline and 28 d after vaccination. Seroconversion was defined as 1) pre-vaccination HI titer < 1:10 and post-vaccination HI titer \geq 1:40, or 2) pre-vaccination HI titer \geq 1:10 and a minimum of 4-fold rise in post-vaccination HI titer. Seroprotection was defined as a post-vaccination HI titer of \geq 1:40. **Conclusions:** A low seroconversion rate to the 2009 H1N1 vaccine in both study groups, corresponding with data from trials in the region, may suggest that the vaccine used in our study is not very immunogenic. Further studies on different vaccines, dosing, adjuvants, or schedule strategies may be needed to achieve effective immunization in HIV-infected population.

18. Influenza A viral loads in respiratory samples collected from patients infected with pandemic H1N1, seasonal H1N1 and H3N2 viruses

Background: Nasopharyngeal aspirate (NPA), nasal swab (NS), and throat swab (TS) are common specimens used for diagnosis of respiratory virus infections based on the detection of viral genomes, viral antigens and viral isolation. However, there is no documented data regarding the type of specimen that yields the best result of viral detection. In this study, quantitative real time RT-PCR specific for *M* gene was used to determine influenza A viral loads present in NS, NPA and TS samples collected from patients infected with the 2009 pandemic H1N1, seasonal H1N1 and H3N2 viruses. Various copy numbers of RNA transcripts derived from recombinant plasmids containing complete *M* gene insert of each virus strain were assayed by RT-PCR. A standard curve for viral RNA quantification was constructed by plotting each Ct value against the log quantity of each standard RNA copy number. Results: Copy numbers of *M* gene were obtained through the extrapolation of Ct values of the test samples against the corresponding standard curve. Among a total of 29 patients with severe influenza enrolled in this study (12 cases of the 2009 pandemic influenza, 5 cases of seasonal H1N1 and 12 cases of seasonal H3N2 virus), NPA was found to contain significantly highest amount of viral loads and followed in order by NS and TS specimen. Viral loads among patients infected with those viruses were comparable regarding type of specimen analyzed. Conclusion: Based on *M* gene copy numbers, we conclude that NPA is the best specimen for detection of influenza A viruses, and followed in order by NS and TS.

19. Infection rate, duration of viral shedding and viral load in an outbreak of novel influenza A (H1N1) 2009 infections among military conscripts in a training center, Thailand, June 2009 (อัตราการติดเชื้อ ระยะเวลาของการขับเชื้อไวรัส และปริมาณเชื้อไวรัส ขณะมีการระบาดของไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 ในกลุ่มทหารเกณฑ์ ศูนย์ฝึกทหารใหม่แห่งหนึ่ง ประเทศไทย เดือนมิถุนายน พ.ศ. 2552)

การระบาดของไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 ในทหารเกณฑ์ชายไทยอายุเฉลี่ย 21 ปี มีอัตราป่วยสูงถึงร้อยละ 29.3 ระยะเวลาการขับเชื้อไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 ในทหารเกณฑ์มีระยะเวลานานเฉลี่ย 5 วัน หลังเริ่มแสดงอาการ แต่สามารถตรวจพบได้ตั้งแต่วันแรกที่เริ่มป่วยจนถึง 11 วัน ซึ่งพบว่าใกล้เคียงกันมาก ซึ่งน่าจะอธิบายได้จากการที่เป็นประชากรอายุใกล้เคียงกันและเป็นการติดเชื้อไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ในระยะต้นของการ

ระบาดใหญ่ ที่ยังมีสารพันธุกรรมใกล้เคียงกัน การเก็บตัวอย่างสารคัดหลังจากคอหอยหลังโรงจมูก (Nasopharyngeal swab) มีโอกาสได้ผลบวกสูง โดยการศึกษานี้พบ ปริมาณเชื้อไวรัสจำนวน 2.6×10^2 copies/ml ถึง 8.1×10^9 copies/ml เฉลี่ย 2.4×10^4 copies/ml ปริมาณเชื้อไวรัสที่พบในผู้ป่วยแต่ละราย ส่วนใหญ่จะมีปริมาณมาก สุดในวันที่ 2 ถึงวันที่ 5 หลังจากเริ่มมีอาการป่วย จึงเป็นระยะเวลาที่ต้องมีมาตรการป้องกันการแพร่เชื้อที่เข้มงวด และต้องป้องกันต่อเนื่องตลอดระยะเวลาที่มีการระบาดเพราผู้ป่วยบางรายอาจจะขับเชื้อได้นานกว่า 10 วันอย่างไรก็ตาม ไม่พบว่ามีความสัมพันธ์ระหว่างปริมาณเชื้อไวรัสกับระยะเวลาของการขับเชื้อไวรัสจากทางเดินหายใจในผู้ป่วยกลุ่มนี้ นอกจากนี้ พบว่าระยะเวลาการขับเชื้อไวรัสในผู้ป่วยที่มีน้ำหนักเกินและเสียชีวิตเท่ากับ 8 วัน และในผู้ป่วยที่กำลังป่วยเป็นวัณโรคปอดเท่ากับ 4 วันเฉลี่ยดังนั้น การเก็บตัวอย่างวิธีนี้จึงมีเหมาะสมหากทำโดยบุคลากรที่มีประสบการณ์และใช้เทคนิคที่ถูกต้อง เพราะเป็นการเก็บตัวอย่างจากจุดที่พบเชื้อไวรัสไข้หวัดใหญ่อยู่ในปริมาณมากปริมาณไวรัสของผู้ป่วยที่ตรวจพบในการศึกษารั้งนี้มี

20. ศึกษาภูมิคุ้มกันข้ามระดับเซลล์ (cellular immune response) และ ระดับสารน้ำ (humoral immune response) ระหว่างเชื้อไข้หวัดใหญ่ และไข้หวัดนก (H5N1)

20.1 ศึกษาภูมิคุ้มกันข้ามในระดับเซลล์ (cross-subtype cellular immunity)

การศึกษาวิทยาภูมิคุ้มกันข้ามระดับเซลล์ระหว่างเชื้อไข้หวัดใหญ่และไข้หวัดนกสายพันธุ์ H5N1 virus เป็นการศึกษาการตอบสนองของระบบภูมิคุ้มกันในระดับ T cell ที่เกิดขึ้นต่อ peptide epitopes ที่มาจากเชื้อไข้หวัดนก การศึกษานี้ได้อาศัยเทคนิค *ex vivo* IFN- γ enzyme-linked immunospot (ELISpot) assay ในการตรวจหา cross-reactive T cells ซึ่งถูกสร้างขึ้นจากการที่ประชากรเคยมีประวัติฉีดวัคซีน หรือเคยได้รับเชื้อไข้หวัดใหญ่ตามถูกต้องมาก่อน โดยคาดว่า memory T cells ที่จำเพาะกับโปรตีนส่วนที่ conserve เช่น nucleoprotein (NP) ของเชื้อไข้หวัดใหญ่สายพันธุ์ H1N1 หรือ H3N2 จะสามารถจดจำและทำปฏิกิริยากับ synthetic overlapping peptide epitopes ที่มาจากเชื้อไข้หวัดนกสายพันธุ์ H5N1 และเพื่อจะจำแนกได้ว่า epitope ใดที่ conserve สามารถทำให้เกิดปฏิกิริยาข้ามระหว่างเชื้อไข้หวัดใหญ่และไข้หวัดนก ซึ่งจะทำการทดสอบโดยใช้เทคนิค ELISpot assay

จากการทดลองด้วยวิธี ELISpot assay โดยใช้ NP overlapping peptides จะทำให้ทราบถึง conserve และ H5N1 specific epitopes แต่ก็ยังไม่ทราบว่า epitope ชนิดนี้ถูกจดจำด้วย T cell ชนิดใด ดังนั้นจึงต้องทำการเลี้ยง peptide-specific T cell line ขึ้นมาเพื่อทำการหา T cell dependency โดยเทคนิค Flow cytometry

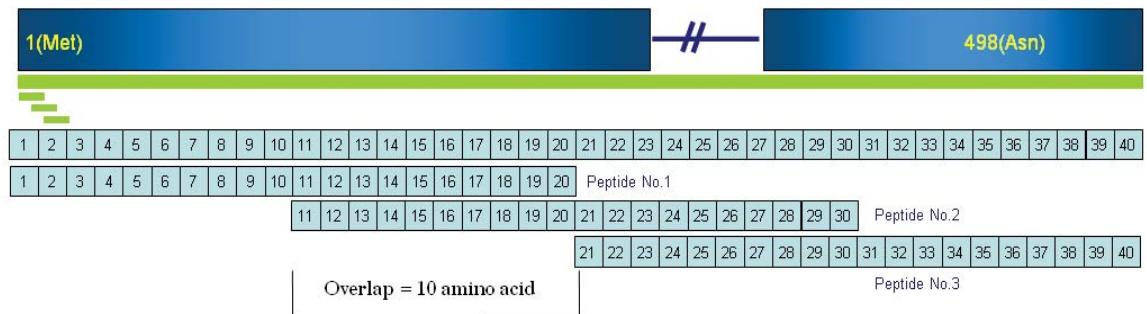
นอกจากนี้ได้ทำการสร้าง recombinant vaccinia viruses 2 ชนิด ที่มี NP และ HA protein insert ในครั้งแรกมีวัตถุประสงค์เพื่อนำไปใช้ใน CTL assay เพื่อศึกษาภูมิคุ้มกันแบบข้าม subtypes แต่มีข้อจำกัดของการทดลองคือ ได้เลือดที่เจาะได้จากผู้ป่วยปริมาณน้อย (ตามข้อกำหนดของคณะกรรมการจุลทรรศน์ของกระทรวงสาธารณสุข) ซึ่งส่งผลให้ได้เซลล์ PBMC

ปริมาณน้อยตามไปด้วย จึงได้เปลี่ยนมาศึกษาด้วยเทคนิค ELISpot assay แทน โดยเลือกศึกษาในกลุ่มคนที่รอดชีวิต (H5N1 survivors) กลุ่มคนปกติทั้งที่เคยและไม่เคยได้รับวัคซีนและกลุ่มคนเป็นไข้หวัดใหญ่ คณะผู้วิจัยได้เลือกศึกษาเฉพาะ NP protein ซึ่งจัดเป็นโปรตีนที่ทำให้เกิด cross-reactive T cell immunity ได้มากที่สุด โดยได้ดำเนินการสังเคราะห์ peptide จำนวน 49 เส้น เพื่อหา common epitope ในกลุ่ม H5N1 survivors และ non-H5N1 subjects ทั้งสิ้น 39 ราย

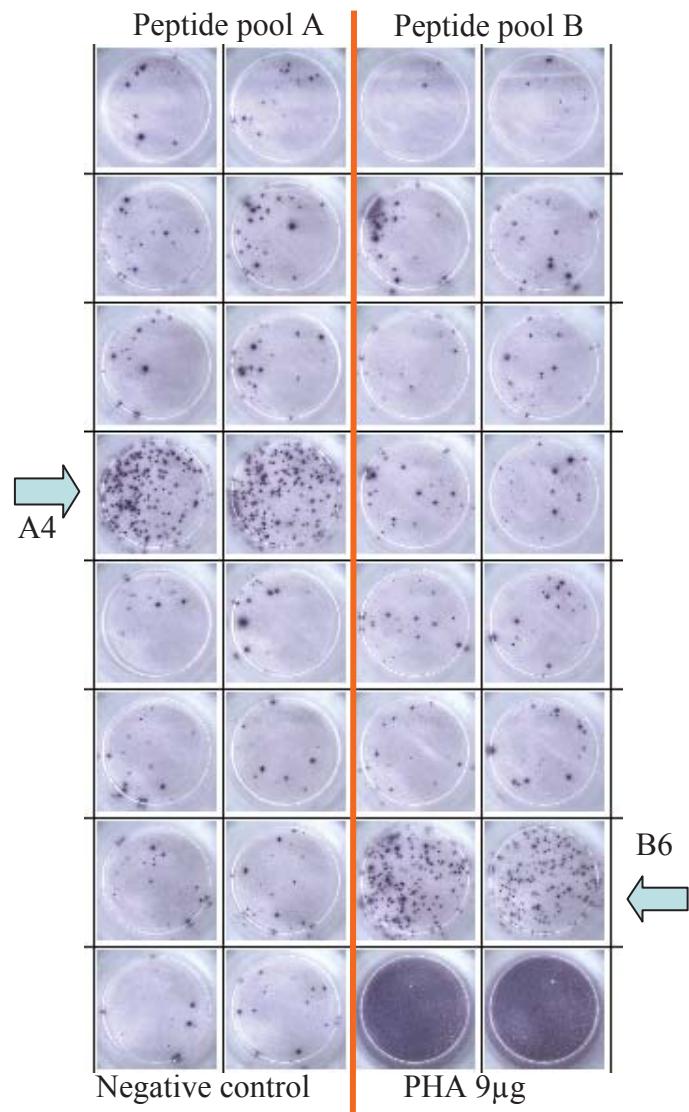
จากการทดลองได้ศึกษาส่วนของ NP protein ของเชื้อ H5N1 ซึ่งมีความอนุรักษ์ (conserve) มากกว่า 90% กับ NP protein ของเชื้อไข้หวัดใหญ่ โดยมี amino acid sequence ดังรูปที่ 1 และได้นำมาสังเคราะห์ overlapping peptides จำนวน 49 เส้น ซึ่งมีความยาวเส้นละ 20 amino acids โดยมี overlapping จำนวน 10 amino acids (รูปที่ 2) แล้วใช้เป็นตัวคัดกรองว่ามี peptide เส้นใดบ้าง ที่ T cells สามารถจดจำได้โดยวัด IFN- γ producing T cell ด้วยวิธี ELISpot assay ดังรูปที่ 3 และทำการยืนยันด้วยการทำ individual peptide ด้วย จากการทดลองในกลุ่ม H5N1 survivors จำนวน 4 คนพบว่า มี 2 ใน 4 คนสามารถจดจำ immunodominant NP epitopes ได้ ดังรูปที่ 4 ทั้งนี้จากการทำ serial blood samples ที่เก็บหลังจากผู้ป่วยเริ่มมีอาการ พบว่า ยังสามารถตรวจ peptide-specific memory T cells ได้หลังจากการติดเชื้อเป็นเวลา อย่างน้อย 4 ปี โดยให้ magnitude (spot forming unit, SFU) ของการตอบสนองในระดับที่สูง พอยกันใน serial blood samples สำหรับในกลุ่ม non-H5N1 subjects พบว่า 16 จาก 35 คน มี memory T cells ที่สามารถจดจำ NP peptide ได้ 1-2 peptides/subject และมี magnitude ของการตอบสนองที่ต่างกันเมื่อเทียบกับในกลุ่ม H5N1 survivors ดังรูปที่ 5 การทดลองนี้ยังพบว่า NP peptide เพียง 2 เส้นเท่านั้นที่อาจจะเป็น H5N1-specific T cell epitope ซึ่งสามารถตรวจพบได้เฉพาะใน H5N1 survivors เท่านั้น และมี 5 เส้นที่จัดว่าเป็น common epitopes ที่สามารถตรวจพบได้ในกลุ่ม non-H5N1 subjects ซึ่งมีอยู่หนึ่ง NP peptide ที่พบได้ทั้งสองกลุ่ม (งานวิจัยในส่วนนี้อยู่ระหว่างการเตรียมต้นฉบับการตีพิมพ์ผลงาน)

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>gi|54610028|gb|AAV35112.1| nucleocapsid protein [Influenza A virus (A/Thailand/1(KAN-1)/2004(H5N1))]  
MASQGTKR SYEQMETGGERQNATEIRASVGRMVSGIGRFYIQMCTELKLSDYEGRLIQNSITIERMVL  
SAFDERRNRYLEEHP SAGKDPKKTGGPIYRRDGKWWRELILYDKEEIRRIWRQANNGEDATAGLTHLMIWH  
SNLNNDATYQRTRALVRTGMDPRMC SLMQGSTLPRRSGAAGAAVKGVGTVMV MELIRMIKRGINDRNFWRGE  
NGRRTRIAYERMCN ILKGKFQTA AQRAMMDQVRESRNP GNAEIEDLIFLARSALILRGSVAHKSCLPACV  
YGLAVASGYDFEREQYSLVGIDPFRL LQNSQVFS LIRPNENPAHKS QLVWMACHSAAFEDL RVSSFIRGT  
R VVPRGQLSTRGVQI ASNENMEA MDSNTL ERSRYWAIRTRSGGNTNQQRASAGQ QISVQPTFSVQRNL  
P FERATIMAAFTGNTEGRTSDMRTEIIRMMESARPEDVS FQGRGVFELSDEKATNP IVPSFDMNNEGSYFFG  
DNAE EYDN
```

รูปที่ 1 Amino acid sequence ของ NP protein ของเชื้อ A/Thailand/1(KAN-1)/2004 (H5N1)

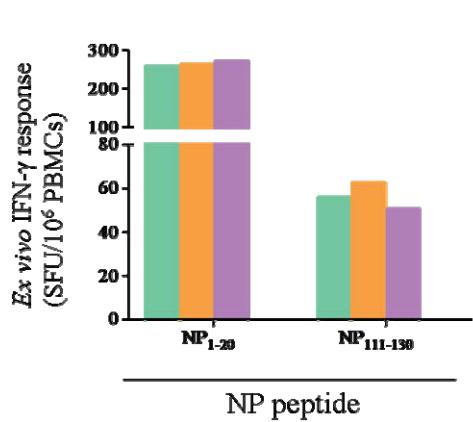


รูปที่ 2 Diagram ของการสร้าง overlapping peptide ขนาด 20 กรดอะมิโน แต่ละเส้นชื่อนับกัน 10 กรดอะมิโน

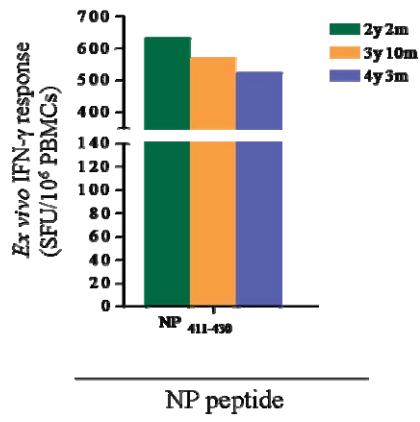


รูปที่ 3 ตัวอย่างผลจากการทำ ELISpot assay ของบุคคลที่รอดชีวิตจากการติดเชื้อ H5N1

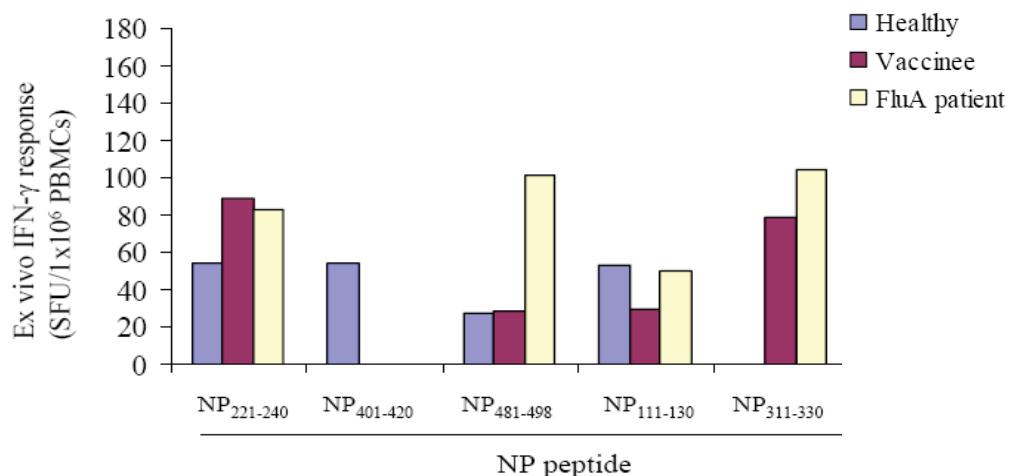
A) H5N1 survivor no.1



B) H5N1 survivor no.2



รูปที่ 4 การตอบสนองต่อ overlapping NP peptides ของกลุ่มตัวอย่างที่เป็น H5N1 survivors พบว่า NP peptides จากทั้งหมด 49 เส้น มีเพียง 1-2 เส้นเท่านั้นที่สามารถถูกจดจำโดย peptide-specific memory T cells จาก blood samples ช่วงเวลาต่างๆ หลังจาก disease onset



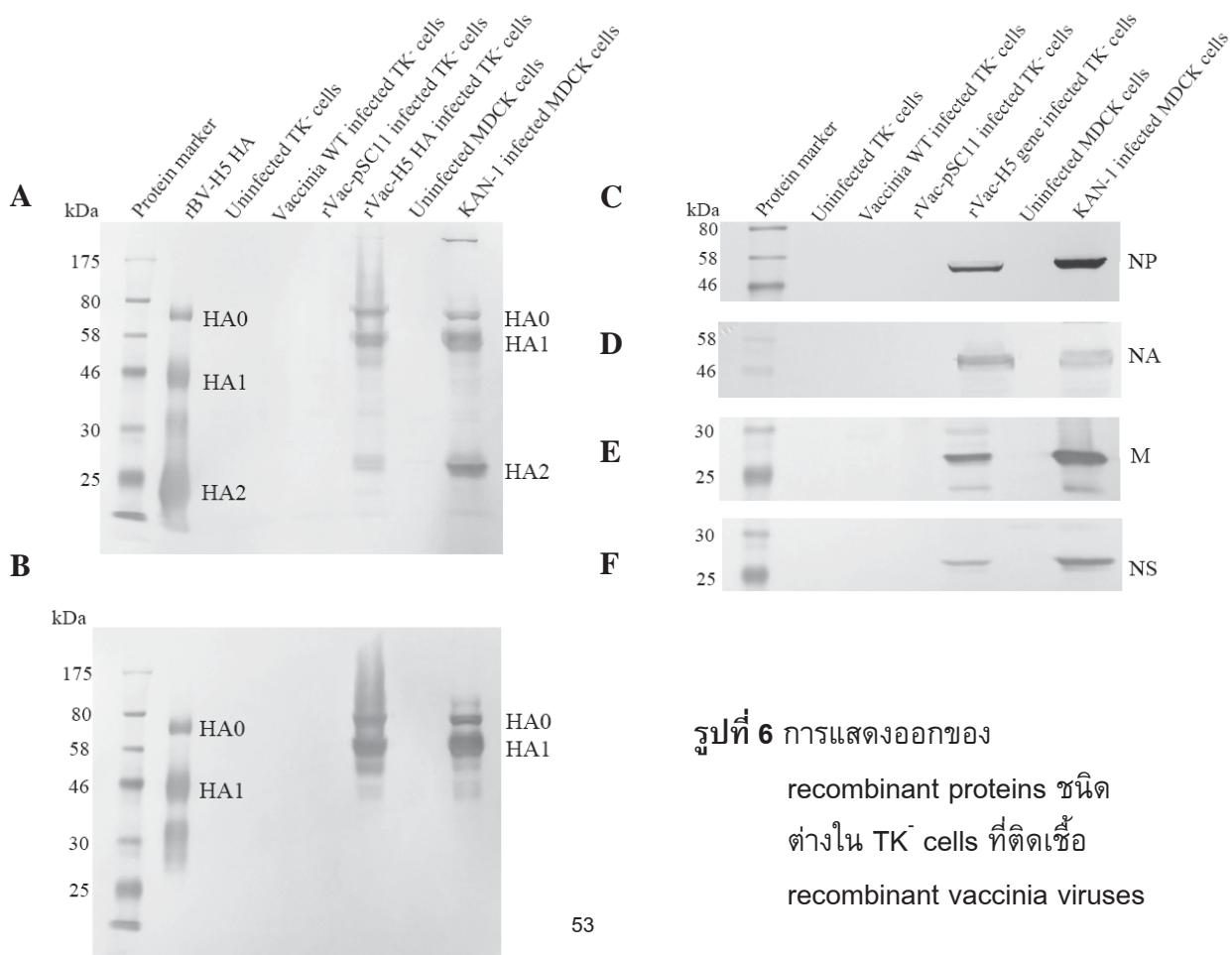
รูปที่ 5 การตอบสนองต่อ overlapping NP peptides ของกลุ่มตัวอย่างที่เป็น non-H5N1 survivors ทั้งสิ้น 35 คน พบว่ามีเพียง 16 คนที่สามารถจดจำ NP peptides 5 เส้นจากทั้งหมด 49 เส้น

20.2 ศึกษาภูมิคุ้มกันข้ามในระดับสารน้ำ (cross-subtype humoral immunity)

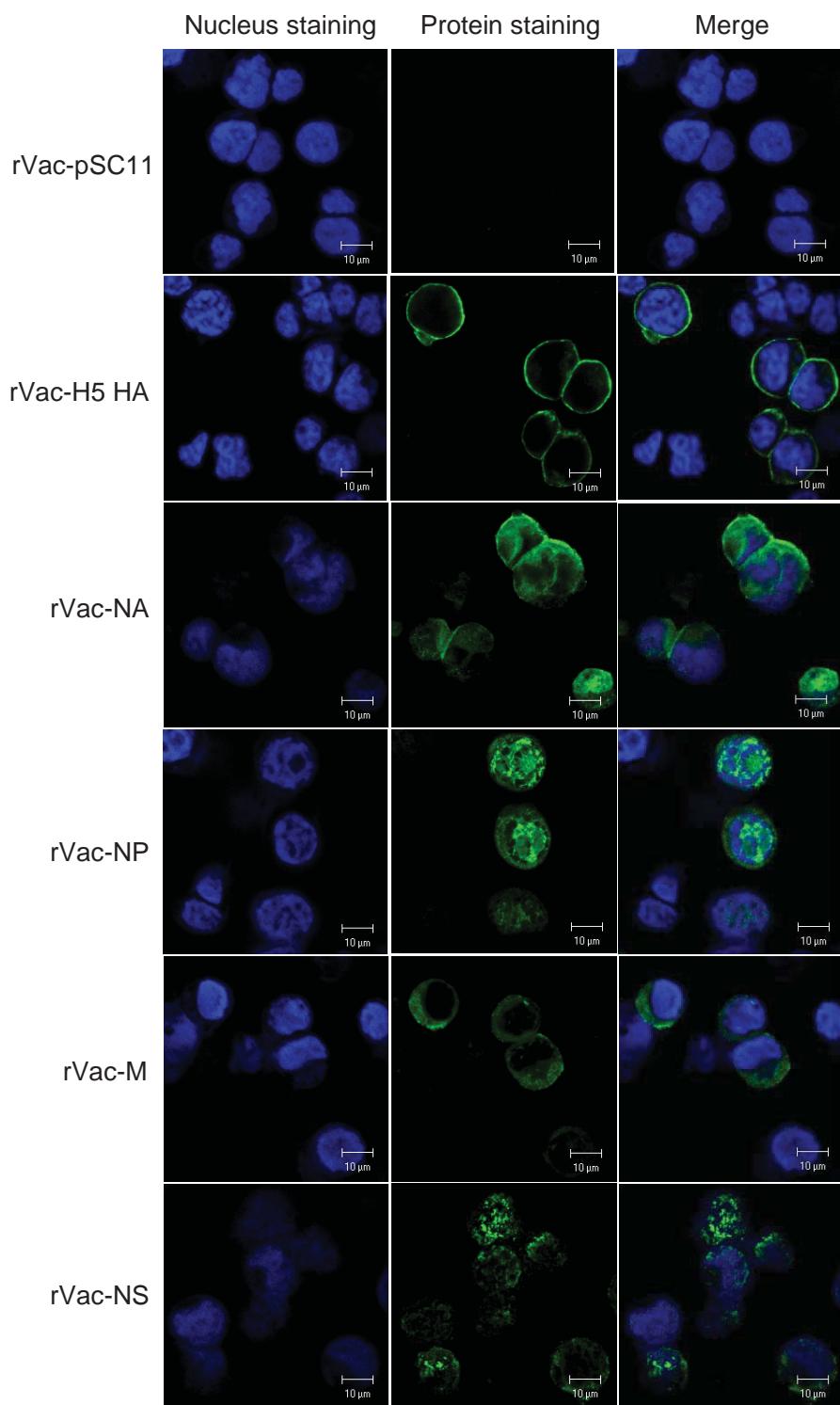
โดยทำการศึกษาภูมิคุ้มกันข้ามระหว่างเชื้อไข้หวัดใหญ่และไข้หวัดนก (H5N1) ของประชากรกลุ่มตัวอย่างที่รอดชีวิตจากการติดเชื้อ H5N1 และในกลุ่มตัวอย่างที่ไม่เคยติดเชื้อ H5N1 มาก่อนต่อโปรตีนต่างๆ ของไวรัสไข้หวัดนกที่เตรียมจาก TK^- cells ที่ติดเชื้อ recombinant vaccinia virus ที่มี insert gene: *M*, *HA*, *NP*, *NS* หรือ *NA* ของเชื้อไวรัส H5N1 โดยใช้เทคนิค immunofluorescence

ผลการทดลองพบว่า สามารถสร้าง recombinant H5 HA, NA, NP, M and NS proteins ใน TK^- cells ที่ติดเชื้อ recombinant vaccinia virus ที่มียีนของเชื้อไข้หวัดนกชนิดต่างๆ อยู่ภายในยีโนม ดังรูปที่ 6 การศึกษาตำแหน่งของการแสดงออกของ recombinant proteins ชนิดต่างๆ ใน TK^- cells ที่ติดเชื้อ พบว่า HA และ NA พบได้ที่ cytoplasm และ cell membrane ของเซลล์ NP และ NS พบได้ที่ nucleus และ cytoplasm ส่วน M พบได้ใน cytoplasm ดังรูปที่ 7

จากการศึกษาแอนติบอดีต่อโปรตีนส่วนต่างๆ ในกลุ่มที่รอดชีวิตจากการติดเชื้อ H5N1 และกลุ่มที่ไม่เคยติดเชื้อ H5N1 มาก่อน พบว่า หั้งสองกลุ่มนี้แอนติบอดีต่อโปรตีนส่วนต่างๆ โดยในกลุ่มที่รอดชีวิตจะมีระดับแอนติบอดีต่อ HA และ NA ที่สูงกว่า ส่วนแอนติบอดีต่อ NP, M และ NS หั้งสองกลุ่มนี้มีระดับที่ใกล้เคียงกัน นอกจากนี้ยังสามารถตรวจพบแอนติบอดีต่อโปรตีนเหล่านี้ได้นานถึง 4 ปี จากการติดตามในผู้ที่รอดชีวิต ดังตารางที่ 1 (งานวิจัยในส่วนนี้อยู่ระหว่างการเตรียมต้นฉบับการตีพิมพ์ผลงาน)



รูปที่ 6 การแสดงออกของ recombinant proteins ชนิดต่างใน TK^- cells ที่ติดเชื้อ recombinant vaccinia viruses



รูปที่ 7 ตำแหน่งของการแสดงออกของแต่ละ recombinant proteins ใน TK^- cells ที่ติดเชื้อ recombinant vaccinia virus

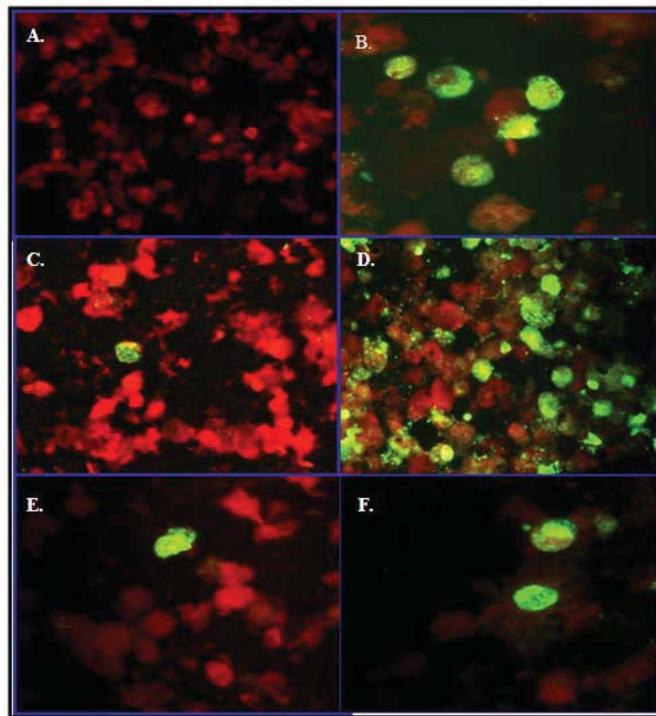
ตารางที่ 1 ระดับและการคงอยู่ของแอนติบอดีต่อโปรตีนส่วนต่าง ๆ ในกลุ่มที่รอดชีวิต

H5N1 survivor	Age (years)	Blood samples	Time at specimen collection after disease onset	NT Ab titer to KAN-1	HI Ab titer to KAN-1	IFA antibody titer to				
						HA	NA	NP	M	NS
No.1	32	1	1y 6m	160	80	640	320	80	160	160
			2	160	80	640	320	80	80	160
			3	80	80	640	160	160	80	160
No.2	29	1	2y 2m	160	80	320	160	80	40	40
			2	160	80	160	320	80	40	160
			3	80	80	320	160	80	40	80
No.3	7	1	20d	640	160	320	320	320	80	160
			11m	80	80	320	160	160	80	160
			2y 2m	80	40	160	80	160	80	160
			3y 1m	40	40	160	80	80	40	160
No.4	2	1	2y 3m	80	80	80	80	40	40	40
			3y 11m	80	80	80	160	40	40	80
			4y 11m	40	40	80	160	40	40	40

21. ตรวจหาการเพิ่มจำนวนของ H5N1 virus ในเซลล์ซึ่งไม่ใช่ respiratory epithelial cells

งานวิจัยในส่วนนี้ได้ทำการศึกษา kinetics การเพิ่มจำนวนและการสร้าง cytokine ของไวรัสไข้หวัดใหญ่ H1N1 และ H3N2 ในเซลล์เยื่อบุเส้นเลือดดำจากสายสะดื้อทารก (Human Umbilical Vein Endothelial Cells; HUVEC) เพื่อศึกษาการแพร่กระจายของไวรัสในระบบทางเดินหายใจ respiratory system เปรียบเทียบกับเชื้อไข้หวัดนก H5N1 และเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ A/H1N1 2009 โดยการตรวจหา viral nucleoprotein ในเซลล์ที่ติดเชื้อด้วยวิธี immunofluorescence assay และตรวจดูปริมาณของไวรัสรุ่นลูกที่ถูกปล่อยออกมานำ้เสียง เซลล์ด้วยวิธี TCID50 ในเซลล์ MDCK รวมทั้งตรวจดูปริมาณ cytokine/chemokine (TNF- α , IP-10, IL-1 β , และ IL-8) โดยวิธี ELISA

การศึกษานี้แสดงให้เห็นว่าเซลล์เยื่อบุเส้นเลือดดำจากสายสะดื้อทารกมีความสามารถในการติดเชื้อไวรัสไข้หวัดใหญ่แต่ละสายพันธุ์ แต่ละสายพันธุ์ซึ่งตรวจพบได้ด้วยวิธี immunofluorescence assay ดังแสดงในรูปที่ 8



รูปที่ 8 การตรวจหาแอนติเจนของเชื้อไวรัสในเซลล์เยื่อบุเส้นเลือดดำที่ถูก inoculate ด้วยเชื้อไวรัสไข้หวัดใหญ่สายพันธุ์ต่างๆ เป็นเวลา 5 วัน (A) Uninfected cells, (B) KAN-1 (H5N1), (C) KK-494 (H5N1), (D) NBL-1(H5N1) (feces), (E) Fujian(H3N2)- like virus, (F) New Caledonia (H1N1) -like virus

การศึกษา kinetic การเพิ่มจำนวนของไวรัสทำโดยการใช้ไวรัสในปริมาณต่ำ ($0.005 \text{ TCID50/cell}$) พบว่าไวรัส H5N1 สายพันธุ์ KAN-1, Nong Khai 1 และ NBL 1 (feces) เพิ่มจำนวนในเซลล์เยื่อบุเส้นเลือดดำอย่างมีประสิทธิภาพ และสร้างไวรัสในปริมาณที่สูงกว่า H5N1 สายพันธุ์อื่น และมากกว่าไวรัสไข้หวัดใหญ่สับไทยอีกด้วย แสดงให้เห็นว่าประสิทธิภาพของการเพิ่มจำนวนของไวรัสไข้หวัดใหญ่ในเซลล์เยื่อบุเส้นเลือดดำมีความแตกต่างกัน ขึ้นอยู่กับ subtype และสายพันธุ์ของไวรัส และเมื่อใช้ไวรัสในปริมาณมาก (1 TCID50/cell) ประสิทธิภาพในการเพิ่มจำนวนของไวรัสไข้หวัดใหญ่ตามถูกต้อง H1N1 และ H3N2 จะสูงขึ้น และการศึกษาไวรัส A/H1N1 2009 จำนวน 3 สายพันธุ์ พบว่าไวรัสทุกตัวสามารถก่อการติดเชื้อ และเพิ่มจำนวนได้ในเซลล์เยื่อบุเส้นเลือดดำจากสายสะดื้อการก ผลการศึกษา kinetic การเพิ่มจำนวนของไวรัสแสดงในตารางที่ 2-4

ตารางที่ 2 Kinetics ของการเพิ่มจำนวนไวรัสในเซลล์เยื่อบุหลอดเลือดดำที่ติดเชื้อไวรัสในปริมาณน้อย (0.005 TCID50/cell)

Viruses	Experiment	Titer of virus progenies at log 10 of TCID50 on				
		No.	Day1	Day3	Day5	Day7
A/Thailand/1(KAN-1)/2004 (H5N1)	1	4.33	5.88	5.5	4.21	
	2	3.74	5	3.88	3	
A/Thailand/2(SP-33)/2004 (H5N1)	1	0	0	2	0	
	2	2.66	1.37	1.17	0	
A/Thailand/3(SP-83)/2004 (H5N1)	1	0	0	0	0	
	2	0	1.86	0	0	
A/Thailand/5(KK-494)/2004 (H5N1)	1	0	0	0	0	
	2	1.23	0	0	0	
A/Thailand/676(NYK)/2005(H5N1)	1	3.16	2	1.83	1.67	
	2	1.74	1.86	0.3	0	
A/Thailand/NBL-1/2006 (H5N1) (trachea)	1	2.74	1.74	1.78	0	
	2	2.58	1.88	1.58	1.88	
A/Thailand/NBL-1/2006 (H5N1) (lung)	1	2	1.83	2	0	
	2	2.25	0	0	0	
A/Thailand/NBL-1/2006 (H5N1) (feces)	1	4.5	4.58	3.83	2.91	
	2	3.88	5.12	4.08	3.25	
A/Laos/Nong Khai 1/2007(H5N1)	1	3.2	6.2	5.2	4.2	
	2	2.88	5.83	4.28	3.66	
A/Fujian/411/2002(H3N2)-like virus (Siriraj 03/04)	1	1.83	3.62	2.62	1.25	
	2	2.16	5.66	4.83	5	
A/Sydney/05/97(H3N2)-like virus (Siriraj-03/98)	1	2.83	2.25	1.32	0	
	2	1.08	1.75	0	0	
A/Moscow/10/99(H3N2)-like virus (Siriraj 06/02)	1	0.25	0.25	0	0	
A/New Caledonia/20/99 (H1N1)-like virus: Siriraj-07/00	1	0	0	0	0	
	2	0	0	0	0	
A/ New Caledonia/20/99 (H1N1)-like virus : Siriraj 10/06	1	0	0	1.66	0	
	2	0	1.51	0	0	
A/ New Caledonia/20/99	1	0	0	0	0	

(H1N1)-like virus : Siriraj 02/06

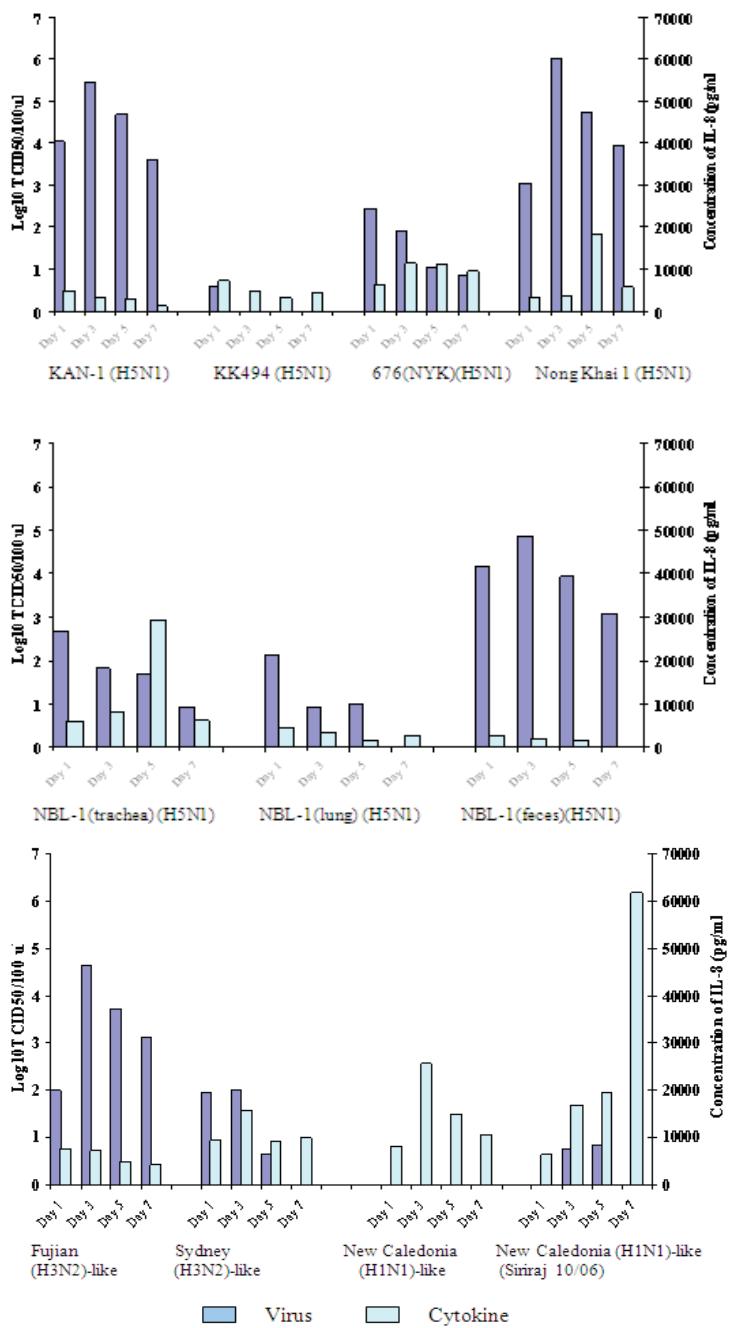
ตารางที่ 3 Kinetics ของการเพิ่มจำนวนไวรัส A/H1N1 A/H3N2 และ A/H5N1 ในเซลล์เยื่อบุหลอดเลือดดำที่ติดเชื้อไวรัสในปริมาณสูง (1 TCID50/cell)

Virus	Titer of virus progenies at log10 of TCID50 on		
	12 hpi	24 hpi	36 hpi
A/Thailand/1(KAN-1)/2004 (H5N1)	3.61	2.33	2.91
A/Thailand/676(NYK)/2005 (H5N1)	2.73	3.37	3.5
A/Laos/Nong Khai 1/2007 (H5N1)	2.75	3.83	3.74
A/Fujian/411/2002 (H3N2)-like virus	2.75	2.5	2.33
A/New Caledonia/20/99 (H1N1)-like virus (Siriraj 07/00)	2.67	3.25	2.71

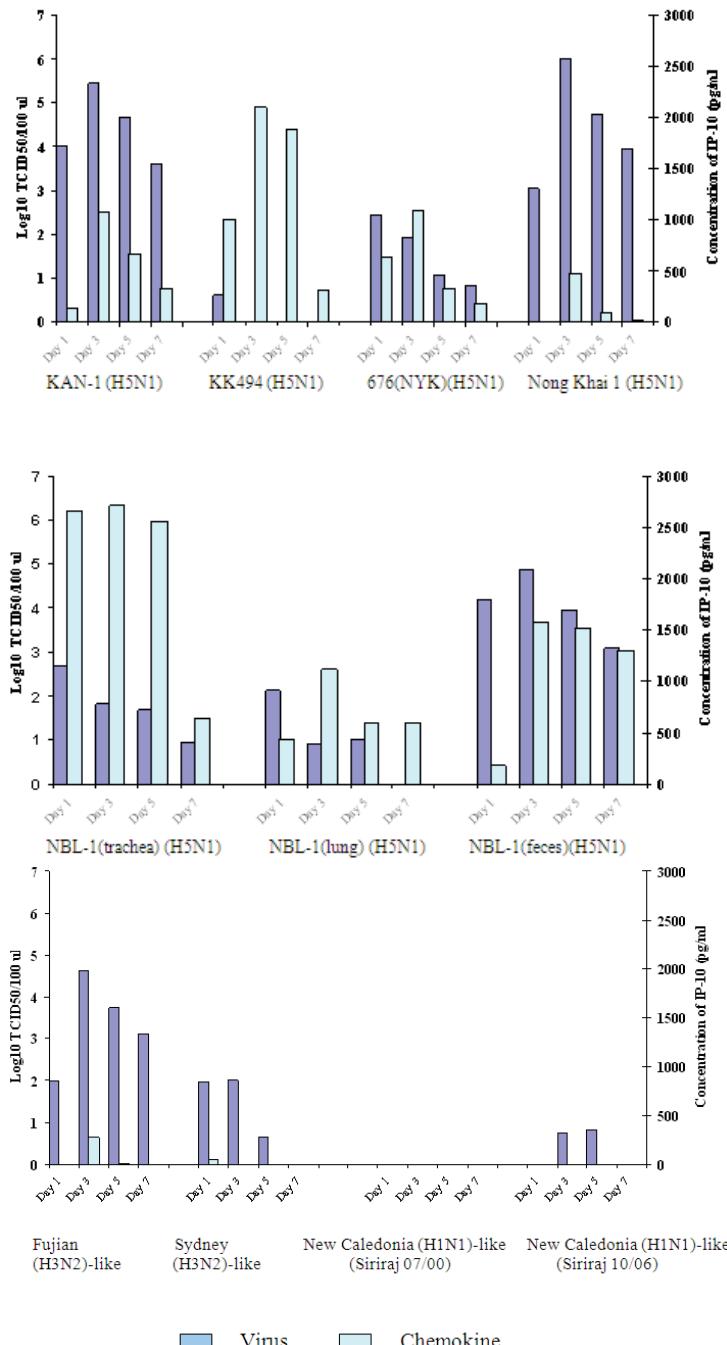
ตารางที่ 4 Kinetics ของการเพิ่มจำนวนไวรัส A/H1N1 2009 ในเซลล์เยื่อบุหลอดเลือดดำที่ติดเชื้อไวรัสในปริมาณสูง (1 TCID50/cell)

Virus	Experiment	Log10 of TCID50 titer		
		No.	12 hpi	24 hpi
A/Nonthaburi/102/09 (H1N1pdm)	1	0	0	0
	2	1.11	1.13	0.25
A/Thailand/104/09 (H1N1pdm)	1	3.38	2.83	3.16
	2	3.08	2.11	2.81
A/Bangkok/ICRC-1/09 (H1N1pdm)	1	3.25	3.11	2.37
	2	4	3.61	3.33

การตรวจหา cytokine/chemokine (รูปที่ 9 และ 10) ทั้งโดยใช้ไวรัสปริมาณต่ำและไวรัสปริมาณสูง ให้ผลอย่างเดียวกัน คือ ไวรัส H5N1 และ A/H1N1 2009 เนื่นี่ยวนำการสร้าง IL-8 และ IP10 ในขณะที่ไวรัสตามฤดูกาล H1N1 และ H3N2 สามารถเนี่ยวนำการสร้าง IL-8 ได้เพียงอย่างเดียว การศึกษานี้แสดงให้เห็นว่าไวรัสที่มีประสิทธิภาพสูงในการเพิ่มจำนวน จะมีความสามารถต่อในการกระตุ้นการสร้าง cytokine หรือตรงข้ามกัน



รูปที่ 9 ความสัมพันธ์ในเชิงผกผันระหว่าง virus progeny titers และ ระดับของ IL-8 ซึ่งทดสอบจากน้ำเลี้ยงเซลล์ที่ติดเชื้อไวรัสในปริมาณต่ำ (0.005 TCID50/cell) ที่ช่วงเวลาต่างๆ กัน



รูปที่ 10 ความสัมพันธ์ในเชิงผกผันระหว่าง virus progeny titers และ ระดับของ IP10 ซึ่งทดสอบจากน้ำเลี้ยงเซลล์ที่ติดเชื้อไวรัสในปริมาณต่ำ (0.005 TCID50/cell) ที่ช่วงเวลาต่างๆ กัน

การศึกษานี้นำไปสู่การเสนอغلไก่ใหม่ในการก่อโรครุนแรง โดยเฉพาะในเชื้อไข้หวัดนก H5N1 การที่ไวรัสสามารถติดเชื้อและเพิ่มจำนวนในเซลล์เยื่อบุเส้นเลือดดำอาจเป็นกลไกหนึ่งที่สามารถอธิบายการแพร่กระจายของเชื้อไวรัสออกไปในระบบทางเดินหายใจ และในรายที่ผู้ป่วยถึงแก่ชีวิต การตายอาจเป็นผลจากการที่เซลล์ถูกทำลาย เนื่องจากติดเชื้อไวรัสที่มีประสิทธิภาพสูงในการเพิ่มจำนวนหรือ การตายอาจเป็นผลจากการสร้าง cytokine มากเกินไปในรายที่ติดเชื้อไวรัสที่มีประสิทธิภาพต่ำในการเพิ่มจำนวน อย่างไรก็ตามเชื้อไข้หวัดนกอาจอาศัยกลไกหลายอย่างที่ทำให้เชื้อมีความรุนแรงในการก่อโรค (งานวิจัยในส่วนนี้อยู่ระหว่างการเตรียมต้นฉบับการตีพิมพ์ผลงาน)

22. การศึกษาและเฝ้าระวังการเกิดเชื้อดื/o ya

22.1 การใช้เทคนิค genotypic based assay โดยการวิเคราะห์ลำดับนิวคลีโอไทด์ของ NA gene เพื่อหาตำแหน่ง mutation ที่ทำให้ไวรัสดื/o ya การศึกษาวิจัยนี้ ยังไม่พบตำแหน่ง mutation ใหม่ ที่ทำให้เชื้อดื/o ต่อ NA inhibitors

22.2 การใช้เทคนิค phenotypic based assays

งานวิจัยนี้ใช้ 3 เทคนิค (MUNANA-based NAI assay, plaque reduction assay, และ ELISA-based NP reduction assay) ในการทดสอบความไวต่อ oseltamivir และ zanamivir ของเชื้อไวรัสไข้หวัดใหญ่/ไข้หวัดนก จำนวน 20 isolates การทดสอบทั้ง 3 วิธี ส่วนใหญ่ให้ผลไปในทิศทางเดียวกัน ดังแสดงในตารางที่ 5 อย่างไรก็ตาม ไวรัสไข้หวัดนก H5N1 ที่แยกได้จากสัตว์จำนวน 3 isolates พบค่า IC50 ที่ได้จาก NAI assay และ NP reduction assay ไม่สัมพันธ์กัน คือ NAI assay พบผลไวต่อ ya แต่ขณะที่ NP reduction assay พบผลดื/o ต่อ ya ทั้ง oseltamivir และ zanamivir เมื่อพิจารณาจาก amino acid sequence ของ NA gene ไม่พบการ mutation ในตำแหน่ง H274Y substitution หรือตำแหน่งอื่นๆ ที่เคยมีรายงานว่าทำให้ดื/o ต่อ ya ซึ่งอาจเป็นเพราะการดื/o ya อาจเกิดจาก mutation ที่ตำแหน่งอื่นหรือยืนยันอื่นที่เกี่ยวข้องที่ยังไม่ทราบก็เป็นได้ แต่เนื่องจากเชื้อ H5N1 ทั้ง 3 isolates นี้มีลักษณะการเกิด plaque ที่มีขนาดเล็กและไม่ชัดเจน (รูปที่ 11) ทำให้ไม่สามารถทดสอบด้วยวิธี plaque reduction assay ได้ จึงอาจเป็นไปได้ว่าไวรัส มีการทำงานของ neuraminidase ที่บกพร่องไปทำให้มีปริมาณ NP สะสมอยู่ในเซลล์ที่ติดเชื้อ ปริมาณสูงซึ่งทำให้ดูเหมือนไวรัสเหล่านี้ดื/o ต่อ ya ในกรณีนี้ ได้มีการเก็บน้ำเลี้ยงเซลล์ของไวรัสหลังจากการ treat ยา ไปทดสอบหาปริมาณไวรัส พบว่าเมื่อ treat ด้วยยาพบปริมาณเชื้อไวรัสในน้ำเลี้ยงเซลล์ ในปริมาณน้อย แสดงว่าแท้จริงแล้วเชื้อนั้นยังคงมีความไวต่อ ya ดังนั้นหากใช้วิธี ELISA-based NP reduction assay ในการคัดกรองหาเชื้อดื/o ya หากพบผลการดื/o ya ด้วยวิธีนี้ อาจต้องมีการทำการทำทดสอบเพิ่มเติมคือ ตรวจหาปริมาณไวรัสในน้ำเลี้ยงเซลล์หากพบว่าไม่สามารถตรวจพบไวรัสในน้ำเลี้ยงเซลล์หรือตรวจพบในปริมาณน้อย นั่นแสดงว่าเชื้อนั้นยังคงมีความไวต่อ ya (งานวิจัยในส่วนนี้อยู่ระหว่างการเตรียมต้นฉบับการตีพิมพ์ผลงาน)

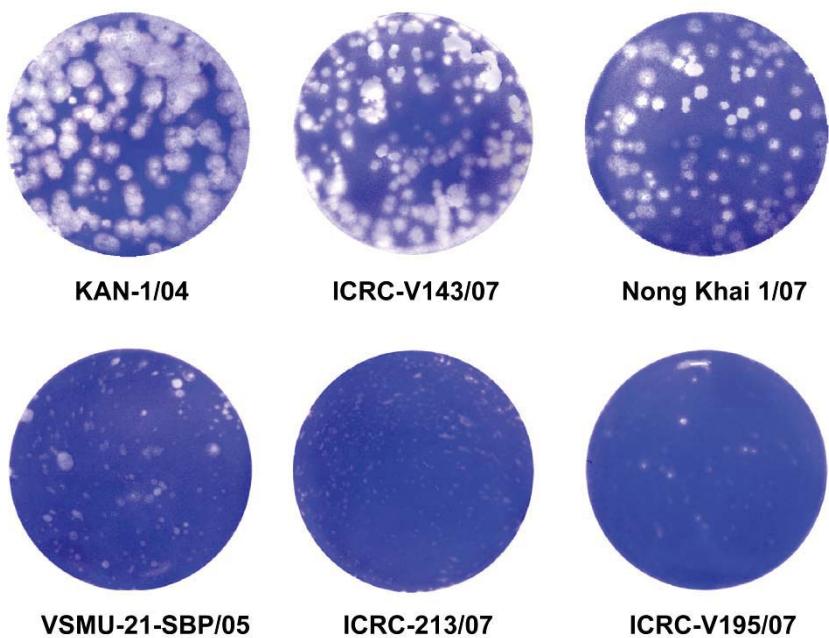
ตารางที่ 5 ค่า IC50 ที่ได้จากการทดสอบความไวต่อยาด้วยวิธีต่างๆ

Viruses	IC50 ^a of oseltamivir carboxylate			IC50 ^a of zanamivir		
	NAI (nM)	Plaque	NP	NAI (nM)	Plaque	NP
		reduction	reduction		reduction	reduction
Reference strains						
Mississippi/01 (NA-274H)	1.799	0.27	0.04	1.27	0.50	0.11
Mississippi/01 (NA-H274Y)	477.76	43.64	108.23	1.33	0.52	0.331
Seasonal strains						
ICRC_SEA-3043/07	875.25	104.44	781.49	3.89	0.39	1.659
ICRC_SEA-3026/07	1.21	0.012	0.833	0.64	0.045	2.205
ICRC_SEA-3613/07	0.85	0.055	0.166	1.82	0.50	1.331
H1N1pdm						
Thailand/104/09	1.02	0.39	1.94	0.60	1.52	4.671
ICRC_CBI_20/09	1.01	0.16	0.41	0.67	1.35	0.71
H5N1 viruses						
KAN-1/04	0.15	0.181	0.447	1.82	4.42	7.92
SP-83/04	0.19	0.003	0.008	1.02	0.017	0.231
KK-494/04	0.26	0.031	0.223	2.21	0.885	0.186
676(NYK)/05	0.17	0.035	0.012	3.12	0.479	0.932
NBL-1/06 (Lung)	0.86	0.006	0.004	2.04	0.009	0.053
NBL-1/06 (Feces)	0.11	0.001	0.013	4.24	0.06	0.145
Nong Khai-1/07	8.05	1.339	5.309	1.13	1.104	3.163
VSMU-11-SPB/04	0.13	0.238	0.4395	0.40	0.042	0.099
AI-1216A/04	0.14	0.003	3.266	0.16	0.038	1.982
VSMU-21-SPB/05	0.18	NA	13.25	0.24	NA	358.3
ICRC-V143/07	1.88	0.002	0.007	7.68	0.013	0.14
ICRC-V195/07	0.53	NA	27.63	4.9	NA	239.7
ICRC-V213/07	0.28	NA	431.3	4.84	NA	271.1

^a IC50 values are means from at least two independent experiments in duplicate wells (for NAI assay) or triplicate wells (for plaque reduction and NP reduction assays).

^b IC50 values of ELISA-based viral NP reduction assay were determined by using the virus inoculum dose at 25 TCID50.

NA, Not applicable because the plaque formation is small and not well defined.



รูปที่ 11 ลักษณะการเกิด plaque ของเชื้อไวรัสไข้หวัดนก H5N1 ซึ่งทดสอบใน 6-well plate พบว่าไวรัส H5N1 3 isolates คือ VSMU-21-SPB/05, ICRC-213/07, และ ICRC-V195/07 มีขนาด plaque ที่เล็กและไม่ชัดเจน

บทวิจารณ์

จุดมุ่งหมายเริ่มแรกของงานวิจัยนี้คือการศึกษาเกี่ยวกับเรื่องของเชื้อไข้หวัดนก H5N1 แต่เนื่องจากผู้ป่วยไข้หวัดนกได้หมดไปจากประเทศไทยตั้งแต่กลางปี พ.ศ. 2549 และในปี พ.ศ. 2552 ได้มีการระบาดทั่วโลกของเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ A(H1N1) ลูกค้ามามากถึงประเทศไทย คณะผู้วิจัยจึงได้ขยายขอบเขตของการศึกษาวิจัยให้ครอบคลุมทั้งไวรัสไข้หวัดนก H5N1 ไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ A(H1N1) และมีการศึกษาเปรียบเทียบกับไข้หวัดใหญ่ตามฤดูกาลด้วย

โครงการวิจัยนี้มีวัตถุประสงค์ที่หลากหลาย ทั้งด้านลักษณะทางอนุชีววิทยาในระดับโมเลกุลของตัวเชื้อ กลไกการก่อโรค ปัจจัยการแพร่กระจายของเชื้อ การตรวจวินิจฉัยการติดเชื้อ การตอบสนองทางภูมิคุ้มกันต่อเชื้อ และรวมถึงการทดสอบการต่อต่อยาต้านไวรัส นอกจากนี้ยังมีการศึกษาเพื่อพัฒนาเทคโนโลยีต่างๆ ที่มีประโยชน์ ซึ่งสามารถทำได้เสร็จสิ้น สมบูรณ์ และเทคนิคที่พัฒนาขึ้นมาเหล่านี้สามารถนำไปใช้ให้เป็นประโยชน์ได้จริง ซึ่งที่มีวิจัยประสบความสำเร็จในการวินิจฉัยและแยกเชื้อไวรัสไข้หวัดนก H5N1 รายแรกของประเทศไทย และจากบทบาทในการเป็นห้องปฏิบัติการคุณนาณกับกรมวิทยาศาสตร์การแพทย์ ทำให้มีวิจัยได้มีโอกาสให้การวินิจฉัยไข้หวัดนกรายที่สำคัญของประเทศไทยในเวลาต่อๆ มา รวมถึงได้ทำการวินิจฉัยและแยกเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่รายแรกของประเทศไทยด้วย

การศึกษาวิจัยในแต่ละด้านมีความละเอียดและค่อนข้างซับซ้อน และในกรณีของการระบาดของเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ข้อมูลเกี่ยวกับลักษณะและคุณสมบัติของตัวเชื้อยังมีอยู่น้อย รวมทั้งต้องมีการพัฒนาเทคนิคที่ใช้ในการตรวจวินิจฉัยให้มีความเหมาะสมกับคุณลักษณะที่มีความจำเพาะเฉพาะเจาะจงกับตัวเชื้อมากขึ้น จึงต้องใช้ระยะเวลาในการศึกษาวิจัย ประกอบกับการเก็บตัวอย่างตรวจจากผู้ป่วยจำนวนมากทำได้ยากและต้องใช้เวลาในการเก็บรวบรวมตัวอย่างเพื่อให้ได้ข้อมูลที่มีความน่าเชื่อถือ ในงานวิจัยบางส่วนอาจต้องอาศัยเวลาในการติดตามเก็บตัวอย่างในระยะยาว เช่น การติดตามเจาะเลือดจากผู้ป่วยที่รอดชีวิตจากการติดเชื้อ H5N1 ที่ใช้ระยะเวลาติดตามนานหลายปี รวมทั้งการติดตามเส้นทางการบินของนกอพยพเป็นต้น ผลการศึกษาจากโครงการวิจัยนี้ได้ถูกนำมาใช้ในสถานการณ์จริง เพื่อประโยชน์ทางการสาธารณสุขของประเทศไทยในการวินิจฉัยโรค การควบคุมโรค และการวางแผนการป้องกันโรค และเป็นการสร้างองค์ความรู้ใหม่ทั้งความรู้พื้นฐานและความรู้ประยุกต์ และสร้างบุคลากรนักวิจัย และนักศึกษา ที่มีศักยภาพสูง เพื่อรับรองการพัฒนาวิจัยทางการแพทย์ในอนาคต

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Output จากโครงการวิจัยที่ได้รับทุนจาก สกอ.

- ผลงานที่มีการ Acknowledgements สกอ. มีจำนวน 23 เรื่อง
 - ผลงานที่ได้รับการตีพิมพ์เผยแพร่เรียบร้อยแล้ว มี 15 เรื่อง
 - ผลงานที่ได้รับการตอบรับให้ตีพิมพ์แล้ว (in gallery proof) มี 1 เรื่อง
 - ผลงานที่มี submit ฉบับ revised version manuscript ไปแล้ว 2 เรื่อง
 - ผลงานที่อยู่ระหว่างการเตรียมฉบับ revised version และตอบข้อซักถามจาก reviewers มี 1 เรื่อง
 - ผลงานที่อยู่ระหว่างการเขียน manuscript มี 4 เรื่อง
- การนำเสนอผลงานในที่ประชุมวิชาการในรูปแบบโปสเตอร์ จำนวน 19 เรื่อง
- การนำเสนอผลงานในที่ประชุมวิชาการแบบปากเปล่า จำนวน 1 เรื่อง
- การผลิตนักศึกษาและนักวิจัยรุ่นใหม่
 - นักศึกษาปริญญาโทจำนวน 4 คน
 - นักศึกษาปริญญาเอกจำนวน 2 คน
 - นักวิจัยหลังปริญญาเอกจำนวน 1 คน
 - นักวิจัยหลังปริญญาโทจำนวน 2 คน
- ผลงานที่เป็นผู้วิจัยร่วมในโครงการอื่นๆ มีจำนวน 28 เรื่อง

Output จากโครงการวิจัยที่ได้รับทุนจาก สกอ.

- ผลงานตีพิมพ์ในวารสารวิชาการนานาชาติ (ระบุชื่อผู้แต่ง ชื่อเรื่อง ชื่อวารสาร ปี เล่มที่ และหน้า)

ผลงานที่ได้รับการตีพิมพ์เผยแพร่เรียบร้อยแล้ว มี 14 เรื่อง คือ

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 - Panaampon J, Ngaosuwankul N, Suptawiwat O, Noisumdaeng P, Sangsiriwut K, Siridechadilok B, Lerdsamran H, Auewarakul P, Pooruk P, **Puthavathana P**. A novel pathogenic mechanism of highly pathogenic avian influenza H5N1 viruses involves hemagglutinin mediated resistance to serum innate inhibitors. *PLoS ONE* 2012;7(5):e36318. (เป็น corresponding author) Impact factor 4.4

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ผลงานที่ได้รับการตอบรับให้ตีพิมพ์แล้ว (in gallery proof) มี 1 เรื่อง คือ

1. Chokephaibulkit K, Asanasaen S, Apisarnthanarak A, Rongrungruang Y, Kachintorn K, Tuntiwattanapibul Y, Judaeng T, **Puthavathana P**. Seroprevalence of 2009 H1N1 virus infection and self-reported infection control practices among healthcare professionals following the first outbreak in Bangkok, Thailand. (Accepted for submission in Influenza and Other Respiratory Viruses, Aug 10th, 2012)

ผลงานที่มี submit ฉบับ revised version manuscript ไปแล้ว 2 เรื่อง คือ

1. Pirom Noisumdaeng, Phisanu Pooruk, Alita Kongchanagul, Susan Assanasen, Rungrueng Kitphati, Prasert Auewarakul, **Pilaipan Puthavathana**. Biological properties of H5 hemagglutinin expressed by vaccinia virus vector and its immunological

reactivity with human sera. (เป็น corresponding author) (Revised version in submission to *Viral Immunology*)

2. Suda Louisirirotchanakul, Pornparn Rojanasang, Kleophant Thakerngpol, Naree Choosrichom, Kridsda Chaichoune, Phisanu Pooruk^a, Aphinya Namsai^a, Robert Webster, **Pilaipan Puthavathana**. Electron micrographs of highly and low pathogenic avian influenza viruses. (เป็น corresponding author) (Revised version in submission to *Asian Biomedicine*)

ผลงานที่อยู่ระหว่างการเตรียมฉบับ **revised version** และตอบข้อซักถามจาก **reviewers** มี 1 เรื่อง คือ

1. Parntep Ratanakorn, Anuwat Wiratsudakul, Witthawat Wiriyarat, Krairat Eiamampai, Adrian H Farmer, Robert G Webster, Kridsada Chaichoune Sarin Suwanpakdee, Duangrat Pothieng, Pilaipan Puthavathana. Satellite tracking on the flyways of Brown-headed gulls and their potential role in the spread of highly pathogenic avian influenza H5N1 virus. (Submitted to *PLoS ONE* with under preparing the revised version)

ผลงานที่อยู่ระหว่างการเขียน **manuscript** มี 4 เรื่อง คือ

1. A pathogenic mechanism of HPAI H5N1 viruses involve active replication and cytokine induction in endothelial cells (ผลงานจากวิทยานิพนธ์นักศึกษาปริญญาโท)

2. Screening for drug resistant influenza A viruses: a comparative study among 3 different phenotypic based assay systems and nucleotide sequencing technique (ผลงานจากวิทยานิพนธ์นักศึกษาปริญญาเอก)

3. Immunological reactivity of specific and cross reactive antibodies against highly pathogenic avian influenza H5N1 viral proteins expresses by vaccinia virus vector (ผลงานจากวิทยานิพนธ์นักศึกษาปริญญาเอก)

4. Homosubtypic and heterosubtypic T cells mediated immune response against nucleoprotein and matrix proteins derived from highly pathogenic avian influenza A (H5N1) virus (ผลงานจากวิทยานิพนธ์นักศึกษาปริญญาเอก)

1.2 ผลงานที่เป็นผู้วิจัยร่วม มี 28 เรื่อง คือ

1. Udompornwattana S, Srajai K, Suwan P, Tangsathapornpong A, Wittawatmongkol O, Phongsamart W, Vanprapar N, Nuntarukchaikul M, Taeprasert P, Sricharoenchai S, Tanchaweng S, **Phuttwattana P**, Taylor WR, Maleesatharn A, Chokephaibulkit K. The clinical features, risk of prolonged hospitalization and household

infections of hospitalized children for pandemic 2009 influenza A (H1N1) virus infection in Thailand. *J Med Assoc Thai.* 2012 Mar;95(3):403-11.

2. Namsai A, Louisirirotchanakul S, Wongchinda N, Siripanyaphinyo U, Virulhakul P, **Puthavathana P**, Myint KS, Gannarong M, Ittапong R. Surveillance of hepatitis A and E viruses contamination in shellfish in Thailand. *Lett Appl Microbiol*. 2011;53:608-13.
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2. การนำผลงานวิจัยไปใช้ประโยชน์

- เป็นการเสริมสร้างศักยภาพให้กับประเทศไทยในการเฝ้าระวังการอุบัติขึ้นของเชื้อใหม่ที่อาจก่อโรครุนแรงกว่าเดิม และเป็นการคงศักยภาพและความพร้อมในการวินิจฉัยโรคไข้หวัดนกให้แก่ประเทศไทยเป็นงานที่ก้มวิจัยได้ทำสืบเนื่องมาตั้งแต่การระบาดครั้งแรก
- เป็นการสร้างองค์ความรู้และความเข้าใจเกี่ยวกับพยาธิกำเนิดของโรคไข้หวัดนก ซึ่งยังขาดข้อมูลทางด้านนี้อยู่อีกมาก
- เป็นการสร้างแนวความคิดใหม่ในการพัฒนาวัคซีนไข้หวัดนก
- เป็นการสร้างบุคลากรรุ่นใหม่ให้มีความรู้เรื่องไข้หวัดนก/ไข้หวัดใหญ่ เพื่อรองรับภาวะวิกฤตของประเทศไทย
- มีการพัฒนาเทคนิคทาง serology เพื่อใช้ในการวินิจฉัยการติดเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ A/H1N1 2009 และเป็นประโยชน์ต่อห้องปฏิบัติการอื่นๆ ในประเทศไทยเพื่อใช้เป็นแนวทางในการวินิจฉัยโรค
- เกิดผลงานตีพิมพ์ในวารสารที่มีชื่อเสียง เป็นการเผยแพร่เชื่อเสียงและเกียรติคุณของนักวิจัยไทย

3. อื่นๆ (เช่น ผลงานตีพิมพ์ในวารสารวิชาการในประเทศไทย การเสนอผลงานในที่ประชุมวิชาการ หนังสือ การจดสิทธิบัตร)

3.1 ผลงานตีพิมพ์ในวารสารวิชาการในประเทศไทย

3.1.1 อดิสรณ์ วรรธนะศักดิ์, จักรรูป พิทยาวงศ์อานันท์, วารินทร์ ปงกันคำ, ราชบัณฑุรัตนศิลป์, วราพร วรรณา, พิไลพันธ์ พุธวัฒนะ, ณัฐมน เงาสุวรรณกุล, พิษณุ ภูรักษ์, ทัยรัตน์ เลิศสำราญ, สมคิด คงอยู่, โสภณ เอี่ยมศิริถาวร. อัตราการติดเชื้อ ระยะเวลาของการขับเชื้อไวรัส และปริมาณเชื้อไวรัส ขณะมีการระบาดของไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 ในกลุ่มทหารเกนท์ ศูนย์ฝึกหหารใหม่แห่งหนึ่ง ประเทศไทย เดือนมิถุนายน พ.ศ. 2552. รายงานการเฝ้าระวังทางระบาดวิทยาประจำสัปดาห์ 2010;41:209-13.

3.1.2 บทความพื้นวิชา:

พิไลพันธ์ พุธวัฒนะ การศึกษาไวรัสไข้หวัดใหญ่ทางห้องปฏิบัติการ ประชุมวิชาการประจำปี ครั้งที่ 19 สมาคมไวรัสวิทยา (ประเทศไทย) วันที่ 20 พฤษภาคม 2552: กรุงเทพฯ. 2552:18-30.

3.2 การเสนอผลงานในที่ประชุมวิชาการในรูปแบบโปสเตรอร์

3.2.1 ประชุมและนำเสนอผลงานวิจัยในงานประชุมวิชาการนานาชาติ Keystone Symposia Conference เรื่อง Respiratory Viruses of Animals Causing Disease in humans โรงแรม Swissotel The Stamford/Biopolis ประเทศไทยสิงคโปร์ วันที่ 10-15 ธันวาคม 2549

3.2.1.1 Lerdsamran H, Louisirirotchanakul S, Wiriyarat W, Sangsiriwut K, Pooruk P, Kijphati R, Chaichoune K, Sawanpanyalert P, Pittayawonganon C, Ungchusak K, Auewarakul P, **Puthavathana P.** Hemagglutinin activity of avian influenza H5N1 viruses.

3.2.1.2 **Puthavathana P.**, pooruk P, Sangsiriwut K, Nateerom K, Prasertsopon J, Chaichoune K, Wiriyarat W, Korkusol A, Auewarakul P, Chokephaibulkit K, Ungchusak K, Sawanpanyalert P, Ratanakorn P. Oseltamivir sensitivity of H5N1 influenza isolates, Thailand.

3.2.2 ประชุมและนำเสนอผลงานวิจัย SEA Influenza Clinical Research Network 3rd Annual Conference ที่ นาหลี ประเทศไทย วันที่ 21-23 พฤษภาคม 2551

Pilaipan Puthavathana, Kulkanya Chokephaibulkit, Chariya Saenasjja, Charoen Chuchottaworn, Phisanu Pooruk, Pisut Komolsiri, Achareeya Korkusol, Suda Louisirirotchanakul, Tawee Chotpityaasunondh, and SEAICRN staffs. Respiratory viruses associated with severe influenza like illness.

3.2.3 ประชุมและนำเสนอผลงานวิจัยในงานประชุม 8th Asia Pacific Congress of Medical Virology ที่ส่องกง วันที่ 26-28 กุมภาพันธ์ 2552

Pisut Komolsiri, Tawee Chotpityasunondh, Kulkanya Chokephaibulkit, Chariya Sangsajja, Charoen Chuchottaworn, Achareeya Korkusol, Rajita Kanyaboon, Phisanu Pooruk, Nirun Vanprapar and **Pilaipan Puthavathana**. Respiratory virus associated with severe pneumonia

3.2.4 ประชุมและนำเสนอผลงานวิจัยในงานประชุม The 2nd Thailand Human Influenza Research Meeting ณ โรงแรมเชอราตัน แกรนด์ สุขุมวิท วันที่ 21-22 ตุลาคม 2552

3.2.4.1 Pirom Noisumdaeng, Thaneeya Duangchinda, Juthathip Mongkolsapaya, Susan Assanasen, Suda Louisirirotchanakul, Prasert Auewarakul, Phisanu Pooruk, Hatairat Lerdsamran and **Pilaipan Puthavathana**. Human influenza

virus-specific T cells mediated cross reactive immune response to nucleoprotein (NP) derived from avian influenza H5N1 virus.

3.2.4.2 Pornparn Rojanasang, Suda Louisirirotchanakul, Kleophant Thakergpol, Naree Choosrichom, Witthawat Wiriyarat, Kridsada Chaichoune, Robert Webster and **Pilaipan Puthavathana**. Electron micrographs of H5N1 viruses and its replication in MDCK cells.

3.2.4.3 Hatairat Lerdsamran, Phisanu Pooruk, Achareeya Korkusol, Pirom Noisumdaeng, Pisut Komolsiri, Kantima Sangsiriwut, Kannika Nateerom, Charoen Chuchottaworn, Chariya Sangsajja, Tawee Chotpitayasanondh, Kulkanya Chokephaibulkit and **Pilaipan Puthavathana**. Surveillance for sensitivity of influenza A and B viruses to neuraminidase inhibitors.

3.2.4.4 Phisanu Pooruk, Hatairat Lerdsamran, Kannika Nateerom, Roongnapa Bunrueng, Pisut Komolsiri, Chakrarat Pittyawonganon, Warin Pongkankham, Sopon Iamsiritaworn, Kulkanya Chokephaibulkit, Tawee Chotpitayasanondh, Chariya Sangsajja, Charoen Chuchottaworn and **Pilaipan Puthavathana**. Hemagglutination-inhibition and microneutralization assays for antibodies to pandemic influenza A (H1N1) 2009 virus.

3.2.4.5 Piyaporn (Nathamom) Ngaosuwankul, Pisut Komolsiri, Pirom Noisumdaeng, Kulkanya Chokephaibulkit, Tawee Chotpitayasanondh, Chariya Sangsajja, Charoen Chuchottaworn and **Pilaipan Puthavathana**. Viral load of pandemic influenza A (H1N1) 2009 virus in various types of respiratory samples.

3.2.4.6 Weena Paungpin, Kanaporn Poltep, Phirom Phompiram, Sarin Suwanpaksee, Tanasak Changbanjong, Chaiyaporn Jakapirom, Poonyapat Sedwisai, Taniyanuch Chamsai, Nam-aoi Toawan, Jarin Chatsiriwech, Parut Suksai, Kridsda Chaichoune, Witthawat Wiriyarat, Arunee Thititanyanon, Kumnuan Ungchusak, Prasert Auewarakul, Parntep Ratanakorn and **Pilaipan Puthavathana**. Seroprevalence to HPAI H5N1 virus in healthy backyards chickens living in repeated outbreak areas of Thailand.

3.2.4.7 Witthawat Wiriyarat, Weena Paungpin, Kanaporn Poltep, Phirom Phompiram, Kridsda Chaichoune, Rassameepen Phonarknguen, Nam-aoi Taowan, Sarin Suwanpakdee, Plern Yongyuttawichai, Anuwat Wiratsudakul, Arunee Thititanyanon2, Kumnuan Ungchusak, Prasert Auewarakul, Parntep Ratanakorn and **Pilaipan Puthavathana**. Seroprevalence of HPAI H5N1 virus in domestic dogs and cats living in repeated outbreak areas in Thailand

3.2.4.8 Anuwat Wiratsudakul, Witthawat Wiriayarat, Kridsada Chaichoune, Sarin Suwanpakdee, Krairat Eiamampai, Adrian Farmer, Tanasak Changbanjong, Kecha Cheewajorn, Pearn Yongyutthawichai, Juthathip Jangjaras, Poonyapat Sedwisai, Tatiyanuch Chamsai, Nam-aoi Taowan, Ladawan Sariya, **Pilaipan Puthavathana** and Parntep Ratanakorn. Satellite telemetry reveals migratory routes of Brown-headed gulls (*Larus brunnicephalus*) captured in Thailand.

3.2.5 ประชุมและนำเสนอผลงานในการประชุมวิชาการประจำปี ครั้งที่ 19 สมาคมวิรัสวิทยา (ประเทศไทย) ณ โรงแรมรอยัลริเวอร์ วันที่ 20 พฤษภาคม 2552

Worawat Dangsagul, Pattaraporn Cheuypratoom, Wanrangkana Aonsoung, Sontana Siritantikorn and **Pilaipan Puthavathana**. Neuraminidase inhibitor resistant seasonal influenza H1N1 viruses in Thailand during 2006 to 2009.

3.2.6 ประชุมและนำเสนอผลงานวิจัยในรูปแบบโปสเตอร์ ในงานประชุมวิชาการด้านวัคซีนไข้หวัดใหญ่และการพัฒนาวัคซีน Options for the Control of Influenza VII Conference จัดโดย The University of Hong Kong ณ Hong Kong Exhibition and Convention Center วันที่ 3-7 กันยายน 2553 ซึ่งนำเสนอผลงานโดยนักศึกษาปริญญาเอก นางสาวหทัยรัตน์ เลิศสำราญ และได้รับรางวัล International Research Scholarship ในการสนับสนุนค่าใช้จ่ายในการเดินทางและค่าเบี้ยเลี้ยง

Hatairat Lerd Samran, Phisanu Pooruk, Kantima Sangsiriwut, Pirom Noisumdaeng, Kannika Nateerom, Kridsada Chaichoune, Witthawat Wiriayarat, Kulkanya Chokephaibulkit, Chariya Sangsajja, Tawee Chotpitayasunondh, Pathom Sawanpanyalert, **Pilaipan Puthavathana**. Susceptibility of influenza A viruses to neuraminidase inhibitors as determined by phenotypic and genotypic-based assays.

3.2.7 ประชุมและนำเสนอผลงานวิจัยในรูปแบบโปสเตอร์ ในงานประชุมวิชาการประจำปีครั้งที่ 20 จัดโดยสมาคมวิรัสวิทยา (ประเทศไทย) ณ โรงแรมจอมเทียนปาล์มบีช รีสอร์ทแอนด์อพาร์ทเม้นต์ พัทยา วันที่ 25-26 พฤษภาคม 2553

3.2.7.1 Jutatip Panaampon, Phisanu Pooruk, Pirom Noisamdaeng, Rungnapa Bunruang, **Pilaipan Puthavatthana**. Normal guinea pig serum mediated inhibitory effects on influenza virus replication. นำเสนอโดยนักศึกษาปริญญาโท นางสาวจุฑาทิพย์ พนอัมพล และชนาการประจำปี ได้รับรางวัลจากสมาคมวิรัสวิทยา (ประเทศไทย)

3.2.7.2 Jarunee Prasertsopon, Prawit Akarasereenont, Kitirat Techatisak, Phisanu Pooruk, Nathamon Ngaosuwankul, Athiwat Thaworn, **Pilaipan Puthavathana**. The 2009 pandemic influenza A (H1N1) virus infection and induction of

cytokines and chemokines in human umbilical vein endothelial cells. นำเสนอโดย นักศึกษาปริญญาโท นางสาวจารุณี ประเสริฐโสกณ

3.2.8 ประชุมและนำเสนอผลงานวิจัยในรูปแบบโปสเตอร์ ในงานประชุมวิชาการ Keystone Symposia เรื่อง Pathogenesis of Influenza: Virus-Host Interactions จัดโดย The University of Hong Kong ณ Sheraton Hong Kong Hotel & Towers, Kowloon, Hong Kong วันที่ 23-28 พฤษภาคม 2554

3.2.8.1 Jarunee Prasertsopon, Prawit Akarasereenont, Kitirat Techatisak, Phisanu Pooruk, Nathamon Ngaosuwankul, Athiwat Thaworn, **Pilaipan Puthavathana**. Influenza A virus infection and induction of cytokines and chemokines in human umbilical vein endothelial cells.

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3.5 การจัดประชุมวิชาการ

3.5.1 จัดประชุมวิชาการเรื่อง “From Human to Avian and Swine-Origin Influenza Viruses” และบรรยายในหัวข้อเรื่อง Virology of influenza viruses และ Laboratory investigation of influenza virus infection ณ คณะแพทยศาสตร์ศิริราชพยาบาล วันที่ 31 พฤษภาคม 2552

3.5.2 จัดประชุมและเป็นวิทยากร ในหัวข้อเรื่อง “Pitfalls in laboratory investigation of influenza viruses” ในการประชุมเชิงวิชาการเรื่อง “Outbreak Situation of the 2009 Pandemic Influenza A (H1N1)” จัดโดยสมาคมไวรัสวิทยา (ประเทศไทย) ร่วมกับ ศูนย์ความร่วมมือการวิจัยไข้หวัดใหญ่ (Siriraj ICRC) ภาควิชาจุลชีววิทยา คณะแพทยศาสตร์ศิริราชพยาบาล โครงการโรคติดเชื้ออุบัติใหม่ ศูนย์ความร่วมมือไทย-สหรัฐด้านสาธารณสุข (Thailand – US.CDC Collaboration, TUC) และทุนเมธีวิจัยอาวุโส สำนักงานกองทุนสนับสนุนการวิจัย (Thailand Research Fund for Senior Research Scholar) โรงแรมรอยัลริเวอร์ กรุงเทพฯ วันที่ 9 สิงหาคม 2553

3.5.3 จัดการอบรมเชิงปฏิบัติการและเป็นวิทยากรบรรยาย 3 หัวข้อ ได้แก่ Immunofluorescence (IF) assay, Cell cultivation and virus isolation techniques และ Serology of influenza viruses: Hemagglutination-inhibition (HI) and microneutralization assays ในการอบรมเชิงปฏิบัติการเรื่อง “Workshop on Laboratory Investigation of Influenza Viruses” ชื่งจัดโดยสมาคมไวรัสวิทยา (ประเทศไทย) ร่วมกับศูนย์ความร่วมมือการวิจัยไข้หวัดใหญ่ (Siriraj ICRC) ภาควิชาจุลชีววิทยา คณะแพทยศาสตร์ศิริราชพยาบาล โครงการโรคติดเชื้ออุบัติใหม่ ศูนย์ความร่วมมือไทย-สหรัฐด้านสาธารณสุข (Thailand – US.CDC Collaboration, TUC) และทุนเมธีวิจัยอาวุโส สำนักงานกองทุนสนับสนุนการวิจัย (Thailand Research Fund for Senior Research Scholar) วันที่ 10-14 สิงหาคม 2553 ณ ตึกจุลชีววิทยา คณะแพทยศาสตร์ศิริราชพยาบาล มหาวิทยาลัยมหิดล ชื่งมีจำนวนผู้รับการอบรม 19 คน จาก 15 สภานบัน

4. การผลิตนักศึกษาและนักวิจัย

4.1 นักศึกษาปริญญาโท

1. นายวรวัฒน์ แดงสกุล หัวข้อวิทยานิพนธ์คือ “การเฝ้าระวังเชื้อไวรัสไข้หวัดใหญ่ตามฤดูกาลชนิด A(H1N1) ที่ดื้อต่อสารยับยั้งเอนไซม์นิวราМИนิดีส, ประเทศไทย 2549 – 2552 (Surveillance for neuraminidase inhibitor resistant seasonal influenza A (H1N1) viruses, Thailand 2006-2009)”

2. นางสาวจารุณี ประเสริฐสิงห์ หัวข้อวิทยานิพนธ์คือ “จลนศาสตร์การเพิ่มจำนวนและการเหนี่ยวนำการสร้างไซโตไคโน/คิโนไคโนในเซลล์เยื่อบุเส้นเลือดดำจากสายสะดื้อทารก (Kinetics of influenza virus replication and cytokine/chemokine induction in human umbilical vein endothelial cells)”

3. นางสาวจุฑาทิพย์ พนอพัน หัวข้อวิทยานิพนธ์คือ “สารในชีรั่มซึ่งมีฤทธิ์ยับยั้งการติดเชื้อของไวรัสไข้หวัดใหญ่ (Serum inhibitory factors against influenza A virus infection)”

4. นางสาวจริง ชัยรัตน์ หัวข้อวิทยานิพนธ์คือ “ความสามารถของรีคอมบีแนนท์แวกซ์เนี่ยไวรัสที่มียีน H5 HA ของไวรัสไข้หวัดนกในการกระตุ้นระบบภูมิคุ้มกันของหนู (Efficiency of recombinant vaccinia virus containing H5 HA gene influenza in the induction of immune response in mice)”

4.2 นักศึกษาปริญญาเอก

1. นางสาวทัยรัตน์ เลิศสำราญ หัวข้อวิทยานิพนธ์คือ “ระบบวิทยาทางชีรั่มของเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 และความไวของเชื้อไข้หวัดใหญ่ต่อยาที่มีฤทธิ์ยับยั้งนิวราМИนิดีส (Seroepidemiology of pandemic influenza A (H1N1) virus and susceptibility of influenza A viruses to neuraminidase inhibitors)”

2. นายภิรมย์ น้อยสำแดง หัวข้อวิทยานิพนธ์คือ “ภูมิคุ้มกันด้านสารน้ำและด้านเซลล์ชนิดจำเพาะและชนิดข้ามสายพันธุ์ต่อเชื้อไวรัสไข้หวัดนกชนิด เอช 5 เอ็น 1 (Homosubtypic and heterosubtypic humoral and cellular immunity against highly pathogenic avian influenza A (H5N1) virus)”

4.3 นักวิจัย

1. นางสาวพิชณุ ภู่รักษ์ (นักวิจัยหลังปริญญาโท)
2. นางสาวกันทิมา แสงศิรุณ (นักวิจัยหลังปริญญาโท ปฏิบัติงานนอกเวลา)
3. นางสาวณัฐมน เงาสุวรรณกุล (นักวิจัยหลังปริญญาเอก)

ภาคผนวก

Immune response to 2009 H1N1 vaccine in HIV-infected adults in Northern Thailand

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Keywords: 2009 H1N1 vaccine, HIV, adults, seroconversion rate, seroprotection rate

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Abstract:

Background: In late 2009, the Thai Ministry of Public Health provided two million doses of the monovalent pandemic influenza H1N1 2009 vaccine (Panenza® Sanofi Pasteur), which was the only vaccine formulation available in Thailand, to persons at risk of more severe manifestations of the disease including HIV infection. Several studies have shown poorer immune responses to the 2009 H1N1 vaccines in HIV-infected individuals. There are limited data in this population in resource-limited countries.

Results: At day 28 post-vaccination, seroconversion was found in 32.0% (95%CI 24.5 - 40.2) of the HIV-infected group and 35.0% (95%CI 15.4-59.2) of the healthy controls ($p = 0.79$). Seroprotection rate was observed in 33.3% (95%CI 25.8-41.6) and 35.0% (95%CI 15.4-59.2) of the HIV-infected group and the control group, respectively ($p = 0.88$). Among HIV-infected participants, the strongest factor associated with vaccine response was age 42 y or younger ($p = 0.05$).

Methods: We evaluated the immunogenicity of a single, 15 μ g/0.5ml dose of a monovalent, non-adjuvanted 2009 H1N1 vaccine in 150 HIV-infected Thai adults and 20 healthy controls. Immunogenicity was measured by hemagglutination inhibition assay (HI) at baseline and 28 d after vaccination. Seroconversion was defined as 1) pre-vaccination HI titer $< 1:10$ and post-vaccination HI titer $\geq 1:40$, or 2) pre-vaccination HI titer $\geq 1:10$ and a minimum of 4-fold rise in post-vaccination HI titer. Seroprotection was defined as a post-vaccination HI titer of $\geq 1:40$.

Conclusions: A low seroconversion rate to the 2009 H1N1 vaccine in both study groups, corresponding with data from trials in the region, may suggest that the vaccine used in our study is not very immunogenic. Further studies on different vaccines, dosing, adjuvants, or schedule strategies may be needed to achieve effective immunization in HIV-infected population.

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Introduction

Thailand was among the first countries in Southeast Asia hit hardest by the 2009 H1N1 influenza pandemic. From May 2009 to December 2010, approximately 226,000 influenza/influenza-like illnesses (ILI) with 47,000 cases of laboratory-confirmed pandemic 2009H1N1 and 347 deaths were reported to the surveillance center at the Bureau of Epidemiology, Ministry of Public Health, Thailand (MOPH).¹ In late 2009, the MOPH purchased two million doses of the monovalent pandemic influenza H1N1 2009 vaccine (Panenza® Sanofi Pasteur), which was the only vaccine formulation available in Thailand. The MOPH provided the vaccine free of charge to persons at risk of more severe manifestations of the disease (pregnant women, persons with obesity, diabetes, cardiopulmonary dysfunction, hematological malignancy, or HIV infection) as well as healthcare personnel.

Clinical studies have been conducted to evaluate the immunogenicity and safety of different types of 2009 H1N1 vaccines in different populations. Results from five studies showed that a single dose of 2009 H1N1 vaccine induced a robust immune response in most healthy adults.²⁻⁶ However, several studies have shown poorer immune responses to the 2009 H1N1 vaccines in HIV-infected individuals.^{7-14,16,17,19-21} There are limited data in the HIV-infected population in resource-limited countries. We, therefore, evaluated the seroconversion and seroprotection rate to a 2009 H1N1 vaccine (Panenza®) in HIV-infected and healthy individuals in Thailand.

Results

One participant in the HIV-infected group developed flu-like illness one day after vaccination. A throat swab for polymerase chain reaction (PCR) performed one day later was positive for Influenza A H1N1 2009. This participant was excluded from subsequent analysis.

Day 28 post-vaccination follow-up was completed in 147 HIV-infected participants and all 20 healthy controls. Baseline characteristics and vaccine response rate by HIV status are shown in **Table 1**. 39% of HIV-infected participants were male and the mean age was 42.1 ± 6.1 y. 98% were on combination antiretroviral therapy and 91.2% of participants had CD4+ cell count above 200 cell/mm³ at time of vaccination. The mean CD4+ cell count was 466 ± 206 cell/mm³. Among the 20 healthy volunteers, 45% was male and the mean age was 32.4 ± 6.3 y. The mean CD4+ cell count was 762 ± 283 cell/mm³. At baseline, 3.4% (5/147) of HIV-infected participants and 5% (1/20) of controls had HI titers $\geq 1:40$.

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Table 1. Baseline characteristics and vaccine response rates by HIV Status.

	HIV Infected (n = 147)	HIV Negative (n = 20)	P-value
Male gender II (%)	57 (38.8)	9 (45.0)	0.59
Mean age (SD)	42.1(6.1)	32.4(6.3)	< 0.05
Number of participant currently receiving HAART II (%)	144(98.0)	-	-
Absolute CD4 count(cell/mm³)			
200 or less II (%)	13 (8.8)	-	-
More than 200 II (%)	134 (91.2)	20 (100)	-
Mean CD4(SD)	465.52(206.09)	761.9(283.43)	< 0.05
Pre-vaccination HI titer ≥ 1:40 II (%)	5(3.4)	1 (5.0)	0.72
Seroconversion rate ¹ II (%)	47 (32.0)	7 (35.0)	0.79
95% CI	24.5–40.2	15.4–59.2	
Seroprotection rate ² II (%)	49 (33.3)	7 (35.0)	0.88
95% CI	25.8–41.6	15.4–59.2	
Mean follow up days (SD)	26.43(1.48)	23.1(1.21)	

¹Seroconversion was defined as: (1) pre-vaccination HI titer < 1:10 and post-vaccination HI titer ≥ 1:40 or (2) pre-vaccination HI titer ≥ 1:10 and a minimum of 4-fold rise in post vaccination HI titer. ²Seroprotection was defined as a post-vaccination HI titer of ≥ 1:40

Seroconversion was found in 47 of 147 (32.0%, 95%CI 24.53 – 40.16) HIV-infected participants and 7 of 20 (35.0%, 95%CI 15.4–59.2) healthy controls ($p = 0.79$). Seroprotection rate was observed in 33.3% (95%CI 25.78–41.57) and 35.0% (95%CI 15.4–59.2) of the HIV-infected group and the control group, respectively ($p = 0.88$).

Factors associated with vaccine response among HIV-infected participants are shown in **Table 2**. In the univariate analysis, baseline HI titer ≥ 1:40 were significantly associated with seroconversion ($p < 0.05$). Age 42 y or younger and baseline CD4+ cell count above 200 cell/mm³ were borderline significant. However, in multivariate analysis, the only significant variable was age 42 y or younger ($p = 0.05$). Since the number of healthy participants was low, we did not analyze for the factor associated with seroconversion for this group.

Table 2. Univariate and multivariate analysis for factors associated with vaccine response among HIV-infected participants.

Characteristics	Number Seroconversion/total (%)	Odd Ratio (95% CI)	P- value	Adjusted Odd Ratio (95%CI)	P-value
Age in years					
≤ 42	32/83 (38.6)	2.05	0.05	2.10	0.05
> 42	15/64 (23.4)	(0.94–4.58)		(0.99–4.45)	
Gender					
Male	17/57 (29.8)	0.85	0.66	-	-
female	30/90 (33.3)	(0.39–1.84)			
Duration of HIV infection					
≤ 8 y	22/66 (33.3)	1.12	0.75	-	-
> 8 y	25/81 (30.9)	(0.53–2.38)			
Initiated Antiretroviral treatment					
Yes	46/144 (31.9)	0.94	0.96	-	-
No	1/3 (33.3)	(0.05–56.57)			
Baseline HIV RNA PCR (copies/ml)					
< 400	46/142 (32.4)	1.92	0.56	-	-
≥ 400	1/5 (20.0)	(0.18–96.40)			
Baseline CD4 count (cell/mm³)					
> 200	46/134 (34.3)	6.27	0.05	5.86	0.10
≤ 200	1/13 (7.7)	(0.87–273.83)		(0.73–47.05)	
Symptomatic or AIDS indicator conditions at baseline					
Yes	2/11 (18.2)	0.45	0.31	-	-
No	45/136 (33.1)	(0.05–2.31)			
Baseline HI titer					
≥ 1:40	4/5(80)	9.21	0.02	8.61	0.06
< 1:40	43/142(30.3)	(0.86–457.91)		(0.91–81.67)	

Discussion

Our study demonstrated low seroconversion and seroprotection rates in response to the non- adjuvanted 2009 H1N1 vaccine in both HIV-infected and healthy participants. These overall response rates were much lower than the expectation since the majority of HIV-infected participants (91%) had CD4+ cell count > 200 cells/mm³ and all the healthy participants had normal immune status. Multiple studies have shown varying but generally high seroconversion rates (from 74 to 98%) to the 2009 H1N1 vaccine in HIV-negative individuals.²⁻⁶ While studies in HIV-infected individuals found lower seroconversion rates (Table 3), despite an immune recovery indicated by increase in CD4+ cell count and full viral suppression indicated by an undetectable plasma HIV-1 RNA after combination antiretroviral therapy. The diversity of seroconversion rates may depend on different type of vaccines used among studies.⁸ There is a trend that the ASO3 adjuvanted vaccine may elicit better immune response in HIV population than other types of vaccine.¹⁵⁻¹⁸

Table 3. Summary of studies of a single dose H1N1 vaccination

Type of vaccine	No. of HIV-infected / control	Age of HIV-infected vaccinees	CD4 count of HIV-infected vaccinees	Seroprotection rate at baseline HIV/Control	Seroprotection rate post vaccination HIV/Control	Seroconversion rate HIV/Control	Author/ Country/ Reference number
Non-adjuvanted 15 µg							
	79/0	40(37–42) ^a	502(449–556) ^a	70/0	92/0	31/0	Lagler et al. / Austria/7
	182/42	47(13) ^b	411(178) ^b	13/12	50/86	39/86	Yanagisawa et al./ Japan/8
	CD4 < 200: 35/0	46(9) ^b	156(97) ^b	21/0	47/0	41/0	Sahly et al./ USA/9
	CD4 ≥ 200: 60/0	46(10) ^b	610(269) ^b	18/0	64/0	52/0	
	104/0	43(34–53) ^c	373(256–520) ^c	12/0	56/0	50/0	Hatakeyama et al./Japan/10
	256/0	45 (22–75) ^c	Not evaluated	9/0	59/0	55/0	Miraglia et al. /Brazil/11
	120/0	46(40–53) ^c	502(307–640) ^c	25/0	69/0	56/0	Tebas et al./ USA/12
	65/66	38(26–45) ^c	581(476–814) ^c	20/33	65/85	68/83	Crum Cianflone et al./ USA/13
	126/0	44 (37–51) ^c	530(400–685) ^c	39/0	87/0	67/0	Maruszak / Australia/14
	150/0	47(40–54) ^c	551(428–702) ^c	10/0	76/0	71/0	Launay et al./France/15
AS03adjuvanted 3.75 µg							
	155/0	47(39–54) ^c	522(387–752) ^c	8/0	93/0	89/0	Launay et al./France/15
	84/0	48(11) ^b	427(178) ^b	8/0	46/0	44/0	Tremblay et al./Canada/16
	160/0	46(11) ^b	514(246) ^b	14/0	75/0	69/0	Bickel et al./Germany/17
	252/0	47(10) ^b	570(266) ^b	26/0	92/0	83/0	Orlando et al./Italy/18
MF59adjuvanted 7.5 µg							
	44/148	46(no SD) ^b	563(505–621) ^d	80/35	98/97	36/79	Kajaste-Rudnitski et al./ Italy/ 19
	57/44	52(11) ^b	507(349–697) ^c	44/23	88/93	53/73	Soonawala et al./ Netherlands/20
	41/0	46(41–55) ^c	528(406–736) ^c	24/0	78/0	61/0	Fabbiani et al./Italy/ 21

^a Median with 95% CI. ^b Mean with Standard deviation. ^c Median with Interquartile range. ^d Mean with 95% CI. Figures are rounded to the nearest whole number: rounded up for half or greater (≥ 0.5), rounded down for less than half (< 0.5).

It is important to investigate the factors responsible for our seroconversion rate being lowest among studies conducted in HIV-infected individuals. Possible explanations include: (1) the vaccine used in our study (Panenza[®]) is less immunogenic than the 2009 H1N1 vaccine used in other studies, (2) imperfect effectiveness of influenza vaccine in field condition caused by factors such as breakdown of the cold chain and improper vaccine management, and (3) the laboratory method used in our study is less sensitive than that employed in other studies in detecting seroconversion.

Results from previous studies using non-adjuvanted 2009 H1N1 vaccine in HIV-infected individuals also showed varying seroconversion rates ranging from 31% to 71% (Table 3). However, the vaccine types used in those studies were different, for instances, inactivated Vero-cell-derived whole virion vaccine by Lagler et al.⁷ and other non-adjuvanted recombinant vaccines produced by several pharmaceutical companies.⁸⁻¹⁵ Therefore, comparison of differences in immunogenicity among those vaccine including that used in our study may not be possible. Nonetheless, a high seroconversion rate in HIV/uninfected group indicated that the immunogenicity of the vaccines employed in those studies were adequate. Conversely, our study failed to demonstrate a desire vaccine efficacy in HIV-negative volunteers. This may support our hypothesis about the immunogenicity of Panenza[®] vaccine.

A literature review was done on the efficacy trials of the Panenza[®]. In the report authored by researchers affiliated with Sanofi Pasteur, two studies were conducted with single standard dose of Panenza[®] in 101 and 100 French healthy volunteers between August 2009 and October 2009 and between March 2010 and April 2010 respectively.²⁵ The seroconversion rate in the first study was 92% and that in the second study was 97%. However, the immunologic response to Panenza[®] was found to be less than that reported in French studies, involving healthy adults in Thailand and Hong Kong. First is a prospective cohort study of a single dose of Panenza[®] in hemodialysis patients and 149 healthy controls by Lerduamrongluk et al.²⁶; the seroconversion rate was 63.1% and protective titers were obtained in 67.1% of the control group at 4 weeks post vaccination. A cross-sectional study conducted in Khon Kaen, Thailand in June 2010, 52.1% of 71 healthcare workers aged 21–75 y who had been vaccinated with Panenza[®] vaccine had HI titers ≥ 40 .²⁷ A similar study conducted in 104 Hong Kong healthcare workers aged 19–64 y receiving Panenza[®] also showed seroprotection rate of 53.8% (95% CI 44.2%–63.2%).²⁸ One of the possible explanations for lower antibody response considered by the authors was imperfect effectiveness of Panenza[®].

The only study of Panenza[®] in HIV-infected individuals in Thailand was done at Siriraj Hospital in Bangkok and Chiang Mai University Hospital in Chiang Mai, Thailand.²⁹ 119 children with a median age of 10.4 y (IQR 7.2–13.7) were given 2 doses of Panenza[®] 28 d apart. The seroconversion rates were 54.2% and 67.8% after the first and second doses, respectively. Our study is the first report of this particular vaccine in HIV-infected adults.

To answer the question of improper vaccine management, the vaccines used in our study were delivered from the Department of Disease Control, MOPH to our institute on January 14, 2010. Vaccine expiration date was September 30, 2010. Vaccinations were started from January 21, 2010 to March 2010. To ensure vaccine quality, all vaccines were stored and delivered under temperature controlled conditions in accordance with the Pharmacy guidelines and Instructions for DAIDS Clinical Trials Networks Division of AIDS pharmaceutical Affairs Branch, July 2008 and the vaccine package insert. Each vaccine vial was only used within a day of first opening. After reviewing the vaccine management records, we did not find any errors that could explain the result of this study. It was also unlikely that cold chain breakdown and improper vaccine management had occurred concurrently in Hong Kong, Khon Kaen, Bangkok and Chiang Mai.

Lastly, considerable variability can be introduced into the laboratory assay used to measure HI antibodies including differences in viral strains and red blood cell types, and the presence of non-specific inhibitors in the assay medium.²⁴ In our study, the HI test was performed according to standard method,³⁰ the only exception is the use of goose erythrocyte instead of turkey erythrocyte. However, a study by Lerdsamran et al.²³ has demonstrated that goose and turkey erythrocytes yielded comparable HI antibody titers. A study by Miraglia JL et al.¹¹ also used the standard HI assay and demonstrated the low seroconversion rate (55%) to Sanofi-Pasteur non-adjuvanted H1N1 vaccine in HIV-infected individuals. Therefore, the method used may not be a potential factor to the low response rate. The fact that the strain used in HI assay in our study, is not identical to the strain included in the vaccine could be a reason for a lower immunogenicity. The A/Thailand/104/2009(H1N1) strain which was also used to evaluate the vaccine response in the other two Thai studies was isolated from a confirmed case of pandemic H1N1 2009 who had recently traveled back from Mexico. The strain was submitted to the GenBank database on June 13, 2009 where full genomic sequence of A/Thailand/104/2009(H1N1) can be retrieved. Its HA gene is 99.7% identical to that of A/California/7/2009 pandemic virus.²³ The author's unpublished data (PP and HL) have shown that the antibody titers against these two viruses were comparable as assayed in 100 individuals without immune deficiency (patients and non-patients). Therefore, the strain used in the HI assay would probably not have a significant influence on the vaccine response rate. To avoid the intra-laboratory variability of the test, we selected the HI assay instead of the viral neutralization assay that may have higher variability in results.³¹ In addition, we performed the tests for all sera in a batch process using the same reagents and by the same lab personnel.

In conclusion, the unexpected low immune response to the single dose of non-adjuvanted 2009 H1N1 vaccine in our study together with similar results in the three other studies²⁶⁻²⁸ suggest that the vaccine formulation Panenza[®] bought by the Hong Kong and Thai government in late 2009 may be the cause of this suboptimal response. Alternatively, there might be problems with cold chain, vaccine management, or the sensitivity of laboratory method. However, these are unlikely to happen in Hong Kong, Bangkok, Chiang Mai, and Khon Kaen concurrently. Further reports from countries that employed Panenza[®] and/or investigation by Sanofi Pasteur of the lot of Panenza[®] marketed in late 2009 are needed. Further studies on different vaccines, dosing, adjuvants, or schedule strategies may be needed to achieve effective immunization in HIV-infected population.

Limitations

Limitations of our study were a small number of HIV-negative controls which may have insufficient power to determine vaccine response in this population and lack of different type of vaccine to compare with Panenza[®] vaccine.

Methods

Participants

Our study was conducted after the first wave of pandemic influenza H1N1 2009 outbreak in Thailand. Between January 2010 and March 2010, we invited and enrolled, on a first-come-first-served basis, a total of 150 HIV-infected individuals aged 18–60 y from the Infectious Disease Clinic, Chiang Mai University Hospital, a 1500-beds tertiary care facility in Chiang Mai, Thailand, where a treatment-cohort of approximately 1,300 HIV-infected patients was under active follow-up. Exclusion criteria were an allergy to eggs or a history of Guillain-Barré Syndrome or family history of Guillain-Barré Syndrome. A total of 20 healthy volunteers were enrolled under the same protocol.

Clinical and laboratory Procedures

The vaccine, Panenza[®], is a monovalent, non-adjuvanted vaccine formulated to contain 15 µg/0.5 mL of hemagglutinin (HA) of influenza A/California/07/2009 (H1N1) v-like virus produced by Sanofi Pasteur. A single 0.5 mL intramuscular dose of the vaccine was administered to all 170 participants. Clinical assessment was performed in HIV-infected individuals prior to vaccination for classification of CDC clinical category.²² Baseline laboratory evaluation included CD4+ cell count and hemagglutination inhibition (HI) antibody titer against 2009 H1N1 virus for both groups and plasma HIV-1 RNA measurement for HIV-infected group. The CD4+ cell count was performed using flow cytometry techniques and plasma HIV-1 RNA was measured by the COBAS Amplicor[™] Analyzer, ROCHE Diagnostic System at the Research Institute for Health Sciences, Chiang Mai University.

The HI assay was performed at the Department of Microbiology, Faculty of Medicine Siriraj Hospital, Mahidol University. The methodology was described previously.²³ Briefly, 50 µL of the test serum were mixed with 150 µL of receptor destroying enzyme (RDE, Denka Seiken) and incubated overnight in water bath at 37°C. This step was followed by heat inactivation at 56°C for 30 min, and removal of nonspecific agglutinator by absorbing with goose erythrocytes for 1 h at 4°C. The replicating virus, A/Thailand/104/2009, at final concentration of 4 HA units/25 µL was used as the test antigen; and goose erythrocytes were used as the indicator. The treated serum was 2-fold serially diluted in duplicate wells of a microtiter V-shaped plate at an initial dilution of 1:10; and 25 µL of the diluted serum were incubated with 25 µL of the test antigen for 30 min at room temperature. Thereafter, the reaction wells were added with 50 µL of 0.5% goose erythrocyte suspension and further incubated for 30 min at 4°C before the HI antibody titers were determined. HI antibody titer is defined as the reciprocal of the highest serum dilution that completely inhibits hemagglutination reaction. Reference/positive control serum with known HI titer, the serum control and back titration of virus antigen were included in each run. The reference human serum was obtained from the National Institute for Biological Standards and Control (NIBSC). The full genomic sequence of the virus, A/Thailand/104/2009, has been deposited with GenBank. Its HA gene is 99.7% identical to that of A/California/7/2009 pandemic virus.²³ This virus was the first strain isolated in Thailand in May 2009 from a case who traveled back from Mexico (PP, personal communication).

Evaluations and endpoints

Any participant who developed influenza-like illness was asked to come to the clinic within 72 h for respiratory specimen collection to confirm the diagnosis of 2009 H1N1 infection. The immunogenicity endpoint was the proportion of participants who had seroconversion and seroprotection from vaccination. Seroconversion was defined in accordance with the US FDA guidance²⁴ as 1) pre-vaccination HI titer < 1:10 and post-vaccination HI titer ≥ 1:40, or 2) pre-vaccination HI titer ≥ 1:10 and a minimum of 4-fold rise in post-vaccination HI titer. Seroprotection was defined as a post-vaccination HI titer of ≥ 1:40.

Ethics

The study protocol was approved by the Research Ethics Committee, Faculty of Medicine, Chiang Mai University.

Statistical methods

For baseline characteristics, continuous variables such as age and absolute CD4+ cell count are presented as mean ± standard deviation. Seroconversion rate and seroprotection rate with the corresponding 95% confidence interval (CI) were calculated. Univariate analyses and multivariate analysis by logistic regression were used to determine factors associated with seroconversion in HIV-infected group. Results were reported by presenting odds ratios and adjusted odds ratios with 95% confidence interval. Level of significance was defined as a p-value of < 0.05.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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A Novel Pathogenic Mechanism of Highly Pathogenic Avian Influenza H5N1 Viruses Involves Hemagglutinin Mediated Resistance to Serum Innate Inhibitors

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Abstract

In this study, the effect of innate serum inhibitors on influenza virus infection was addressed. Seasonal influenza A(H1N1) and A(H3N2), 2009 pandemic A(H1N1) (H1N1pdm) and highly pathogenic avian influenza (HPAI) A(H5N1) viruses were tested with guinea pig sera negative for antibodies against all of these viruses as evaluated by hemagglutination-inhibition and microneutralization assays. In the presence of serum inhibitors, the infection by each virus was inhibited differently as measured by the amount of viral nucleoprotein produced in Madin-Darby canine kidney cells. The serum inhibitors inhibited seasonal influenza A(H3N2) virus the most, while the effect was less in seasonal influenza A(H1N1) and H1N1pdm viruses. The suppression by serum inhibitors could be reduced by heat inactivation or treatment with receptor destroying enzyme. In contrast, all H5N1 strains tested were resistant to serum inhibitors. To determine which structure (hemagglutinin (HA) and/or neuraminidase (NA)) on the virus particles that provided the resistance, reverse genetics (rg) was applied to construct chimeric recombinant viruses from A/Puerto Rico/8/1934(H1N1) (PR8) plasmid vectors. rgPR8-H5 HA and rgPR8-H5 HANA were resistant to serum inhibitors while rgPR8-H5 NA and PR8 A(H1N1) parental viruses were sensitive, suggesting that HA of HPAI H5N1 viruses bestowed viral resistance to serum inhibition. These results suggested that the ability to resist serum inhibition might enable the viremic H5N1 viruses to disseminate to distal end organs. The present study also analyzed for correlation between susceptibility to serum inhibitors and number of glycosylation sites present on the globular heads of HA and NA. H3N2 viruses, the subtype with highest susceptibility to serum inhibitors, harbored the highest number of glycosylation sites on the HA globular head. However, this positive correlation cannot be drawn for the other influenza subtypes.

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Introduction

Human and H5N1 avian influenza viruses are different in terms of pathogenesis and severity of the disease. While the infections by influenza A(H1N1), A(H3N2) and influenza B viruses are confined mostly to the upper respiratory tract, the infection caused by highly pathogenic avian influenza (HPAI) H5N1 viruses frequently invades lower respiratory tract, induces cytokine storm, and causes severe pneumonia which progresses to acute respiratory distress syndrome and multi-organ failure [1,2]. Dissemination of H5N1 virus beyond the respiratory tract is well documented. The viral RNA could be detected in the autopsies of several organs [3], cerebrospinal fluid [4], and fetal tissues [5]. In addition, HPAI H5N1 virus could be isolated from a plasma sample of a Thai patient [6]. This information indicates that the propensity to

undergo viremic phase is not uncommon for HPAI H5N1 virus infection. On the other hand, there has been just one recent report on viremia in patients infected with the 2009 pandemic A(H1N1) (H1N1pdm) virus [7]. Moreover, viremia associated with seasonal influenza H1N1 and H3N2 viruses is very rare [8–10]. These findings indicate that various influenza subtypes are different in the capability to exhibit viremic phase.

Sera and respiratory fluids of mammals contain several innate soluble factors that exhibit anti-influenza activity, for examples, members of the collectin superfamily such as surfactant protein A (SP-A), surfactant protein D (SP-D), conglutinin and mannose-binding lectin (MBL) [11–13], member of the pentraxin superfamily such as pentraxin 3 (PTX3) [14], and serum amyloid P component [15]. The binding of human SP-D and MBL to both hemagglutinin (HA) and neuraminidase (NA) can inhibit influenza

virus hemagglutinating activity, interfere with virus release through inhibition of viral neuraminidase activity, and hinder viral infection by preventing viral attachment to the cell receptor. The anti-influenza activities of human SP-D and MBL do not involve other complement factors [16]. Interestingly, the highly glycosylated seasonal H1N1 strains are sensitive to inhibition by both SP-D and MBL, while the poorly glycosylated A/Puerto Rico/8/1934(H1N1) (PR8) and H1N1pdm are resistant to either one of them [17]. The long chain pentraxin, PTX3 inhibits several strains of seasonal influenza A(H1N1), A(H3N2) and influenza B viruses [14], though the susceptibility to PTX3 may be strain-specific as some seasonal human influenza isolates including PR8 virus and the H1N1pdm viruses are resistant to PTX3 [17]. Complement, the major component of innate immunity, may play anti-influenza activity independently or in adjunct with other components. Activation of the complement system results in virus aggregation, virolysis or opsonization [18]. It can lead to increased vascular permeability and recruitment of phagocytic cells to destroy the pathogens. MBL, together with complement in guinea pig serum, exerted lytic activity on influenza virus infected-BHK-21 cells through the classical pathway [19]. MBL also binds influenza HA and activates complement through lectin pathway [20]. Moreover, complement together with natural IgM antibody can destroy virus through the classical pathway [21].

In the other system, non-specific inhibitors against influenza viruses present in normal sera of various animal species were classified into three types: α -, β -, and γ -inhibitors based on their chemical composition and several biological properties [22,23]. α -inhibitors are heat-stable, but receptor destroying enzyme (RDE)-sensitive glycoproteins. It inhibited influenza virus hemagglutination, but not influenza virus infectivity. The examples of α -inhibitors found in serum are soluble mucoproteins. β -inhibitors are non-sialylated, Ca^{2+} dependent and heat-labile but RDE-resistant. Study in bovine and mouse serum suggested that MBL and SP-D belonged to β -inhibitors [24]; and MBL was serologically cross reactive with human mannose-binding protein (MBP) [20]. γ -inhibitors are heat-stable and RDE-sensitive sialylated glycoproteins which compete with cellular receptor for binding with HA; these inhibitors neutralize viral infectivity by blocking the attachment step in the influenza virus replication cycle [23,25]. In horse, guinea pig and mouse sera, γ -inhibitor had been identified as α 2-macroglobulin [25,26]. In addition, the study in murine model also demonstrated that the α 2-macroglobulin could inhibit hemagglutination inhibition (HI) assay, but its activity on microneutralization (microNT) assay against various viruses expressing H3N2 HA was varied among H3N2 isolates [26].

For the influenza viruses to exhibit viremic phase, they should be able to overcome the inhibition by innate serum inhibitors. Therefore, the ability of HPAI H5N1 viruses to spread beyond the respiratory tract is suggestive of their ability to resist the serum inhibitors. Herein, guinea pig sera were used as the model to study serum innate immunity against various influenza viruses of human and avian origins, including seasonal H1N1, H3N2, H1N1pdm, and HPAI H5N1 viruses. The nature of inhibitors was characterized by their sensitivity to heat or RDE treatment. We demonstrated that HPAI H5N1 virus was the only subtype that could resist the inactivation by serum innate inhibitors. Using reverse genetics, the viral resistance to serum inhibitors could be mapped to HA. Our finding suggested a novel pathogenic mechanism on H5N1 virus dissemination beyond the respiratory system.

Results

Biological properties of the guinea pig sera

In order to determine role of serum inhibitors against influenza viruses, it is necessary to screen that the test guinea pig sera contained no specific antibodies against the study viruses. Otherwise, it would be difficult to differentiate between inhibitory effects mediated by the serum specific inhibitors and specific antibodies. Sera of three guinea pigs from different batches of animals were screened for specific antibody against all 14 influenza virus isolates and 4 reassorted viruses by HI and microNT assays. The result showed that none of the test sera contained pre-existing HI or NT antibody as screened at the initial serum dilution 1:10 (data not shown).

It has been known that some serum innate inhibitors are heat-labile and some are heat-stable. There is no control measure to determine stability of those unknown heat-labile components in the stored sera during the on going experiments. Therefore, our study used complement as the representative of heat-labile components based on its abundant amount in guinea pig sera and availability of the measurement method. We assumed that if complement in the test sera did not deteriorate, the other heat-labile components should remain in good condition. Each guinea pig serum was measured for complement titer by complement fixation test using hemolysin sensitized-sheep red blood cells (SRBCs) as the indicator system. We also showed that the three guinea pigs used in our experiments contained comparable serum concentrations of complement, i.e., 32–64 complement hemolytic units; in another word, the serum dilution of 1:32 or 1:64 contained one complement hemolytic unit. The native sera and heat-inactivated sera were assayed in parallel for their lytic activity on hemolysin sensitized-SRBCs. The result demonstrated that the native sera completely lysed the sensitized-SRBCs, while the lytic activity was eradicated after heat inactivation.

Furthermore, the sera were diluted to contain the complement concentrations of 0.25, 0.5, 1, 2, 4 and 8 hemolytic units and assayed against the seasonal A(H1N1) (SI-RA-TT/04), seasonal A(H3N2) (SI 03/04), H1N1pdm (Nonth/102/09) and HPAI H5N1 (KAN-1) viruses in order to determine the optimal dilutions that could exert anti-influenza activity. The result showed a slight increase in the percentages of viral inhibition when serum complement concentrations were greater than two hemolytic units (Figure 1). Therefore, the concentration of 2 complement hemolytic units was employed in subsequent experiments.

Determination for activity of serum innate inhibitors against various influenza subtypes

Guinea pig sera were used as source of innate inhibitors in the assay for infection inhibition against influenza viruses. The study viruses at concentration of 1,000 TCID50/50 μ l (TCID50; 50% tissue culture infectious dose) were incubated with native guinea pig serum at working dilution which contained complement concentration of 2 hemolytic units. The virus-serum mixture in quadruplicate was inoculated onto Madin-Darby canine kidney (MDCK) cell monolayers for overnight. Infectivity of the viruses which were susceptible to serum innate inhibitors should be inhibited and resulted in the decreased amount of viral nucleoprotein produced in the infected MDCK cells as determined by enzyme-linked immunosorbent assay (ELISA). Based on the percentages of viral infection inhibition as compared to the virus control, H3N2 viruses were the subtype most susceptible to serum inhibitors (81–100% inhibition); and followed in order by H1N1pdm (34–89% inhibition) and seasonal H1N1 viruses (21–62% inhibition) (Table 1 and Figure 2). In contrast, all HPAI

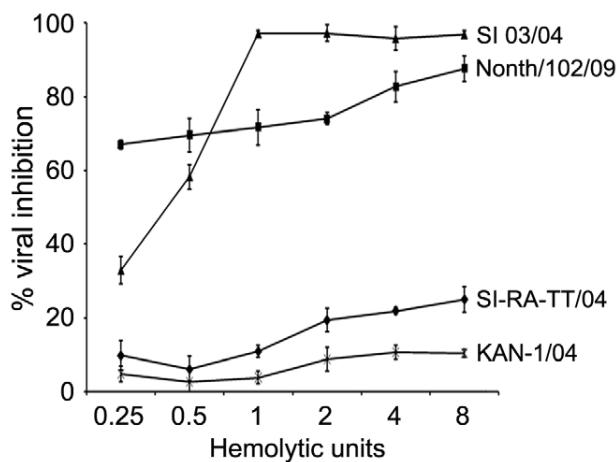


Figure 1. Anti-influenza activities of guinea pig sera at various complement hemolytic units. Native guinea pig sera at various complement hemolytic units were incubated with seasonal H1N1 (SI-RA-TT/04), H3N2 (SI 03/04), H1N1pdm (Nonth/102/09) or HPAI H5N1 (KAN-1/04) virus followed by inoculation the serum-virus mixture onto MDCK cell monolayers. After an overnight incubation, the viral inhibitory activity of the test serum was measured by determining the amount of viral nucleoprotein produced in the inoculated MDCK cells by ELISA. The results are shown as mean of the percentages of viral inhibition derived from quadruplicate experiments. Error bars represent the standard deviation.

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H5N1 viruses were resistant to serum inhibitors with the percentages of inhibition of less than 10, except one serum which exerted 19% inhibition against KAN-1, and 12% inhibition against NBL (feces in origin) viruses (Table 1).

Biochemical nature of serum innate inhibitors and the viral susceptibility

Heat-inactivated serum or RDE-treated+heat-inactivated serum was assayed for their viral inhibitory effect against various influenza subtypes/strains in comparison with the native serum control. Statistically significant difference in the percentage of inhibition was considered at $p \leq 0.05$. Each serum was assayed in quadruplicate and the percentages of viral inhibition of all 3 guinea pig sera were averaged. The viral inhibition effects exerted by native sera, heat-inactivated sera and RDE-treated+heat-inactivated sera are shown as the histograms in Figure 2.

Among H1N1 viruses (Figure 2A), PR8 virus was the most susceptible to serum inhibitors (62% viral inhibition) and followed in order by SI 3043/09 and SI-RA-TT/04. Nevertheless, the inhibitory activity against PR8 decreased to almost 4% when the viruses were treated with either heat-inactivated sera or RDE-treated+heat-inactivated sera. Thus, the PR8 virus was susceptible to heat-sensitive inhibitors only, as the addition of RDE (in the RDE-treated+heat-inactivated sera) did not further decrease the percentages of viral inhibitory activity. Similarly, SI 3043/09 was also inhibited by native serum; and percentages of viral inhibition decreased from 31% to 15% with heat-inactivated sera, and to 12% with RDE-treated+heat-inactivated sera. As the decrease in the percentages of inhibition from 15 to 12% was not statistically significant, it is interpreted that SI 3043/09 was susceptible to heat-labile inhibitors, but susceptibility to RDE-sensitive inhibi-

Table 1. Presence of inhibitory factors against influenza viruses in guinea pig sera.

Subtype	Virus name	Abbreviations	% inhibition of viral infection mediated by guinea pig sera		
			No. 1	No. 2	No. 3
Seasonal H1N1	A/PR/8/34 (reassorted virus)	PR8	47.7	56.9	62.1
	A/Thailand/Siriraj-Rama-TT/04 (A/New Caledonia/20/ SI-RA-TT/04 99-like virus)	SI-RA-TT/04	21.9	23.3	21.0
	A/Thailand/Siriraj3043/09 (A/Brisbane/59/07-like virus)	SI 3043/09	37.9	31.8	30.7
Seasonal H3N2	A/Thailand/Siriraj-08/98 (A/Sydney/05/97-like virus)	SI 08/98	82.6	82.2	80.9
	A/Thailand/Siriraj-06/02 (A/Moscow/10/99-like virus)	SI 06/02	88.7	87.0	100
	A/Thailand/Siriraj-02/03 (A/Fujian/411/02-like virus)	SI 02/03	99.5	97.1	96.2
	A/Thailand/Siriraj-03/04 (A/Fujian/411/02-like virus)	SI 03/04	94.9	97.2	96.9
H1N1pdm	A/Thailand/104/09	Thai/104/09	51.6	65.0	34.2
	A/Nonthaburi/102/09	Nonth/102/09	81.2	80.8	83.7
	A/California/07/09	CA/07/09	86.7	85.3	88.7
HPAI H5N1	A/Thailand/1(KAN-1)/04	KAN-1	8.9	18.6	5.5
	A/Thailand/676(NYK)/05	676(NYK)	0	2.9	6.0
	A/Thailand/NBL-1/06 (feces)	NBL feces	6.8	12.0	9.8
	A/Thailand/NBL-1/06 (lung)	NBL lung	7.3	6.5	5.2
	A/Laos/Nong Khai 1/07	Nong Khai 1	3.4	7.6	0.8
H5 reverse genetics	rgPR8-H5 HANA (KAN-1)	rgPR8-H5 HANA	1.9	7.1	6.4
	rgPR8-H5 HA (KAN-1)	rgPR8-H5 HA	0	4.6	1.6
	rgPR8-H5 NA (KAN-1)	rgPR8-H5 NA	80.0	41.6	84.9

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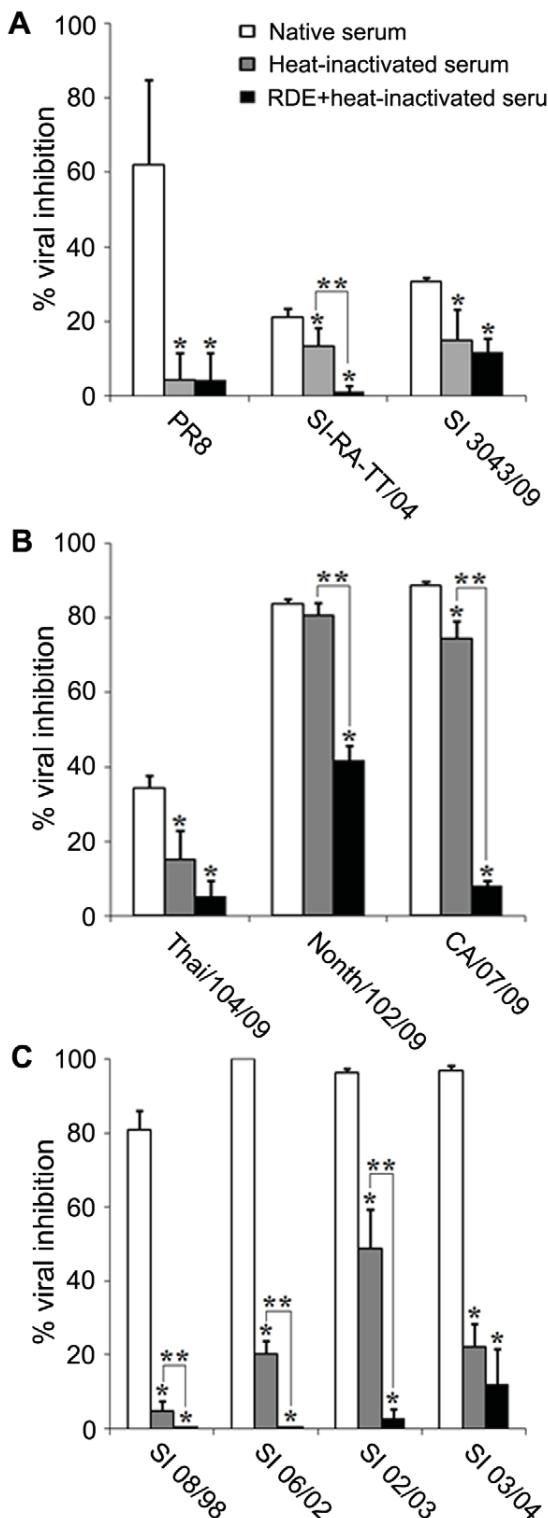


Figure 2. Inhibitory activities of native guinea pig serum, heat-inactivated serum, and RDE-treated+heat-inactivated serum against influenza viruses. Guinea pig sera were incubated with (A) H1N1 viruses, (B) H1N1pdm viruses, or (C) H3N2 viruses. The viral inhibitory activities of the test sera were determined in MDCK cells inoculated with the serum-virus mixtures by ELISA. The results are shown as mean of the percentages of viral inhibition derived from quadruplicate experiments. Error bars represent the standard deviation.

* There are statistically significant differences between the inhibitory activity of the native serum and the heat-inactivated serum or the native serum and the RDE-treated+heat-inactivated serum ($p \leq 0.05$).
 ** There are statistically significant differences in the inhibitory activity between heat-inactivated serum and RDE-treated+heat-inactivated serum ($p \leq 0.05$).
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tors, if any, should be very minute. On the other hand, SI-RA-TT/04 was susceptible to both heat-sensitive inhibitors and RDE-sensitive inhibitors as the percentages of viral inhibition dropped from 21% to 13% or 1% after treatment with heat-inactivated sera or RDE-treated+inactivated sera, respectively.

Among H1N1pdm (Figure 2B), percentages of inhibition of Thai/104/09 virus as assayed against native sera, heat-inactivated sera and RDE-treated+heat-inactivated sera were 34, 15 and 5%, respectively. This result showed that Thai/104/09 virus was susceptible to heat-labile serum inhibitors; however, its susceptibility to RDE-sensitive inhibitors could not be drawn statistically. On the other hand, percentages of inhibition of Nonth/102/09 virus as assayed with native sera, heat-inactivated sera and RDE-treated+heat-inactivated sera were 84, 81 and 42%, respectively. The data suggested that Nonth/102/09 virus was partially susceptible to RDE-sensitive inhibitors. The percentages of viral inhibition of CA/07/09 virus as assayed with native sera, heat-inactivated sera and RDE-treated+heat-inactivated were 89, 74, and 8%, respectively. The result suggested that CA/07/09 virus was slightly susceptible to heat-labile inhibitors, but highly susceptible to RDE-sensitive inhibitors.

Interestingly, all H3N2 viruses were highly susceptible to native serum with percentages of viral inhibition greater than 80% (Figure 2C). SI 08/98, SI 06/02 and SI 02/03 were susceptible to both heat-labile inhibitors and RDE-sensitive inhibitors. Such that the percentages of viral inhibition dropped from 81 to 5% for SI 08/98, from 100 to 20% for SI 06/02, and from 96 to 49% for SI 02/03, as the results obtained from the assays with native sera were compared with those employed heat-inactivated sera; and also, the percentages of viral inhibition dropped from 5 to 0% for SI 08/98, from 20 to 0% for SI 06/02, and from 49 to 3% for SI 02/03, as the results obtained from the assay with heat-inactivated sera were compared with those employed RDE-treated+heat-inactivated sera. The statistical analyses were significantly different for those comparisons. On the other hand, SI 03/04 was susceptible to heat-labile inhibitors alone as shown by the significant decrease in the percentages of viral inhibition from 97 to 22% as the assays with native sera were compared with those employed heat-inactivated sera. In contrast, the percentages of viral inhibition which decreased from 22% (as assayed with heat-inactivated sera) to 12% (as assayed with RDE-treated+heat-inactivated sera) was not significantly different.

Owing to low susceptibility of the HPAI H5N1 viruses to native guinea pig sera (the mean percentage of viral inhibition of 11, 3, 10, 6, and 4 for KAN-1, 676(NYK), NBL feces, NBL lung, and Nong Khai 1, respectively), the assays employing heat-inactivated serum as well as RDE-treated+heat-inactivated serum were not performed.

Role of HA on viral resistance to serum innate inhibitors

Owing to the difference in susceptibility to serum innate inhibitors among various influenza subtypes, it is speculated that HA and/or NA play a key role in this difference. To elucidate this speculation, reassorted PR8 virus together with three reverse genetic viruses harboring *HA* and/or *NA* genes from HPAI H5N1 (KAN-1) viruses in PR8 backbone, i.e., rgPR8-H5 HANA (6+2

virus), rgPR8-H5 HA (7+1 virus), and rgPR8-H5 NA (7+1 virus) were tested against guinea pig sera. The result showed that reassorted PR8 parental virus and rgPR8-H5 NA could be inhibited by serum innate inhibitors with 48–62% and 42–85% viral inhibition, respectively (Table 1). In contrast, rgPR8-H5 HA and rgPR8-H5 HANA could resist the serum inhibitors with percentages of viral inhibition of only 0–5% for rgPR8-H5 HA and 2–7% for rgPR8-H5 HANA, similarly to the H5N1 wild type viruses. When the viral inhibitory activity of native serum, heat-inactivated serum and RDE-treated+heat-inactivated serum were compared, the result showed that efficiency to inhibit reassorted PR8 parental virus and rgPR8-H5 NA viruses were almost completely lost simply by heat inactivation alone; and thus, the inhibitory effect from RDE could not be seen (Figure 3). No significant change in percentages of viral inhibition was observed with rgPR8-H5 HA and rgPR8-H5 HANA viruses when reacted with either heat-inactivated serum or RDE-treated+heat-inactivated serum. The results were reproducible with all three guinea pig serum samples tested (Table 1). In conclusion, it was the HA not NA that rendered HPAI H5N1 viruses the resistance to serum inhibitors.

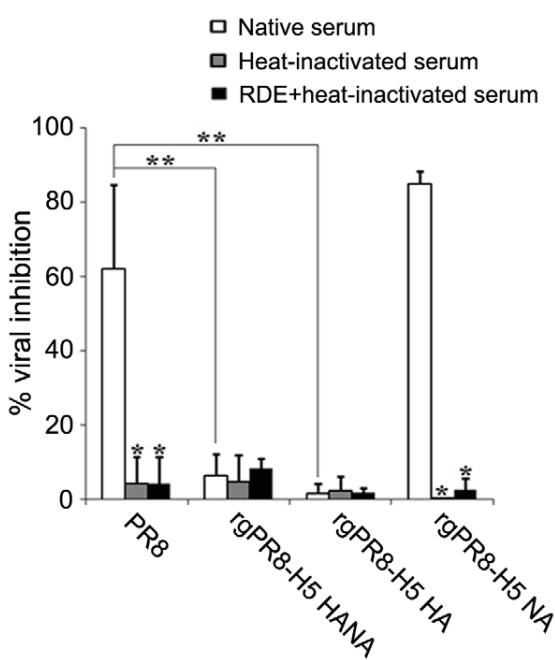


Figure 3. Inhibitory activities of native guinea-pig serum, heat-inactivated serum, and RDE-treated+heat-inactivated serum against reverse genetic viruses. Guinea pig sera were incubated with rgPR8 viruses that contain HPAI H5N1 HANA, HA alone or NA alone. The viral inhibitory activities of the test sera were determined in MDCK cells inoculated with the serum-virus mixtures by ELISA. The results are shown as mean of the percentages of viral inhibition derived from quadruplicate experiments. Error bars represent the standard deviation. * There are statistically significant differences between the inhibitory activity of the native serum and the heat-inactivated serum or the native serum and the RDE-treated+heat-inactivated serum ($p \leq 0.05$). ** There are statistically significant differences in the serum inhibitory activity as compared between the reassorted PR8 virus and the rgPR8-H5 HA virus or the reassorted PR8 virus and the rgPR8-H5 HANA ($p \leq 0.05$).

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Prediction of the potential N-linked glycosylation sites on HA and NA globular domains

Our previous experiments demonstrated that HA determined the viral susceptibility or resistance to serum innate inhibitors. Additionally, previous groups of investigators reported that an increase in glycosylation site in HA protein resulted in the increased susceptibility to innate inhibitory factors such as SP-D and collectins [27,28]. Therefore, our study viruses were predicted for their potential sites of glycosylation in HA and NA molecules by CountGS application in BioEdit program version 7.0.4.1 [29]. HA and NA sequences of the study viruses are retrieved from the GenBank database using the accession numbers as shown in Table 2. The potential N-linked glycosylation motif was defined as Asn-X-Ser/Thr, where X may represent any amino acids except proline. The present study determined number of glycosylation sites in the HA globular head of the study viruses, defining that the globular head is situated between the loop region flanked with a conserved disulfide bond in the cysteine bridge in HA1 domain [30]. With methionine as the start position, the globular heads are situated between amino acid position 59 to 291 (reassorted PR8 and seasonal H1N1 viruses), 59 to 292 (H1N1pdm viruses), 68 to 293 (seasonal H3N2 viruses), and 58 to 290 (HPAI H5N1 viruses).

The results showed that H3N2 viruses, the most susceptible subtype to serum inhibitors, contained highest number of glycosylation sites in HA. On the other hand, reassorted PR8 and H1N1pdm viruses which were moderately susceptible to serum innate inhibitors contained one glycosylation site on the HA globular head, while the resistant H5N1 viruses harbored 2 glycosylation sites (Table 2). A homology-based structural model of the HA molecules of seasonal H1N1 (SI-RA-TT/04), H1N1pdm (Thai/104/09), seasonal H3N2 (SI 03/04) and HPAI H5N1 (KAN-1) viruses were constructed using HA crystal structures of PR8, A/California/04/09, A/X-31 (H3N2) or A/HK/212/03 (H5N1) (PDB codes: 1RU7, 3LZG, 1HGF and 3FKU, respectively) as the template. All three-dimensional models are generated by Chimera program version 1.5.3 [31] as shown in Figure 4. Amino acid positions that are the potential *N*-linked glycosylation sites on globular head of HA were predicted for reassorted PR8 (Asn285), seasonal H1N1 (Asn71, Asn104, Asn142 and Asn176), H1N1pdm (Asn104), seasonal H3N2 (Asn79, Asn138, Asn142, Asn149, Asn160, Asn181 and Asn262, but Asn160 was not found in SI 08/98 (H3N2)), and H5N1 (Asn170 and Asn181).

Number of glycosylation sites on NA of the study viruses is shown in Table 2. Based on NA crystal structures of A/Brevig Mission/1/18 (H1N1) and A/Memphis/31/98 (H3N2) (PDB codes: 3BEQ and 2AEP, respectively) with methionine as the start position, the globular head domain of N1 NA starts at position 83 to 468 (N1 numbering) and that of N2 NA starts at position 82 to 469 (N2 numbering). Amino acid positions that are the potential *N*-linked glycosylation sites on globular head of NA were predicted for reassorted PR8 (Asn88 and Asn235), seasonal H1N1 (Asn88, Asn146, Asn235, Asn434 and Asn455), H1N1pdm (Asn88, Asn146, Asn235 and Asn385), seasonal H3N2 (Asn86, Asn146, Asn200, Asn234, Asn392 and Asn402, but additional site, Asn93, was found in SI 06/02), and H5N1 viruses (Asn126, Asn215, but additional site, Asn321, was found in 676(NYK), and Asn366 was found in Nong Khai 1 virus).

Discussion

Most of human sera contain pre-existing anti-influenza antibodies as the results of vaccinations or past infections with some influenza subtypes. Therefore, guinea pig sera instead of human sera were used as the model to study innate immunity

Table 2. Potential glycosylation sites on HA and NA proteins of the study viruses.

Virus name	Accession number		Number of glycosylation sites on			
	HA	NA	HA	Globular head of HA	NA	Globular head of NA
A/PR/8/34 (reassorted virus H1N1)	EF467821	EF467823	7	1	4	2
A/Thailand/Siriraj-Rama-TT/04 (H1N1)	JN676132	JN676133	10	4	9	5
A/Thailand/Siriraj3043/09 (H1N1)	JN676130	JN676131	10	4	9	5
A/Thailand/104/09 (H1N1)	GQ169382	GQ169381	8	1	8	4
A/Nonthaburi/102/09 (H1N1)	GQ150342	GQ150343	8	1	8	4
A/California/07/09 (H1N1)	FJ969540	HM138502	8	1	8	4
A/Thailand/Siriraj-08/98 (H3N2)	JN617980	JN617985	11	6	8	6
A/Thailand/Siriraj-06/02 (H3N2)	JN617982	JN617984	12	7	9	7
A/Thailand/Siriraj-02/03 (H3N2)	JN617979	JN617983	12	7	8	6
A/Thailand/Siriraj-03/04 (H3N2)	JN617981	JN617986	12	7	8	6
A/Thailand/1(KAN-1)/04 (H5N1)	AY555150	AY555151	8	2	3	2
A/Thailand/676(NYK)/05 (H5N1)	DQ360835	DQ360836	8	2	4	3
A/Thailand/NBL1/06 (H5N1) lung	GQ466176	GQ466177	8	2	3	2
A/Laos/Nong Khai 1/07 (H5N1)	EU499372	EU499378	8	2	4	3
rgPR8-H5 HANA (KAN-1)	AY555150	AY555151	8	2	3	2
rgPR8-H5 HA (KAN-1)	AY555150	-	8	2	4	2
rgPR8-H5 NA (KAN-1)	-	AY555151	7	1	3	2

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against influenza viruses in order to avoid interference effect from human specific antibody which might create miss-interpretation in the viral infection inhibition assay. Nevertheless, it has been shown that the serum components such as MBL and SP-D are presented in both guinea pig and human sera [11–13]. To some extents and with a careful interpretation, our results from guinea pig should be able to extrapolate to humans. Additionally, to ascertain that the guinea pig sera were also free from anti-influenza antibodies, the sera were tested negative against all study viruses at the screening dilution of 1:10 by HI and microNT assays.

Our viral infection inhibition assay demonstrated that among 10 human influenza viruses (reassorted PR8, 2 seasonal H1N1, 4 seasonal H3N2 and 3 H1N1pdm viruses) tested, 5 were susceptible to both heat-inactivated sera and RDE-treated+heat-inactivated sera, 4 were susceptible to heat-inactivated sera only and 1 was susceptible to RDE-treated+heat-inactivated sera only, with degree of inhibition varying to virus subtypes and strains within the same subtype. H3N2 subtype was the most susceptible to serum inhibitors, while seasonal H1N1 and H1N1pdm viruses were moderately susceptible. All HPAI H5N1 isolates tested were highly resistant to serum inhibitors. While the identities of the serum inhibitors were not determined in our study, the class of serum innate immunity could be estimated from the viral inhibition effects after the sera were treated with heat or RDE+heat. Since α -inhibitors can inhibit only hemagglutination but not virus infection [22,23], they are likely not contributing to the virus inhibition observed in our experiments. On the other hand, our results suggested that serum innate inhibitors against the non H5N1 influenza viruses could be β -inhibitors which are heat-labile and RDE-resistant, γ -inhibitors which are heat-stable and RDE-sensitive, and complement which is heat-labile.

While most of investigators utilized individual serum factors such as SP-D, SP-A, MBL or PTX-3 to study influenza innate immunity, serum factors are likely to work together to exert their

anti-influenza activities. In addition, there might be several more anti-influenza factors in sera that have not been discovered yet; thus, complicating the interpretation of the results in broader picture of pathogenesis. The activity of individual factor may not represent overall inhibitory activity observed in the native serum. For example, investigators previously reported that PR8 virus was resistant to MBL [17], and SP-D [27]; however, the present study demonstrated that our reassorted PR8 virus was sensitive to native guinea pig sera with 48–62% viral inhibition activity. The effect of reverse genetics manipulation on susceptibility to serum inhibitors has been excluded as our rgPR8-H5 NA was sensitive while rgPR8-H5 HA and rgPR8-H5 HANA were resistant to the serum inhibitors. Therefore, our system of using whole serum to examine anti-influenza innate serum inhibitors provides a suitable platform to dissect how the HPAI H5N1 virus could disseminate to distal organs.

Number of glycosylation sites on the envelope glycoprotein, HA in particular, has been correlated to the susceptibility of influenza viruses to innate serum inhibitors [28]. Our study showed that H3N2, the most susceptible subtype, has the highest number of glycosylation sites on HA as compared to the other virus subtypes, with 11–12 sites on the H3N2 complete HA amino acid sequences and 6–7 sites on the globular head. A previous study demonstrated that high degree of *N*-linked glycosylation could attenuate H3N2 influenza viruses. The addition of oligosaccharide moieties to globular head of HA had been linked to increased sensitivity of H3N2 viruses to SP-D and MBL [32]. Glycosylation sites on HA have accumulated in the human influenza H3N2 virus since its appearance in 1968. This gain of sites and their long-term maintenance are presumed to be due to a selective advantage of glycosylation [33]. Extensive evidences indicated that glycosylation plays important roles in the life cycle of influenza viruses by conferring structural integrity and stability of virus particles as well as modulating the functions of HA and NA in the recognition of

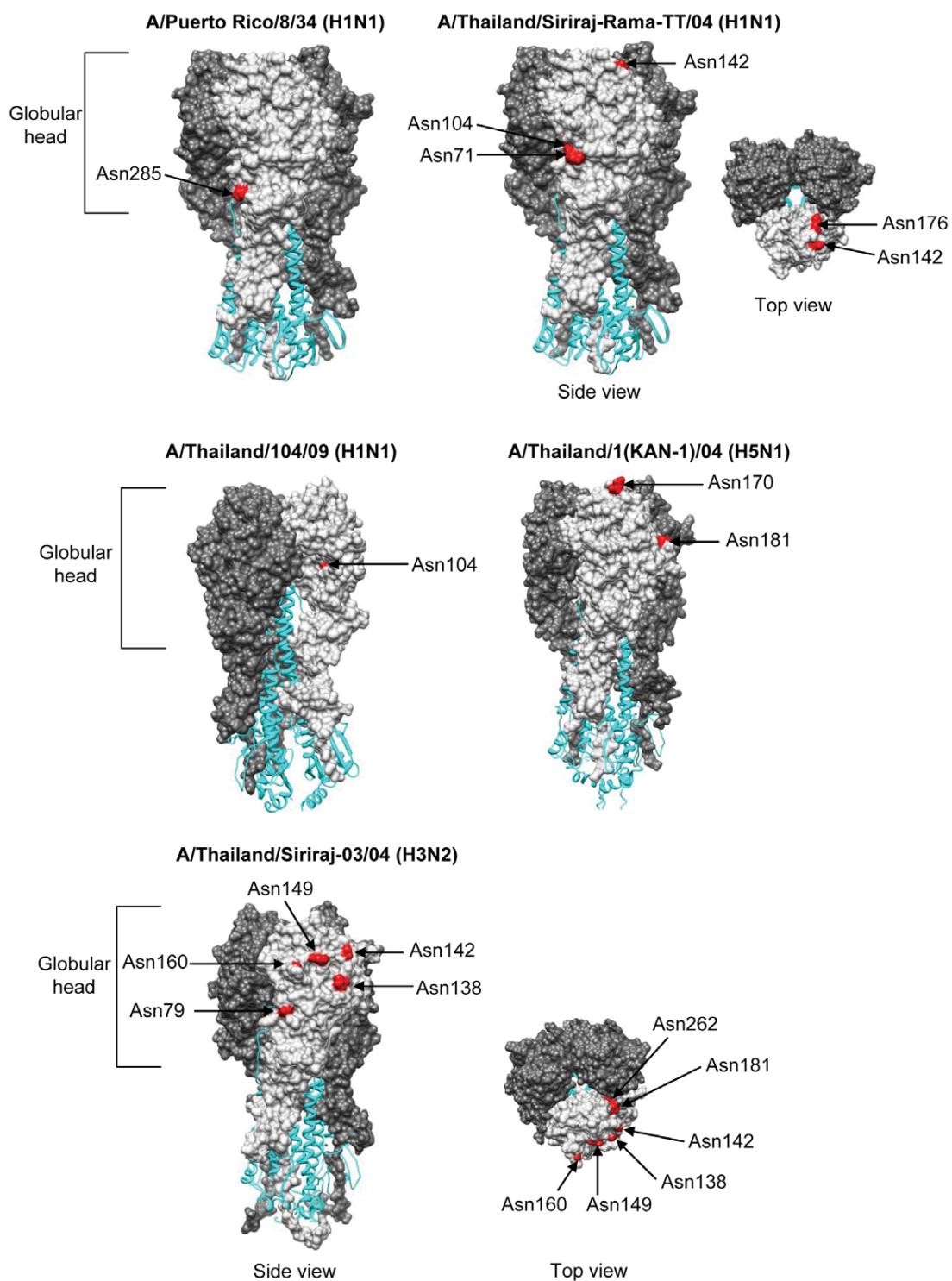


Figure 4. Potential *N*-linked glycosylation sites on HA globular domain. HA1 chains are displayed as space-filling models in HA trimer, while HA2 chains are displayed as ribbon. One of the three HA1 chains is highlighted in lighter shade than the other two HA1 chains. Model of H1N1pdm is related to models of PR8 by 60-degree counterclockwise rotation on vertical axis. The top view is related to the side view by 90-degree rotation on horizontal axis.

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host cell receptors, in particular [34]. Mannose-containing oligosaccharides on the virus envelope were shown to be a target for recognition and destruction by lectins of the innate immune

system [35]. Based on the data obtained from H3N2 viruses, it is likely that the degree of viral neutralizing activity of our guinea pig sera was positively correlated to number of glycosylation sites

present on HA globular head. Nevertheless, our data from other human influenza subtypes does not support this hypothesis. Our reassorted PR8 and H1N1pdm viruses, which are moderately susceptible to serum inhibitors, contain only one glycosylation site on the HA globular head; while HPAI H5N1 viruses, which are the most resistant subtype, contain two sites. These findings suggested that the viral domains other than glycosylation sites on HA globular head could be the target for binding with serum innate inhibitors. In addition, our previous work also suggested that receptor binding site might not be the target of recognition by the serum inhibitors as 676(NYK) which preferred human type receptor (sialic acid-linked α 2,6-galactose) was as resistant as the other H5N1 isolates which preferred avian type receptor (sialic acid-linked α 2,3-galactose) [36].

Previous studies have shown genetic elements that contribute to the H5N1 viral virulence such as glutamine to lysine substitution at amino acid position 627 in PB2, the presence of multiple basic amino acids at the HA cleavage site, and the presence of a sequence motif, Glu-Ser-Glu-Val at the carboxyl terminus of NS1 protein [37]. Herein, our study suggests a novel mechanism to virulence of HPAI H5N1 viruses through their ability to resist serum innate immunity, enabling the viruses to disseminate beyond the respiratory tract, the primary organ of infection, to various visceral organs. The disseminated viruses may subsequently exert their immunopathological effect via an induction of cytokine storm and multi-organ failure, the hallmarks of HPAI H5N1 in humans.

Materials and Methods

Guinea pig sera

Guinea pig blood was purchased from the National Laboratory Animal Center, Mahidol University. When the blood clot retracted, serum was separated by spinning at 2,000 rpm in a refrigerated centrifuge, and then aliquoted and stored at -80°C . Guinea pig sera were negative for antibody to all study influenza viruses as determined by HI and microNT assays.

The viruses

Influenza A viruses in this study including seasonal H1N1 and H3N2, H1N1pdm and HPAI H5N1 viruses (Table 1), were propagated in MDCK cells (obtained from the American Type Culture Collection; CCL-34). These virus isolates were kindly provided by Siriraj Influenza Cooperative Research Center; and the routine service laboratory, Department of Microbiology, Faculty of Medicine Siriraj Hospital, Mahidol University.

Construction of influenza reassortants by reverse genetics

The pHW reverse genetic system [38] comprising 8 recombinant plasmids containing *PA*, *PB1*, *PB2*, *NP*, *HA*, *NA*, *M* or *NS* genomic segments derived from the parental PR8 virus were kindly provided by Prof. Robert Webster and Dr. Erich Hoffman, St. Jude Children Research Hospital, Memphis, Tennessee, USA. Three kinds of reverse genetic viruses harboring *HA*, *NA*, or both *HA* and *NA* genes derived from A/Thailand/1(KAN-1)/04 (H5N1) viruses were constructed. *HA* and *NA* genomic segments were amplified by RT-PCR using universal primers [39] and cloned individually into pHW2000 vector. *HA* segment (accession number AY555150) was engineered to eliminate the multiple basic amino acids at HA cleavage site (337-PQRERRRKRR-346 was changed to 337-PQ---IETR-346, H5 numbering) which mimics the cleavage site of the low pathogenic avian H6 virus before cloning; while the *NA* segment (accession number AY555151) was

cloned unmodified. To construct the reverse genetic viruses, rgPR8-H5 HA (7+1), rgPR8-H5 NA (7+1) and rgPR8-H5 HANA (6+2) viruses, 1 μg of each of the 8 recombinant plasmids were transfected into HEK-293 cells co-culturing with MDCK cells using *TransIT*[®]-LT1 Transfection Reagent (Mirus Bio LLC, Madison, WI). After 24 hours, the reassortants were rescued by adding with 1 ml of Opti-MEM[®] I Reduced Serum Medium (Invitrogen, Carlsbad, CA) containing 2 $\mu\text{g}/\text{ml}$ of TPCK-treated trypsin (Sigma, St. Louis, MO). The culture plate was further incubated at 37°C for 24–48 hours, observed for cytopathic effect and screened for progeny viruses released in the culture supernatant by hemagglutination assay. In addition, all 8 pHW recombinant plasmids containing each gene of PR8 origin were transfected into HEK-293 cells co-culturing with MDCK cells to generate reassorted PR8 virus as the control of the experiments. The reassortants were propagated and titrated in MDCK cells.

HI assay

HI assay was performed based on the protocol as described in the WHO manual [40]. Goose RBCs were employed in the assay for antibody to HPAI H5N1 and H1N1pdm. On the other hand guinea pig RBCs were employed in the assay for antibody to the other human influenza viruses. Briefly, 50 μl of guinea pig serum was mixed with 150 μl of RDE (Denka Seiken Co. Ltd., Tokyo, Japan) and incubated at 37°C for 16–18 hours to eliminate the nonspecific inhibitors. The treated serum was inactivated at 56°C for 30 minutes and absorbed with the test RBCs to remove nonspecific agglutinators. The replicating influenza virus at the final concentration of 4 hemagglutination units/25 μl was used as the test antigen. The treated serum was serially two-fold diluted at an initial dilution of 1:10 into a final volume of 25 μl per well before 25 μl of the test antigen was added. After incubation at room temperature for 30 minutes, 50 μl of 0.5% goose RBCs (for HI antibody to H1N1pdm and H5N1 viruses) or 0.75% guinea pig RBCs (for HI antibody to seasonal H1N1 and H3N2 viruses) were added into every well and further incubated the reaction plate at 4°C 30 minutes (for goose RBCs) or 60 minutes (for guinea pig RBCs). HI titer was defined as the reciprocal of the last serum dilution that completely inhibited hemagglutination of RBCs.

MicroNT assay

Guinea pig sera were screened for the antibodies to the test influenza viruses by microNT assay using the protocol as described previously [40]. Guinea pig serum was treated with RDE before heat inactivation at 56°C for 30 minutes. The treated sera were serially two-fold diluted with 1X EMEM at an initial dilution of 1:10 in a microtiter plate. The diluted serum was incubated with the test virus at the final concentration of 100 TCID₅₀/100 μl for 2 hours at 37°C . Then, 100 μl of each virus-antibody mixture was transferred onto the MDCK cell monolayer maintained in EMEM supplemented with trypsin TPCK (Sigma, St. Louis, MO), and incubated overnight at 37°C , 5% CO₂. The inoculated MDCK cell monolayers in the reaction plates were fixed with 80% acetone prior to determining for presence of viral nucleoprotein by ELISA. Antibody titer was defined as the highest serum dilution that yielded a 50% reduction in the amount of nucleoprotein as compared to the virus infected cell control.

Complement titration

Guinea pig serum contains many soluble factors, including complement factors that confer activity against influenza virus. The amount of complement present in each guinea pig serum can be measured by titration against hemolysin-sensitized SRBCs [41]. Equal volume of 2% SRBCs was mixed with appropriate

concentration of hemolysin (Sigma-Aldrich, St. Louis, MO) for 1 hour with shaking at intervals to obtain hemolysin sensitized SRBCs. The test guinea pig serum was serially two-fold diluted with veronal buffer to obtain a volume of 25 μ l per well in a U-shaped microtiter plate. Then, the serum was incubated with hemolysin sensitized SRBCs for 45 minutes with shaking at intervals. In the presence of serum complement, the sensitized SRBCs would be lysed; while the SRBCs and sensitized SRBC controls appeared as a red button at the bottom of the well. One hemolytic unit was defined as the highest dilution of complement which yielded complete hemolysis of the sensitized SRBCs. Owing to heat-labile nature of the complement proteins, guinea pig sera were stored at -70°C ; and complement titration was conducted prior to each use.

Assay for inhibition of influenza virus infection by soluble factors in guinea pig serum

Guinea pig serum at the working concentration of 2 complement hemolytic units was incubated with the test virus at a final concentration of 1,000 TCID₅₀/50 μ l at 37°C for 45 minutes in quadruplicate wells. Then, the mixtures were transferred onto MDCK cell monolayers and incubated overnight at 37°C prior to measuring the amount of viral nucleoprotein in the infected MDCK cell monolayers by ELISA. In the presence of serum inhibitors, viral infection was blocked, resulting in the decreased amount of viral nucleoprotein synthesized in the inoculated culture as compared to the infected MDCK cell controls. In the case where serum inhibitors could not inhibit viral infection, the high O.D. values indicating viral nucleoprotein synthesis would be observed. The percentages of viral inhibition were calculated based on the O.D. values as compared to the virus control without serum.

The assay employed native guinea pig serum was conducted in parallel with the heat-inactivated serum and together with the RDE-treated+heat-inactivated serum. Heat treatment to inactivate the β -inhibitors was performed by treating the guinea pig

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ELISA

ELISA for influenza viral nucleoprotein was performed with mouse specific monoclonal antibody against influenza nucleoprotein (Catalog number MAB8257, Millipore Corporation, Temecula, CA) as the primary antibody. Horseradish peroxidase (HRP)-conjugated goat anti-mouse Ig (Catalog number 1010-05, Southern Biotech, Birmingham, AL) was used as the secondary antibody. The optical density was measured at dual wavelengths of 450/630 in a spectrophotometer.

Statistical analysis

Statistical analysis was done with PASW Statistics 18 software. The percentages of viral inhibition by native sera, heat-inactivated sera and RDE-treated+heat-inactivated sera were analyzed using analysis of variance (ANOVA). Difference between two data sets was examined using Student's *t*-test. The significance level was set at $p \leq 0.05$.

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Author Contributions

Conceived and designed the experiments: P. Puthavathana. Performed the experiments: JP NN OS KS P. Pooruk. Analyzed the data: NN PN BS HL. Contributed reagents/materials/analysis tools: P. Puthavathana PA. Wrote the paper: P. Puthavathana.

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The difference in IL-1 β , MIP-1 α , IL-8 and IL-18 production between the infection of PMA activated U937 cells with recombinant vaccinia viruses inserted 2004 H5N1 influenza HA genes and NS genes

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Summary

Background: The severity of avian influenza H5N1 disease is correlated with the ability of the virus to induce an over production of pro-inflammatory cytokines from innate immune cells. However, the role of each virus gene is unknown. To elaborate the function of each virus gene, the recombinant vaccinia virus inserted HA and NS gene from the 2004 H5N1 virus were used in the study.

Methods: U937 cells and PMA activated U937 cells were infected with recombinant vaccinia virus inserted with HA or NS gene. The expressions of HA and NS proteins in cells were detected on immunofluorescence stained slides using a confocal microscope. The cytokine productions in the cell supernatant were quantitated by ELISA.

Results: The recombinant vaccinia virus inserted with HA genes induces the production of IL-1 β , MIP-1 α , IL-8 and IL-18 cytokines from PMA activated U937 cells significantly more than cells infected with wild type vaccinia, whereas the recombinant vaccinia virus inserted with NS genes it was similar to that with the wild type vaccinia virus. However, there was no synergistic nor antagonistic effect of HA genes and NS genes in relation to cytokines production.

Conclusion: Only the HA gene from the 2004 H5N1 virus induces IL-1 β , MIP-1 α , IL-8 and IL-18 cytokine productions from activated U937 cells. The same HA gene effect may or may not

be the same in respiratory epithelial cells and this needs to be explored. (*Asian Pac J Allergy Immunol* 2011;29:349-56)

Key words: H5N1 influenza viruses, cytokines, U937 cells, HA, NS

Abbreviations

H5N1 influenza	=	Influenza A virus subtype of hemagglutinin type 5 and neuraminidase type 1 surface antigens
HA	=	Hemagglutinin gene
NS	=	Non-structural gene
PMA	=	Phorbol myristate acetate
r-HA	=	Recombinant hemagglutinin gene
r-NS	=	Recombinant non-structural gene

Introduction

Avian influenza in humans is severe and fatal. The severity of the disease correlates with an ability of the virus to induce an over production of pro-inflammatory cytokines.¹⁻⁵ The cytokine response occurs, whereas a specific immune response has hardly been detected. Thus, a cytokine storm is the immunopathology mediated by innate immunity in H5N1 infection. Pro-inflammatory cytokines are produced in bronchial epithelial cells infected with H5N1 viruses⁶ and it is also well documented that innate mononuclear cells, monocytes and macrophages, are the major cell types that release a variety of cytokines.^{1,7} Information elucidated from these studies was derived from using whole virions, either wild type or reverse genetic viruses. It can not be ruled out that the interplay between different genes or their products, either RNA-RNA interaction or RNA-protein interaction, may influence certain

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gene expression and function. The only way to study individual gene function is to create a recombinant virus containing the gene of interest.

This study aimed to investigate cytokine released in culture supernatants of PMA activated U937 cells infected with recombinant vaccinia virus inserted with HA (r-HA vaccinia) or NS (r-NS vaccinia) genes from the 2004 H5N1 virus by using the ELISA technique. Confocal microscopy of immunofluorescence staining for HA or NS protein and RT-PCR for mRNA in infected cells was performed. The results show that (compared to the wild type vaccinia) chemokines; MIP-1 α and IL-8, antiviral cytokine; IL-18 and proinflammatory cytokine; IL-1 β are significantly released in the supernatant of PMA activated U937 cell infected with r-HA vaccinia whereas TNF α , another proinflammatory cytokine, is not. This effect on cytokines production is not observed for r-NS infection. This study demonstrates the direct effect of either HA or NS without any interference by other influenza genes in cytokines production in activated monocytes. Moreover, the results suggest the absence of NS gene suppressive effect and an antagonistic effect on cytokines production induced by HA gene expression.

Methods

Cell preparation

U937, a human monocyte cell line, was cultured in RPMI 1640, supplemented with 10% heat-inactivated fetal bovine serum, 2.5 mM glutamine, 10mM HEPES, 10,000U/ml penicillin and 10,000 μ g/ml streptomycin. The cells were activated by incubating them with 10 nM of phorbol myristate acetate (PMA) (Sigma, Mo. U.S.A) for 24 hours (activated U937 cell).

Viruses

The viruses used in this study were: Vaccinia virus Lister strain (wild type control), recombinant vaccinia virus inserted with HA (r-HA vaccinia) and recombinant vaccinia virus inserted with NS (r-NS vaccinia). Both the HA and NS genes of the two recombinant viruses were derived from A/Thailand/1(KAN-1)/04 (H5N1) (sequences of both genes can be accessed from GenBank with accession numbers AY555150 and AY626146 for HA and NS respectively). These viruses were propagated and titrated in TK cells. Titers were presented as plaque forming units /ml.

Virus infection in U937 cell culture

Resting (no PMA) or activated (with PMA) U937 cells at a concentration of 1×10^6 cells/ml in 2% FBS RPMI 1640 were infected in triplicate with wild type vaccinia or r-HA vaccinia or r-NS vaccinia at a multiplicity of infection (M.O.I.) of 0.05 in a 96 well- tissue culture plate. An M.O.I. of 0.1 was obtained by double infection with both types of the recombinant viruses. Infection was carried out for 24 hours at 37°C in a humidifying CO₂ incubator. Thereafter, culture supernatants were harvested and kept at -80°C for cytokine assays by ELISA. Meanwhile; cell pellets were washed once with PBS and divided into two portions; one portion was used for RNA extraction by TRIzol® Reagent (Invitrogen, Carlsbad, CA., USA.) and another portion was smeared on microscopic slides for immune-fluorescence staining.

Semiquantitation for HA or NS mRNA by RT-PCR

Total RNA extracts were reverse transcribed into cDNA by using AMV reverse transcriptase™ first-strand kit (Invitrogen, Carlsbad, CA., USA.). The cDNA was further used as template in polymerase chain reactions (PCR). The primer pairs were: HA-H5f: 5'-ACTCCAATGGGGCGATAAA-3', HA-H5r: 5'-CAACGGCC TCAAAC TGAGTGT-3' and SNSF: 5'-GATAAGGC ACTTAAATGCCG-3' and SNSR: 5'-ACGGTGAGATTCTCCCACG-3'. The β -actin gene was amplified as the internal control 5'-ATC TGG CAC CAC ACT TCT ACA-3' as the forward primer and 5'-GTT TCG TGG ATG CCA CAG GAC T-3' as the reverse primer. Amplicons were analysed by densitometer (Amersham Biosciences, England) using Image Scanner Software (Image MasterTotal Lab version 2.01) analysis. The percentage of gene expression originating from HA and NS mRNA were semiquantitated by comparing them to that of the β -actin gene.

Immunofluorescence assay for HA or NS protein

Slides of cell deposits were air-dried and fixed in pre-cooled acetone at -20°C for 10 minutes. The slides were stained immediately, or otherwise kept at -70°C until staining by the indirect immunofluorescence technique. Goat antiserum against H5N1 HA (kindly provided by Dr. Richard Webby, St Jude Children Research Hospital) or goat anti-NS peptides antiserum (Santa Cruz Biotechnology Inc., CA., USA) was used as the primary antibody, FITC conjugated rabbit anti-goat Ig was used as the second antibody. Uninfected cells and cells infected

with wild type vaccinia virus were used as negative controls. The stained slides were observed for fluorescence using a Confocal Laser Scanning Biological Microscope (FV1000 Fluoview, Olympus, Tokyo, Japan).

Cytokine quantitation by ELISA

Culture supernatants were assayed for pro-inflammatory cytokines: TNF α and IL-1 β , chemokines: MIP-1 α and IL-8, and antiviral cytokines: IFN α and IL-18 by ELISA kits (R&D Systems Inc., Minneapolis, USA.). The test protocols followed those described in the kit instructions. The reproducibility of the results was confirmed by repeating the experiments in culture supernatants collected from the three separate experiments.

Statistical analysis

The cytokine concentrations from ELISA (in triplicate) were analysed using Prism software (GraphPad prism 4 Software). Nonparametric, one tailed Mann Whitney u test was used; a p value < 0.05 was considered statistically significant.

Results

HA or NS proteins are more strongly expressed in PMA activated U937 cells than in resting/non-activated U937 cells

Compared to the results of semi-quantitation of mRNA for HA and NS band density of RT-PCR (% band density for HA from PMA activated U937 is 152.5 and non-activated is 96), the amount of positive immunofluorescence staining in PMA activated U937 cells was higher and more intense than in non-activated U937 cells as shown in Figure 1A and 1B for anti HA staining, whereas there was negative staining in wild type vaccinia infected cells.

A similar pattern is observed for anti NS staining as shown in Figure 2A and 2B (% band density for NS from PMA activated U937 is 41.7 and non-activated is 12.4).

Cytokine productions in resting/non-activated U937 cell

There were no differences in cytokines production from non activated U937 cells infected with r-HA vaccinia or r-NS vaccinia or both or wild vaccinia. Three groups of cytokine effector functions were investigated; these are pro-inflammatory cytokines (TNF α and IL-1 β), chemokines (MIP-1 α and IL-8) and antiviral cytokines (IFN α and IL-18). The concentrations of these 6 cytokines in the

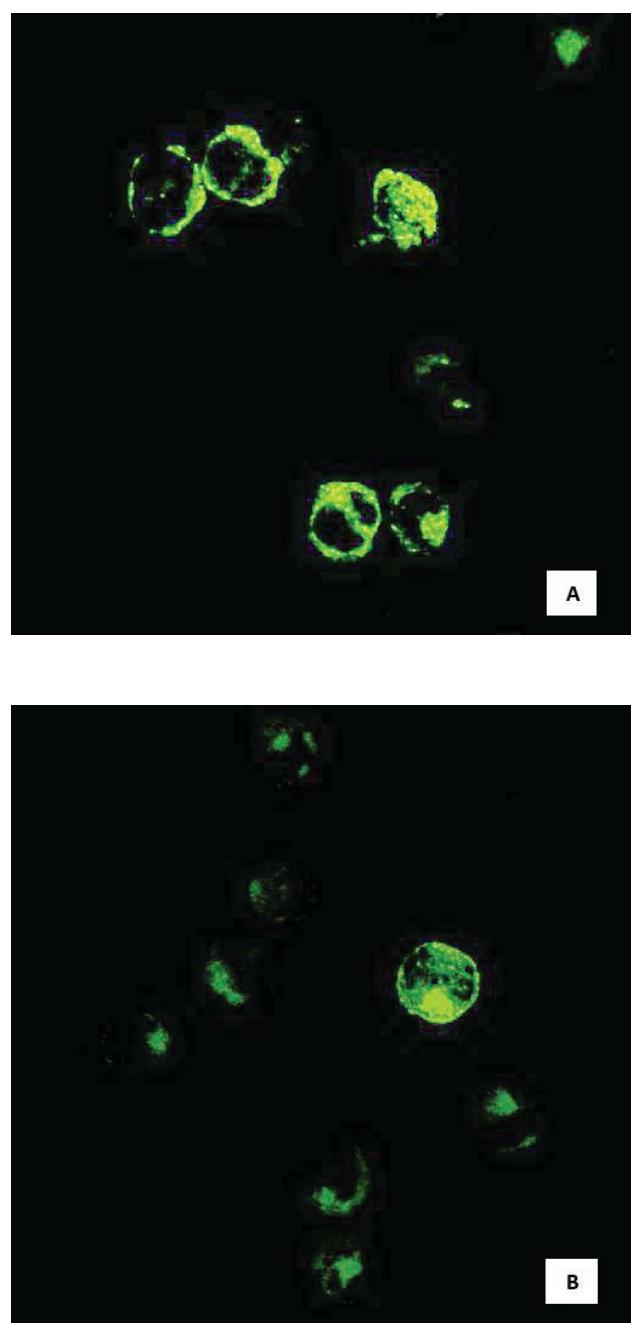


Figure 1. A. Anti HA immunofluorescence staining of PMA activated U937 cells infected with recombinant HA vaccinia (r-HA vaccinia), observed by UV light under a confocal microscope (400 magnification). B. Anti HA immunofluorescence staining of U937 cells infected with recombinant HA vaccinia (r-HA vaccinia), observed by UV light under a confocal microscope (400 magnification).

supernatants of non activated U937 cells were not different in all infections, the average cytokine concentrations from 3 separate infections (n=3) of r-HA, r-NS and dual vaccinia infections were not different from wild type vaccinia infection.

Cytokine production in activated U937 cell

Cytokine production from r-HA vaccinia or r-NS vaccinia or both infected PMA activated U937 cells were different. The cytokine concentrations in the supernatants of infected PMA activated U937 cells were different in rHA vaccinia, rNS vaccinia or dual infections. rHA vaccinia infection induces increased production of TNF α , IL-1 β (significantly), MIP-1 α (significantly), IL-8 (significantly) and IL-18, compared to wild vaccinia infection. On the contrary, the rNS vaccinia infection did not induce any effect. The cytokine concentrations in rNS vaccinia infection supernatants were the same as in wild vaccinia infection. Furthermore, in supernatants of the dual infections with rHA and rNS vaccinia, the TNF α , IL-1 β , MIP-1 α and IL-18 levels were significantly higher than in the supernatant of wild vaccinia infection, but the levels of the cytokine concentrations were almost the same as observed in supernatants of rHA vaccinia infections, as shown in Figure 3A-F.

Discussion

Cytokine dysregulation is proposed to be a mechanism explaining the unusual severity of avian influenza. High levels of inflammatory cytokines such as TNF α , IL-1 and IL-6 or chemokines such as IL-8 and CCL2 were detected in the patients' serum.^{2,3,5} *In vitro* studies had demonstrated hyper-production of pro-inflammatory cytokines in macrophages infected with H5N1 viruses.¹ Excessive infiltration of macrophages and neutrophils together with significantly higher levels of pro-inflammatory cytokines were noted in the lungs of mice infected with 1918 H1N1 virus and in those had had recent H5N1 virus infection with A/Thailand/SP/83/2004 and A/Thailand/16/2004.⁸ Based on the knowledge that macrophages could be infected by H5N1 viruses and macrophage is the major source of innate cytokine, the present study used U937 as the cell source to explore the effect of the H5N1 HA gene and the NS gene, and their interaction, on cytokine production. An advantage of this study was the use of recombinant vaccinia viruses, so that the influence of the HA or NS gene could be studied

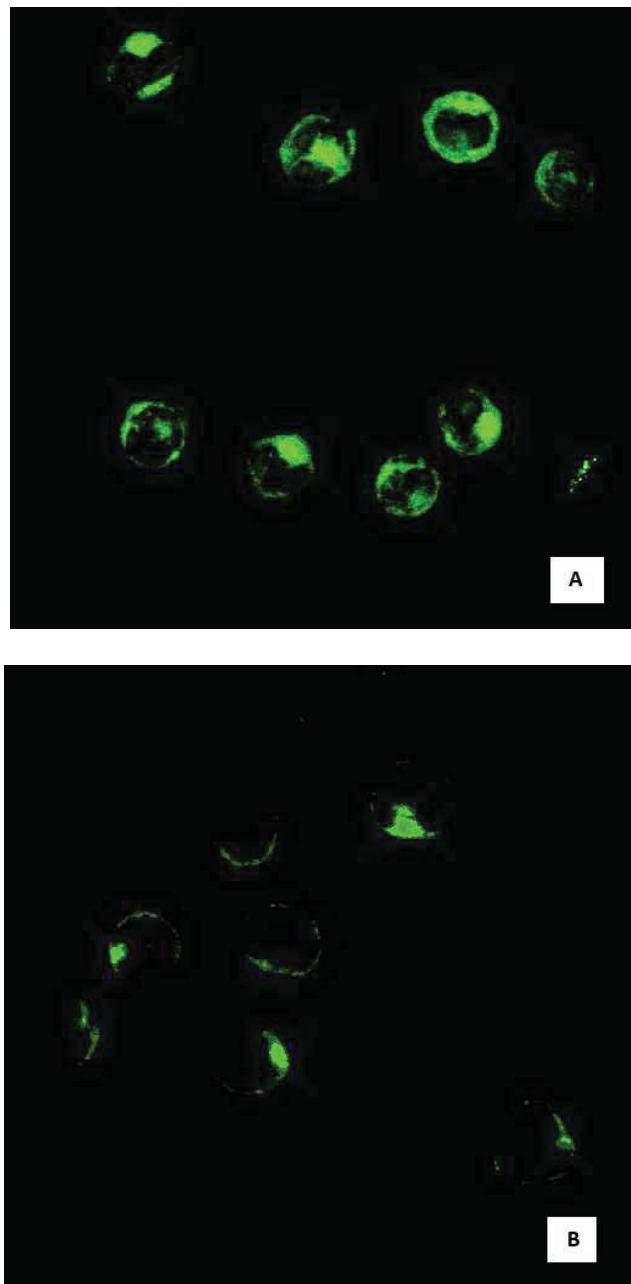


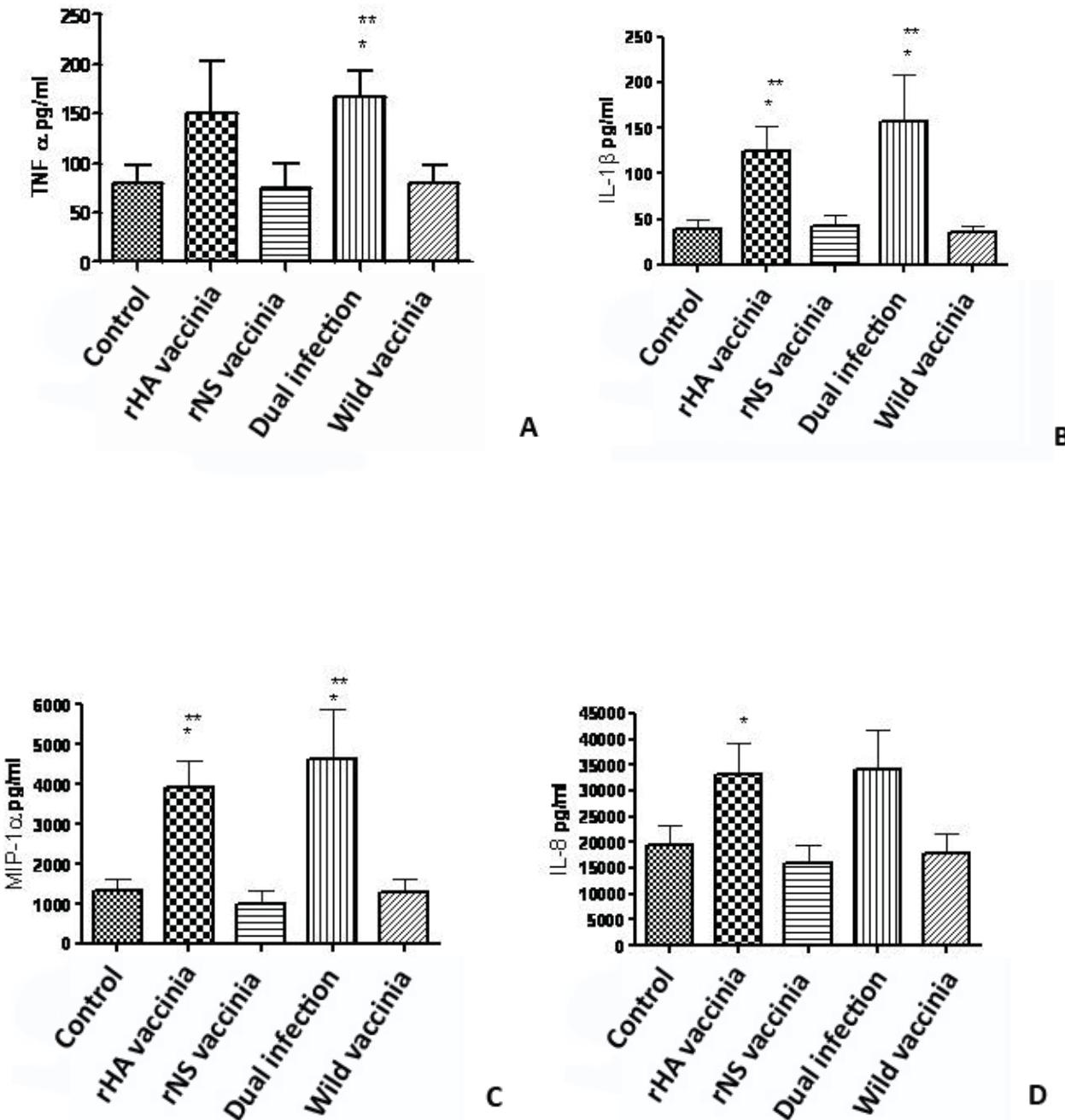
Figure 2. A. Anti NS immunofluorescence staining of PMA activated U937 cells infected with recombinant NS vaccinia (r-NS vaccinia), observed by UV light under a confocal microscope (400 magnification).

B. Anti NS immunofluorescence staining of U937 cells infected with recombinant NS vaccinia (r-NS vaccinia), observed by UV light under a confocal microscope (400 magnification).

without interference from the other influenza genes. Wild type vaccinia virus, as the parent of recombinant virus, provided the background levels of the cytokines released. In addition, using U937 cells provided advantages as well, since the essentials of the cell condition in HA or NS gene expression and cytokine production can be elucidated. The PMA stimulated U937 cells were demonstrated to exhibit increased expression of a variety of cellular molecules, including the ability to mediate chemotaxis and phagocytosis, i.e., the stimulated cells became activated and mature.⁹ The present study showed that viral infection in activated U937 cells induced higher levels of influenza specific mRNA, protein expression and of all the cytokines studied, when compared with the infection in resting cells. No cell death was observed either in resting or activated cells under the conditions of infection at an M.O.I. of 0.05 or 0.1 in case of double infection for 24 hours. This study suggests that activation of U937 cells or the monocyte maturation may provide biochemical conditions that allow the HA or NS gene to exert their influence on the cytokines synthesis. This effect may or may not be the same as that of dendritic cells, which was reported by other investigators.¹⁰ A low amount of the chemokine, MIP-1 α , was detected in the cell supernatant of rHA-vaccinia infected non-activated U937 cells, which was the same level in cell supernatant of wild vaccinia infection. This is normally detected in virus infection such respiratory virus infection.¹¹ However, significantly increased production of both detected chemokines, MIP-1 α and IL-18 levels was observed in the cell supernatant of rHA vaccinia infected activated U937 cells (Figure 3C and 3D). This may suggest that chemokines are cytokines produced to influence the immune cell recruitment to influenza infected cells. TNF α is a cytokine that plays this role or functions as "intracrine".¹² TNF α probably plays this role in H5N1 influenza infection too. Others have reported the hyper-production of TNF α in human macrophages infected with the 1997 H5N1 virus and the high production of MIP-1 α , IL-1 α , KC (mouse equivalent to human IL-8), IL6, MCP-1 and IFN- γ lung of mice infected with 1918 influenza virus or recent H5N1 virus.⁸ Our results show non-significant production of TNF α in 24 hours the supernatant of rHA-vaccinia infection in activated U937 cells but significant production of MIP-1 α and IL-8, Figure 3A, 3C, 3D. This may indicate that during the 24 hr period of rHA-vaccinia infection TNF α effected

chemokines induction and was then used as an autocrine. The cytokine storm is hypothesized to be the major cause of the unusual disease severity in avian influenza and during that period of time TNF α should be produced from dendritic cells; however, cytokine inhibition did not protect mice against lethal challenge with H5N1 virus.¹³

In contrast to the increase in cytokines production in rHA-vaccinia infection, this study demonstrated that rNS-vaccinia was a poor cytokine inducer. Levels of cytokines induced by rNS-vaccinia were not significantly different from those induced by wild type vaccinia virus. Moreover, the levels of cytokines synthesized in cells infected with both rHA-vaccinia and rNS-vaccinia, the dual infection, were not different from those released from cells infected with rHA-vaccinia. This result implies that the NS gene transcription and translation processes do not exert any antagonistic nor synergistic effect in cytokine induction mediated by processes in the HA gene, at least in activated U937 cells. The first H5N1 avian influenza outbreak in 1997 caused the disease in 18 human cases with six deaths, or a fatality rate of 33%.¹⁴ The current H5N1 avian influenza epidemic is even more disastrous and covers a wide geographical area. Even though cytokine dysregulation is proposed to be the mechanism of disease severity in patients from both outbreaks, the NS protein of H5N1 viruses that caused the recent outbreak does not possess Glu92, but Asp92 instead. Nevertheless, the recent viruses possess Ala149.¹⁴ Role of Glu92 and Asp149 on the virulence and pathogenicity of avian influenza are in doubt as a result of the study done by Perrone, et al.⁸ The study involved two recent isolates from fatal cases: A/Thailand/16 and A/Thailand/SP/83, which both possess Glu92 and Asp149.^{8,15} A/Thailand/16 was highly virulent in the mouse model with a mouse lethal dose 50 (MLD50) of 1.7, while A/Thailand/SP/83 was of low virulence with an MLD50 of 5.5.⁸ These previous studies together with our results have led to the suggestion that the NS1 gene alone is not enough to elicit cytokine dysregulation. Moreover, the interplay between HA and NS genes in double infected cultures did not lead to an enhancement of cytokine synthesis. The results of the present study suggests that the severity of avian influenza might be derived from the interplay between genes, apart from HA and NS genes, within cassette of the viral genome. Essentially, this study demonstrated an important role for HA in certain cytokine inductions.



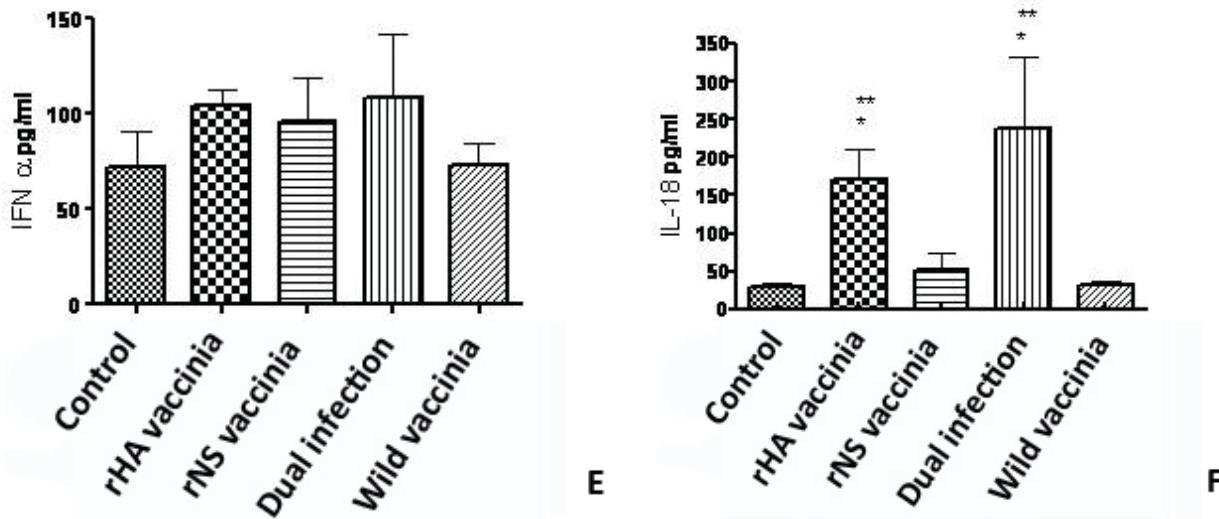


Figure 3. A. Histogram shows TNF α cytokine levels (from 3 separate experiments) in supernatants of infected PMA activated U937 cells with r-HA Vaccinia, r-NS Vaccinia, r-HA and r-NS vaccinia (dual infection), Wild vaccinia and non-infected (control).

B. Histogram shows IL-1 β cytokine levels (from 3 separate experiments) in supernatants of infected PMA activated U937 cells with r-HA Vaccinia, r-NS Vaccinia, r-HA and r-NS vaccinia (dual infection), Wild vaccinia and non-infected (control).

C. Histogram shows MIP-1 α cytokine levels (from 3 separate experiments) in supernatants of infected PMA activated U937 cells with r-HA Vaccinia, r-NS Vaccinia, r-HA and r-NS vaccinia (dual infection), Wild vaccinia and non-infected (control).

D. Histogram shows IL-8 cytokine levels (from 3 separate experiments) in supernatants of infected PMA activated U937 cells with r-HA Vaccinia, r-NS Vaccinia, r-HA and r-NS vaccinia (dual infection), Wild vaccinia and non-infected (control).

E. Histogram shows IFN α cytokine levels (from 3 separate experiments) in supernatants of infected PMA activated U937 cells with r-HA Vaccinia, r-NS Vaccinia, r-HA and r-NS vaccinia (dual infection), Wild vaccinia and non-infected (control).

F. Histogram shows IL-18 cytokine levels (from 3 separate experiments) in supernatants of infected PMA activated U937 cells with r-HA Vaccinia, r-NS Vaccinia, r-HA and r-NS vaccinia (dual infection), Wild vaccinia and non-infected (control).

*statistically significant against wild vaccinia infection,

**statistically significant against non-infected control (PMA activated U937 cell).

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Full Length Research Paper

Monitoring the influenza pandemic of 2009 in Thailand by a community-based survey

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As an international traveling hub of South-East Asia, Thailand was one of the countries hardest and earliest hit by the influenza A (H1N1) 2009 pandemic. In order to understand the epidemic spread in the country, we conducted community-based surveys in metropolitan, urban, and rural areas using questionnaire interviews. We also determined sero-positive rates from randomly selected samples within the surveyed population. Recalled incidences of fever and acute respiratory symptoms in the survey correlated well with systematic reports of 2009 pandemic influenza cases from hospitals in the same areas, giving a ratio of total cases extrapolated from the surveyed data for persons who sought medical attention reported in the hospital-based surveillance system at 275:1. Conducting a large scale survey of the influenza outbreak is time consuming and also can be difficult to complete in a short time. Therefore, we used the survey for monitoring the outbreak of respiratory disease in the early pandemic phase. The seroprevalence rate was 8 to 10%, with higher rate for younger age groups, and suggests that sufficient herd immunity may have been reached in Thailand, especially in urban areas, while others may still be vulnerable to the second wave of the pandemic.

Key words: Pandemic, influenza, survey, Thailand.

INTRODUCTION

Influenza epidemics can be unpredictable and vary enormously in severity (Bramley et al., 2009). Novel influenza A (H1N1) 2009 was first reported in the USA and Mexico in April 2009 (CDC, 2009). The World Health Organization announced Phase 6 of the influenza pandemic on June 11, 2009. The virus is new to humans, so there are uncertainties about transmission efficiency and disease severity as pandemic influenza continues to evolve rapidly (AlMazroa et al., 2009).

As an international traveling hub of South-East Asia, Thailand was one of the countries hardest and earliest hit by the influenza A (H1N1) 2009 pandemic. The initial cases of laboratory-confirmed influenza A (H1N1) 2009 in Thailand were among travelers and students returning

from epidemic area of the American Continent, The Thai Ministry of Public Health (MOPH) reported. In Thailand, locally acquired epidemics of pandemic influenza were first detected in June 2009. In the early epidemic, wide and rapid spreads of influenza transmission primarily occurred in schools in Bangkok metropolitan and major tourist cities (Apisarnthanarak, 2009; Suchada, 2009; Jongchedchootrakul, 2010).

Having accurate and timely information on the extent of spread of outbreaks is crucial to informed decisions, and to deployment of proper interventions and mitigating measures. Thailand has a well-developed public health infrastructure, however, getting accurate information on numbers of cases and their distribution is often difficult in a widespread outbreak situation (Fraser et al., 2009).

Most public health authorities have relied on systematic reporting of laboratory-confirmed cases, influenza-like illnesses in out-patient settings, hospitalized patients with severe cases, and deaths (Kitler et al., 2002; Rao, 2003;

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Flahault, 2006). Having estimated the total cases based on available data, one has to assume fixed proportions of total cases to the surveyed population, which can be acquired from studies at the beginning of the outbreak when the number of total cases is small enough to be tracked.

In addition, the proportion of patients who seek medical attention can be strongly affected by perception about disease severity, for instance, information gathering through the media, however, this perception can vary with time depending on several factors. The proportion of admitted cases and deaths can also vary as the severity of the virus changes while it evolves. Community-based active survey seems reasonable alternative (Ghosh, 2008; Levy-Bruhl, 2009). However, it is difficult to get accurate data from a large-scale clinical-based survey, because influenza symptoms are mostly non-specific, and other infectious and non-infectious illnesses can confound the findings. To overcome this problem, we designed a community-based survey to monitor the situation of influenza-like illnesses and tested its reliability to detect pandemic influenza infections by serological testing.

METHODS

Questionnaire and survey

The tool we used in the survey was a structured questionnaire, which was tested for feasibility and practicality in a district of the Bangkok Metropolitan Administration (BMA) called Dusit. The set of questions on demographic information of respondents and their families included gender, age, education level, religion, number of household members, and type of property resided in. Also, questions about the trend of the influenza outbreak comprised the number of household members who had influenza-like symptoms in the immediately preceding 2 weeks and in the 3 months prior to the survey; details of influenza-like illness and chronic diseases of each household member; behavior of sick individuals to prevent transmission to others; behavior to prevent oneself from getting influenza; and willingness to receive vaccination. For quality control of the interview process, a group of interviewers were trained, educated, and observed by an investigator as they moved step-by-step to follow the guideline for the survey.

Population and sampling method

The initial outbreaks of influenza A (H1N1) 2009 occurred at Thailand at different times. Areas of the country can be categorized into four groups on the basic of timing of outbreaks as May, June, July and August. We selected the province that first reported an outbreak of pandemic influenza in each of the four time-based groups for our survey including Bangkok Metropolitan Administration, NakhonRatchasima, ChiangMai, and Nakhonsrithammarat, respectively. The household survey by poll method (Poll-1), cluster sampling technique, in urban and suburban areas of BMA was conducted by a poll conducted by experienced interviewers in October 2009. For the other three provinces, their cities were purposively chosen, and rural areas were simply randomized to be surveyed with similar periods and techniques.

We also conducted a serologic survey based on a proportional-cluster sampling technique classified by number of households in

sub-districts of ChiangMai and Nakhonsrithammarat. Since the prevalence of Influenza A (H1N1) 2009 in the Thai population was estimated at 20% with 5% as worst acceptable value, a total of 246 respondents should be tested. Face-to-face interviews and blood sample collection was done by an investigator and a team of health professionals. Exclusion criteria for recruitment for blood sample collection was a person who was <5 years old, and when fewer than 75% of family members in the household agreed to provide blood samples.

Case definition

An acute respiratory illness (ARI) case was defined as one affecting a person who had history of at least two of the following symptoms; fever, cough, sore throat, and running noses within recent three months prior to the survey.

Serologic testing

Hemagglutination-inhibition assay (HI assay) was performed as previously described (Iconic et al., 2009). The protocol called for A/Thailand/104/2009(H1N1) live virus as the test antigen; and 0.5% goose erythrocytes were used as the detector. The test sera were rid of non-specific inhibitors by pre-treatment with receptor destroying enzyme (Denka Seiken, Tokyo, Japan), at 37°C overnight, followed by heat inactivation at 56°C for 30 min; nonspecific agglutinator was removed by addition of 50% goose erythrocytes and incubated at 4°C for 1 h. Two-fold serial dilutions of test sera were prepared in duplicate, followed by incubation with the test antigen at a working concentration of 4 HA-units, the highest dilution of antigen that gives complete haemagglutination of cells, for 30 min at room temperature. Erythrocyte suspension was added to the reaction plates, and further incubation at 4°C for 30 min was performed before the result was read. HI antibody titer was defined as the reciprocal of the highest serum dilution that completely inhibited hemagglutination.

A microneutralization assay (MicroNT) was performed as previously described (Kitphati et al., 2009). The assay was based on a reduction in the amount of nucleoprotein produced in the virus-infected Madin-Darby Canine Kidney Cells (MDCK) monolayer as infectivity of the test virus is neutralized by specific antibody. A/Thailand/104/2009 pandemic strain was used as the test virus. The test sera were two-fold serially diluted, added with the test virus at a final concentration of 100TCID50 for 2 h at 37°C. The serum-virus mixture was then added onto the MDCK cell monolayer and further incubated for 24 h at 37°C. The reaction plate was fixed and tested by enzyme-linked immunosorbent assay (ELISA) for presence of the viral nucleoprotein using mouse monoclonal antibody (Chemicon, Temecula, CA) as the primary antibody and goat anti-mouse IgG (Southern Biotech, Birmingham, AL) as the secondary antibody. Antibody titer was defined as reciprocal of the highest serum dilution that could reduce ≥50% of the amount of nucleoprotein when compared with the virus control.

RESULTS

The surveyed incidence of ARI correlated with systematically reported ARI

We initially conducted a small exploratory survey to test tools in a district of Bangkok in August 2009. A total of 90 households were recruited with data for each household member obtained in an interview with a family member

Table 1. Demographic characteristics and practices of prevention measures in community based survey (Pol-1) in 8 areas, Thailand, July - September 2009

Characteristics	Bangkok		ChiangMai		NakhonRatchasima		NakhonSriRatthammarat	
	City	Suburb	City	Rural	City	Rural	City	Rural
Population* (mid-year 2009)	99,994	150,166	238,460	21,405	329,531	83,639	254,261	30,816
Interviewed family (n = 826)	100	115	101	106	103	98	101	102
Family members (n = 3,351)	479	450	352	373	429	434	408	426
- Median of member in family [range]	4 [2-25]	3 [1-20]	3 [1-15]	3 [1-8]	4 [1-10]	4 [1-12]	4 [2-7]	4 [2-8]
Any member developed ARI between July and September 2009 (n = 460) (%)	48 (10)	62 (14)	36 (10)	29(8)	101 (24)	60 (14)	66 (16)	58 (14)
- Male (%)	16 (33)	34 (55)	13 (36)	15 (52)	42 (42)	32 (53)	28 (42)	30 (52)
- Median of age (year) [range]	21 [1-67]	25 [1-55]	24 [2-65]	23 [1-71]	18 [1-76]	7 [1-62]	16 [1-70]	12 [1-52]
Interviewee developed ARI (n = 128) (%)	18 (18.0)	22 (19.1)	14 (13.9)	6 (5.7)	35 (34.0)	6 (6.1)	18 (17.8)	9 (8.8)
- Mask use by interviewee (%)	38.9	63.6	71.4	83.3	31.4	16.7	11.1	22.2
- Mask use by family members (%)	5.6	22.7	0.0	50.0	11.4	33.3	5.6	0.0
- Take a sick leave (%)	33.3	59.1	57.1	50.0	60.0	50.0	83.3	55.6
- Hand covers mouth when cough (%)	77.8	63.6	100.0	83.3	82.9	66.7	94.4	88.9
- Not sharing bedroom (%)	22.2	31.8	21.4	50.0	25.7	0.0	33.3	44.4
- Frequent hand washing (%)	83.3	59.1	92.9	100.0	77.1	50.0	100.0	88.9

* Mid-year 2009 Thai population from Department of Provincial Administration, Ministry of Interior, Thailand.

whose age was higher than 15 years. Report for those households indicated that 62.2% had experienced symptoms of acute respiratory infections, example, fever and/or respiratory tract symptoms during the previous 3-month period. The highest frequency of illness was reported for children and young adults (ages 0 to 19 years). We subsequently conducted surveys (Pol-1) in two areas each of ChiangMai, Nakhonratchasima, and NakhonsriRatthammarat (BMA), Bangkok Metropolitan Administration (BMA), simultaneously in October 2009. These eight areas represented different levels of impact by pandemic influenza according to the national surveillance system for ARI. A total of 826 families were recruited in the eight survey sites. Among those, a member of each family was randomly selected for interview. Table 1 shows population density and characteristics of the surveyed areas, as well as demographic data of the surveyed subjects. Of all 460 persons who reported having ARI in the surveyed households, 128 (28%), one from each household, were interviewed for their practice of personal hygiene and their family members' preventive measures, example, a face mask wearing, home rest, personal hygiene practice, bedroom separation, and frequent hand washing (Table 1). The survey showed a cumulative incidence of ARI since the beginning of the epidemic to be just under 14%. Concurrent illnesses of two or more members in the same household were reported in 39% of all reported illnesses. Younger age groups had higher incidence of ARI, with cumulative incidence of ARI up to 43% for children <5 years old (Figure 1). The surveyed ARI incidence was extrapolated to the total population in the eight survey areas. Total numbers of ARI by age group correlate well with numbers of reported pandemic influenza A (H1N1) 2009 by age group in the MOPH system ($r^2 = 0.733$, $p < 0.005$) (Figure 2) giving a ratio of total community-based ARI cases to the reported pandemic H1N1 cases seeking medical attention in the MOPH system was estimated to be 275:1. We repeated the survey in ChiangMai and

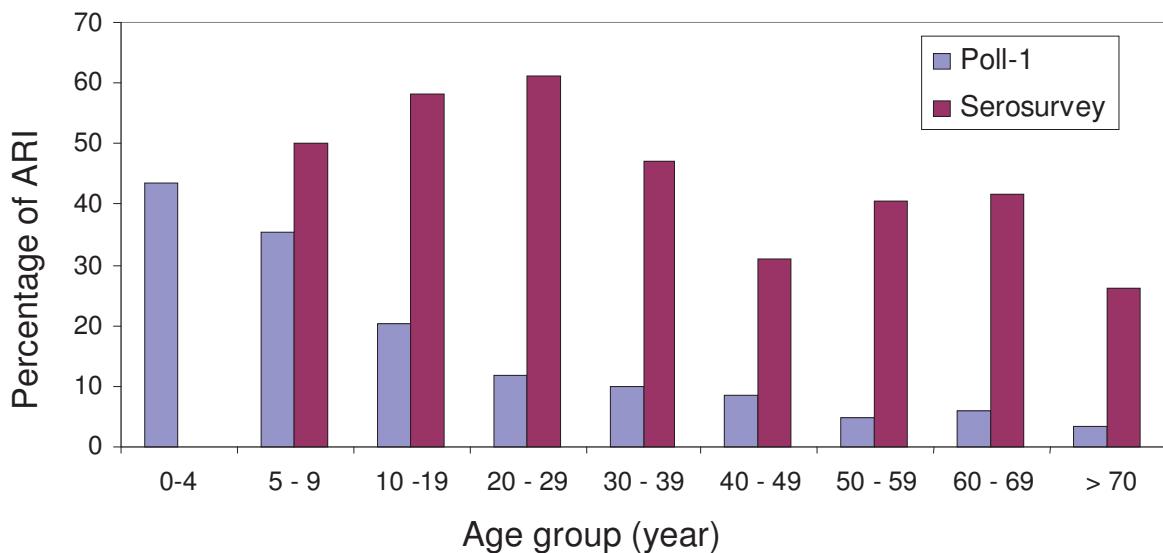


Figure 1. Prevalence of acute respiratory illnesses (ARI) by age-group, community based survey. (Poll-1) in October 2009 (n=3,351) and sero-survey in December 2009 (n=222).

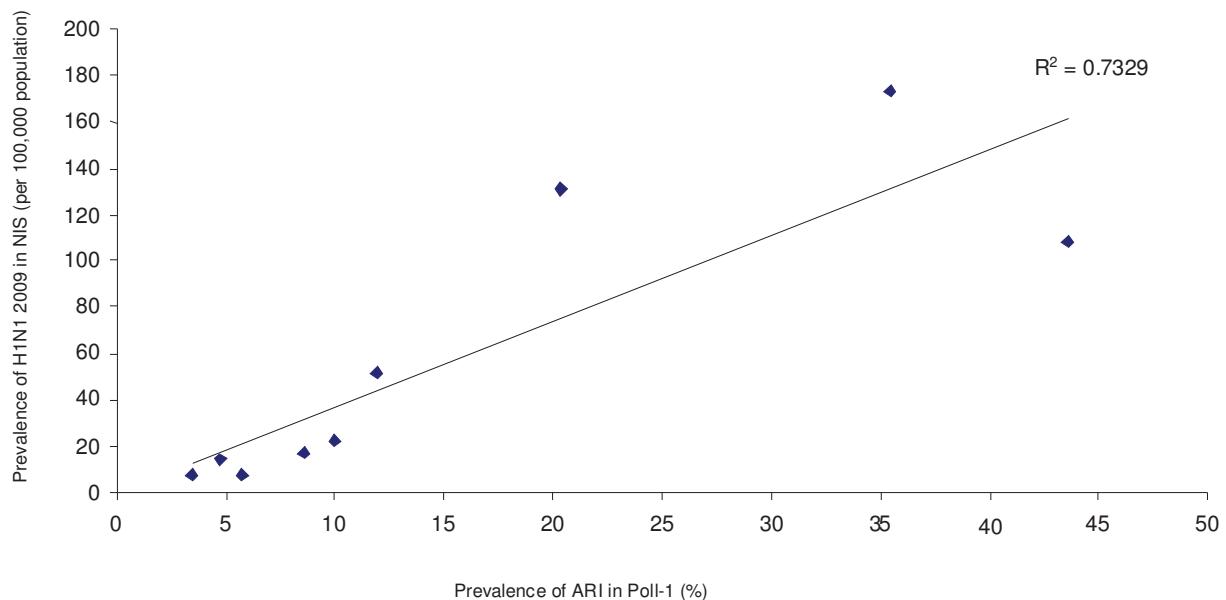


Figure 2. Correlation between prevalence of ARI and prevalence of reported pandemic H1N1 2009 infections by age group in 4 provinces of Thailand, July - September 2009.

Nakhonsrithammarat city in December 2009. The cumulative incidence of ARI increased to 43%, but the incidence of ARI during the 2-week period prior to the survey was 16%.

Antibody detection

In the second survey, we performed serologic tests for

antibody to the influenza A (H1N1) 2009 targeted to 246 subjects. Only 222 (90%) subjects from 40 households in ChiangMai city and 44 households in Nakhonsrithammarat city had blood samples taken. Among the 222 subjects, a total of 20 serologically positive cases were detected with HI and MicroNT assays, and the proportion of serologically positive subjects was 9% (95%CI: 5.6 to 13.6%). Among the 96 ARI cases, the proportion of serologically positive cases was 14.6% (95%CI: 8.2 to

Table 2. Characteristics of respondents in sero-survey for a novel influenza H1N1, Thailand, December 2009

Factor	All respondents (n=222)	ILI cases (n=49)	ARI cases (n=96)	Seropositive cases (n=20)
Study area				
- ChiangMai city (%)	110 (50)	23 (47)	52 (54)	11 (55)
- Nakornsithammarat city (%)	112 (50%)	26 (53%)	44 (46%)	9 (45%)
Median of age (years)	45 (range 5 - 89)	35 (range 7 - 70)	39 (range 7 - 89)	12 (range 7 - 57)
Male : Female	0.57 : 1	0.75 : 1	0.58 : 1	0.43 : 1
Education				
- Primary school (%)	86 (39)	17 (35)	32 (33)	12 (60)
- Secondary school (%)	73 (33)	16 (33)	29 (30)	4 (20)
Had history of any chronic illness (%)	85 (38)	16 (33)	40 (42)	4 (20)
Type of house				
- Separated house (%)	154 (69)	32 (65)	64 (67)	13 (65)
- Dormitory / Apartment (%)	64 (29)	17 (35)	32 (33)	7 (35)
Got seasonal influenza vaccine within 6 months (%)	11 (5)	0	3 (3%)	1 (5)

23.3%). Among 126 non-ARI cases, the proportion of serologically positive cases was 4.8% (95%CI: 1.8 to 10.1%).

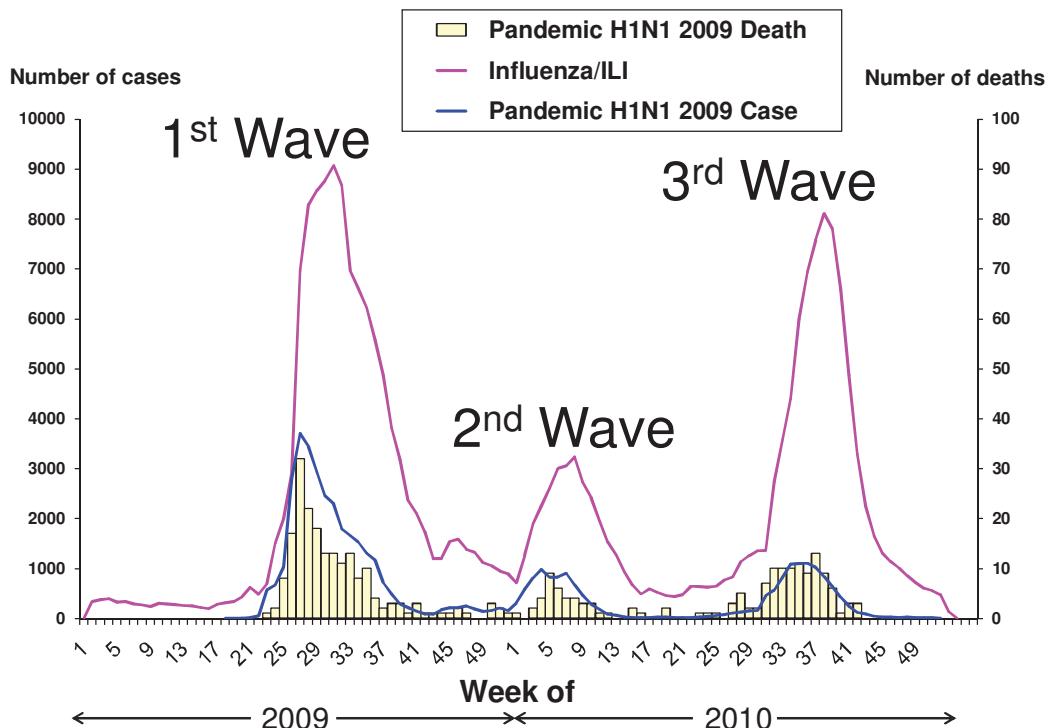
The demographic findings for all respondents with reported ARI cases, and with sero-positive cases are shown in Table 2. None of the 222 individuals had a history of pneumonia, hospitalization, and Oseltamivir administration. Only 10 (4.5%) individuals had a history of seasonal influenza A vaccination in the previous year, and 162 (73%) of them stated that they would like to get a novel influenza A (H1N1) vaccination. Age-distribution of the sero-positive cases indicates that children and young adults were most affected by the virus. Subjects living in households with more family members had higher of seropositivity rates, indicating the importance of intra-household transmission. Among 20 case families, 11 families had 1 case each, 3 families had 2 cases each, and 1 family had 3 cases. Among the 11 families with 1 case each, the mean attack rate was 30%. Among the other 4 families, the mean attack rate was 58%. The difference in seropositivity rates among the areas is consistent with the survey data (Table 2). Using serologic data as a gold standard, our survey showed that ARI has a sensitivity of 70%, a specificity of 59%, and a positive predictive value of 15%.

DISCUSSIONS AND CONCLUSIONS

In Thailand, the first wave of the 2009 H1N1 influenza pandemic peaked in mid-July, and the low level of transmission activities lasted until October 2009. During late

December 2009 to early January 2010, the rising trend in the influenza pandemic signaled an upcoming second wave of the pandemic in Thailand (Figure 3). In all the studied areas, the outbreaks subsided to an insignificant level by the time blood samples were obtained. So the seroprevalence rate reflected the cumulative incidence of the novel H1N1 influenza infections toward the end of the first wave.

It is not clear why the epidemic declined with herd immunity levels of as low as <10%. Behavioral changes caused by increased awareness and public campaigns may have contributed to this pattern (Neumann et al., 2009; Wiwanitkit, 2009). Weather changes, including reduced rainfall, which usually synchronizes with reduction in seasonal influenza outbreaks, may have also played a role. Another possibility is that the H1N1 pandemic may not have been able to sustain itself in the general population but required continuous sources with higher transmission rates and reproduction numbers of greater than one within the subpopulations. With enough herd immunity within these subpopulations, outbreaks might have been interrupted. Our data that show higher sero-positive rates among children support this hypothesis. However, pharmaceutical and non-pharmaceutical preventions and controls were implemented countrywide during the first pandemic wave. The different levels of saturated infection and immunity in different areas may reflect different timing of deployment of interventions, as areas with delayed onset of outbreak could start interventions earlier in the outbreak, or they may reflect different contact rates and transmission rates, thereby required different levels of herd immunity to stop



Source: Bureau of Epidemiology, Ministry of Public Health, Thailand

Figure 3. Three waves of the 2009 H1N1 influenza pandemic in Thailand. Source: Bureau of Epidemiology, Ministry of Public Health, Thailand.

an outbreak.

Our study showed that the rural areas had smaller proportion of ARI cases than cities did. This finding seems to support the pattern of a spread of pandemic influenza from cities to rural area in the early phase of pandemic, and similar patterns have been observed in many countries (Hien et al., 2009; Lopez-Cervantes et al., 2009; Yasuda and Suzuki, 2009). However, the different perceivable to ARI symptoms between city and rural people and the survey without serologic confirmation in countrywide were not allowed to conclude the spread of pandemic influenza A (H1N1) 2009 from cities to rural area. In addition, we found inadequacy of non-pharmaceutical prevention measures in the families that reported at least one ARI case. Therefore household transmission of influenza virus was inevitable, and sick children served as effective spreaders in families (Appuhamy et al., 2009; Health Protection Agency, 2009).

The limited sensitivity of a questionnaire to detect pandemic influenza infection was likely due to asymptomatic infections or mild infections, which may have been discounted. In an outbreak in a military camp in Thailand, in which all subjects were tested for H1N1 pandemic influenza-specific antibody response, we found an asymptomatic infection rate to be just under

30% of all reported infections (Wattanasak, 2010). Nevertheless, survey results are predictive enough to show good correlation with data in official reporting system. This gave a rather constant ratio of extrapolated total cases to reported cases of 275:1. This ratio is very useful for estimation of total cases and of the impact of the outbreak from the existing reporting system all over the country. This information is important for policy makers and for strategic implementation of outbreak control measures.

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Serological Response to the 2009 Pandemic Influenza A (H1N1) Virus for Disease Diagnosis and Estimating the Infection Rate in Thai Population

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Abstract

Background: Individuals infected with the 2009 pandemic virus A(H1N1) developed serological response which can be measured by hemagglutination-inhibition (HI) and microneutralization (microNT) assays.

Methodology/Principal Findings: MicroNT and HI assays for specific antibody to the 2009 pandemic virus were conducted in serum samples collected at the end of the first epidemic wave from various groups of Thai people: laboratory confirmed cases, blood donors and health care workers (HCW) in Bangkok and neighboring province, general population in the North and the South, as well as archival sera collected at pre- and post-vaccination from vaccinees who received influenza vaccine of the 2006 season. This study demonstrated that goose erythrocytes yielded comparable HI antibody titer as compared to turkey erythrocytes. In contrast to the standard protocol, our investigation found out the necessity to eliminate nonspecific inhibitor present in the test sera by receptor destroying enzyme (RDE) prior to performing microNT assay. The investigation in pre-pandemic serum samples showed that HI antibody was more specific to the 2009 pandemic virus than NT antibody. Based on data from pre-pandemic sera together with those from the laboratory confirmed cases, HI antibody titers ≥ 40 for adults and ≥ 20 for children could be used as the cut-off level to differentiate between the individuals with or without past infection by the 2009 pandemic virus.

Conclusions/Significance: Based on the cut-off criteria, the infection rates of 7 and 12.8% were estimated in blood donors and HCW, respectively after the first wave of the 2009 influenza pandemic. Among general population, the infection rate of 58.6% was found in children versus 3.1% in adults.

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Introduction

There were 3 influenza pandemics occurring in the last century, i.e., Spanish influenza A (H1N1) in 1918, Asian influenza A (H2N2) in 1957 and Hong Kong influenza A (H3N2) in 1968 [1]. The influenza pandemic phase of this century, as declared by the World Health Organization (WHO) on 11th June 2009, was caused by A (H1N1) virus [2], a reassortant derived from influenza viruses of 4 origins: classical swine, European swine, avian, and human influenza viruses [3]. Epidemiological studies of the 2009

pandemic showed that the disease is more common in children [4,5]. Death mostly occurred in patients with underlying conditions, such as pregnancy, obesity, diabetes, hematological malignancy and cardiopulmonary dysfunction [6–9].

It is necessary to estimate and predict the magnitude of the pandemic in various regions worldwide, either by case based or serological based surveillance. However, the serological surveys were estimated to be approximately 10 times more sensitive than the clinical surveillance for determining infection rate of the pandemic virus [10,11]. HI assay employing turkey erythrocytes

was conducted; and the HI antibody titers ≥ 32 or ≥ 40 were established as the cut-off levels to estimate the infection rates in populations by various groups of investigators [10–13]. This cut-off titer was established based on the WHO guideline for vaccine evaluation which suggested HI antibody titers ≥ 40 as the levels indicating 50% protection [14,15]. Moreover, microNT assay had been conducted in parallel in order to determine the protection correlation, and it was suggested that the HI antibody titer 40 was correlated to the NT titer 160 in adults or 40 in children [13].

On 10th August 2010, WHO announced the beginning of the post-pandemic phase of the 2009 pandemic influenza. Nevertheless, epidemiological data from the Bureau of Epidemiology of Thailand suggested that only one fourth of the Thai population had been infected by this novel virus after it was introduced into Thailand at the beginning of May 2009 until December 2009. The data suggested that Southeast Asian countries and some other parts of the world might still be vulnerable to the new attack by that time.

The present study aimed to establish the cut-off HI and NT antibody titers that could differentiate between individuals with or without past infection by the 2009 pandemic influenza. We demonstrated that erythrocytes from goose yielded comparable HI antibody titers as those from turkey, an animal species that is not common in Southeast Asian countries. Moreover, we showed that it is necessary to treat human sera with receptor destroying enzyme (RDE) before running microNT assay. This RDE treatment is usually not included in the microNT protocol generally employed for testing human sera in most laboratories [10,13,16,17]. Our established cut-off titers were applied in the seroepidemiological surveillance to estimate the infection rate in different groups of the Thai populations after subsidence of the first epidemic wave.

Materials and Methods

Ethical issues

This study was approved by two Ethical Committees: Siriraj Institutional Review Board, Faculty of Medicine Siriraj Hospital, Mahidol University and the Ministry of Public Health Review Board. Adult subjects signed in consent form for participation. With ascent from children subjects, their parents signed the consent form for them.

Subjects

Serum samples tested in this study were collected from 5 groups of subjects. The first group comprised 80 patients with 2009 pandemic influenza as confirmed by real time reverse transcription-polymerase chain reaction employing the protocol of the US, Centers for Disease Controls [18]. Part of these patients were sent for disease diagnosis by the Bureau of Epidemiology, Department of Disease Control, Ministry of Public Health under public health emergency service; and part of them were sent anonymously from the clinic sites under the Southeast Asia Infectious Disease Clinical Research Network, Thailand. The second group comprised 100 anonymous blood donors of the National Blood Center, the Thai Red Cross Society, Bangkok. All were bled within the same day in September 2009. Small aliquots of blood were subjected to anti-HIV testing; and the leftovers were provided for this study. The third group comprised 258 healthcare workers (HCW) from two hospitals: Siriraj Hospital, Bangkok and Thammasat University Hospital in Pathum Thani, the neighboring province of Bangkok. These HCW were exposed to patients suspected of the 2009 pandemic influenza and/or to the laboratory confirmed cases during their duty. The fourth group comprised 222 general

population from two provinces, Chiang Mai (696 km. north from Bangkok) and Nakhon Si Thammarat (780 km. south from Bangkok), whose ages were older than 5 years. These two provinces were selected based on highest numbers of reported cases in the region; and in each province, the random samples were collected in the community-based setting during the opinion survey in a district that high number of cases was reported. The test samples also included anonymously archival sera collected during pre-pandemic period from vaccinees whose ages were at range of 21–49 years. The vaccinees received inactivated influenza vaccine of the 2006 season which contained 15 µg of hemagglutinin antigen of A/New Caledonia/20/1999(H1N1)-like strain (A/New Caledonia), A/Wellington/1/2004(H3N2)-like strain, and B/Shanghai/361/2002-like strain (Government Pharmaceutical Organization-Merieux Biological Products Co., Ltd., Bangkok). Details regarding subjects who participated in this study are shown in Table 1.

Blood samples

Paired bloods were collected from the patients, and single blood samples were collected from the other groups of subjects. Acute blood samples were collected mostly within 7 days; meanwhile, the convalescent samples were collected at between 11 to 54 days after onset of illness. Serum was separated, aliquot and kept frozen at -20 C until tested.

Regarding archival sera, the pre-vaccinated blood samples were collected just before vaccination; and the post-vaccinated blood samples were collected at one month later.

The study virus

A/Thailand/104/2009(H1N1) propagated in MDCK cells was used as the test virus for both HI and microNT assays. Full genomic sequence of this isolate can be retrieved from the GenBank database. The H genomic sequence of this virus was 99.7% identity to that of A/California/7/2009 pandemic virus (data not shown).

Reference serum

A reference human serum from the National Institute for Biological Standards and Control (NIBSC), UK was used for standardizing our serological methods. Based on the investigation performed by various laboratories under the International Collaborative Study, this reference serum had the overall geometric mean titer (GMT) of 183 by HI and 516 by microNT assays (NIBSC package insert). The HI GMT titer 183 implies that the results of HI titers obtained from those laboratories varied between 160 and 320. Similarly, the NT GMT titer 516 implies that the results of NT titers varied between 320 and 640.

Hemagglutination (HA) assay

HA assay was performed in order to measure the amount of hemagglutinin antigen present in the test virus suspension prior to running HI assay [17]. The test virus was serially twofold diluted with phosphate buffered saline (PBS) in a volume of 50 µl/well in duplicate. Fifty µl of 0.5% goose or 0.5% turkey erythrocyte suspension was added into the test wells and incubated for 30 minutes at 4 C before hemagglutinating result was determined. One HA unit of the test virus was defined as the highest virus dilution that displayed complete hemagglutinating activity.

Hemagglutination inhibition (HI) assay

HI assay was performed as previously described [17,19–21]. Fifty µl of the test serum were mixed with 150 µl of RDE (Denka

Table 1. Subjects and time of specimen collection.

Subjects	No. of subjects	Age (years)			Time at specimen collection
		Mean	Median	Range	
Vaccinees who received seasonal influenza	71	33.6	31	21–49	Dec 2005 - Mar 2006 (pre-vaccination) Jan - Apr 2006 (post-vaccination)
Patients					
- Pediatrics	36	10.6	12.5	2–15	June 2009 – Feb 2010
- Adults	44	23.6	21	18–62	June 2009 – Feb 2010
Blood donors	100	35.7	34.5	17–60	Sep 2009
Health care workers	258	35.3	34	20–61	Oct 2009
General population (Chiang Mai)					
- Children	11	9.8	10	7–13	Dec 2009
- Adults	99	49.3	52	15–89	Dec 2009
General population (Nakhon Si Thammarat)					
- Children	18	10.1	10.5	5–14	Dec 2009
- Adults	94	49.5	48	15–87	Dec 2009

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Seiken, Tokyo, Japan) and incubated overnight in water bath at 37°C for eliminating the nonspecific inhibitors. This step was followed by heat inactivation at 56°C for 30 minutes, and removal of nonspecific agglutinator by absorbing with the test erythrocytes for 1 hour at 4°C. The replicating virus at final concentration of 4 HA units/25 µl was used as the test antigen; and goose or turkey erythrocytes were used as the indicator. The treated serum was twofold serially diluted in duplicate wells of a microtiter V shaped plate at an initial dilution of 1:10; and 25 µl of the diluted serum were incubated with 25 µl of the test antigen for 30 minutes at room temperature. Thereafter, the reaction wells were added with 50 µl of 0.5% goose or 0.5% turkey erythrocyte suspension and further incubated for 30 minutes at 4°C before the HI antibody titers were determined. HI antibody titer is defined as the reciprocal of the highest serum dilution that completely inhibits hemagglutination reaction. Reference/positive control serum with known HI titer, the serum control and back titration of virus antigen were included in each run. For calculating GMT, the antibody titer <10 was assigned as 5, and the titer ≥2560 was assigned as 2560.

Microneutralization (microNT) assay

ELISA based microNT assay was performed as described previously [17,19–21]. The test sera were treated by any of the following two protocols. The first one was the standard protocol employing only heat inactivation of the native sera at 56°C for 30 minutes; and the second one employed RDE treatment similar to that mentioned above for HI assay. Briefly, 50 µl of the test serum were mixed with 150 µl of RDE and incubated overnight in water bath at 37°C followed by heat inactivation at 56°C for 30 minutes. The treated sera were twofold serially diluted in duplicate and incubated with the test virus at final concentration of 100TCID50/100 µl for 2 hours at 37°C. The serum-virus mixture was transferred onto MDCK monolayer maintained in minimum essential medium supplemented with trypsin TPCK (Sigma, St.Louis, MO) for 24 hours. The reaction plate was tested by ELISA for presence of the viral nucleoprotein using mouse specific monoclonal antibody (Chemicon, Temecula, CA) as the primary antibody and goat anti-mouse IgG (Southern Biotech, Birmingham,

AL) as the secondary antibody. Antibody titer is defined as reciprocal of the highest serum dilution that reduces ≥50% of the amount of viral nucleoprotein in the reaction wells as compared to the virus control wells. For calculating GMT, the antibody titer <10 was assigned as 5, and the titer ≥2560 was assigned as 2560.

Results

Goose and turkey erythrocytes yielded comparable HI antibody titers

In order to determine that goose and turkey erythrocytes yielded comparable HI antibody titers, the reference human serum from the NIBSC which contains HI antibody at GMT 183 was assayed in duplicate by 6 scientists using goose and turkey erythrocytes in parallel experiments. The HI antibody titer 160 was obtained from all 6 scientists as using either one of both erythrocyte species. The comparison was further extended to include the acute and convalescent serum samples from 53 patients as well as single serum samples from 100 HCW. The analysis on the total number of 206 serum samples showed that goose and turkey erythrocytes yielded comparable HI titers with $r=0.96$ (Spearman's rank, $p<0.0001$) (Figure 1). The number of samples with HI antibody titers ≥40, as well as the ratio between convalescent to acute antibody titers, and the number of samples showing a fourfold or greater rise in HI antibody titer, were similar when goose or turkey erythrocytes were used (Table 2). Based on comparable HI titers obtained by the two erythrocyte species as well as our convenience to obtain goose erythrocytes; therefore, goose erythrocytes were employed in the subsequent experiments of our HI assay.

RDE treated serum was required for microNT assay

We recognized that microNT assay using RDE untreated sera yielded an unusually high level of NT antibody to the 2009 pandemic virus in the test sera which had no HI antibody. Therefore, the serum samples were treated with RDE and retested again. The result showed that the RDE treated sera from all serum settings showed a marked decrease in level of NT antibody titer when compared to the RDE untreated samples (Wilcoxon Signed

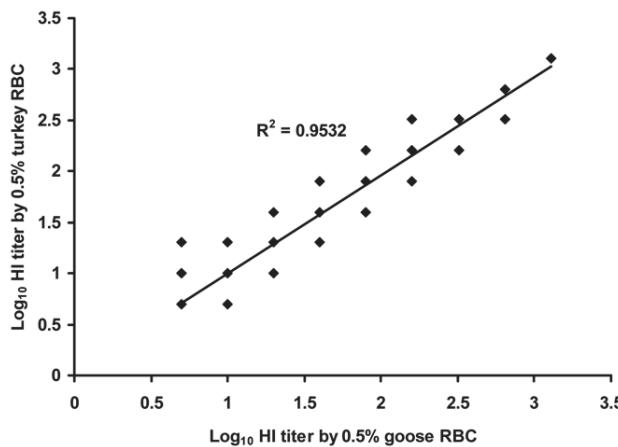


Figure 1. Correlation between HI antibody titers obtained from goose and turkey erythrocytes by HI assays.

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Ranks test, $p < 0.05$) (Table 3). Therefore, the RDE treated sera were employed subsequently.

Moreover, the reference human serum from NIBSC which harbored NT antibody at GMT 516 was assayed in parallel by our two scientists using RDE treated serum as well as the untreated serum control in triplicate experiments. The GMT 640 was obtained either with the RDE treated or untreated serum.

Cross-reactive antibody to the 2009 pandemic virus in pre-pandemic serum samples

Information about serological response in our vaccinees who received influenza vaccines during the pre-pandemic period had been published previously [22]. Among 71 tested sera, 98.6% developed a fourfold or greater rise in HI antibody titer against A/New Caledonia, a component of the immunizing vaccine (Table 4). Herein, those serum samples were investigated for serological response against the 2009 pandemic virus; and it was found that 16.9% of the vaccinees developed seroconversion as determined by HI assay. Six (8.4%) subjects seroconverted with HI titer rising from ≤ 10 to ≥ 40 . Cross-reactive HI antibody titer 80 was found

in one (1.4%) pre-vaccinated serum sample; nevertheless, post-vaccinated serum from this subject did not increase in antibody titer against the 2009 pandemic virus. At post-vaccination, number of subjects with the cross-reactive HI antibody ≥ 40 increased to 8 (11.3%). Regarding microNT assay, 16 (22.5%) developed a fourfold or greater rise in antibody titer (convalescent titer ≥ 40) in post-vaccination sera. Our study demonstrated broader cross-reactivity of NT antibody than HI antibody.

HI and NT antibody response in patients infected with the 2009 pandemic influenza virus

HI and NT antibody response in the patients by days after onset of illness is shown in Figure 2. Positive correlation with $r = 0.85$ (Spearman's rank, $p < 0.0001$) was found between the two assays. Seroconversion or a fourfold or greater rise in HI or NT antibody titers could be demonstrated when convalescent blood samples were collected at 11 days earliest after disease onset. Among 36 pediatric cases, 32 (88.9%) developed seroconversion (Table 5). The other 4 cases already contained high HI titers ≥ 40 in their first blood samples. And among 32 seroconverters, 5 cases (13.9%) seroconverted with HI titers rising from < 10 to 20; and the remaining 29 cases seroconverted with convalescent titers ≥ 40 . Therefore, the HI titers ≥ 20 were found in 100%, and HI titer ≥ 40 were found in 86.1% of the pediatric patients. Similarly, the NT titers ≥ 20 were found in 97.2% and NT titer ≥ 40 were found in 94.4%.

Among 44 adult patients, 43 (97.7%), developed HI titers ≥ 40 in their convalescent sera. There was one adult patient who could not develop significant HI antibody response (HI titer < 10 and 10), although he possessed NT antibody titer of 20 and 80. The convalescent NT titers ≥ 80 were found in all adult patients.

Estimation of the infection rate of the 2009 pandemic influenza after the first epidemic wave

Regarding titers of HI antibody found in the patients together with the data showing the absence of HI antibody in all except one pre-pandemic serum samples, the cut-off HI antibody titers ≥ 20 for pediatric cases and ≥ 40 for adult patients were established to indicate past infection by the 2009 pandemic virus. The established criteria had been used to estimate the infection rate of the 2009 pandemic influenza in various groups of populations;

Table 2. Comparison between HI antibody titers obtained from goose and turkey erythrocytes.

Subjects	HI assay with	Number of sera test	Blood	GMT (95% CI)	No. with HI titers ≥ 40	No. with 4-fold rising Ab titer (%)	Ratio Conv./Acute
Patients	0.5% turkey RBC	Children = 29	Acute	14 (8–25)	7		
			Convalescent	111 (78–158)	28	23 (79.3)	7.6
		Adults = 24	Acute	15 (7–29)	6		
			Convalescent	87 (53–141)	22	19 (79.2)	5.8
	0.5% goose RBC	Children = 29	Acute	15 (8–27)	8		
			Convalescent	106 (72–157)	27	24 (82.8)	6.9
Health care workers	0.5% turkey RBC	Adults = 100	Acute	14 (7–28)	6		
			Convalescent	89 (55–145)	22	19 (79.2)	6.4
	0.5% goose RBC	Adults = 100	Single blood	9 (7–10)	14	NA	NA
			Single blood	9 (7–11)	15	NA	NA

Note: A/Thailand/104/2009(H1N1) was used as the test virus. GMT = geometric mean titer, CI = confidence intervals, RBC = red blood cells,

NA = Not applicable

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Table 3. Comparison between NT antibody titers obtained from RDE treated and RDE untreated sera.

Subjects	No. of subjects	Blood samples	RDE treatment	Number of cases at NT antibody of										GMT* (95% CI)
				<10	10	20	40	80	160	320	640	≥1280		
Patients	80	Acute	Yes	9	30	8	3	8	12	3	4	3		33 (23–47)
			No	0	0	0	7	18	21	22	5	7		191 (155–236)
	80	Convalescent	Yes	0	1	1	3	14	23	22	9	7		214 (172–267)
			No	0	0	0	1	2	11	36	22	8		380 (326–443)
General population	222	Single blood	Yes	15	87	46	33	24	10	5	2	0		21 (18–24)
			No	0	0	0	103	88	22	5	3	1		66 (61–72)
Vaccinees	71	Pre-vaccination	Yes	22	34	6	7	0	1	0	1	0		10 (8–13)
			No	0	0	1	5	33	27	2	3	0		110 (95–127)
	71	Post-vaccination	Yes	3	19	24	16	6	1	1	1	1		23 (18–28)
			No	0	0	0	0	24	34	8	4	1		152 (131–176)
Blood donors	100	Single blood	Yes	10	40	19	16	6	7	2	0	0		19 (16–24)
			No	0	0	0	1	29	60	10	0	0		138 (126–150)
Health care workers	258	Single blood	Yes	14	116	61	35	15	12	1	4	0		19 (16–21)
			No	0	0	0	10	81	127	34	5	1		138 (129–148)

*There are significant differences between GMT of NT antibodies in RDE treated and untreated sera from all 7 serum settings (Wilcoxon Signed Ranks test, $p<0.05$).
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and it was found that 7.0% of blood donors and 12.8% of HCW had been infected with the pandemic virus by the end of the first epidemic wave (Table 6). Magnitude of the infection in the general population residing in the North and the South of Thailand was similar. In these two populations, the infection rates were much higher in children (17 of 29) than adults (6 of 193), i.e., 58.6 versus 3.1%, respectively.

It was not easy to establish the cut-off NT antibody titer owing to presence of cross-reactive NT antibody at high titers in the pre-pandemic serum samples collected from vaccinees whose ages were under 50 years, and also in general people who had no HI antibody against the 2009 pandemic virus. Poorer correlation

between HI and NT antibody was found in this group of subject ($r=0.32$: Spearman's rank, $p<0.0001$) (data not shown).

Discussion

Herein, HI and microNT assays that were suitable for a Southeast Asian country had been established to estimate the infection rate of the 2009 pandemic influenza in Thai people after subsidence of the first epidemic wave. HI assay has long been used for serodiagnosis of influenza virus infection, vaccine evaluation, and vaccine strain selection [16,23,24]. It was noted that sensitivity of the HI assay could be affected by the erythrocyte species

Table 4. Cross-reactive antibody to the 2009 pandemic A (H1N1) influenza virus in vaccinees who received trivalent influenza vaccine of the 2006 season (N = 71).

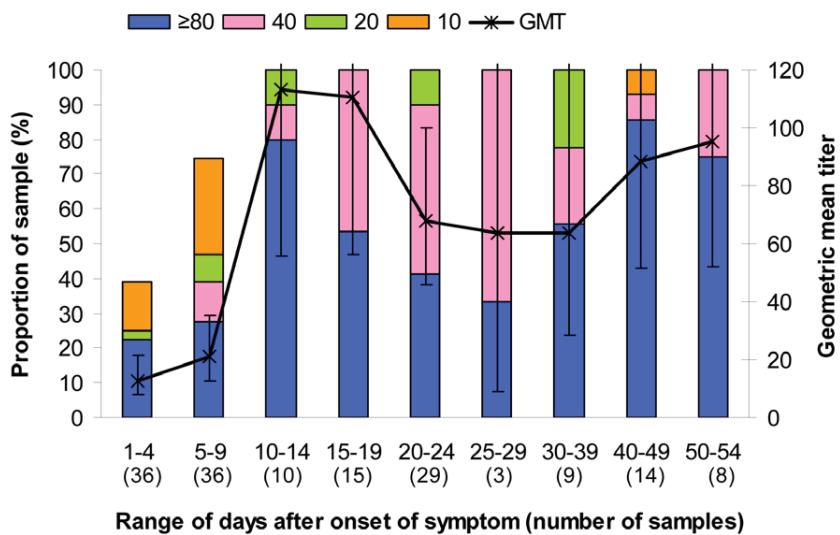
Test viruses	Assays	Number of cases with antibody titer of										Post- to pre-vaccination ratio	No. with ≥4 folded rise in Ab titer ^a (%)
		<10	10	20	40	80	160	320	640	GMT (95% CI)			
A/New Caledonia/20/99-like (H1N1)													
Pre-vaccination	HI	43	8	9	10	0	0	1	0	9 (7–11)			
Post-vaccination	HI	0	0	1	1	8	13	15	33	310 (254–379)	34		70 (98.6) ^b
A/Thailand/104/09 (H1N1)													
Pre-vaccination	HI	64	5	1	0	1	0	0	0	5 (5–6)			
Post-vaccination	HI	43	12	8	2	3	2	1	0	9 (7–11)	2		6 (8.4)
Pre-vaccination	microNT	22	34	6	7	0	1	0	1	10 (8–13)			
Post-vaccination	microNT	3	19	24	16	6	1	1	1	23 (18–28)	2		16 (22.5)

^aSeroconversion with post-vaccination antibody titer ≥ 40 to the 2009 pandemic virus.

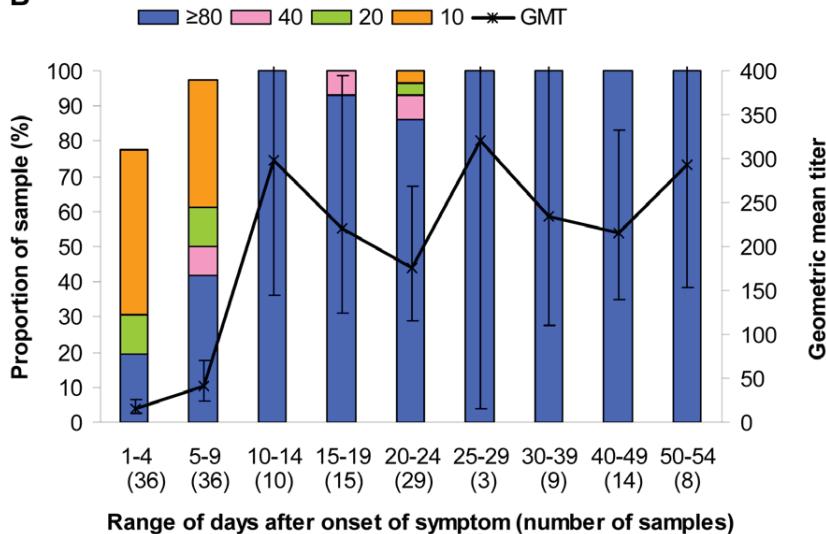
^bA/New Caledonia/20/99 was used as the test antigen.

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A

Range of days after onset of symptom (number of samples)

B

Range of days after onset of symptom (number of samples)

Figure 2. Antibody titers by date after onset of symptom. (A) HI antibody titer; (B) NT antibody titer. Colored stacked bars give the proportion with titers of 10, 20, 40 and ≥ 80 while the line denotes the geometric mean titer with error bars indicating 95% confidence intervals.
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employed. Stephensen, et al [25] previously reported that horse erythrocytes were more sensitive than turkey erythrocytes in the detection of HI antibody to H5N1 highly pathogenic avian influenza (HPAI) virus. Since there was difficulty in accessing both horse and turkey erythrocytes in Thailand, we previously looked for the alternative erythrocyte species and found that goose erythrocytes yielded comparable results in both HA and HI assays [19]. Similarly, the present study showed that goose erythrocytes could replace turkey erythrocytes for detection of HI antibody to the 2009 pandemic influenza virus. Our preliminary study on 206 serum samples as well as the reference serum from NIBSC demonstrated good correlation between HI titers employing either goose or turkey erythrocytes. This finding is an advantage for laboratories in Southeast Asian countries where goose erythrocytes have long been used in HI assay for diagnosis of dengue,

chikungunya and Japanese encephalitis, the endemic diseases in this region. It was also demonstrated that the hemagglutination pattern of goose was also clearer than that of turkey erythrocytes.

A number of laboratories performed microNT in adjunct with HI assay in a seroepidemiological study, but the step of serum treatment with RDE was not included [10,13]. In contrast, our study showed that NT GMT titer in the test sera without RDE treatment was significantly higher than that employed the RDE treated sera. Collectively, RDE is used for removal of nonspecific inhibitor from the test sera, in which its presence may lead to false positive result in HI as well as microNT assays as shown by this study. On the other hand, the presence of this nonspecific inhibitor did not affect our result on using RDE untreated sera in microNT assay for antibody against H5N1 HPAI virus. Cross-reactive H5N1 antibody, even at low level, was rare [20,21,26]. Therefore,

Table 5. HI and NT antibody response in patients infected with the 2009 pandemic influenza virus.

Patients	Assays	Blood samples	No. of cases at antibody titer of											Ratio of Conv./Acute	No. with ≥ 4 folded rise in Ab titers (%)
			<10	10	20	40	80	160	320	640	1280	2560	GMT (95% CI)		
Children (N = 36)	HI	Acute	19	8	1	2	1	3	2	0	0	0	12 (7–19)	6.3	32 (88.9%)
		Conv.	0	0	5	12	10	3	1	4	1	0	78 (53–114)		
	microNT	Acute	5	20	2	1	5	3	0	0	0	0	16 (11–23)	10.9	31 (86.1%)
		Conv.	0	1	1	3	9	6	8	4	4	0	179 (119–269)		
Adults (N = 44)	HI	Acute	15	4	4	3	8	5	2	2	1	0	29 (17–48)	38.1	24 (54.5%)
		Conv.	0	1	0	16	15	6	3	2	1	0	83 (63–111)		
	microNT	Acute	4	10	6	2	3	9	3	4	2	1	58 (33–100)	4.3	23 (52.3%)
		Conv.	0	0	0	0	5	17	14	5	3	0	248 (199–310)		

Note: Number of pediatric patients with convalescent HI titers $\geq 20 = 36/36$ (100.0%).Number of adult patients with convalescent HI titers $\geq 40 = 43/44$ (97.7%).

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it is postulated that HPAI H5N1 and the 2009 pandemic viruses bind to different species of nonspecific inhibitor.

Investigation in pre-pandemic serum samples demonstrated that NT antibody is broader in activity than HI antibody; however, both cross-reactive HI and NT titers could be increased by seasonal influenza vaccination. Similarly, Hancock, et al. [13] previously reported a fourfold or greater increase in cross-reactive antibody to the 2009 pandemic virus in archival serum samples from adult recipients of trivalent inactivated influenza vaccines during 2007–2009 seasons. A fourfold or greater increase in cross-reactive HI antibody was found in 7% among vaccinees of age 18–64 years, but it was as high as 22% for cross-reactive NT antibody. This cross-reactive antibody was rarely found in young children in

their study. Our group previously reported that 5.2% of the elderly who received seasonal influenza vaccine seroconverted to HPAI H5N1 virus as determined by microNT assay [27]. Nevertheless, the studies from U.S. and Australia concluded that vaccination with seasonal influenza vaccine did not protect against the current pandemic [13,28]. In contrast, partial protection conferred through seasonal influenza vaccination was reported by the other group of investigators [29]. Frequency of cross-reactive NT antibody was high in Thai and U.S. population [13]; and it was as low as 0.3% in Chinese [12]. However, it is well accepted that NT antibody activity is broader than HI antibody. HI antibody recognizes small epitopes in erythrocyte binding site, while NT antibodies recognize the epitopes in HA1 variable domain of the

Table 6. Estimation on the infection rates of the 2009 pandemic influenza in different groups of subjects after the first epidemic wave.

Subjects	Assays	No. of cases at antibody titer of								Infection rate (%)	GMT (95% CI)
		<10	10	20	40	80	160	320	640		
Blood donors (N = 100)	HI	81	7	5	7	0	0	0	0	7 (7.0)	6 (5–7)
	microNT	10	40	19	16	6	7	2	0	33 (12.8)	8 (7–9)
Health care workers (N = 258)	HI	177	26	22	16	12	5	0	0		
	microNT	14	116	61	35	15	12	1	4	19 (16–21)	19 (16–21)
General population (Chiang Mai, N = 110)											
- Children (N = 11)	HI	2	0	1	4	2	2	0	0	9 (81.8)	37 (17–82)
- Adults (N = 99)	HI	86	8	2	3	0	0	0	0	3 (3.0)	5 (5–6)
- Children (N = 11)	microNT	0	1	1	0	2	2	3	2	141 (57–348)	141 (57–348)
- Adults (N = 99)	microNT	2	40	24	16	11	4	2	0		
General population (Nakhon Si Thammarat, N = 112)											
- Children (N = 18)	HI	10	0	2	2	4	0	0	0	8 (44.4)	13 (7–24)
- Adults (N = 94)	HI	81	6	4	3	0	0	0	0	3 (3.2)	5 (5–6)
- Children (N = 18)	microNT	2	7	4	2	1	2	0	0	19 (11–32)	19 (11–32)
- Adults (N = 94)	microNT	11	39	17	15	10	2	0	0		

Infection rate is determined by HI titer ≥ 40 in adults or ≥ 20 in children.

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hemagglutinin molecule as well as the epitopes in HA2 domain which is conserved across influenza A subtypes [30–32].

Only one (2.3%) of our 44 adult patients failed to mount HI antibody titers ≥ 40 in their convalescent blood. Meanwhile, Miller, et al [10] demonstrated that HI assay failed to diagnose 10.9% of laboratory confirmed cases in their setting as the cut-off point ≥ 32 was employed. According to Millers, et al, the adult and pediatric patients were not separately analyzed; and the HI titers 32 or greater were found in 89.1% of their patients. In our study, if the data from pediatric and adult patients was pooled and analyzed together, the HI titer 40 or greater will be found in 92.5% of our patients. Regarding the study by Chen, et al [33], the HI titers 40 or greater were found in 93% of their adult patients if the convalescent blood samples were collected at peak between 25 and 29 days after onset of symptom.

Our study decided to use the HI antibody at cut-off titers ≥ 40 for adults and ≥ 20 for children to differentiate between individuals with and without past infection by the 2009 pandemic influenza. The cut-off titer for NT antibody could not be established because frequency of the cross-reactive NT titers was high as shown from the result of investigation in pre-pandemic sera obtained from vaccinees of age younger than 50 years, and additionally, from the high number of general adult population who had no HI antibody, but possessed NT titer ≥ 40 . Based on our criteria, magnitudes of the 2009 pandemic influenza after the first epidemic wave were around 7% in blood donors and 12.8% in HCW. Eventually, the infection rate in general population was much higher in children than adults, i.e., 58.6% (17/29) versus 3.1% (6/193), which is suggestive of susceptibility of children and partial protection from pre-existing immunity in Thai adults. In United Kingdom, seroincidence rate of the 2009 pandemic influenza was also high in children [10]. Seroepidemiological data from Pittsburgh, U.S. showed that approximately 21% of population was infected following the second epidemic wave [34]. Estimation on the infection rates based on serological data may be affected by confounding factor of cross-reactive antibody-rising from seasonal influenza vaccination; and probably from pre-existing antibody against the 1957 influenza A (H1N1) virus. Nevertheless, this effect may be not drastic in the Thai population

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owing to less than 1% coverage of seasonal influenza vaccination among the Thai population. In addition, most of our adult subjects were younger than 50 years, therefore, cross-reactive antibody owing to previous infection by the 1918 influenza A (H1N1) virus was excluded.

Thailand reported the first two imported cases from Mexico in the beginning of May 2009. Subsequently, the virus was reintroduced into the country both by groups of tourists and Thai students who returned from Europe and America. The first epidemic wave began in late May, peaked in July and almost disappeared in November 2009. The first wave was followed by a short period of the second epidemic wave during December 2009 to April 2010 with peak in February. The third epidemic wave which lasted between June and October with peak in August 2010 was more serious than the second one. Serosurveillance nationwide will help the estimation for number of vulnerable people and immunity of the population to this pandemic virus. The 2009 pandemic monovalent vaccine was introduced into Thailand in December 2009; and trivalent vaccine containing the 2009 pandemic virus as a component has been introduced into the country in June 2010. Nevertheless, the vaccine coverage was less than 3% of the Thai population. Therefore, cross-reactive HI antibody due to the pandemic virus might have least effect on the estimated infection rate in the present study.

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Author Contributions

Conceived and designed the experiments: P. Puthavathana. Performed the experiments: HL P. Pooruk SK PN. Analyzed the data: HL P. Puthavathana. Wrote the paper: P. Puthavathana HL SI. Specimen providers: CP AM SI PT UK PA KC SO WP PS TC CS SL. Processing on ethical issue: PA. Veterinarian: WW.

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Short communication

Erythrocyte binding preference of 16 subtypes of low pathogenic avian influenza and 2009 pandemic influenza A (H1N1) viruses

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ABSTRACT

All 16 subtypes of avian influenza viruses of low pathogenicity (LPAIV) as well as their hemagglutinin (H) antigens, and four 2009 pandemic influenza A (H1N1) virus isolates were assayed for hemagglutinating activity against 5 erythrocyte species: goose, guinea pig, human group O, chicken and horse. Of all viruses and antigens assayed, the highest hemagglutination (HA) titers were obtained with goose and guinea pig erythrocytes. Hemagglutinating activity of replicating LPAIV and LPAIV antigens decreased, in order, with chicken and human group O; meanwhile, horse erythrocytes yielded lowest or no HA titer. Moreover, the 2009 pandemic viruses did not agglutinate both horse and chicken erythrocytes. Our study concluded that goose and guinea pig erythrocytes are the best in HA assay for all subtypes of influenza viruses.

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1. Introduction

Hemagglutinating activity of influenza viruses is mediated by binding of hemagglutinin surface glycoprotein and sialic acid receptors on erythrocyte surface membrane; that can be measured by HA assay which is the basis for recognition of the virus isolates (Ito et al., 1997). Additionally, adhering of erythrocytes on the cell monolayer inoculated with clinical sample is also suggestive of positive virus isolation; this reaction is known as hemadsorption assay. HA assay is performed for virus titration prior to running hemagglutination-inhibition (HI) assay for specific antibody detection (Webster et al., 2002). The importance of erythrocyte species in HA and HI assays has come into consideration after several occasions of

cross-species transmission of avian influenza viruses to human populations (Subbarao and Shaw, 2000).

At present, 16 H subtypes and 9 neuraminidase (N) subtypes of influenza A viruses have been discovered. All of these subtypes are found in aquatic birds; therefore, it is believed that these viruses are ancestors of all those that cause infection in man and other animal species (Webster, 1998). However, most of avian viruses are of low virulence, with exception of some isolates in H5 and H7 subtypes that are recognized as highly pathogenic avian influenza viruses (HPAIV). Both subtypes were evidenced for cross-species transmission from avian to man (Liu, 2006; Myers et al., 2007). However, the subtypes that are currently known as human viruses comprise only H1N1 and H3N2 subtypes (Brockwell-Staats et al., 2009). Humans are seldom vulnerable to LPAIV. Nevertheless, sporadic human infections with LPAIV H7N2, H7N3, H7N7, H9N2 and H10N7 had been reported without death (Kalthoff et al., 2010). On the other hand, it is well documented that LPAIV was the ancestors of HPAIV.

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Through reassortment events, the avian virus H5N1 which originated in Hong Kong in 1997 received *H* gene from A/goose/Guangdong/1/1996 (H5N1) (A/Gd), *N* gene from A/teal/Hong Kong/W312/1997 (H6N1)-like viruses and the 6 internal genes from A/quail/Hong Kong/G1/1997 (H9N2)-like or A/teal/Hong Kong/W312/1997 (H6N1)-like viruses (Hatta and Kawaoka, 2002; Subbarao and Shaw, 2000). A/Gd was also the gene donor for *H* and *N* genomic segments of the current H5N1 virus.

Our group previously investigated hemagglutinating activity of HPAIV H5N1 against 5 erythrocyte species: horse, goose, chicken, guinea pig and human O cells and found that goose cells yielded the highest HA titer, and was followed in order by chicken, guinea pig, human O and horse cells. Meanwhile, human viruses H1N1 and H3N2 could agglutinate guinea pig erythrocytes at highest titers, but none could agglutinate horse erythrocytes. Additionally, human virus H3N2 isolated in 1998 could agglutinate chicken erythrocytes, but this activity was lost with the 2003 and 2004 H3N2 viral isolates (Louisirirotchanakul et al., 2007; Medeiros et al., 2001; Nobusawa et al., 2000). The present study, then, further explored the hemagglutinating activity of all 16 subtypes of replicating LPAIV, LPAIV antigens as well as the replicating 2009 pandemic A (H1N1) viruses against all 5 erythrocyte species mentioned above.

2. Materials and methods

2.1. Viruses

All 16 subtypes of LPAIV investigated in this study were kindly provided by St. Jude Children Research Laboratory, Tennessee, U.S.A. These viruses were further propagated in embryonated eggs in Thailand; and the replicating viruses were used as the test antigens in HA assay. H antigens from LPAIV used in the assay were purchased from the Veterinary Laboratory Agency, Weybridge, UK. The four 2009 pandemic A (H1N1) viruses were isolated and propagated in MDCK cells at the Siriraj Cooperative

Research Center, Department of Microbiology, Faculty of Medicine Siriraj Hospital, Mahidol University.

2.2. Erythrocyte species

Five erythrocyte species: goose, guinea pig, chicken, horse and human blood group O, were employed in the study. Fresh blood was mixed with Alsever's solution at equal volumes and kept at 4 °C until used within 2 weeks.

2.3. Hemagglutination assay

The procedure was performed as described previously (Louisirirotchanakul et al., 2007; Medeiros et al., 2001; Webster et al., 2002). Different erythrocyte species were tested at different concentrations, i.e., 1% horse, 0.5% goose, 0.5% chicken, 0.75% guinea pig and 0.75% human blood group O cells. These erythrocyte species were suspended in phosphate buffered saline (PBS), pH 7.2, except for that of horse erythrocytes which were suspended in PBS plus 0.5% bovine serum albumin. The same aliquot of each virus subtype was titrated against all 5 erythrocyte species. HA assays employing goose and chicken erythrocytes were performed in V-shaped bottom microtiter plates, while those employing guinea pig, human blood group O and horse erythrocytes were performed in U-shaped bottom microtiter plates. The test viruses/antigens were twofold serially diluted, starting from the dilution 1:2/1:8 and proceeding to 1:1024. A reaction well consisting of 50 µl of test viruses/antigens and 50 µl of erythrocyte suspension was incubated at 4 °C for approximately 45 min before determining the HA titer which is defined as the highest virus dilution that yielded complete hemagglutination of the test erythrocytes.

3. Results

With each LPAIV subtype, three erythrocyte donors from each species were employed in three separate experiments, except that two separate experiments were

Table 1
Hemagglutinating activity of replicating LPAIV.

Viruses	HA titers as determined by erythrocytes from				
	Goose	Guinea pig	Human	Chicken	Horse
A/aquatic bird/Hong Kong/DI25/2002 (H1N1)	256	256	128	128	64
A/wild duck/Shan Tou/992/2000 (H2N8)	256	256	128	128	64
A/duck/Shan Tou/1283/2001 (H3N8)	256	256	128	64	128
A/duck/Shan Tou/461/2000 (H4N9)	512	512	256	256	128
A/duck/Jiangxi/6151/03 (H5N3)	256	256	128	256	64
A/heron/Hong Kong/LC10/2002 (H6N8)	1024	1024	256	256	128
A/strich/Zimbabwe/222/1996 (H7N1)	512	512	256	256	128
A/mallard/Alberta/242/2003 (H8N4)	512	512	256	256	256
A/quail/Hong Kong/G1/1997 (H9N2)	1024	512	256	1024	<2
A/chicken/Hong Kong/G9/1997 (H9N2)	512	512	256	512	<2
A/duck/Hong Kong/Y280/1997 (H9N2)	1024	1024	512	512	<2
A/duck/Shan tou/1796/2001 (H10N8)	256	256	128	128	128
A/duck/Shan tou/1411/2000 (H11N2)	256	512	128	128	128
A/red-necked stint/Australia/5745/1981 (H12N9)	512	512	128	256	128
A/gull/MD/704/1977 (H13N6)	128	128	64	128	<2
A/mallard/Gurjev/263/1982 (H14N5)	1024	1024	256	512	256
A/duck/Australia/341/83(H15N8)	128	256	128	128	32
A/shore bird/DE/172/2006 (H16N3)	128	128	64	128	64

Table 2
Hemagglutinating activity of hemagglutinin antigen of LPAIV.

Viruses ^a	HA titers as determined by erythrocytes from				
	Goose	Guinea pig	Human	Chicken	Horse
A/duck/Alberta/35/1976 (H1N1)	512	512	256	256	<8
A/duck/Germany/1215/1973 (H2N3)	512	512	512	512	128
A/turkey/England/1969 (H3N2)	1024	1024	512	512	256
A/duck/Czech/1956 (H4N6)	512	512	256	512	128
A/ostrich/Denmark/72420/1996 (H5N2)	512	512	256	512	64
A/turkey/England/647/1977 (H7N7)	512	512	256	512	64
A/turkey/Ontario/6118/1968 (H8N4)	64	128	32	64	16
A/duck/England/1956 (H11N6)	32	64	32	64	<8
A/duck/Alberta/60/1976 (H12N5)	256	512	256	256	16
A/mallard/Astrakhan/244/1982 (H14N6)	64	128	64	32	<8
A/she/WA/2576/1979 (H15N6)	512	512	256	512	128
A/gull/Denmark/68110/2002 (H16N3)	16	16	8	16	<8

^a Hemagglutinin titers of some subtypes are too low for performing HA assay.

Table 3
Hemagglutinating activity of the 2009 pandemic A (H1N1) viruses.

Virus name	Passage history	HA titers as determined by erythrocytes from				
		Goose	Guinea pig	Human	Chicken	Horse
A/Nonthaburi/102	MDCK4	128	128	32	<2	<2
A/Thailand/104	MDCK4	64	64	32	<2	<2
A/Bangkok/SI 614	MDCK2	16	16	8	<2	<2
A/Bangkok/SI 618	MDCK2	16	16	8	<2	<2

conducted for the 2009 pandemic viruses. Each experiment was run in duplicate. In total, 4 or 6 titer values were obtained for each virus/antigen; these values were equal or were within twofold differences. Therefore, the HA titer shown in Tables 1 and 2 represented the result for each erythrocyte species. The highest HA titers were obtained with goose and guinea pig erythrocytes for most of the LPAIV subtypes assayed. Chicken erythrocytes were slightly more sensitive than human group O erythrocytes, and horse erythrocytes were least sensitive. Particularly, it was demonstrated that quail H9N2, chicken H9N2, duck H9N2 and H13N6, could not agglutinate horse erythrocytes (Table 1).

With regard to usage of commercial H antigen, the amount supplied for some subtypes were inadequate for running an assay. The HA titers using H antigens from 12 subtypes are shown in Table 2. Again, the result showed that goose and guinea pig erythrocytes yielded the highest HA titers; chicken erythrocytes were more sensitive than human group O erythrocytes, while horse erythrocytes yielded the lowest titers.

Additionally, four 2009 pandemic influenza A (H1N1) virus isolates were assayed against these 5 erythrocyte species. It was similarly demonstrated that goose and guinea pig erythrocytes were the most sensitive, followed by human O erythrocytes. Meanwhile, the viruses did not agglutinate either chicken or horse erythrocytes (Table 3).

4. Discussion

Upon the isolation of influenza viruses in cell cultures or embryonated eggs, various erythrocyte species have been applied for recognition of the isolated viruses by HA assay.

However, no rigid data has discovered differences in sensitivity of the assay when different erythrocyte species are employed. Even though turkey erythrocyte has been recommended, this animal species is seldom found in Thailand; and thus, it is not included in this study. All viruses preferentially bind sialic acid- α 2,3-galactose (SA α 2,3Gal) receptor, while human viruses prefer SA α 2,6-Gal receptor, and swine viruses have a propensity for both (Ito et al., 1997). Some mutational change in the receptor binding site might lead to change in binding property of the viruses to certain erythrocyte species (Auewarakul et al., 2007; Nobusawa et al., 2000). Of 5 erythrocyte species, all 16 subtypes of LPAIV preferentially bound guinea pig and goose erythrocytes and yielded the highest HA titers. Meanwhile, horse erythrocyte was least sensitive in recognizing the test viruses or H antigens (Table 1). Interestingly, H9N2 virus, regardless of host of origin (quail, chicken or duck), as well as H13N6 virus, could not agglutinate horse erythrocytes. Binding between influenza viral hemagglutinin and cellular receptor is influenced not only by the type of galactosyl linkage, but also the species of sialic acid, i.e., N-acetylneurameric acid (NeuAc) or N-glycolylneurameric acid (NeuGc). While the other erythrocyte species contain both NeuAc α 2,3Gal and NeuA- α 2,6Gal, horse erythrocytes contain only NeuGc α 2,3Gal (Stephenson et al., 2003). As avian viruses preferentially bind SA α 2,3Gal, failure of some avian virus subtypes to agglutinate horse erythrocytes might possibly be explained by a loss of ability to recognize sialic acid residue.

Our study with the 2009 pandemic A (H1N1) virus demonstrated that all 4 isolates could not agglutinate both chicken and horse erythrocytes; whereas, highest HA titers

were observed with goose and guinea pig erythrocytes. Genetic analysis revealed that the *H* genomic segment of the 2009 pandemic viruses was derived from classic American swine influenza A (H1N1) virus (Smith et al., 2009). Complete genomic sequences of two pandemic strains in our study (A/Nonthaburi/102/2009 and A/Thailand/104/2009) can be accessed through GenBank.

Our study also demonstrated that the HA titers for each virus as obtained from three different donors within the same species were comparable; therefore, we can draw the conclusion that different genetic allotypes within species do not affect hemagglutinating reaction.

Collective data obtained with our LPAIV and 2009 pandemic A(H1N1) viruses as well as our previous work on HPAIV H5N1, demonstrated that goose and guinea pig erythrocytes are the best erythrocyte species in HA assay, and are then followed by chicken erythrocytes for LPAIV or human O cells for the pandemic A (H1N1) viruses. Our study thus exerts its importance on an increase in sensitivity for recognizing the virus isolates in the virus isolation technique when the appropriate erythrocyte species is chosen. Viruses that replicate slowly and yield low levels of viral progenies could be picked-up. Additionally, the sensitive HA assay will consequently result in the sensitive HI assay. When a smaller amount of viruses is needed to prepare the working dilution of H antigen, a smaller amount of molecules of HI antibody will be required to completely inhibit the hemagglutinating activity of the test virus.

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Induction of Cross-Neutralizing Antibody Against H5N1 Virus After Vaccination with Seasonal Influenza Vaccine in COPD Patients

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Abstract

Archival serum samples from elderly individuals with underlying chronic obstructive pulmonary disease (COPD) who were enrolled in a double-blind case-control study of seasonal influenza vaccine efficacy were assayed for cross-neutralizing antibody formation to avian influenza A (H5N1) virus. Of 118 serum samples, 58 were collected from influenza vaccinees (mean age 68.5 y), and 60 from placebo controls (mean age 68.4 y) who received vitamin B injections. Blood samples were collected before and at 1 mo after seasonal influenza vaccination from all subjects; in addition, for a longitudinal follow-up period of 1 y paired-blood samples were collected again from subjects who developed acute respiratory illness. Hemagglutination inhibition assay for antibodies to influenza A (H1N1), influenza A (H3N2), and influenza B viruses was carried out to determine the serological response to vaccination, and to diagnose influenza viral infection, while microneutralization assays were performed to detect cross-reactive antibody to H5N1 virus. Pre-existing cross-reactive H5N1 antibody at reciprocal titer 10 was found in 6 (10.3%) vaccinees and 4 (6.7%) placebo controls. There was no change in H5N1 antibody titer in these subjects after vaccination. On the other hand, 3 (5.2%) vaccinees developed seroconversion to H5N1 virus at 1 mo after vaccination, even though they had no pre-existing H5N1 antibody in their first blood samples. No cross-neutralizing antibody to H5N1 virus was detected in the placebo controls or in the 22 influenza patients, suggesting that influenza vaccination, but not influenza virus infection, induces cross-neutralizing antibody against avian influenza H5N1 virus.

Introduction

DIRECT TRANSMISSION OF HIGHLY PATHOGENIC AVIAN INFLUENZA (HPAI) H5N1 virus from poultry to humans was first reported in Hong Kong in 1997, and it caused 18 cases with 6 deaths, for a 33% fatality rate (3). Its re-emergence since 2003 has spread across continents, producing a higher fatality rate of about 60% in infected humans (24). Thailand reported the first human case on January 23, 2004, and the last case occurred in July 2006 (9). Nevertheless, human cases of avian influenza were seen in the People's Republic of China, Vietnam, Indonesia, and Egypt in 2009 (24). The elderly succumbed to avian influenza to a lesser extent than young children, which may be a result of cross-immunity elicited by repeated infection with other human influenza A virus subtypes (26).

A few pieces of evidence have suggested that heterosubtyping immunity may be able to confer protection

across influenza subtypes, but the mechanism of this cross-protection, if it is mediated by cellular or humoral immunity, and from which antigenic domain, is not well defined (12,13). Theoretically, cross-immunity can be induced either by hemagglutinin (HA) or neuraminidase (NA) antigen. The hypothesis of cross-protection mediated by NA immunity was derived from the observation that the 1968 pandemic influenza caused by the H3N2 virus, which came after the 1957 pandemic caused by the H2N2 virus, produced fewer deaths (8,21). Increasing levels of anti-NA antibody have been associated with decreasing frequency of viral infection and suppression of clinical manifestations (11). In an animal model, mice immunized with DNA vaccine containing a human N1 NA gene survived lethal challenge with H5N1 virus (18). On the other hand, HA antigen might also play a role in heterosubtypic immunity. In a previous study researchers reported that children with primary infection by H1N1 or H3N2 virus developed HA antibody to the

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contemporary subtypes, as well as cross-reactive antibody to H8 as assayed by ELISA (1).

During 1997 and 1998, our group conducted a double-blind controlled trial to demonstrate the efficacy of human influenza vaccination in patients with chronic obstructive pulmonary disease (COPD) aged >60 y (10,22). Serum samples were collected from these subjects before and at 1 mo after vaccination to determine the serological response to influenza vaccine. These vaccinees were longitudinally followed up for a year, and paired-blood samples were collected from the individuals who developed acute respiratory illness (ARI) for serodiagnosis of influenza by hemagglutination inhibition (HI) assay. In the present study we aimed to detect neutralizing antibody against HPAI H5N1 virus in the aforementioned serum samples by microneutralization (microNT) assay. In this study we demonstrated that the elderly subjects developed cross-neutralizing H5N1 antibody as the result of vaccination, but not from influenza illness. Since our archival serum samples were collected before the occurrence of the avian influenza outbreak, H5N1 infection in the subjects was excluded.

Materials and Methods

Subjects

A total of 118 COPD patients who attended the COPD clinic at Siriraj Hospital, Bangkok, Thailand, were enrolled in a double-blind case-control study to evaluate the efficacy of seasonal influenza vaccine between 1997 and 1998. Fifty-eight subjects (mean age 68.5 y) received vaccine, whereas 60 subjects (mean age 68.4 y) received vitamin B injection as the placebo control. Venous blood samples (10 mL) were collected from each subject prior to vaccination or vitamin B injection; the second blood samples were collected 1 mo thereafter to determine the serological response to vaccination. No subject developed influenza-like illness during this 1-mo period. Furthermore, the subjects were longitudinally followed-up for 1 y for ARI. In those cases, paired-blood samples at 4- to 6-wk intervals were collected for serodiagnosis of influenza by HI assay using the vaccine strains as the test antigens. Serum samples were kept frozen at -20°C until testing. The study was approved by the Institutional Review Board of the Committee on Ethics, Faculty of Medicine, Siriraj Hospital, Mahidol University.

Vaccines

The seasonal influenza vaccine used in this study was the split-typed trivalent vaccine from Pasteur Mérieux, Lyon, France. A 0.5-mL dose of vaccine contained influenza A/Texas/36/91 (H1N1), A/Nanchang/933/95 (H3N2), and B/Harbin/07/94, at concentration of 15 µg of HA for each virus. A 0.5-mL dose of vitamin B₁ was used as placebo.

Hemagglutination inhibition test

The procedure for the HI assay was as described elsewhere (10,23). Briefly, non-specific inhibitor in the test sera was eliminated by treatment with receptor-destroying enzyme from *Vibrio cholerae* (Denka Seiken, Niigata, Japan) overnight at 4°C, followed by inactivation at 56°C for 30 min. Then non-specific agglutinator was removed by absorption with 50% chick red blood cells. The test antigen panel, in-

fluenza A/H1N1, influenza A/H3N2, and influenza B viruses, was kindly provided by the World Health Organization (WHO). Serum with HI antibody titer $\geq 1:10$ was considered positive for influenza antibody. A positive seroresponse to influenza vaccine was obtained when paired-blood samples collected before and after vaccination showed a fourfold or greater rise in HI antibody titer against any of the test antigens. Similarly, influenza diagnosis by HI assay was given based on the same criteria.

Microneutralization assay

The ELISA-based microNT assay protocol was based on that described in Kitphati *et al.* (9) and the WHO manual (23). The experiments were conducted in a laboratory with biosafety level 3. Influenza A/Thailand/1 (KAN-1)/2004 (H5N1) was used as the test virus. Briefly, a serum sample was twofold serially diluted from the dilution of 10 to 1280; then 60 µL of each serum dilution was mixed with an equal volume of the test virus at a concentration of 200 TCID₅₀/100 µL and incubated at 37°C for 2 h. A 100-µL volume of the virus-serum mixture was inoculated onto a Madin-Darby canine kidney (MDCK) cell monolayer in a well of a microtiter plate and further incubated for 18–20 h in a CO₂ incubator. The assays were run in duplicate. The reaction plate was tested by ELISA to determine the amount of influenza nucleoprotein produced in the infected MDCK cells. Mouse monoclonal antibody (Chemicon International, Temecula, CA) was used as the primary antibody, anti-mouse Ig conjugated with horseradish peroxidase (Southern Biotechnology Associates, Birmingham, AL) was used as the second antibody, and TMB (KPL Inc., Gaithersburg, MD) was used as the chromogenic substrate. The reaction plate was read under a spectrophotometer at the wavelengths of 450 and 630 nm. Wells with uninfected cells and virus back-titration were included as the control sets in every test plate. The serum dilution that reduced more than 50% of the amount of viral nucleoprotein compared to the virus control was considered to be positive for anti-H5N1 antibody. The cut-off titer for positive H5N1 antibody was set at 10.

Statistical analysis

Data were analyzed by SPSS version 11.5 software (SPSS, Inc., Chicago, IL). Comparison of geometric mean titer (GMT) values and fold increase in titers between the two groups was performed by the Mann-Whitney *U* test. Comparison of prevalence between two groups was performed by chi-square testing. The level of statistical significance was set at *p* < 0.05.

Results

H5N1-neutralizing antibody after seasonal influenza vaccination

Elderly subjects with COPD were immunologically intact, as shown by the fact that 85% of the vaccinees, but not the placebo controls, developed a fourfold or greater rise in HI antibody titer to the influenza A/H1N1 and H3N2 vaccine strains (Table 1). GMTs of H5N1-neutralizing antibodies prior to vaccination in both groups were not statistically significantly different (5.37 versus 5.24; *p* = 0.558). Meanwhile, pre-existing H5N1-neutralizing antibody at titer 10 was found in 6 (10.3%) of 58 vaccinees, and in 4 (6.7%) of 60

TABLE 1. DISTRIBUTION OF ANTIBODY RESPONSE TO H1N1 AND H3N2 VACCINE STRAINS IN PAIRED-BLOOD SAMPLES FROM VACCINE AND PLACEBO GROUPS

Virus	Group	Vaccination	Antibody titer									% Vaccine responders ^a
			<10	10	20	40	80	160	320	640	1280	
H1N1	Vaccine (n = 58)	Pre	33	5	9	8	2	0	1	0	0	85
		Post	3	3	8	5	10	9	7	4	9	
	Placebo (n = 60)	Pre	24	12	8	10	4	1	0	1	0	0
		Post	23	14	7	11	2	2	0	1	0	
H3N2	Vaccine (n = 58)	Pre	27	10	5	7	5	2	1	1	0	85
		Post	3	1	7	7	10	13	4	2	11	
	Placebo (n = 60)	Pre	28	8	7	4	5	4	1	0	3	0
		Post	28	8	7	4	6	4	0	0	3	

^aA responder is defined by at least a fourfold rise in antibody titers in the paired serum samples.

placebo controls (Table 2). The numbers of subjects who had pre-existing H5N1 antibody in the two groups were also not statistically significantly different ($p = 0.637$). After influenza vaccination, 3 (5.2%) vaccinees who had no pre-existing H5N1 antibody in their initial blood samples did develop a fourfold or greater rise in H5N1-neutralizing antibody titers. The increase in GMT of H5N1 antibody in the vaccine group was not statistically significantly different (5.37 versus 6.05; $p = 0.10$). However, a slight increase in GMT was observed in the vaccine group, but not in the placebo group (Table 2). Two of these three subjects seroconverted to both H1N1 and H3N2, while the third one seroconverted to H1N1 virus only (Table 3).

Lack of H5N1-neutralizing antibody after natural influenza illness

During 1 y of longitudinal follow-up, 102 episodes of ARI occurred among vaccinees and placebo controls. Influenza was diagnosed in 5 (8.6%) vaccinees and 17 (28.3%) placebo controls (Table 4). Nevertheless, no increase in cross-reactive neutralizing H5N1 antibody was detected in these influenza patients. There was one placebo control that had an H5N1 antibody titer of 20 in paired sera. The results demonstrated that acute influenza virus infection did not elicit detectable cross-H5N1 antibody in the study subjects.

Discussion

In the present study we demonstrated pre-existing cross-neutralizing antibody against H5N1 virus in 10 (8.5%) of 118

subjects, as well as induction of a fourfold or greater rise of this cross-reactive antibody in 5.2% of elderly individuals with underlying COPD who were vaccinated with seasonal influenza vaccine. The data on the induction of cross-neutralizing antibody against H5N1 virus by seasonal influenza vaccine are controversial. In our previous unpublished work, cross-neutralizing antibody against H5N1 virus was not detected in 42 young people aged 25–40 y with a history of seasonal influenza vaccination, and also not in 140 healthy subjects aged 20–45 y, of which approximately 70% had neutralizing antibody to A/New Caledonia/20/99 (H1N1) and A/Fujian/411/02 (H3N2). Gioia *et al.* (4) demonstrated a rise in H5N1-neutralizing antibody titer to >20-fold over baseline in 13 (34.2%) of 38 vaccinees (aged 27–59 y, with an average age of 43 y), while their H5N1 HI antibody titers remained at undetectable levels. In contrast, Tang *et al.* (19) did not detect cross-reactive antibody to influenza H5N1 virus, either by microNT or HI assay, in serum samples collected at intervals from 10 vaccinees (aged 20–40 y) who received seasonal influenza vaccine, even though they could elicit a serological response with high HI antibody titers to the vaccine strains. During the 1997 avian influenza outbreak, Rowe *et al.* (17) found that an H5N1-neutralizing antibody titer of 80 was suggestive of avian influenza infection. However, this appeared to apply only to people aged <50 y. Moreover, the H5N1 microNT assay may be less specific in adults aged 60 y and older (17). Results of that study and ours suggest that elderly persons may have cross-reactive antibody to avian H5N1 virus as a result of seasonal

TABLE 2. DISTRIBUTION OF H5N1 NT ANTIBODIES IN PAIRED-BLOOD SAMPLES FROM VACCINE AND PLACEBO GROUPS

Group	No. of positive samples at NT antibody titers					GMT	Number of subjects with pre-existing antibody
	<10	10	20	40	80		
Vaccine (n = 58)	B1	52	6	0	0	5.37 ^{a,c}	6 ^b
	B2	49	6	0	2 ^d	6.05 ^c	
Placebo (n = 60)	B1	56	4	0	0	5.24 ^a	4 ^b
	B2	56	4	0	0	5.24	

^a $p = 0.558$ for the comparison of pre-vaccination GMT.

^b $p = 0.637$ for the comparison of frequencies of subjects with pre-existing H5N1 antibodies.

^c $p = 0.100$ for comparison of GMT between pre- and post-vaccination in the vaccine group.

^dWithout acute respiratory infection.

Abbreviations: B1, pre-vaccination; B2, post-vaccination; GMT, geometric mean titer; NT, neutralizing antibody.

TABLE 3. ANTIBODY RESPONSES TO H1N1, H3N2, AND B VIRUSES IN VACCINEES WHO DEVELOPED A FOURFOLD RISE IN ANTIBODY TO H5N1 VIRUS

Code No.	Group	Antibody to subtype	Antibody titers to influenza viruses	
			Pre-vaccination (B1)	Post-vaccination (B2)
15	V	H5N1 NT	<10	80
		H1N1 HI	<10	40
		H3N2 HI	<10	160
		B HI	<10	20
29	V	H5N1 NT	<10	40
		H1N1 HI	<10	160
		H3N2 HI	<10	320
		B HI	<10	<10
37	V	H5N1 NT	<10	40
		H1N1 HI	10	640
		H3N2 HI	160	160
		B HI	20	80

Abbreviations: NT, neutralizing antibody; HI, hemagglutination inhibition antibody; V, vaccination; B1, pre-vaccination; B2, post-vaccination; H5N1, influenza A/Thailand/1 (KAN-1)/2004; H1N1, influenza A/Texas/36/91; H3N2, influenza A/Nanchang/933/95; B, influenza B/Harbin/07/94.

influenza vaccination or repeated infection by human influenza viruses. The inducible H5N1 antibody may be the result of immunologic priming that occurred in children infected with seasonal influenza viruses bearing common epitopes to the H5N1 strain, as previously reported (16). Preschool-age children were more susceptible due to their lack of immunity against influenza virus infections (2). During the 2003–2004 influenza season approximately 43% of cases occurred in 10-year-old children, while only 12% occurred in those aged 65 and older (14). The attack rate of seasonal influenza is approximately 5–10% per year (25). Therefore elderly persons have most likely experienced natural influenza virus infections several times in their lives. Data from the current outbreak also indirectly support the theory that the elderly, who may have experienced influenza disease several times in their lives, died from H5N1 infection at lower rate than younger people (26).

Based on the *in-vitro* microNT assay results, it is possible that the H5N1-neutralizing antibodies detected may be induced by the common epitopes present in HA proteins, but less likely to those in NA proteins. It is generally accepted that antibody to HA blocks viral entry and confers neutralizing activity and protective immunity, whereas antibody to NA blocks virus release and confers only partial protective immunity. Cross-neutralizing antibodies induced by common epitopes in HA from different influenza subtypes has been reported. Monoclonal antibodies against conserved antigenic sites on H1 or H2 could neutralize both the H1 and H2 subtypes (15). Using the phage display library technique together with panning by recombinant H5 HA, two sets of researchers showed that gene pools from peripheral blood mononuclear cells of healthy subjects could produce heterosubtypic monoclonal antibodies directed against epitopes in the HA2 domain of the HA molecule that were able to

TABLE 4. DISTRIBUTION OF H5N1 NT ANTIBODIES IN PAIRED-BLOOD SAMPLES FROM PATIENTS WITH ACUTE RESPIRATORY ILLNESS

Illness	Group (no. episodes/no. case)	Sample	No. of positive samples at NT antibody titers					
			<10	10	20	40	80	GMT
Flu	Vaccine (5/5)	BA	5	0	0	0	0	5.00
		BC	5	0	0	0	0	5.00
	Placebo (17/17)	BA	16	1	0	0	0	5.21
		BC	16	1	0	0	0	5.21
	Total (22/22)	BA	21	1	0	0	0	5.16
		BC	21	1	0	0	0	5.16 ^a
Non-Flu	Vaccine (39/35)	BA	34	4	1	0	0	5.56
		BC	34	4	1	0	0	5.56
	Placebo (41/33)	BA	40	1	0	0	0	5.09
		BC	40	1	0	0	0	5.09
	Total (80/68)	BA	74	5	1	0	0	5.31
		BC	74	5	1	0	0	5.31 ^a

^a $p = 0.952$ for comparison of GMT between influenza and non-influenza patient groups.

Abbreviations: BA, acute blood sample; BC, convalescent blood sample; GMT, geometric mean titer; NT, neutralizing antibody.

neutralize HPAI H5N1 virus, as well as other influenza virus subtypes (5,6). Although seasonal influenza vaccine induced a fourfold or greater rise in cross-neutralizing H5N1 antibody in the three vaccinees who did not have pre-existing H5N1 antibody in their initial blood samples, the vaccine failed to boost the anamnestic response in vaccinees who had pre-existing H5N1 antibody. It is unclear whether the population of memory lymphocytes and the common epitopes present in vaccines are well matched; perhaps pre-existing H5N1 antibody had bound the common epitopes in the vaccine and diminished its boosting effect.

Regarding serologic surveys for H5N1 virus infection in Hong Kong, Treanor *et al.* (7,20) reported that the an H5N1-neutralizing antibody titer of 40 was the primary immunogenic threshold to distinguish between infected and uninfected persons. Neutralizing H5N1 antibody titers of 40–80 were also found in our three vaccinees. Since this study was carried out on archival blood samples collected before the avian influenza outbreak, it appears that the cross-H5N1-neutralizing antibody that developed in our subjects was induced by vaccination, not by natural H5N1 infection.

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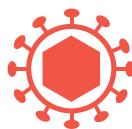
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RESEARCH

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Influenza A viral loads in respiratory samples collected from patients infected with pandemic H1N1, seasonal H1N1 and H3N2 viruses

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Abstract

Background: Nasopharyngeal aspirate (NPA), nasal swab (NS), and throat swab (TS) are common specimens used for diagnosis of respiratory virus infections based on the detection of viral genomes, viral antigens and viral isolation. However, there is no documented data regarding the type of specimen that yields the best result of viral detection. In this study, quantitative real time RT-PCR specific for *M* gene was used to determine influenza A viral loads present in NS, NPA and TS samples collected from patients infected with the 2009 pandemic H1N1, seasonal H1N1 and H3N2 viruses. Various copy numbers of RNA transcripts derived from recombinant plasmids containing complete *M* gene insert of each virus strain were assayed by RT-PCR. A standard curve for viral RNA quantification was constructed by plotting each Ct value against the log quantity of each standard RNA copy number.

Results: Copy numbers of *M* gene were obtained through the extrapolation of Ct values of the test samples against the corresponding standard curve. Among a total of 29 patients with severe influenza enrolled in this study (12 cases of the 2009 pandemic influenza, 5 cases of seasonal H1N1 and 12 cases of seasonal H3N2 virus), NPA was found to contain significantly highest amount of viral loads and followed in order by NS and TS specimen. Viral loads among patients infected with those viruses were comparable regarding type of specimen analyzed.

Conclusion: Based on *M* gene copy numbers, we conclude that NPA is the best specimen for detection of influenza A viruses, and followed in order by NS and TS.

Background

Influenza A viruses are classified into 16 hemagglutinin (H) and 9 neuraminidase (N) subtypes [1]. Since the emergence of Russian influenza A (H1N1) in 1977 [2] to the emergence of pandemic influenza A (H1N1) in April 2009, only A/H1N1, A/H3N2 and influenza B viruses have been recognized as human or seasonal influenza. Influenza virus spreads via respiratory secretion. After an incubation period of about 1-3 days, the viruses are shed from various kinds of respiratory samples. Upper respiratory tract specimens, such as nasopharyngeal wash (NPW) or nasopharyngeal aspirate (NPA), nasal swab (NS), throat swab (TS), endotracheal swab, bronchoal-

veolar lavage and tissues, are recommended for virus detection in patients with respiratory tract infection. These specimens could be used for viral antigen detection, virus isolation and molecular methods for genome detection. Nevertheless, there is no documented data which addresses the type of specimen that gives the best yield for the disease diagnosis [3].

Genomes of influenza A and B viruses are composed of 8 negative sense, single-stranded RNA segments encoded for 10-11 proteins essential for infection and replication [1]. The genomic RNA has been used as targets for amplification by conventional and real time reverse transcription-polymerase chain reaction (RT-PCR). The highly conserved *M* gene-derived primers are usually utilized for diagnosis of all influenza A subtypes, whereas specific subtype identification targets *H* or *H* and *N* genes. In this

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study, the protocol established by the U.S., Center for Disease Control (CDC) for detection of *M* gene [4] in adjunct with the standard curves of known copies of *M* RNA transcripts derived either from H1N1, H3N2 or the 2009 pandemic A (H1N1) viruses was used to quantify the viral loads in specimens collected from patients with severe influenza prior to receiving anti-viral drug. Our study provided the information on the clinical specimens that yielded the best diagnostic result; and the viral loads in patients infected with different influenza subtypes and strains were also compared.

Methods

Subjects and Specimen Collection

This study was approved by the Institutional Review Boards of the Committee on Ethics, Faculty of Medicine Siriraj Hospital, Mahidol University and the Ministry of Public Health, Thailand. NPA, NS and TS samples were collected in viral transport medium (MicroTest™ Multi-Microbe Media; Remel, Lenexa, KS) from patients with severe influenza. The collection of NPA was performed by flushing through a nasopharyngeal tube with 2 ml of sterile normal saline using a sterile NG-tube or sterile butterfly needle tube, inserted through the floor of nose. The NPA yield at approximately 0.5 ml volume was then added with VTM and the 3.5 ml final volume was obtained. The nose and throat swabbing were performed right after the NPA collection from nostrils and throat, respectively, using MicroTest™ kit with 3 ml of VTM.

Quantitative Real time Reverse Transcription-Polymerase Chain Reaction

Real time RT-PCR protocols established by CDC as well as viral antigen detection by QuickVue (Quidel Corporation, San Diego, CA), virus isolation in MDCK cell culture and serodiagnosis, were used to diagnose influenza

virus infection in these patients. Positive results from at least two diagnostic tests were obtained for each case. A total of 29 patients enrolled in this study comprised 12 cases of pandemic influenza A/2009 (H1N1), 5 cases of A/Brisbane/59/2007(H1N1) like- and 12 cases of A/Brisbane/10/2007 (H3N2) like-virus infection. All respiratory specimens were kept at -70°C until tested.

In the preparation of standard *M*-RNA, viral RNA extracted from A/Nonthaburi/102/2009 (H1N1), A/Brisbane/59/2007-like (H1N1) and A/Brisbane/10/2007-like (H3N2) viruses were reverse transcribed into complementary DNA (cDNA) in a 20 μ l reaction comprised 8 μ l of viral RNA, 1 \times RT buffer, 5 mM MgCl₂, 10 mM DTT, 50 ng of random hexamers, 0.5 mM dNTPs, 40 units of RNaseOUT™ (Invitrogen Corporation, Carlsbad, CA) and 200 units of SuperScript™ III reverse transcriptase (Invitrogen) following the manufacturer's instruction. Thereafter, cDNA was subjected to PCR amplification in a 50 μ l reaction mixture containing 5 μ l of cDNA target, 5 μ l of 10 \times High Fidelity PCR buffer, 1 mM dNTP mixture, 2 mM MgSO₄, 0.4 μ M forward primer, 0.4 μ M reverse primer (universal *M* primers, Bm-M-1 and Bm-M-1027R [5]; sequences as shown in Table 1) and 0.5 μ l of High Fidelity Platinum™Taq DNA polymerase (Invitrogen). The PCR amplification cycle was set as 94°C for 2 min for initial denaturation, followed by 35 cycles of 94°C for 30 sec, 55°C for 30 sec, and 68°C for 90 sec, and followed by final extension at 68°C for 10 min. The PCR product of complete *M* segment of 1,056 base pairs in size was gel-purified and cloned into pGEM® T-Easy plasmid (Promega Corporation, Madison, WI). Thereafter, *M* RNA was *in vitro*-transcribed from the recombinant plasmid using Riboprobe® combination system-SP6/T7 (Promega), followed by step of RNase-free DNase (Promega) digestion in order to remove out the recombinant plasmid DNA

Table 1: Sequences of primers and probes for PCR and real time RT-PCR.

Primer and probe	Sequence (5'>3')	Reference
Bm-M-1	TAT TCG TCT CAG GGA GCA AAA GCA GGT AG	Hoffmann E et al.
Bm-M-1027R	ATA TCG TCT CGT ATT AGT AGA AAC AAG GTA GTT TTT	Hoffmann E et al.
FluA Forward	GAC CRA TCC TGT CAC CTC TGA C	CDC
FluA Reverse	AGG GCA TTY TGG ACA AAK CGT CTA	CDC
FluA Probe ¹	TGC AGT CCT CGC TCA CTG GGC ACG	CDC
RnaseP Forward	AGA TTT GGA CCT GCG AGC G	CDC
RnaseP Reverse	GAG CGG CTG TCT CCA CAA GT	CDC
RnaseP Probe ¹	TTC TGA CCT GAA GGC TCT GCG CG	CDC

¹TaqMan® probes are labeled at the 5'-end with the reporter molecule 6-carboxyfluorescein (FAM) and with the quencher, Blackhole Quencher 1 (BHQ1) at the 3'-end.

templates. *M* transcripts obtained were kept at -70°C until assayed.

To minimize the test variation, standard curves of *M* RNA transcripts were constructed in parallel with the detection of viral *M* RNA in clinical samples in the quantitative real time RT-PCR. The *M* RNA transcripts were measured by Quant-iT™ RNA Assay Kit (Invitrogen) and diluted to various copy numbers in a ten folded serial dilution manner; and each known *M* RNA copy number was assayed by real time RT-PCR according to that described by the 2009 CDC protocol [4]. The sequences of primer and probe sets used in this study are shown in Table 1. A 25 μ l reaction mixture of real time RT-PCR comprised 5 μ l of total RNA, 12.5 μ l of 2x reaction mix, 0.5 μ l of SuperScript™ III Platinum™ Taq Mix (Invitrogen), each 0.8 μ M of forward and reverse primers and 0.2 μ M of labeled probe, and H₂O was added to bring up the final volume. The amplification was carried out in DNAEngine® Peltier Thermal Cycler with Chromo4™ Real-Time PCR Detector (Bio-Rad Laboratories, Inc., Hercules, CA) using the amplification cycles of 50°C for 30 min for reverse transcription, 95°C for 2 min for *Taq* polymerase activation, followed by 45 cycles of PCR amplification (95°C for 15 sec and 55°C for 30 sec). Fluorescence signal was obtained at 55°C. The results were analyzed by MJ OpticonMonitor™ Analysis Software version 3.1 (Bio-Rad). A standard curve was constructed by plotting each cycle threshold (C_t) value against the log quantity of standard RNA copy numbers. Total RNA was extracted from the NPA, NS and TS specimens by QIAamp® Viral RNA Mini Kit (QIAGEN Inc., Valencia, CA) following the manufacturer's instruction. Real time RT-PCR for detection of influenza A *M* gene and the *RnaseP* (RNP) house keeping gene, was carried out. To obtain amount of viral load present in each clinical sample, the test C_t value was extrapolated against the standard curve derived from each virus subtype or strain (Fig. 1). The sensitivity of the assay for all 3 subtypes and strain was 100 copies of target *M* RNA/real time RT-PCR reaction when the cut-off for positive result was set at 40 cycles.

Data Analysis

Statistical analysis was performed with SPSS program. Pair *t*-test was used to compare the mean log₁₀ viral loads among different types of specimens collected from the same subjects and at the same time. Student *t*-test was used to analyze the mean log₁₀ viral copy numbers in contemporary specimens from patients infected with different virus subtypes and strain.

Results and Discussion

Real time RT-PCR protocol was analyzed for its applicability to amplify *M* genes derived from H1N1, H3N2 and

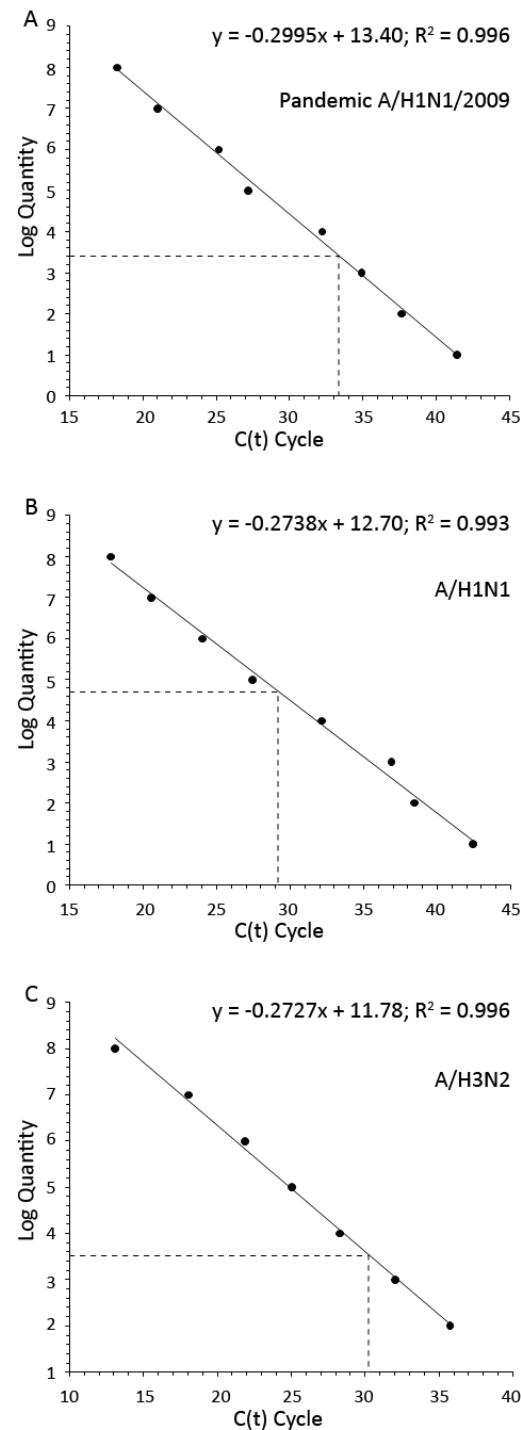


Figure 1 *M* transcript standard curve for quantitative detections of the pandemic A/H1N1 (A), seasonal A/H1N1 (B) and seasonal A/H3N2 viruses (C). The standard curve of *M* RNA copy numbers was generated by plotting the C_t value (X-axis) against log₁₀ copy numbers of *M* transcripts (Y-axis). The amount of *M* copy number in clinical specimens was obtained by extrapolation of the C_t of the test sample against the standard curve.

the 2009 pandemic viruses by aligning the primers and probe nucleotide sequences against those *M* genes of various influenza subtypes and strains using BioEdit Sequence Alignment Editor (Fig. 2, Table 2). The forward and reverse primers bound to those *M* genes with higher than 90% identity, while the probe bound with 100% identity. This suggested that the CDC primers/probe set can be universally used for detection of *M* segments or viral loads of the novel influenza A/2009 (H1N1), seasonal H1N1 and seasonal H3N2 viruses.

Three standard curves of *M* RNA transcripts were constructed with the R^2 of 0.996, 0.993 and 0.996 for pandemic A/2009 (H1N1), seasonal H1N1 and seasonal H3N2, respectively (Fig 1). The *M* copy numbers per ml of VTM from patients infected with pandemic H1N1 or H3N2 viruses were significantly highest in NPA samples (pair *t*-test; $P \leq 0.05$) (Table 3). However, number of patients infected with seasonal H1N1 virus was too small for data analysis. Additionally, viral load levels in patients infected with either subtype or strain was comparable (student *t*-test, $P > 0.05$). *M* RNAs were detected in all NPA and NS, but not in all TS samples collected from patients infected with any one of the virus subtypes/strain. The detection rate was shown in Table 4.

RT-PCR for diagnosis of influenza viruses is generally more sensitive than viral isolation method. The technique detected the viral genome present in dead and alive viruses including excess viral RNA present in the infected cells; however, virus isolation detected only live virus particles. RT-PCR is a high through-put and less time con-

suming method. In addition, only RT-PCR can differentiate type, subtype and strain of influenza viruses. Sensitivity of RT-PCR to diagnose the disease not only depends on the protocol, but also the type of clinical sample used in the diagnosis. Our study has two advantages that are not commonly conducted in previous reports. Firstly, we had an opportunity to investigate 3 types of clinical specimens collected from the same individuals at the same time, e.g., NPA, NS and TS. Secondly, we had employed full length *M* RNA transcripts derived from A/H1N1, A/H3N2 and the 2009 pandemic viruses to construct 3 standard curves for quantifying viral RNA copy numbers of the contemporary subtype and strain present in the test specimens, with the assumption that the full length *in vitro* *M* RNA transcripts closely mimics the native structure of the viral *M* genomic segments. Regardless of viral subtypes and strains (H1N1, H3N2 and 2009 pandemic H1N1 virus), we found that all NPA and NS specimens were positive for viral genome detection, while the positive rate was lower in TS specimens.

Previous investigators reported that viral RNA concentration in respiratory samples and long duration of virus shedding were correlated with influenza disease severity [6]. Amount and duration of viral shedding are important in the disease treatment and control of virus spread. Different type of specimens contained different amount of viral RNA concentration; therefore, using different type of clinical specimens may yield different information. In addition, there is no reference method for viral load assay. Peiris et al. [7] reported that viral load in NPA samples of

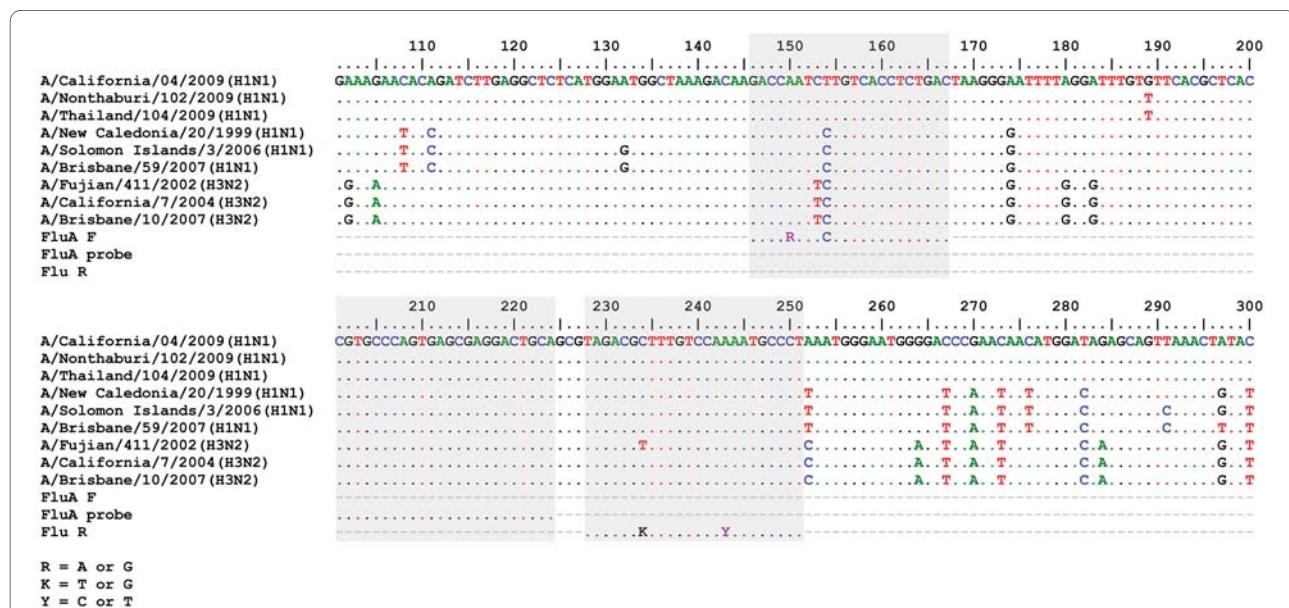


Figure 2 Alignment of *M* gene fragment from the pandemic A/H1N1, seasonal A/H1N1 and seasonal A/H3N2 viruses against CDC real time RT-PCR primers and probe sequences. BioEdit Sequence Alignment Editor was used to locate the region of real time RT-PCR primers and probe binding site within *M* gene of various subtypes of influenza A viruses.

Table 2: Percentages of identity of primers and probe with the *M* sequences derived from different virus subtypes and strain.

Virus	% identity with		
	Forward primer	Reverse primer	Probe
Pandemic A/H1N1/2009	95.45	91.67	100
A/H1N1	100	91.67	100
A/H3N2	95.45	91.67-95.83	100

H5N1 patients was lower than those of H3N2 patients. The finding was further extended by Ward et al. [8] that viral load in throat swab samples of H5N1 patients in 1997 and 2004 was 10-fold lower than that observed in H3N2 patients, i.e., 1.5×10^6 TCID₅₀/ml versus 1.6×10^5 TCID₅₀/ml (*t*-test, $P < 0.05$). On the other hand, de Jong et al. [9] found that viral load in TS from H5N1 patients was significantly higher than that from H3/H1 patients; and, additionally, TS contained significantly higher H5N1 viral load than nasal swab samples; meanwhile, viral load in TS and nasal swab samples from H1/H3 patients was not statistically different. The difference in results obtained from different groups of investigators might reflect process of specimen collection and also the different protocols for viral load measurement.

It has been reported that the 2009 pandemic virus preferentially binds sialic acid receptor with α 2, 6 linkage to galactose (SA α 2,6 Gal), the same as human influenza H1N1 and H3N2 viruses [10]. Fatality rate in patients infected with the novel virus is less than 1%, except in that which occurs in patients with underlying conditions, e.g., cardiovascular disease, hypertension, asthma and diabetes, etc. [11,12]. However, the study in a mammalian model demonstrated that the 2009 pandemic H1N1 virus was more pathogenic than the seasonal H1N1 virus [13]. Our study, therefore, explored the viral load in respiratory secretions collected prior to anti-viral treatment, and found that the level of viral RNA in cases infected with the 2009 pandemic H1N1 virus was not statistically different from those infected with seasonal H1N1 and

Table 3: Influenza viral loads in various types of clinical specimens collected from patients infected with different virus subtypes.

Virus	Number of cases	Statistics	Age	Days after onset	Log ₁₀ <i>M</i> RNA copy number in		
					NPA	NS	TS
Pandemic A/H1N1/2009	12	Mean	12	5	7.5 ^{a, b}	6.5 ^{a, c}	4.1 ^{b, c}
		Median	8	5	7.5	6.9	4.9
		Range	3-53	2-10	5.8-8.9	2.7-8.7	Und.-6.9
A/H1N1	5	Mean	5	5	7.8	7.2	7.4
		Median	4	4	8.5	6.4	7.7
		Range	1-12	2-10	4.7-8.9	5.5-9.3	5.8-8.7
A/H3N2	12	Mean	17	5	8.0 ^{a, b}	6.6 ^a	5.6 ^b
		Median	4	5	8.1	7.2	6.8
		Range	1-69	2-6	5.8-9.2	3.5-8.3	Und.-7.7

The viral loads are reported as log₁₀ of *M* segment copy number/1 ml of VTM. Pair *t*-test was used to compare the mean log₁₀ viral loads in different types of specimens collected from the same subjects and at the same time.

^aindicates a significant difference of the viral loads in NPA and NS, ^bin NPA and TS and ^cin NS and TS (Pair *t*-test, $P < 0.05$).

Und., below detection limit; NPA, Nasopharyngeal aspirate; NS, Nasal swab; TS, Throat swab.

Table 4: Genome detection rate by type of clinical specimens.

Virus	Number of positive cases		
	NPA	NS	TS
Pandemic A/H1N/2009	12 (100%)	12 (100%)	9 (75%)
A/H1N1	5 (100%)	5 (100%)	5 (100%)
A/H3N2	12 (100%)	12 (100%)	11 (91.67%)

NPA, Nasopharyngeal aspirate; NS, Nasal swab; TS, Throat swab.

H3N2 viruses. Mean \log_{10} copies/ml of viral RNA of 7.5-8.0 in NPA, 6.5-7.2 in NS and 4.1-7.4 in TS samples were found in our study. It is to be kept in mind that all of our patients had severe influenza at time of specimen collection, and most of them were pediatric patients (24 children and 5 adults). Duration of viral shedding of the seasonal influenza as reported by the other groups of investigators was 4-5 days in average [6,14]. A recent report by To et al. [15], showed that the level of the 2009 pandemic viral load of $8 \log_{10}$ copies/ml was found in respiratory specimens collected before oseltamivir treatment; and the viral shedding peaked at the day of onset of symptom with median duration of 4 days [15]. On the other hand, when using plasmid containing amplification target to construct the standard curve together with using pool of throat and nasal swab as the test samples, the other study demonstrated that the H1/H3 viral loads of $5.06 \pm 1.85 \log_{10}$ copies/ml were found in patients with major co-morbidities and $3.62 \pm 2.13 \log_{10}$ copies/ml in patients without co-morbidities [6].

Conclusions

Our study suggested that when complete facilities are accessible, such as in clinics and hospitals, NPA will be the best specimen of choice; and in field investigation, NS will be the second choice, followed by TS specimen. Using the appropriate specimen will provide the highest diagnostic rate and the precise strategy for disease treatment and prevention control.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

PP designed the research study; NN, PN, PK and PhP performed research; NN, PN and PK analyzed data; NN and PP wrote the manuscript. KK, TC, CS, CC and JF provided specimens. All authors read and approved the final manuscript.

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Kinetics and Longevity of Antibody Response to Influenza A H5N1 Virus Infection in Humans[†]

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Anti-H5N1 antibody was determined by microneutralization, hemagglutination inhibition, and Western blotting assays in serial blood samples collected from eight Thai patients, including four fatal cases and four survivors. The antibody was detected as early as 5 days and, typically, with an increase in titer in paired blood at about 15 days after disease onset. The anti-H5 antibody response was long-lasting, for almost 5 years in cases which can be followed that far. In addition, cross-neutralizing activity to related clade 1 viruses was observed.

During the first outbreak of human highly pathogenic avian influenza (HPAI) virus H5N1 disease in Hong Kong in 1997, the microneutralization (microNT) assay was used to detect acute antibody responses in virologically confirmed cases, but the durability of the response was not assessed (4). The microNT assay was more sensitive than the traditional hemagglutination inhibition (HI) assay, which used erythrocytes from avian species in detecting human antibodies induced by H5 viruses (7). The sensitivity and specificity of microNT could be improved when it was combined with a confirmatory Western blot (WB) assay (7).

Since late 2003, highly pathogenic avian influenza (HPAI) H5N1 viruses have caused unprecedented outbreaks in poultry in 61 countries (10). Human disease has accompanied the global spread of the virus, and as of 14 January 2009, 394 human H5N1 virus infections had been reported by the World Health Organization (WHO), with an overall fatality rate of over 60% (13). Despite these case numbers, information on the kinetics, and in particular the persistence of H5 virus-specific antibody in humans infected with H5N1 viruses, is lacking. This information could guide H5N1 vaccine studies and the optimal design of seroepidemiological investigations to better understand the extent of and risk factors associated with human H5N1 infection. In 2006, WHO included serodiagnosis as one among other criteria for an H5N1 confirmed case, i.e., (i) a fourfold or greater rise in neutralizing antibody titer in paired blood samples of which the acute blood has been collected within 7 days after symptom onset and the convalescent sample achieves a titer of $\geq 1:80$, or (ii) presence of a neutralizing antibody titer of $\geq 1:80$ in a single serum sample collected 14 or more days after symptom onset together with a positive

result using a different serological assay, such as the horse erythrocyte HI assay or an H5-specific WB positive result (12).

Thailand reported the first human case of H5N1 disease on 23 January 2004. No human case has occurred after July 2006; in total, there have been 25 human cases with 17 deaths. The diagnosis of H5N1 infection in human cases in Thailand is primarily based on results of conventional and real-time reverse transcription-PCR (RT-PCR) and virus isolation methods. Serological tests have been introduced more recently. The present study reports the results of serological analyses conducted by using the microNT, HI, and WB assays to explore the kinetics and longevity of the antibody response to H5N1 virus infection in fatal cases and survivors.

MATERIALS AND METHODS

Ethical issues. This study has been approved by two Ethical Committee for Human Research panels: one from the Faculty of Medicine Siriraj Hospital, Mahidol University, and the second one from the Ministry of Public Health, Thailand. Subjects or parents gave consent to participate in the follow-up blood collection.

Subjects. Eight individuals, four fatal cases and four survivors, were included in this study. All of them were diagnosed with H5N1 virus infection by both RT-PCR and virus isolation methods. Nucleotide sequencing showed that all of the isolated viruses belonged to clade 1. The demographic data for these subjects are shown in Table 1. Serial blood samples from the four survivors were collected at approximately 6-month intervals. Serum or plasma samples were kept frozen at -20°C until tested.

Viruses. Two human H5N1 isolates belonging to genotype Z, clade 1, were used for serodiagnosis in this study. A/Thailand/1(KAN-1)/04 (KAN-1), the first human virus isolated in the country, was isolated in January 2004, and A/Thailand/676(NYK)/05 (NYK) was isolated in December 2005 during the third wave of the epidemic. The latter virus contains two mutational changes: A134V in the receptor binding site and R325K in the cleavage site of the hemagglutinin (HA) molecule (1, 6). Complete genomic sequences of the two virus isolates used in this study are available through GenBank. KAN-1 preferentially binds sialic acid $\alpha 2,3$ -linked galactose (SA $\alpha 2,3$ Gal), while NYK preferentially binds sialic acid $\alpha 2,6$ -linked galactose (SA $\alpha 2,6$ Gal) (1). The viruses were propagated in MDCK cell monolayers without serum supplement. Experiments related to infectious viruses were conducted in biosafety level 3 facilities.

Microneutralization assay. An enzyme-linked immunosorbent assay (ELISA)-based microNT assay was conducted for detection of NT antibody. The test protocol followed what is described in the WHO manual, with a small modifi-

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TABLE 1. Demographic data for H5N1 patients

Subject no.	Age (yrs)	Gender	Estimated incubation period (days)	Disease outcome	Yr of infection
1	6	M		Death	2004
2	2	M	5	Survival	2004
3	29	M	3	Survival	2004
4	32	F		Survival	2004
5	48	M	12	Death	2005
6	7	M	8	Survival	2005
7	5	M	10	Death	2005
8	59	M		Death	2006

cation (11). The test serum was heat inactivated at 56°C for 30 min and then twofold diluted with maintenance medium starting from a dilution of 1:5 to 1:2,560. The assay was performed by mixing 60 µl of the diluted serum with 60 µl of the virus suspension at a concentration of 200 50% tissue culture infective doses (TCID₅₀) and incubated at 37°C for 2 hours. Then, 100 µl of the mixture was transferred onto an MDCK cell monolayer and further incubated at 37°C for 18 to 20 h. In order to verify the amount of virus inoculum, virus back-titration at doses of 0.1, 1, 10, and 100 TCID₅₀ were included in every assay plate, together with the positive control serum and cell culture control. The test reaction was run in duplicate. Viral nucleoprotein produced in the infected MDCK cells was detected by indirect ELISA using mouse monoclonal antibody to influenza A virus nucleoprotein (Chemicon International, Inc., CA) as the primary antibody and goat anti-mouse immunoglobulin (Ig) conjugated with horseradish peroxidase (Southern Biotechnology Associates, Inc. Birmingham, AL) as the second antibody. The tetramethylbenzidine (TMB) peroxidase substrate system (Kirkegaard & Perry, Gaithersburg, MD) was used as the chromogenic substrate. The color product was read for the optical density (OD) at dual wavelengths of 450 and 630 nm. The corrected OD value of the test serum was obtained after subtracting the cell control OD from the original OD value. The corrected OD value of the virus control at a working concentration of 100 TCID₅₀ was also obtained in the same manner. A positive microNT result was obtained when the test serum yielded a ≥50% reduction in the corrected OD value compared with that of the virus control. The antibody titer was defined as the reciprocal value of the highest serum dilution that gave ≥50% neutralization of 100 TCID₅₀ of the test virus. It should be noted that the antibody titer value as determined by our definition was twofold lower than that defined by WHO and CDC, such that our titer of 1:40 is equivalent to 80 as defined by WHO and CDC. In our assay protocol, the volume of the test virus in the reaction well was not taken into account in the calculation for the NT antibody titer; meanwhile, this volume is included in the WHO/CDC protocol (I. Stephenson, WHO manual on influenza microneutralization assay: CDC Influenza Training Course at Faculty of Medicine Siriraj Hospital, Mahidol University, November 2004). In addition, we found no significant difference in the NT titers, as the CDC reference serum samples were assayed in an MDCK cell monolayer or cell suspension such that under two types of cell conditions, a test serum showed the same antibody titer or the variation was within twofold of the difference.

Hemagglutination inhibition test. The two H5N1 isolates and horse and goose erythrocytes were used for antibody detection by an HI test. The protocol was as described previously (8, 11). A test serum was mixed with receptor-destroying enzyme (Denka Seiken, Japan) to obtain a dilution of 1:4, followed by incubation for 16 h at 37°C, heat inactivation at 56°C for 30 min, and adsorption with packed red blood cells (RBC) for 60 min at 4°C. The treated serum was serially diluted twofold to yield the starting dilutions of 1:20 to 1:2,560 and then added with 4 HA units of the test virus. One HA unit is defined as the highest virus dilution that yields complete hemagglutination. A reaction well containing 25 µl of the diluted serum and 25 µl of the virus suspension was incubated at room temperature for 30 min before adding 50 µl of the erythrocyte suspension and further incubated for 1 hour at 4°C. Either a 0.5% goose red blood cell (GRBC) or 1% horse red blood cell (HRBC) suspension was employed in our HI assay. Hemagglutination patterns of the test wells were examined. The HI antibody titer was defined as the reciprocal of the highest serum dilution that gave complete inhibition of hemagglutination.

Western blot assay. Based on WHO criteria, a human serum sample that possesses an NT antibody titer of ≥80 (or ≥40 by our assay) should be further confirmed for its specificity to H5 HA in a WB assay. The serum sample at the dilution of 1:100 was tested against baculovirus recombinant H5 HA antigen (Protein Sciences Corporation, CT). According to the product brochure, the

HA1 and HA2 subunits possess molecular masses of 45 and 25 kDa, respectively. Goat antiserum against purified HA of A/Vietnam/1203/04(H5N1), kindly provided by Robert G. Webster and Richard Webby, St. Jude Children's Research Hospital, and a commercial monoclonal antibody to H5 HA (US Biological, Swampscott, MA) was used as the reference antibody control. The nitrocellulose membrane blotted with antigens was blocked with 5% skim milk in Tris-buffer saline plus 0.1% Tween 20 (TBS-T). The test sera were incubated with the blotted membrane overnight at 4°C before washing three times with TBS-T, followed by the secondary antibody, horseradish peroxidase enzyme conjugated with either rabbit anti-goat Ig (Dako Cytomation, Denmark), goat anti-mouse IgG (Santa Cruz Biotechnology Inc., Santa Cruz, CA), or goat anti-human IgG (Zymed Laboratories Inc., San Francisco, CA) for 2 hours at room temperature. Diaminobenzidine (Sigma-Aldrich, St. Louis, MO) mixed with NiCl₂ and H₂O₂ was used as the chromogenic substrate.

RESULTS AND DISCUSSION

A fourfold rise in antibody titer either by microNT or HI assay was noted in paired blood specimens, typically when the second specimen was collected 15 or more days after onset of disease (patient nos. 1, 4, and 6). The highest microNT and HI titers of 1:1,280 were detected in sera collected at 15 days (patient no. 6) or 21 days (patient nos. 1 and 4) after onset of disease (Table 2). In one surviving subject from whom repeated serial blood specimens were collected (patient no. 6), the early peak antibody level was followed by a marked decrease in titer about 5 months later, after which the antibody titer remained stable for at least another year. Similarly, all four survivors (patient nos. 2, 3, 4, and 6) also demonstrated microNT titers of ≥1:40 that persisted in all serial serum samples collected at over 3 or almost 5 years after disease onset, the longest periods that we could follow for an individual subject. Our titer of 1:40 was a critical value for indicating previous H5N1 infection, because it was not found in the general Thai population. When establishing the microNT assay, we had investigated more than 200 serum samples from healthy subjects. The results showed that 70% of the subjects had NT antibody to H1N1 virus as tested against A/New Caledonia/20/99 (H1N1) but none had antibody to KAN-1 virus (data not shown). We previously reported the result of an ELISA-based microNT assay in 901 residents of four villages with H5N1 human cases and found that 888 (98.6%) had no NT antibody titer to KAN-1 virus as screened at the serum dilution of 1:5. Among 13 positive cases, 11 had an NT titer of 5 and the other 2 had titers of 10 and 20 (2).

There were two patients (nos. 5 and 7) who died before convalescent blood samples were collected. No anti-H5 antibody was detected in patient no. 7, whose acute blood was collected 9 days after onset of disease; even the NT assay was performed against NYK, which was the autologous virus. On the other hand, patient no. 5, who had a single serum sample collected 5 days after onset of disease, remarkably exhibited a serum antibody titer of about 1:320 by either microNT or HI assay. Finally, patient no. 8 had no detectable anti-H5 antibody in two blood samples collected at 24 and 27 days after onset of symptoms, beyond the time when a response was typically seen in other patients. Patient no. 8 was negative for anti-human immunodeficiency virus and anti-hepatitis C virus antibodies and was naturally immune to hepatitis B virus infection (positive anti-HBs, positive anti-HBc, and negative HBs antigen). However, he was an alcohol abuser, an underlying condition that might lead to the inability to develop high antibody re-

TABLE 2. Kinetics and longevity of antibody response to H5N1 virus infection

Subject no.	Blood sample No.	Specimen collection (time after disease onset)	Antibody titer to:					
			A/Thailand/1(KAN-1)/04 ^a as determined by:			A/Thailand/676(NYK)/05 ^b as determined by:		
			NT	HI with:		NT	HI with:	
1	1	10 days	<5	20	20	1,280	20	20
	2	21 days	1,280	640	1,280		1,280	640
2	1	2 yrs, 3 mos	80	80	160	160	160	80
	2	2 yrs, 9 mos	160	80	160	160	160	160
	3	3 yrs, 3 mos	80	80	80	160	160	160
	4	3 yrs, 11 mos	80	80	160	160	160	160
	5	4 yrs, 5 mos	40	40	160	160	160	160
	6	4 yrs, 11 mos	40	40	160	160	160	160
3	1	2 yrs, 2 mos	160	80	160	80	160	80
	2	2 yrs, 8 mos	160	80	160	160	160	160
	3	3 yrs, 2 mos	160	80	160	160	160	160
	4	3 yrs, 10 mos	160	80	160	160	160	160
	5	4 yrs, 3 mos	80	80	160	160	160	160
	6	4 yrs, 10 mos	80	80	160	160	160	160
4	1	10 days	<5	20	20	1,280	20	20
	2	12 days	5	20	20		20	20
	3	21 days	1,280	20	20		20	20
	4	1 yrs, 6 mos	160	80	80	320	160	160
	5	2 yrs	160	80	160	320	160	160
	6	2 yrs, 6 mos	160	80	160	160	80	160
	7	3 yrs, 3 mos	80	80	80	160	160	160
	8	3 yrs, 8 mos	80	80	80	160	160	160
	9	4 yrs, 2 mos	80	80	80	160	160	160
5	1	5 days	320	80	320	160	640	640
6	1	4 days	5	<20	<20	<10	20	<20
	2	15 days	1,280	320	640	2,560	1,280	1,280
	3	20 days	640	160	320	640	640	640
	4	5 mos	80	80	160	80	160	160
	5	11 mos	80	80	160	80	160	160
	6	1 yrs, 5 mos	40	80	80	80	160	160
	7	2 yrs, 2 mos	40	40	40	80	80	80
	8	2 yrs, 7 mos	40	40	40	80	80	80
	9	3 yrs, 1 mos	40	40	40	80	80	80
7	1	9 days	<5	<20	<20	<5	20	20
8	1	24 days	5	<20	<20	<20	<20	<20
	2	27 days	5	<20	<20		<20	<20

^a Autologous virus of patient no. 1.^b Autologous virus of patient no. 7.

spouse. He received standard oseltamivir treatment beginning 14 days after onset of symptoms but died 13 days later. We further tested these two blood samples against autologous virus (A/Thailand/1(NBL)/06 (H5N1), but still no NT antibody titer was detected (data not shown). Katz et al. (4) previously reported an adult H5N1 patient in whom no H5-specific antibody response was detected, despite the collection of appropriately timed paired blood specimens. The diagnosis of H5N1 virus infection in this case was similarly based on positive RT-PCR and virus isolation. However, in this case, the inability to mount an H5 antibody response was attributed to the immunocompromised status of the patient due to systemic lupus erythematosus.

Interestingly, we found that sera obtained from patients infected in 2004 could cross-neutralize the two virus isolates to comparable antibody titers. Similarly, sera collected in 2005 cross-neutralized the earlier H5N1 strain, despite the two viruses sharing 96% amino acid identity in the HA sequence (GenBank accession nos. AAS65615 and ABC72655) and 90% identity in NA sequence (GenBank accession nos. AAS65616 and ABC72646) and the difference in receptor site binding preference of SA α 2,3Gal or SA α 2,6Gal (1, 6). These results suggest that the two H5N1 viruses examined were antigenically closely related with respect to the human antibody response.

This study used infectious viruses as the test antigens in the HI assay. The protocol as described previously employed ei-

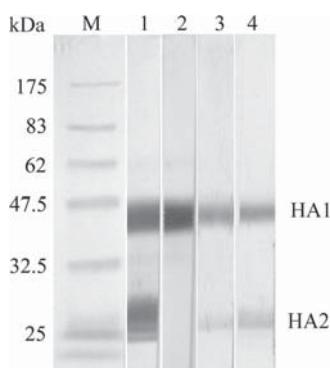


FIG. 1. Detection of anti-H5 HA antibody by WB assay using H5 HA recombinant protein as the test antigen. Lane M, protein molecular mass markers; lane 1, goat antiserum to purified H5 HA; lane 2, mouse monoclonal antibody to H5 HA; lane 3, serum from patient no. 4 at 1 year 6 months after disease onset; lane 4, serum from patient no. 6 at 11 months after disease onset.

ther 1% horse or 0.5% goose erythrocytes (5, 8). Even though horse erythrocytes have been recommended by previous investigators and WHO (8, 11) for detection of antibody to AI virus by HI assay, we did not see a marked difference in the antibody titers obtained when either kind of erythrocytes was used (Table 2). Our finding provides an alternative choice of erythrocytes that can be accessed more easily for Asian countries. We previously reported this finding in a smaller number of blood samples (5).

The result from the WB assay in 20 serum samples from healthy subjects was clearly negative, including the serum sample with anti-H5N1 NT antibody titers of 10 and 20 (data not shown). On the other hand, sera from all four survivors, including when using goat anti-H5 HA, reacted with both HA1 and HA2 domains of the H5 HA, while the monoclonal antibody reacted with the HA1 domain only. The WB assay confirmed the persistence of H5N1 antibody in serial serum samples collected at all time points in all survivors. Examples of serum specimens from patients 4 and 6 are shown in Fig. 1.

Our study was limited by the amount and number of blood specimens available for investigation for several reasons: diagnosis of H5N1 virus infection is generally performed on respiratory samples, not sera; criteria for serologic diagnosis have only been established more recently and are not useful for acute clinical care; based on early disease manifestations, clinicians were more likely to suspect other more common diseases, such as dengue, resulting in only small volumes of sera remaining after dengue serodiagnosis; most important is the high fatality rate of human H5N1 disease. Another limitation was the inability to obtain the exact time of exposure and infection of an individual. During a poultry die-off in a village, it was difficult to pinpoint the exact date of exposure, and some cases may have experienced multiple exposures. The incubation period for H5N1 virus infection in humans after exposure to infected poultry in many cases is 2 to 5 days and is generally 7 days or less. In clusters with probable human-to-human transmission, the incubation period appeared to be approximately 3 to 5 days but in one instance was estimated to be 8 to 9 days (3, 9, 14).

In summary, our study demonstrated high neutralizing anti-

body titers were achieved 2 to 3 weeks after disease onset in the majority of H5N1-infected symptomatic individuals tested. Furthermore, the anti-H5 neutralizing antibody response was long-lasting and cross-neutralizing for related clade 1 viruses. To what extent these features are implicated among asymptomatic individuals remains to be determined.

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Codon volatility of hemagglutinin genes of H5N1 avian influenza viruses from different clades

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Abstract Codon volatility is a method recently developed to estimate selective pressures on proteins on the basis of their synonymous codon usage. Volatility of a codon was defined as the fraction of single nucleotide substitutions that would be nonsynonymous. Higher volatility may indicate that the gene has been under more positive selection in the recent past. We analyzed volatility of hemagglutinin genes of H5N1 viruses in the recent outbreaks and observed differences in the volatility among viruses of different clades. The codon volatility of subclade 2.1 viruses from Indonesia was the lowest among all H5N1 clades and subclades. Time series analyses since the beginning of the epidemic in 2004 showed that codon volatility of subclade 2.1 has gradually decreased, while those of other major clades have been increasing. This may reflect differences in the recent evolution of these viruses.

Keywords Avian influenza · H5N1 · Clade · Codon volatility · Selection · Evolution

Avian influenza H5N1 virus is a highly pathogenic influenza A virus that has emerged and caused wide-spread outbreaks in many countries [1]. The ability to infect and cause severe disease in human poses a serious threat that the virus may further evolve to the point that it can transmit efficiently from person to person [2]. This would

potentially cause a catastrophic influenza pandemic, which could kill millions of people worldwide [3].

All influenza A viruses are believed to have a common reservoir source in water fowls, which are considered a natural host of the virus [4]. Avian influenza viruses have been transmitted to other avian and mammalian host species and have established several host-specific lineages [4]. The virus evolves differently in natural avian hosts than it does in non-reservoir species [5]. Immunological pressure and adaptation to new host species are probably the major driving forces of viral evolution [6]. All the highly pathogenic H5N1 viruses that are causing outbreaks in various countries have hemagglutinin (HA) genes that originated from the common ancestral strain that caused an outbreak in geese in Southern China in 1996, A/goose/Guangdong 1/1996 (H5N1) (GsGd) [7]. The virus has gone through many reassortment events giving rise to multiple genotypes [7]. The HA gene of H5 subtype has diverged into clades and subclades, some of which are different in the geographical distribution [8]. Viruses of clade 1 are responsible for the outbreaks in Thailand and Vietnam, whereas clade 2 viruses have a more wide-spread distribution and can be further classified into 5 subclades. Subclade 2.1 is responsible for the outbreak in Indonesia, while subclade 2.2 belongs to the Qinghai lineage that spread to Europe and Africa [8]. Clade 2.3.4 has recently replaced clade 1 viruses in northern Vietnam [9]. The ancestral GsGd and its closely related sequences are defined as clade 0. Other subclades of clade 2 (2.3–2.5) and clade 3–9 are confined to China and some neighboring countries [1, 10]. It is not clear whether the diversification among clades was merely a result of geographical separation or there is a more fundamental difference in the evolution of the clades. We sought to understand the evolutionary pattern of the clades and subclades by analyzing their codon bias. We used a

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recently developed method called codon volatility, which assesses selective pressure by looking at codon usage of the gene [11–13]. We chose to analyze the HA1 portion of the hemagglutinin (HA) gene of the viruses. HA1 is a viral surface protein with high variability and has been previously shown to have high codon volatility, which indicates positive selection [14].

Codon volatility can be defined loosely as the proportion of a codon's point mutations that result in a nonsynonymous substitution [11]. Although there are several possible definitions of volatility, we used the formal definition described in Plotkin et al. [11] where the volatility of a gene is the summed volatility of its codons. Because codons with high volatility also have neighboring codons with high volatility, nonsynonymous substitutions are more likely to result in codons with high volatility. Therefore, after a positive selection has occurred, a site is more likely to be occupied by a codon of greater than average volatility. On the other hand, proteins containing a larger number of sites under negative selection will exhibit a statistical bias towards less volatile codons, after controlling for their amino acid content [13].

Whether codon volatility can be used to detect positive selection has been a controversial issue. Criticisms on the ability of codon volatility to detect positive selection include the fact that it is under influence from other factors, such as amino acid and nucleotide frequencies [15–19]. Nevertheless, the ability of codon volatility to detect relative positive selection has been shown in a number of models including influenza virus, *Mycobacterium tuberculosis*, and protozoan parasite *Trypanosoma cruzi* [11, 14, 20]. Although comparative method using the ratio of non-synonymous/synonymous changes (dN/dS) is the most widely used approach for analysis of positive selection, it can be affected by time since divergences of the compared sequences and population size when closely related sequences are analyzed [21]. Therefore, dN/dS can be biased by how well the compared sequences represent the population structure in the timeline of evolution in each clade. In contrast, codon volatility is a function of individual sequence, and not dependent on the selection of comparison pair.

Volatility calculation was performed using the Codon Volatility Computation Server (v1.0), Harvard University Bauer Center for Genomic Research (<http://volatility.cgr.harvard.edu/cgi-bin/volatility.pl>). Volatility of a codon is strongly influenced by the amino acid which it encodes. Therefore, in order to get rid of the bias caused by amino acid content of the gene, we used the “volatility *P*-values” that control for the amino acid sequence of each gene [13]. The volatility *P*-value for a gene is computed using a statistical test that evaluates whether or not its volatility is significantly elevated or depressed compared to the rest of

the sequences in the set, controlling for its length and amino acid composition. The *P*-value can be calculated using a randomization procedure or by direct formulae based upon a normal approximation. This web-implementation uses the normal approximation, which produces *P*-values that are virtually identical to those obtained by the randomization procedure. *P*-values near zero indicate significantly elevated volatility where *P*-values near one indicate significantly depressed volatility.

HA1 sequences were retrieved from the NCBI Influenza Virus Resource. The sequences include all influenza A virus of subtype H5N1 of the year 2003–2007 with full-length HA1 coding region. In order to classify the retrieved sequences into clades and subclades, we performed a phylogenetic analysis using maximum likelihood method in PHYLIP 3.66 package. The retrieved HA1 sequences clustered into clades and subclades according to their geographical origins as previously described [1, 8, 10] (data not shown). Comparing codon volatility of HA1 from various clades and subclades revealed that the subclade 2.1 (2.1.1–2.1.3) from Indonesia had lower codon volatility (higher volatility *P*-value), while all other clades and subclades had comparable *P*-values (Fig. 1). The difference between the mean *P*-value of subclade 2.1 (0.710) and that of all other clades and subclades (0.457) was statistically significant ($P < 0.0001$, *t*-test). All the differences between the *P*-value of subclade 2.1 and that of each individual clade and subclade were also statistically significant at $P < 0.0001$ by Bonferroni test. Since all the H5N1 viruses of different clades are related and believed to diversify from a common group of ancestral viruses of GsGd lineage in the recent past, we asked whether the observed difference in codon volatility was present at the beginning of diversification as a result of founder effect or has developed over the years after the separation between clade and subclade founders. To address this issue, we separated codon volatilities by the year of viral isolation. The codon volatilities of clade 2.1 viruses decreased (with the codon volatility *P*-values increasing) gradually over the years since the beginning of the epidemic in 2003. In contrast, codon volatilities of closely related viruses of clade 2.2–2.5 increased (with the codon volatility *P*-values decreasing) steadily during the same period. There were significant correlations between year of viral isolation and the means of codon volatility *P*-values. The correlation coefficient (R^2) was 0.8959 and 0.8381 for clade 2.1 and clade 2.2–2.5, respectively (Fig. 2). For the other major clade (clade 1), we also observed a trend of increasing codon volatility over the years, but the correlation did not reach statistical significance ($R^2 = 0.3518$). Therefore, the difference in codon volatilities became more prominent in the more recent years. This suggested that the difference in codon volatility occurred as a result of different

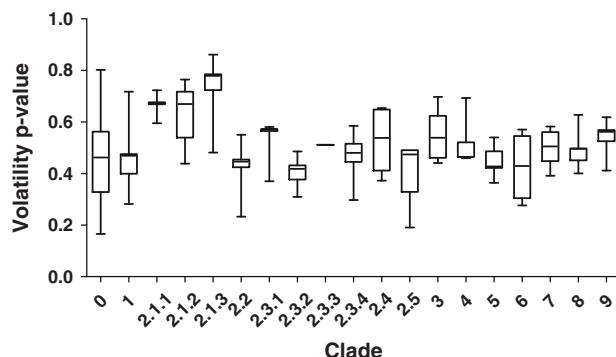


Fig. 1 HA1 volatility P -value of H5N1 viruses from different clades and subclades. Error bars, quadrangles, and horizontal lines inside the quadrangles represent ranges, 2nd and 3rd quartiles, and modes of codon volatility P -values of clades and subclades

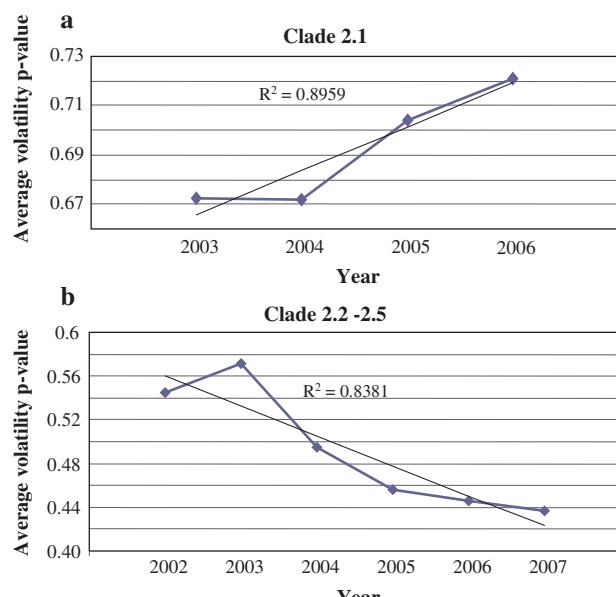


Fig. 2 Regression lines showing trends of decreasing codon volatility (increasing volatility p -value) over the recent years in HA1 of clades 2.1 (a) and increasing codon volatility of HA1 of clade 2.2–2.5 over the same period (b)

evolutionary pattern among the viruses as they separately evolved.

Our analyses indicate that H5N1 avian influenza viruses of clade 2.1 from Indonesia may be under a lower positive selective pressure or under a higher negative selection as compared to viruses of other clades. It is unclear what caused this differential selection. Certain environments of the transmission either intra-species or inter-species, especially avian-mammalian inter-species transmission, may impose a positive selective pressure on the virus in order to adapt to the new transmission environment. The environment and nature of transmission in Indonesia may be different from those in other countries and may require

less viral adaptation. Because of the persistent outbreaks and continuous transmission in poultry in this country, the virus may not need to jump from species to species in order to maintain the transmission chain. This may provide the virus the ability to persist and spread without having to evolve rapidly. On the other hand, it is also possible that the HA1 of clade 2.1 viruses may be under a higher negative selection because of either its own structural constraint or any constraint required for effective spreading in specific environmental conditions in this country.

With the assumption that codon volatility reflected the level of positive selection in these HA1 sequences, the higher codon volatility of HA1 for all other clades and subclades as well as the continuously increasing codon volatility for clades 2.2–2.5 suggests that most of the current H5N1 viruses, except for the clade 2.1 from Indonesia, have been under positive selection since the beginning of the epidemic and still continue to evolve rapidly. This is in agreement with a recently published analysis showing rapid evolutionary dynamics in avian influenza viruses including H5N1 [22]. Another study also showed evidence of positive selection in HA genes of H5N1 viruses that might be different among viral lineages [23]. Since high codon volatility indicates viruses with high ability to evolve, it may pose a higher risk of successful viral adaptation to human host. Therefore, we have to maintain vigilance and continuous monitoring and control in order to prevent the emergence of a pandemic virus.

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Indigenous sources of 2007–2008 H5N1 avian influenza outbreaks in Thailand

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Outbreaks of H5N1 avian influenza show strong seasonality. It is not clear where the source of virus originates from in each new outbreak season. This study sought to understand the nature of viral resurgence in recent outbreak seasons in Thailand, where the epidemic is relatively well controlled. In such a situation, indigenous viruses surviving the inter-outbreak season would have to pass through a bottleneck. In order to look for evidence of the bottleneck effect, viral genome sequences from recent outbreaks in the country were analysed. H5N1 avian influenza viruses were isolated from six outbreaks in the rainy season and winter of 2007 through to early 2008. Most of the outbreaks were in the Yom–Nan River basin in the southern part of the northern region of the country. Sequences of these viral isolates were identified as clade 1, genotype Z, similar to viruses from previous years in the central region of the country. The sequences clustered into two groups, one of which was closely related to viruses isolated from the same area in July 2006. These analyses indicated that there was a strong bottleneck effect on the virus population and that only a few lineages remained in the area. In addition, evidence of reassortment among these viruses was found. These indicated re-emergence of viruses from a small pool of indigenous sources that had been silently perpetuated over the dry summer months. Therefore, an approach to eradicate H5N1 avian influenza from the area by eliminating these local reservoirs may be feasible and should be seriously considered.

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INTRODUCTION

Thailand has suffered several rounds of H5N1 avian influenza (AI) outbreaks in poultry. The outbreaks in 2004–2005 were explosive and caused severe economic loss to the poultry industry. Poultry outbreaks, as well as human cases, in Thailand have a clear seasonal pattern. Each year, cases appear with the start of the rainy season in

The GenBank/EMBL/DDBJ accession numbers for the avian influenza sequences are EU233413–EU233420, EU497919–EU497921, EU547798–EU547801, EU669187–EU669201, EU676306–EU676321 and EU875388–EU875397; details are available with the online version of this paper.

July, peak at the end of the rainy season and the start of winter in September–October, and disappear with the start of summer in February (Tiensin *et al.*, 2005). The outbreaks in 2004–2005 were widespread, covering all regions of the country (Buranathai *et al.*, 2007; Tiensin *et al.*, 2005). After massive campaigns and vigorous outbreak control by culling and movement restrictions, the epidemic subsided. Subsequent outbreaks in 2006 and later were limited to small clusters of backyard chickens and ducks. These outbreaks were concentrated in the central part (lower northern region) of the country and were caused by clade 1 viruses. Although a few limited outbreaks were reported in the north-eastern region of the

country bordering Laos in July 2006 and January 2007, they were caused by a different group of viruses, belong to clade 2 (Chutinimitkul *et al.*, 2007). Interaction or exchange of the clade 1 and clade 2 viruses between these two areas has never been detected. In this study, we confined our analyses to the outbreaks in the central part of the country, which has been suffering repeated H5N1 AI outbreaks since the beginning of the epidemic in 2003–2004. The provinces with repeated H5N1 outbreaks in poultry in 2006–2008 include Sukhothai, Phitsanulok, Pichit and Nakhonsawan in the lower northern region. In the rainy season and winter of 2007 through to early 2008, there were several reports of backyard chicken die-off in these provinces. Despite intensive control and the apparent complete disappearance of outbreak in the dry summer months, outbreaks reappeared in the rainy season of 2006 and 2007. This indicated either the existence of locally persistent viral reservoirs or the reintroduction of viruses from other countries. Although introduction of a new viral strain (clade 2.3.4) into the north-eastern region of the country was reported, the viral sequences from the north/central region remained clade 1, genotype Z (Chutinimitkul *et al.*, 2007; Keawcharoen *et al.*, 2005). This indicated that yearly re-emerging viruses in central Thailand belong to a similar lineage and suggested that they originate from a locally persistent reservoir (Amonsin *et al.*, 2006; Buranathai *et al.*, 2007). The disappearance of the virus in summer suggested that there might be only a small number of viruses surviving the inter-outbreak period, causing a bottleneck

effect. Although previously published analyses of viral sequences in 2004–2005, when the epidemic was extensive and did not completely subside in summer, did not suggest any bottleneck effect (Amonsin *et al.*, 2006; Buranathai *et al.*, 2007), we questioned whether the situation would be different in 2006–2008, when the epidemic was better controlled. In order to understand the nature of viral perpetuation and resurgence, we analysed nucleotide sequences from viruses isolated between 2006 and 2008 in the lower northern provinces of Thailand, where outbreaks have taken place repeatedly in every outbreak season.

METHODS

Outbreaks. We investigated six episodes of poultry die-off. All but one occurred in backyard chicken flocks with limited spread. One outbreak in the Chumsaeng district of Nakhonsawan province was in a broiler chicken farm. These outbreaks were located in the Yom–Nan River basin. The Yom and Nan Rivers are branches of the Chao Phraya River, the main river of the central plain of Thailand. The locations of the outbreaks are shown in Fig. 1, and characteristics of the outbreaks are given in Table 1.

Virus isolation and sequencing. Tracheal and cloacal swabs collected from backyard chickens and ducks were inoculated into Madin–Darby canine kidney cells. The subtype of viruses was identified by RT-PCR using H5- and N1-specific primers (Lee *et al.*, 2001). RT-PCR was performed on RNA samples extracted from haemagglutination-positive culture supernatants and the PCR

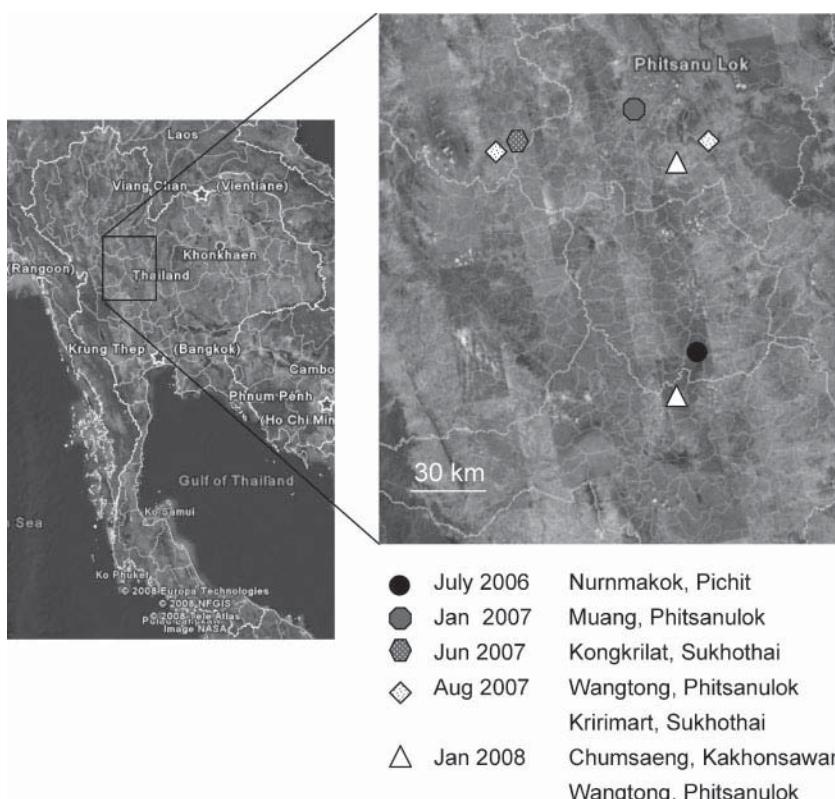


Fig. 1. Location of H5N1 outbreaks in poultry in 2007–2008, with the date of sample collection from the outbreaks.

Table 1. Characteristics of the poultry outbreaks in 2006–2008

Location (district, province)	Type of poultry	No. birds*	Time span	Virus name
Nurmmakok, Pichit	Backyard chickens	Unknown	24 July 2006	A/chicken/Thailand/PC-168/2006, A/chicken/Thailand/PC-170/2006
Muang, Phitsanulok	Ducks	207 died (30 backyard chickens, 177 ducks)	15 January 2007	A/duck/Phitsanulok/NIAH6-5-0001/2007
Kongkrilat, Sukhothai	Backyard chickens	Unknown	May–June, 2007	A/chicken/Thailand/ICRC-V143/2007
Wangtong, Phitsanulok	Backyard chickens	Eight died from 70 birds (11.4%)	17–23 August 2007	A/chicken/Thailand/ICRC-V195/2007
Kririwat, Sukhothai	Backyard chickens	19 died from 70 birds (27.1%)	21–23 August 2007	A/chicken/Thailand/ICRC-V213/2007
Chumsaeng, Nakhonsawan	Broiler	4085 died from 14 000 birds (29.2%)	22–29 January 2008	A/chicken/Thailand/ICRC-V586/2008
Wangtong, Phitsanulok	Backyard chickens	127 died from 250 chickens (50.8%)	24–29 January 2008	A/chicken/Thailand/ICRC-V618/2008
	Backyard ducks	A small flock of 10 apparently healthy ducks in the outbreak area		A/duck/Thailand/ICRC-V629/2008
Supanburi	Captive pheasant	One died from 500 captive wild birds (0.2%)	17 January 2008	A/pheasant/Thailand/VSMU-1-SPB/2008

*Data from the Department of Livestock Development (http://www.dld.go.th/home/bird_flu/history.html).

products were directly sequenced as described previously (Puthavathana *et al.*, 2005). The sequences of A/chicken/Thailand/PC168/06, A/chicken/Thailand/PC170/06 and A/duck/Phitsanulok/NIAH6-5-0001/2007 were obtained from GenBank. All sequences determined in this study were submitted to GenBank; the accession numbers are shown in Supplementary Table S1, available in JGV Online.

Phylogenetic reconstruction. Sequence alignment was carried out using MUSCLE version 3.6 and adjusted manually using BioEdit version 7.0.9. The maximum-likelihood (ML) method from the PhyML package was applied to generate a phylogenetic tree of the aligned sequences. Bootstrap analyses were performed on the ML trees for 1000 pseudo-replicates.

RESULTS

We sequenced all of the genomic fragments of the isolated viruses. The sequences were inspected for unusual changes. We found no mutations at key determinant residues, including receptor-binding preference in the haemagglutinin (HA) gene at positions 138, 186, 196 and 226–228 (H3 numbering system) (Auewarakul *et al.*, 2007; Stevens *et al.*, 2006; Yamada *et al.*, 2006); adaptation to mammalian hosts and growth at lower temperatures in the polymerase basic gene (PB2) at position 627 (Hatta *et al.*, 2007); innate immunity escape and cytokine induction in the non-structural gene (NS1) at position 92 (Lipatov *et al.*, 2005; Seo *et al.*, 2004); and oseltamivir resistance in the neuraminidase (NA) gene at position 274 (Le *et al.*, 2005).

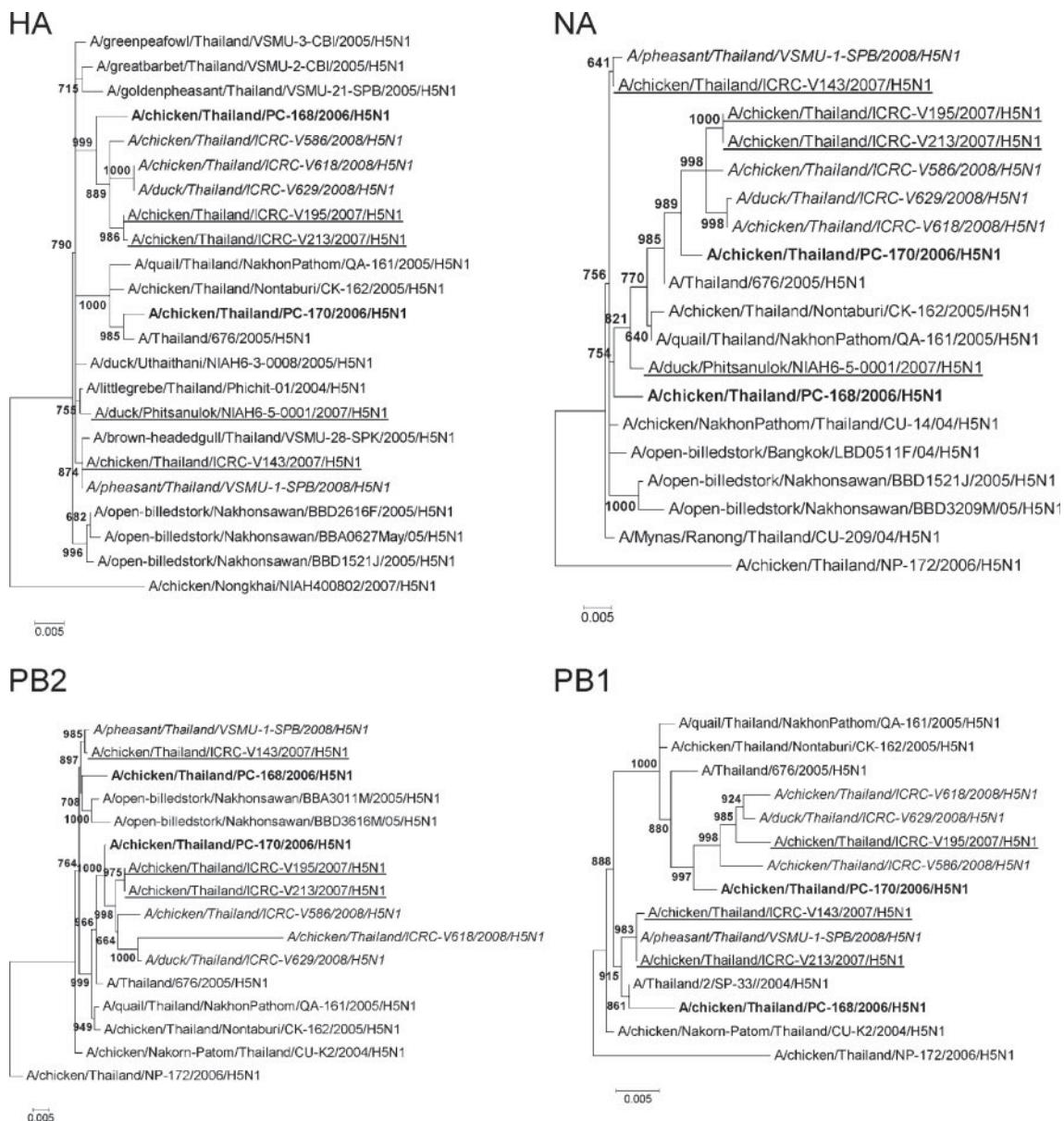
We performed phylogenetic analyses of all of the genomic segments using the ML algorithm. All of the sequences clustered with clade 1, genotype Z viruses isolated previously in the central region of Thailand, and could be clearly separated from the previously reported clade 2.3.4 from north-eastern Thailand (Chutinimitkul *et al.*, 2007) (Fig. 2). When we looked at the relationship among the newly isolated viruses, the HA sequences of ICRC-V143 and ICRC-V213 did not appear to be more related to each other than to other Thailand sequences (Fig. 2). This was unexpected, as the two viruses were isolated from neighbouring areas over consecutive time periods. In contrast, sequences with clear epidemiological linkage clustered closely and formed separated branches, e.g. sequences from open-billed storks in Nakhonsawan in 2005, which indicated a common origin of viruses within the same outbreak cluster. On the other hand, the HA sequence of ICRC-V213 was closely related to that of ICRC-V195 (Fig. 2). The two viruses were isolated in the same week of August 2007 but from areas about 60 km apart. Surprisingly, the patterns of relationship among these three viruses were not consistent for some other genomic segments. The polymerase subunits PB1 and PA of ICRC-V213 were closely related to those of ICRC-V143 rather than ICRC-V195. This suggested that ICRC-V213 could be a reassortant between ICRC-V143- and ICRC-V195-like viruses. Interestingly, the HA, matrix (M),

nucleoprotein (NP) and PA genes of ICRC-V195 were closely related to those of A/chicken/Thailand/PC-168/2006 (PC-168), a virus isolated in a neighbouring province, Pichit, 1 year earlier. Moreover, the NA, NS, PB1 and PB2 genes of ICRC-V195 were closely related to those of A/chicken/Thailand/PC-170/06 (PC-170), a virus isolated in the same area and time period as PC-168 (Fig. 2). Although PC-168 and PC-170 were from the same area in the same time period, these two viruses were not more related to each other than to other clade 1 Thailand viruses. This suggested a reassortment event between the PC-168 and PC-170, which might have given rise to ICRC-V195. Another 2007 virus, A/duck/Phitsanulok/NIAH6-5-0001/2007, was identified in January 2007, but its HA and NA sequences did not show any closer relationship to other recent isolates than to other clade 1 isolates, suggesting that this HA/NA lineage may have been extinct after January 2007. However, as sequences of other genomic segments of this virus are not available, we do not know whether the virus passed on some of its other genomic segments to other viruses via reassortment. In January 2008, outbreaks reappeared in Nakhonsawan, Phitsanulok and Supanburi. The viruses A/chicken/Thailand/ICRC-V586/2008, A/chicken/Thailand/ICRC-V618/2008 and A/duck/Thailand/ICRC-V629/2008, and A/pheasant/Thailand/VSMU-1-SPB/2008 were isolated from Nakhonsawan, Phitsanulok and Supanburi, respectively. The virus A/pheasant/Thailand/VSMU-1-SPB/2008 was isolated from a zoo in an area where poultry die-off had occurred. All of the genomic segments of this virus clustered closely with those of ICRC-V143, whereas sequences of the other viruses isolated in January 2008 were closely related to those of ICRC-V195. In summary, viruses from a cluster of outbreaks in January 2008 (ICRC-V586, ICRC-V618 and ICRC-V629) appeared to be direct descendants of a virus similar to an isolate from August 2007 (ICRC-V195), which was probably a reassortant of two viruses similar to those identified in July 2006 (PC-168 and PC-170). Another isolate from January 2008 (A/pheasant/VSMU-1-SPB/2008) seemed to be a descendant of a virus similar to a chicken isolate from June 2007 (ICRC-V143) (Fig. 3). These data indicated that at least two varieties of H5N1 virus persisted silently over the dry summer months and gave rise to outbreaks in the 2007–2008 season, and that reassortment among these viruses may have occurred. The two varieties were probably responsible for all of the outbreaks in season 2007–2008. Other strains from 2004–2005 were not detected after 2006, suggesting that they were extinct, resulting in a strong bottleneck effect on the virus population.

DISCUSSION

A bottleneck effect is an evolutionary event in which a substantial fraction of a population is eliminated, leaving the surviving minority to repopulate the milieu.

Population bottlenecks can increase genetic drift. The re-emergence of H5N1 viruses of similar lineage every year in the rainy season after a silent period in the summer suggests that either there is an unrecognized infected reservoir or there is a low-level transmission chain during the summer months. Either way, if the reservoir or the level of the transmission chain during the summer is small enough, there would be a bottleneck effect on the virus population after re-emergence, as only a few viruses would re-emerge each year and give rise to a few branches, leaving other branches extinct. In this case, phylogenetic trees would show subclusters with some chronological and spatial correlations. However, if the reservoir or the transmission chain during summer was large, the emerging virus population structure would be similar to that of the previous season. In this case, phylogenetic trees would show no specific pattern. Previously published phylogenetic analyses of H5N1 sequences from central Thailand in 2004–2005 did not show any specific sublineage within the virus population (Amonsin *et al.*, 2006; Buranathai *et al.*, 2007; Keawcharoen *et al.*, 2005). This suggested that the virus was endemic in the area throughout the year without interruption, despite the brief periods of undetectable transmission during the summer months. In contrast, the outbreaks in 2006–2008 were much smaller in their geographical extent and the number of birds affected. This reduced the size of the virus population in the outbreak season and also in the inter-outbreak period. The virus populations in the summers of 2006 and 2007 were probably small enough to cause a bottleneck effect. Our data support this model. Despite the evidence supporting the existence of a bottleneck, our analyses did not indicate where this bottleneck might be. Mild or asymptomatic infection with limited virus shedding is ideal to render transmission chains undetectable. One of the recent isolates in this study was from an apparently healthy duck, and ducks have been shown to be infected with mild disease by some H5N1 strains (Sturm-Ramirez *et al.*, 2005). Free-grazing duck raising is still common practice in the Yom–Nan River basin, and previous risk analyses have shown that populations of free-grazing ducks correlate well with the risk of AI outbreak (Gilbert *et al.*, 2006, 2007, 2008). It is therefore likely that free-grazing ducks served as the viral reservoir and that limitation of transmission chains within duck populations in inter-outbreak periods caused the observed bottleneck effect. Infection of vaccinated animals can also make the infection asymptomatic and render the transmission undetectable. Although poultry vaccination is prohibited in Thailand, illegal vaccination is believed to be widespread in the area, especially in fighting cocks. However, accurate information on poultry vaccination in Thailand is not available. The extent and role of poultry vaccination in this country needs to be clearly elucidated. Accurate identification of the reservoir and bottleneck requires more detailed surveillance, especially in the inter-outbreak periods. Such intensified surveillance would



greatly benefit our understanding and future control of H5N1 AI epidemics.

The similarity between ICRC-V143 and A/pheasant/Thailand/VSMU-1-SPB/2008 was intriguing, as the locations of the two outbreaks were 280 km apart. This suggests that a long-range carrier, such as birds or the poultry trade, might be involved in the transmission. Understanding how the virus spreads over long distances is crucial to the successful control of the epidemic and deserves further investigation.

H5N1 AI outbreaks have been occurring repeatedly in the Yom–Nan River basin in recent years. The area has a good

irrigation system and the water supply is abundant all year round. Rice cultivation is also carried out in the summer in this area, whilst it is limited to the rainy season in most other areas of the country. The largest freshwater lake in Thailand, Bung Borapet, with an area of over 200 km², is also located in this area. Whether these geographical characteristics contribute to the repeated AI outbreaks requires further investigation. The limited geographical area of the sporadic outbreaks in 2006–2008 to the Yom–Nan River basin suggests that future attempts at controlling the virus reservoirs and outbreaks should be focused in this area.

The small pool of viruses surviving inter-outbreak periods may be amplified periodically in the outbreak seasons. It is

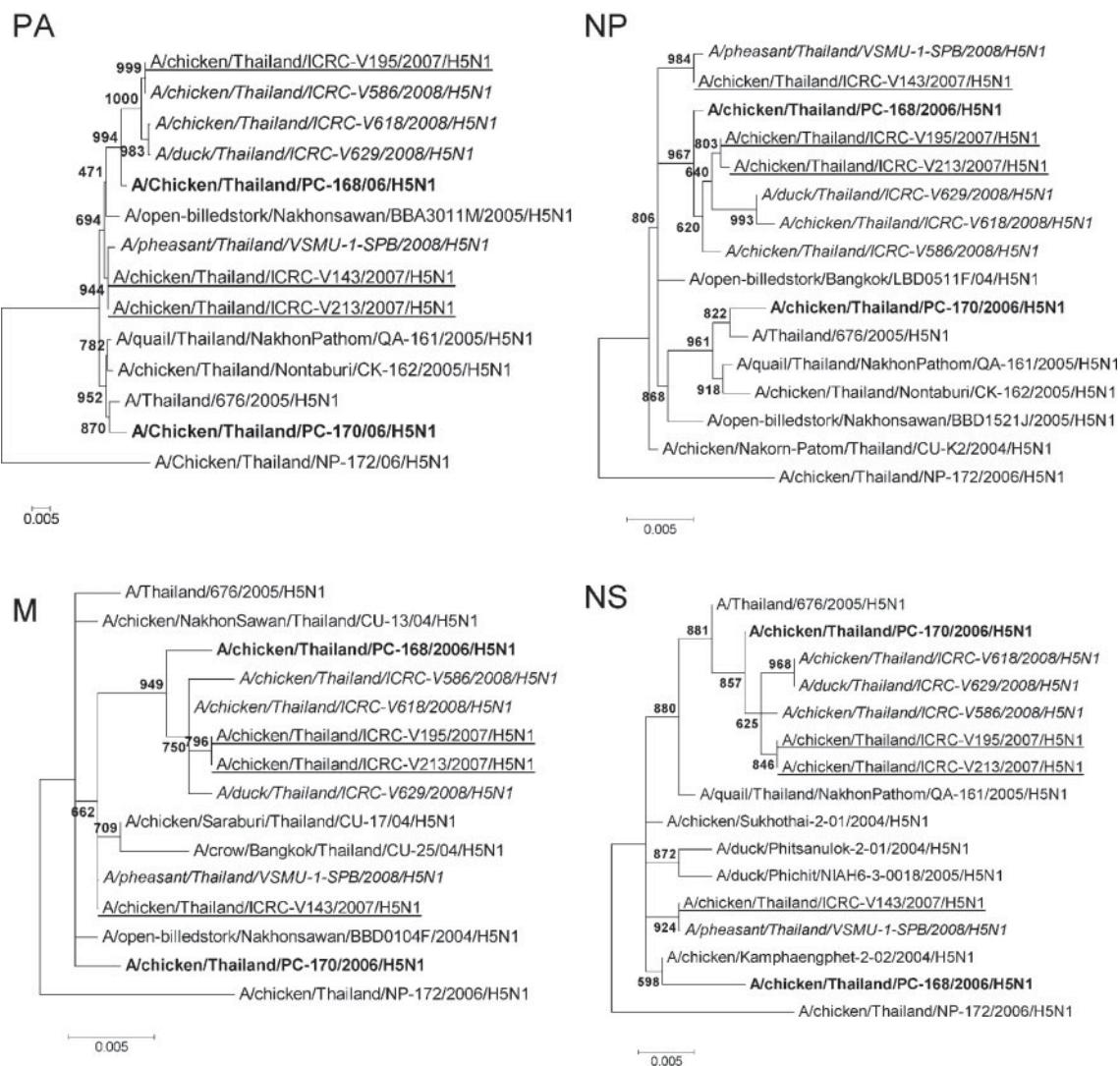


Fig. 2. ML trees with bootstrap values of genes of recent H5N1 viruses from Thailand. The viral sequences isolated in 2006, 2007 and 2008 are bold, underlined and italicized, respectively.

plausible that the cycle of low-level perpetuation in the summer and amplification in the rainy season and winter may together play crucial roles in persistence of the virus in this area. Our analyses suggest that the virus population during the inter-outbreak period may be quite small and could be the weak link in the cycle. Targeting this weak link by both extensive surveillance for virus reservoirs in summer and disrupting transmission chains at the end of the outbreak season to prevent the establishment of virus reservoirs may be the most appropriate strategy in the current situation in Thailand. Such a strategy could potentially lead to the eradication of the virus from this country.

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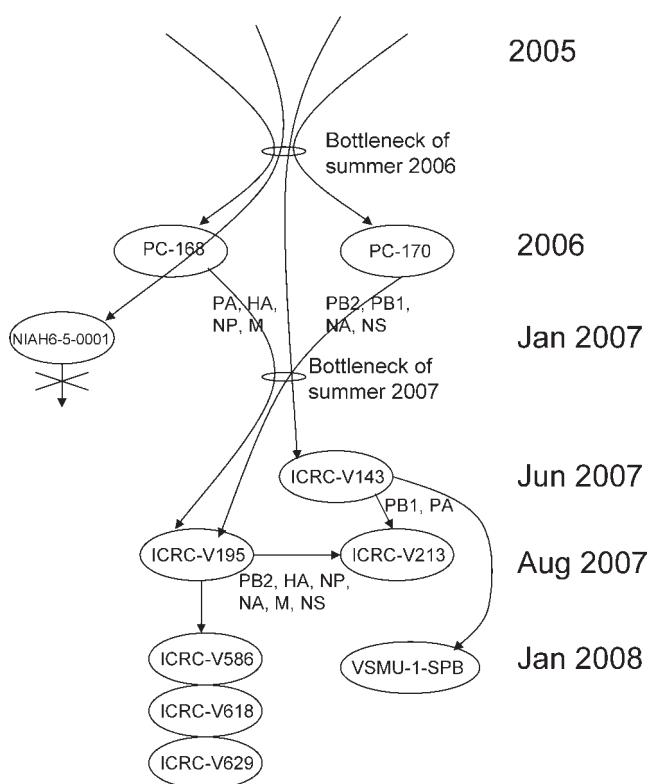


Fig. 3. Schematic diagram showing the predicted evolutionary paths of recent H5N1 isolates in Thailand and the proposed bottlenecks. The linear relationships among viruses were derived from the clustering of their genomic segment sequences in the phylogenetic trees in Fig. 2.

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Supplementary Table S1. List of GenBank accession numbers of the viral sequences

Virus name	GenBank accession number for gene							
	PB2	PB1	PA	HA	NP	NA	M	NS
A/chicken/Thailand/PC-168/2006	DQ99988 4	DQ99988 6	DQ99988 5	DQ99988 0	DQ99988 3	DQ99988 1	DQ99988 2	DQ99987 9
A/chicken/Thailand/PC-170/2006	DQ99989 3.1	DQ99989 2	DQ99989 4	DQ99988 7	DQ99989 1	DQ99988 8	DQ99988 9	DQ99989 0
A/duck/Phitsanulok/NIAH6-5-0001/2007	—	—	—	EF50199 7	—	EF50199 6	—	—
A/chicken/Thailand/ICRC-V143/2007(H5N1)	EU23341 3	EU23341 4	EU23341 5	EU23341 6	EU23341 7	EU23341 8	EU23341 9	EU23342 0
A/chicken/Thailand/ICRC-V195/2007(H5N1)	EU66919 2	EU66919 1	EU66919 0	EU49792 0	EU66918 9	EU66918 8	EU66919 3	EU66919 4

A/chicke n/Thailan d/ICRC- V213/20 07(H5N1)	EU87539 1	EU87539 2	EU87539 3	EU49792 1	EU87539 4	EU87539 5	EU87539 6	EU87539 7
A/chicke n/Thailan d/ICRC- V586/20 08(H5N1)	EU66919 5	EU66919 6	EU66919 7	EU49791 9	EU66919 8	EU66919 9	EU66920 1	EU66920 0
A/chicke n/Thailan d/ICRC- V618/20 08(H5N1)	EU87539 0	EU87538 9	EU54780 0	EU54779 8	EU54779 9	EU87538 8	EU66918 7	EU54780 1
A/duck/T hailand/I CRC- V629/20 08 (H5N1)	EU67631 2	EU67631 3	EU67630 6	EU67630 7	EU67630 8	EU67631 1	EU67630 9	EU67631 0
A/pheasa nt/Thaila nd/VSM U-1- SPB/200 8 (H5N1)	EU67631 4	EU67631 5	EU67631 6	EU67631 7	EU67632 0	EU67631 8	EU67631 9	EU67632 1

Chaichoune, K., Wiriyarat, W., Thitithanyanont, A., Phonarknguen, R., Sariya, L., Suwanpakdee, S., Noimor, T., Chatsurachai, S., Suriyaphol, P., Ungchusak, K., Ratanakorn, P., Webster, R. G., Thompson, M., Auewarakul, P. and Puthavathana, P. (2009). Indigenous sources of 2007–2008 H5N1 avian influenza outbreaks in Thailand. *J Gen Virol* **90**, 216–222.

P. jirovecii independent of environmental hazards.

Isolation of pathogens from an aborted fetus does not necessarily mean that they have caused the death of the fetus because many agents appear to pass through the fetal-placental unit and cause little damage. However, fungal infection is a major worldwide cause of abortion in cattle (10), and the surprising high prevalence of *P. jirovecii* infection found in dead fetuses in our study emphasizes the need to study the possible role of this fungal organism in human abortion.

Our findings could be of potential clinical importance and could open a new field of research, which should be explored. Further research should assess the scope of the problem and design rational preventive strategies, if necessary.

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Avian Influenza Virus (H5N1) in Human, Laos

To the Editor: The first avian influenza (H5N1) outbreak in poultry in Laos occurred in 2003 and subsided in March 2004 after massive killing of poultry to contain the disease. Extensive surveillance from July 2005 through January 2006 did not detect any influenza virus subtypes in chicken, ducks, quails, and pigs in live bird markets in the Vientiane, Champasak, and Savannakhet Provinces (1). Avian influenza virus (H5N1) was reintroduced into Laos in February 2006 but showed a lower incidence. Viruses isolated in this country in 2004 belonged to genotype Z, clade 1, and 2006 isolates belonged to clade 2.3.4 (online Appendix Figure, panel A, available from www.cdc.gov/EID/content/15/1/127-appF.htm) (1).

Avian influenza (H5N1) had not been reported in humans in Laos until February 27, 2007 (2). Our patient was a 15-year-old adolescent girl who lived in a suburb of Vientiane where an outbreak of influenza (H5N1) in poultry had been confirmed on February 7, 2007. Influenza-like symptoms developed in the patient on February 10. She was hospitalized in Vientiane with fever and respiratory symptoms on February 15. On February 17, her parents brought her to a private hospital in Nong Khai Province, Thailand. Oseltamivir was prescribed on February 19. On February 20, she was transferred to the Nong Khai Provincial Hospital because of rapid, progressive, severe pneumonia with acute respiratory distress syndrome. When we suspected avian influenza in this patient, clinical specimens were tested.

A diagnosis of infection with avian influenza (H5N1) was based on positive results obtained by reverse transcription-PCR (RT-PCR), viral isolation in MDCK cells inoculated with an endotracheal suction specimen

collected on February 22, and a 4-fold increase in neutralizing antibody titers from 80 to 320 in paired blood specimens collected on February 25 and March 1, as assayed against autologous virus. This virus isolate was named A/Laos/Nong Khai 1/07(H5N1). Subsequent samples were collected on February 25 and March 7 (day of death). Results of RT-PCR were positive for the sample collected on February 25 only; virus isolation results were negative for both samples.

The virus was screened for a novel reassorted gene by a multiplex RT-PCR and 8 primer pairs specific for each genomic segment of genotype Z, clade 1 virus (3). All segments except the polymerase A (PA) segment were amplified, which indicated that the new virus was different from genotype Z viruses. The viral genome was sequenced and submitted to GenBank (accession nos. EU499372–EU499379 for hemagglutinin, nonstructural protein, matrix protein, nucleoprotein, PB1, PB2, neuraminidase, and PA genes, respectively). Phylogenetic analysis showed that this virus belonged to genotype V (online Appendix Figure, panel B) (4); phylogenetic analysis of the hemagglutinin gene (www.who.int/csr/disease/avian_influenza/smalltree.pdf) showed that it belonged to clade 2.3.4 (online Appendix Figure, panel A).

Protein sequence at the hemagglutinin cleavage site harbored many basic amino acids (RERR_RKR). One amino acid deletion and 1 amino acid change were found when compared with RERRRKRR, which is present in most avian influenza viruses (H5N1). There was no change in receptor binding site. This virus had glutamic acid at aa 627 in the PB2 protein, aspartic acid at aa position 92 in nonstructural protein 1, and 5 aa deletions at positions 80–84 in the nonstructural protein 1. Analysis of the neuraminidase gene showed a 20-aa deletion in the stalk protein; there was no mutation of histidine to tyrosine at aa position 274,

a position shown to be the oseltamivir resistance marker in the neuraminidase 1 viral genome (5). Mutations in the matrix 2 gene showed that amantadine resistance was not present in our virus (6). Our in vitro assay (7) showed that this virus was sensitive to oseltamivir and amantadine.

Since 2003, genotype V influenza viruses (H5N1) have been reported in some East Asian countries. Genetic diversity in the hemagglutinin gene has classified those genotype V viruses into distinct clades. Viruses from avian species in South Korea in 2003 and Japan in 2004 (8,9) belong to clade 2.5. A/chicken/Shanxi/2/2006 isolate belonged to clade 7. Human cases in People's Republic of China, i.e., A/China/GD01/06, A/Shenzhen/406H/06, A/Jiangsu/1/2007, and A/Jiangsu/2/2007, belong to clade 2.3.4, the same clade as A/chicken/Thailand/NP-172/2006 and the virus from our study.

Highly pathogenic avian influenza viruses (H5N1) that caused outbreaks in Thailand since 2004 belong to genotype Z, clade 1. Introduction of genotype V clade 2.3.4 virus, A/chicken/Thailand/NP-172/2006, to Nakhon Phanom Province occurred in November 2006 (10), the same year that clade 2.3.4 virus was introduced into Laos (online Appendix Figure, panel A). On the basis of hemagglutinin gene phylogeny, A/Laos/Nong Khai 1/2007 is closely related to A/chicken/Nongkhai/NIAH 400802/2007 and A/chicken/Thailand/NP-172/2006. Phylogenetic analysis suggested that viruses from these 2 countries shared the same origin. There was extensive movement across the Mekong River even before the bridge linking Nong Khai from Vientiane was opened. However, the route of transmission of genotype V viruses from east Asian to Southeast Asian countries could not be elucidated.

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Fatal HIV Encephalitis in HIV-Seronegative Patients

To the Editor: Acute encephalitis is rarely seen in patients infected with HIV (1). In addition, HIV in patients who are seronegative is extremely rare, particularly in the setting of current screening ELISAs (2). We report a case of encephalitis and HIV in the same patient, which resulted in death.

A 44-year-old Caucasian woman sought treatment at our hospital with a 1-week history of fever, unsteady gait, and progressive confusion. Her medical history included hypothyroidism, depression, and chronic alcohol abuse. The patient's first tests for HIV were negative at 19 and 12 months prior to admission during routine intake screening for jail inmates (Abbott HIV AB HIV-1/HIV-2 [rDNA] enzyme immunoassay [EIA] kit; Abbott Laboratories, Abbott Park, IL, USA). Six months before admission, the patient had a viral exanthem of blistering rash on her lips, palate, and chest. Two weeks later, she had oral thrush and a leukocyte count of 1,700 cells/ μ L. An HIV ELISA result was negative. Three months before admission, she was admitted to a different hospital for weakness, abdominal pain, intermittent fever, diarrhea, persistent oral candidiasis, and ethanol withdrawal. She had leukopenia and thrombocytopenia. A fourth HIV ELISA result was negative. The patient had been admitted to our hospital one week before the current admission with symptoms of fever, confusion, and urinary tract infection. Lumbar puncture showed an elevated protein level (106 mg/dL). A fifth HIV test result 6 days before most recent admission was negative. Five days before admission, she had been discharged to a rehabilitation facility.

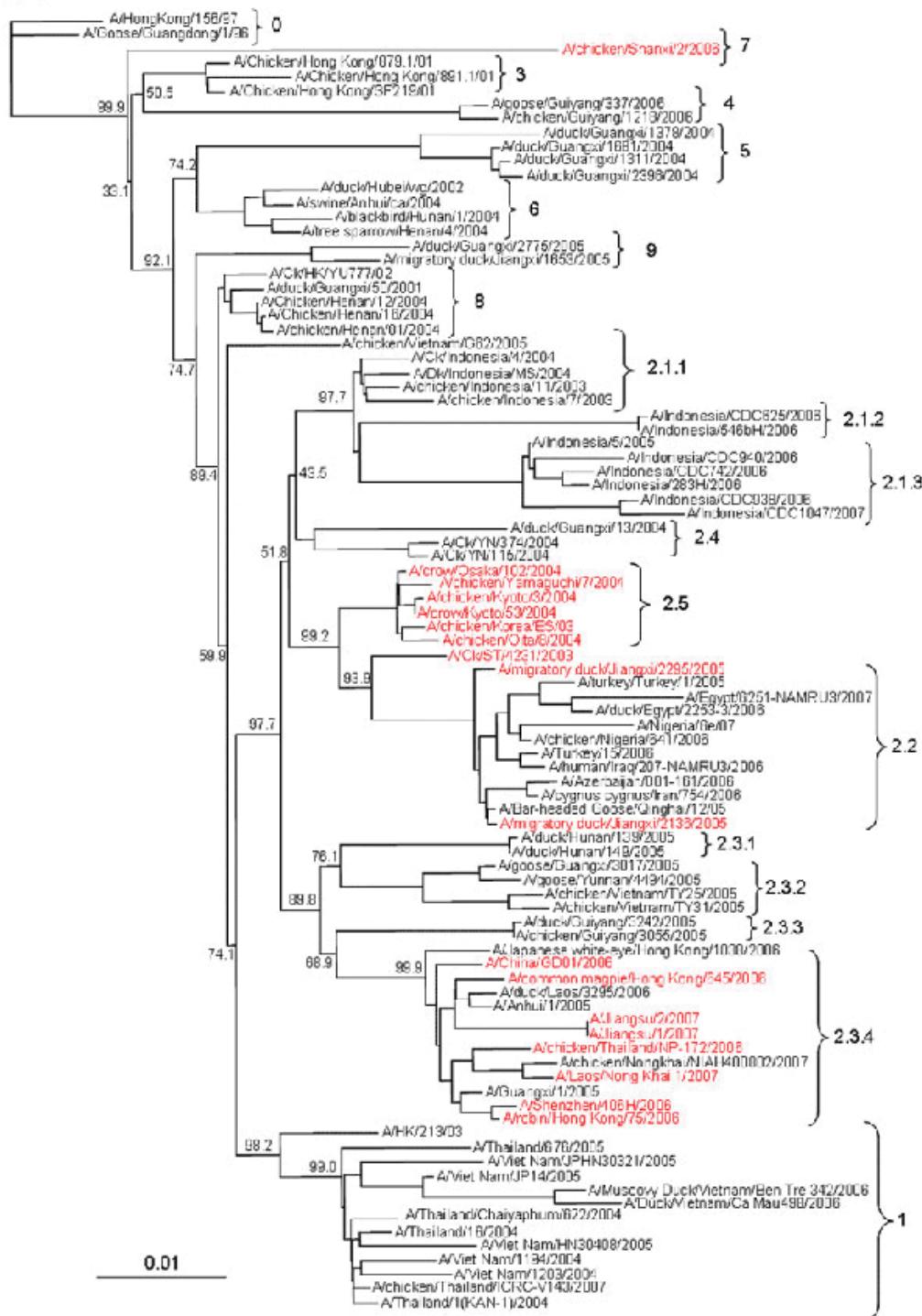
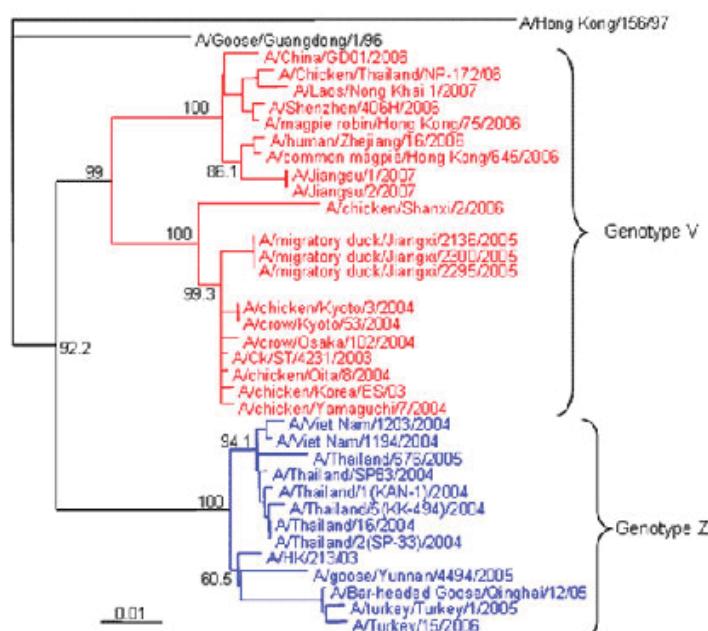
On this hospitalization, she had fatigue, headache, disequilibrium, dysarthria, and blurred vision. Initial

examination showed fever of 101.3°F, poor word recall, and a wide-based gait. Laboratory tests showed mild anemia and a leukocyte count of 2×10^3 cells/ μ L.

Over the next few days the patient's fever persisted and her mental status fluctuated. Tests on hospital day 2 showed a CD4 count of 101/mL (16.9%). Magnetic resonance imaging (MRI) of the brain showed diffuse symmetric white matter disease (Figure, panel A). Samples sent on hospital day 9 eventually showed wild-type HIV with a viral load $>500,000$ copies/mL. Repeat cerebrospinal fluid (CSF) test results were negative for cryptococcus antigen, and PCR results were negative for cytomegalovirus, herpes simplex virus (HSV), and JC polyoma virus. The next day, a sixth HIV ELISA result was negative. The serum level of HIV p24 antigen was 202 pg/mL.

On hospital day 13, the patient began treatment with zidovudine, lamivudine, didanosine, and nevirapine. Within 24 hours, seizures and catatonia developed in the patient. An electroencephalogram showed diffuse wave form slowing. A repeat MRI showed worsened white matter disease (Figure, panel B). The result of a seventh HIV screening ELISA performed on hospital day 15 was negative. Two days later, the HIV viral load was 241,789 copies/mL. On hospital day 19, her serum levels were within normal limits: immunoglobulin (Ig) M level (164 mg/dL), IgG level (1,440 mg/dL), a 3 \times normal IgA level (1,060 mg/dL), and no oligoproteins. The CSF had an IgG level $>10 \times$ normal (72 mg/dL), elevated IgG levels for HSV1 (1:160) and HSV2 (1:40), was negative for virus culture, and showed a negative PCR result for JC polyoma virus. On hospital day 23, the eighth HIV ELISA result was negative. The Abbott HIVAB HIV-1/HIV-2 (rDNA) EIA was used throughout the hospitalization. On hospital day 24, supportive care was withdrawn and the patient

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Erythrocyte Binding Preference of Avian Influenza H5N1 Viruses^{▽†}

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Five erythrocyte species (horse, goose, chicken, guinea pig, and human) were used to agglutinate avian influenza H5N1 viruses by hemagglutination assay and to detect specific antibody by hemagglutination inhibition test. We found that goose erythrocytes confer a greater advantage over other erythrocyte species in both assays.

Endemicity of H5N1 avian influenza in Southeast Asian countries since late 2003 has led to the application of various techniques to diagnose the disease. For the isolation technique, influenza virus progenies released from the infected cells are primarily recognized by hemagglutination (HA) test. In addition, HA is employed to quantify the amount of hemagglutinin antigen used in HA inhibition (HI) assay (7). Importantly, the World Health Organization (WHO) has specified the presence of a horse erythrocyte HI titer of ≥ 160 in adjunct with a microneutralization (microNT) antibody titer of ≥ 80 in a single serum collected at day 14 or later as one among other criteria for a confirmed case of H5N1 infection (8).

Agglutination of erythrocytes by influenza viruses is mediated by the interaction between the receptor binding site (RBS) in hemagglutinin molecule and the sialyl receptor. Human influenza H1N1 and H3N2 viruses preferentially bind to a sialic acid receptor, the oligosaccharide side chain of which is linked with $\alpha 2,6$ -galactose linkage (SA α 2,6Gal), while avian and equine influenza viruses prefer an $\alpha 2,3$ -galactose linkage (SA α 2,3Gal). Horse and cow erythrocytes contain mainly an SA α 2,3Gal linkage but no SA α 2,6Gal (1). Chicken and goose erythrocytes contain more SA α 2,3Gal linkage than SA α 2,6Gal, while this is reversed with human O cells and pig, guinea pig, and turkey erythrocytes (1, 2).

Herein, five erythrocyte species (horse, goose, chicken, guinea pig and human O cells) were tested by HA assay against 14 H5N1 clade 1 isolates from Thailand, including five from humans, seven from wild and domestic birds, one from a tiger and, one from a clouded leopard, together with one human

H1N1 isolate and five H3N2 isolates. Final concentrations of 0.5% goose, 0.5% chicken, 0.75% guinea pig, 0.75% human group O, and 1% horse erythrocytes were used. Except for those from the horse, erythrocytes were suspended in phosphate-buffered saline, pH 7.2. Horse erythrocytes were suspended in phosphate-buffered saline plus 0.5% bovine serum albumin. These protocols were followed as described previously (6, 7). A reaction well, consisting of 50 μ l of diluted virus and 50 μ l of erythrocyte suspensions, was incubated for 1 h at 4°C before the agglutination pattern was read. One HA unit is defined as the highest virus dilution that yields complete HA.

The experiments demonstrated that 13 of 14 H5N1 isolates could agglutinate erythrocytes from all five species with a statistical difference in the extent of titer (Friedman test, $P < 0.05$). Interestingly, an isolate from the clouded leopard could not agglutinate horse erythrocytes (Table 1). The result was consistent, as repeatedly tested with erythrocytes from three donors within one species. Goose erythrocytes yielded the highest HA titer, followed in order of sensitivity by chicken, guinea pig, human, and horse erythrocytes (Wilcoxon's signed-rank test, $P < 0.005$).

Hemagglutinin amino acid sequences of our H5N1 isolates were compared with those of A/Goose/Guangdong/1/96 (the ancestor) and with Hong Kong virus 1997 (5) (see Fig. S1 in the supplemental material). No change in RBS was found, except for one isolate, A/Thailand/676(NYK)/05, which contained a mutational change A134V in RBS. However, this mutational change did not relate to erythrocyte binding preference. It remains to be elucidated why the isolate from the clouded leopard could not agglutinate horse erythrocytes while there were no change in RBS and no difference in the deduced amino sequence of hemagglutinin. Receptor specificity of influenza viruses is influenced by both the galactose linkage and species of sialic acid: *N*-acetylneurameric acid (NeuAc) or *N*-glycolyneurameric acid (NeuGc). Horse erythrocytes contained only NeuGc α 2,3Gal (1, 3). Therefore, loss of the ability to agglutinate horse erythrocytes may be related to loss of the ability to recognize either NeuGc or galactose linkage (1, 3).

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TABLE 1. HA titers of influenza A viruses as assayed with erythrocytes from different species

Influenza A virus and HA GMT	Passage history	Accession no.	HA titer by erythrocyte source ^a				
			Goose	Chicken	Guinea pig	Human	Horse
H1N1 human influenza virus							
A/New Caledonia/20/99-like virus (Siriraj 07/00)	MDCK7	EF568930	128	64	128	64	<2
H3N2 human influenza viruses							
A/Sydney/05/97-like virus (Siriraj 08/98)	MDCK4	EF568929	64	64	128	64	<2
A/Fujian/411/02-like virus (Siriraj 03/04)	MDCK6	EF568924	32	<2	64	64	<2
A/Fujian/411/02-like virus (Siriraj 01/03)	MDCK3	EF568925	32	<2	32	32	<2
A/Fujian/411/02-like virus (Siriraj 02/03)	MDCK2	EF568926	4	<2	32	32	<2
A/California/07/04-like virus (Siriraj 12/04)	MDCK4	EF568927	4	<2	16	32	<2
H5N1 influenza viruses							
A/Thailand/1(KAN-1)/04	LLC-MK2, MDCK8	AY555150	512	512	128	128	128
A/Thailand/2(SP-33)/04	MDCK6	AY555153	64	64	64	32	16
A/Thailand/3(SP-83)/04	MDCK5	AY577314	64	64	16	32	16
A/Thailand/5(KK-494)/04	MDCK4	AY627885	128	64	32	64	32
A/Thailand/676(NYK)/05	MDCK9	DQ360835	256	256	512	256	32
A/Great Barbet/Thailand/ VSMU-2-CBI/2005	MDCK2	EF206697	128	128	64	64	32
A/Green Peafowl/Thailand/ VSMU-3-CBI/2005	MDCK2	EF206700	256	128	64	64	64
A/Gray-Crowned Crane/ Thailand/VSMU-4-CBI/2005	MDCK2	EF206696	512	256	128	128	128
A/Tree Sparrow/Thailand/ VSMU-16-RBR/2005	MDCK4	EF178506	64	64	32	32	16
A/Golden Pheasant/Thailand/ VSMU-21-SPB/2005	MDCK1	EF178517	128	64	32	16	32
A/Pigeon/Thailand/VSMU-25-BKK/2005	MDCK3	EF206698	64	64	32	16	16
A/Chicken/Thailand (Suphanburi)/137/05	MDCK4	EF568922	512	512	64	64	128
A/Tiger/Thailand/VSMU-11-SPB/2004	Egg 1	EF178531	512	512	256	256	256
A/Clouded Leopard/Thailand (Chonburi)/AI-1216A/2004	Egg 1	EF568923	512	512	256	256	<2
HA GMT of H5N1 viruses			190.21	156.03	74.25	67.25	33.62

^a The most frequent titer obtained from three erythrocyte donors within the same species is presented.

The study of human influenza H1N1 and H3N2 viruses showed that all six isolates could not agglutinate horse erythrocytes (Table 1). An A/Sydney/05/97(H3N2)-like isolate could agglutinate chicken erythrocytes, while all three A/Fujian/411/02(H3N2)-like isolates and one A/California/07/04(H3N2)-like isolate could not. This result supported previous findings that current H3N2 isolates have lost their agglutinating activity with chicken erythrocytes (2, 4). However, all of the data, including ours, were discrete and could not conclude that there was a correlation between certain mutational positions and loss of the agglutinating activity (data not shown).

Fourteen serum samples from seven H5N1 patients, including the survivors, were assayed for H5N1 antibody. Two H5N1 strains, A/Thailand/1(KAN-1)/04 which was the first human isolate from the country (5), and A/Thailand/676(NYK)/05, as described above, were selected as the test antigens. This study was approved by the Institution Ethical Committee for Human Research.

In the HI test, serum was pretreated with a receptor-destroying enzyme (Denka Seiken, Japan) at final dilution of 1:4 for 16 h at 37°C followed by heat inactivation for 30 min at 56°C and absorbed with a 50% erythrocyte suspension for 60 min at 4°C. A mixture of 25 µl of the diluted serum and 25 µl of the test virus at a concentration of 4 HA units was incubated for 30

min at room temperature before addition of 50 µl of erythrocyte suspension. The end result was read after incubation for 1 h at 4°C. HI antibody titer is defined as the final serum dilution that completely inhibits HA. Again, three donors from each of the five erythrocyte species were tested in separate runs with consistent results.

The results demonstrated that horse erythrocytes, which were the least sensitive in HA, gave the highest geometric mean titer (GMT) of antibody when A/Thailand/1(KAN-1)/04 was used as the test antigen (Wilcoxon's signed-rank test, $P < 0.005$). Goose erythrocytes were ranked second, followed by human, guinea pig, and chicken erythrocytes. In contrast, when A/Thailand/676(NYK)/05 was used as the test antigen, goose erythrocytes yielded the highest GMT, followed in order by chicken, horse, human, and guinea pig erythrocytes. However, a statistically significant difference was not found (Wilcoxon's signed-rank test, $P > 0.005$) (Table 2). Collectively, the level of HI antibody titer was dependent on both the erythrocyte species and the test antigen used. We also showed that HI is more sensitive for strain differentiation than microNT.

Our study proposes that goose erythrocytes confer a greater advantage for recognition of H5N1 viruses and HI antibody

TABLE 2. H5N1 HI antibody titers as tested by different erythrocyte species

Patient, sequential sample no., and HI antibody GMT	Time after onset of illness	A/Thailand/1(KAN-1)/04(H5N1) ^a					A/Thailand/676(NYK)/05(H5N1) ^b					NT antibody titer	
		HI antibody titer by erythrocyte source					NT antibody titer	HI antibody titer by erythrocyte source					
		Goose	Chicken	Guinea pig	Human	Horse		Goose	Chicken	Guinea pig	Human	Horse	
Patient 1													
1	8 days	20	<20	20	<20	20	<5	20	<20	<20	<20	20	
2	17 days	640	640	640	640	1,280	1,280	1,280	1,280	1,280	1,280	640	
Patient 2	2 yr, 2 mo	20	<20	20	20	40	80	160	80	80	80	80	40
Patient 3	2 yr, 1 mo	20	<20	20	20	40	160	160	80	80	80	80	80
Patient 4													
1	10 days	20	<20	<20	20	20	<5						
2	12 days	20	<20	20	<20	20	5	20		20		20	
3	6 mo	40	20	20	40	80	160	160	320	160	80	320	
4	1 year	40	20	20	40	80	160	160	160	80	160	160	80
Patient 5	7 days	<20	<20	<20	<20	<20	<5	20	<20	<20	<20	20	
Patient 6													
1	4 days	<20	<20	<20	<20	<20	5	<20	<20	<20	<20	<20	
2	15 days	320	160	160	160	640	1,280	1,280	1,280	1,280	1,280	1,280	
3	21 days	160	80	80	160	320	640	640	1280	640	640	640	
4	5 mo, 9 days	20	20	20	20	40	80	160	80	80	40	40	80
Patient 7	5 days	80	40	80	160	320	320	640	640	320	320	640	
GMT of HI antibody		40.00	24.38	31.23	36.26	65.63		136.35	134.54	93.88	100.79	110.16	

^a A/Thailand/1(KAN-1)/04 was isolated from patient 1.^b A/Thailand/676(NYK)/05 was isolated from patient 5.

assay. Whether this finding is also generalized for H5N1 clade 2 viruses need to be investigated.

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Multiplex Reverse Transcription-PCR
Specific for Eight Genomic Segments of
Avian Influenza A H5N1 Viruses**

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Surveillance for Reassortant Virus by Multiplex Reverse Transcription-PCR Specific for Eight Genomic Segments of Avian Influenza A H5N1 Viruses[†][▽]

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Avian influenza H5N1 virus is a global threat. An emergence of a reassortant virus with a pandemic potential is a major concern. Here we describe a multiplex reverse transcription-PCR assay that is specific for the eight genomic segments of the currently circulating H5N1 viruses to facilitate surveillance for a virus resulting from reassortment between human influenza virus and the H5N1 virus.

The genome of influenza A viruses is composed of eight gene segments, which encode polymerase (PB1, PB2, and PA), nucleocapsid (NP), hemagglutinin (HA), neuraminidase (NA), matrix (M) protein, and nonstructural (NS) protein. Since influenza viruses have segmented genomes, they are able to evolve through reassortment (1). Both the 1957 and 1968 pandemic strains are believed to be reassortants in which HA and PB1 genes, with or without the NA gene, were replaced by the corresponding genomic segments of avian influenza virus strains (5). The reassortments provided the viruses with new HA and NA antigenic profiles and the ability to spread efficiently from human to human. The ongoing outbreak of the highly virulent avian influenza virus H5N1 is concerning because of the possibility of a reassortant virus emerging with pandemic potential (3). Monitoring for a reassortant with mixed genomic segments from human and avian viruses is therefore very important. However, detection of a reassortant requires sequencing of all eight genomic segments, a process which is laborious and time consuming. Therefore, we developed a simple and high-throughput screening method using multiplex reverse transcription-PCR (RT-PCR) specific for eight genomic segments of recent H5N1 viruses to detect the probable reassortant viruses worthy of further characterization.

For the primer design, 100 full-length sequences arbitrarily selected from the Influenza Virus Resource Database (National Center for Biotechnology Information; <http://www.ncbi.nlm.nih.gov/genomes/FLU/>) were used to search for the sequence(s) that was conserved in H5N1 and that differed from

those of other subtypes. The viruses used in this study comprised 28 human influenza virus isolates and 103 H5N1 isolates from various animal species (94 isolates from poultry and other birds, 6 isolates from tigers, 2 isolates from leopards, and 1 isolate from a cat). These viruses have been collected since the beginning of the epidemic in the country. In 2003, 2004, 2005, and 2006, 7, 34, 60, and 2 animal H5N1 virus isolates were collected, respectively. The human viruses comprised 6 H5N1, 3 H1N1, 8 H3N2, and 11 influenza B viruses. These viruses were propagated in MDCK cells or embryonated eggs. The H5N1 viruses were originally subtyped by RT-PCR. The subtyping was confirmed by sequencing for all human H5 and some animal H5 viruses (2). Available accession numbers of some of the H5N1 virus isolates used in this study are shown in Table S1 in the supplemental material and also in a report by Puthavathana et al. (4). The human H1, H3, and influenza B viruses were characterized and confirmed with respect to their subtypes by hemagglutination inhibition assay at the WHO Reference Laboratories, Melbourne, Australia, or the Centers for Disease Control and Prevention of the United States via the National Reference Laboratory on Influenza, NIH, Thailand.

RNA was extracted by using a QIAamp viral RNA Mini kit (QIAGEN, Valencia, CA). A 140- μ l volume of virus suspension from the infected culture or embryonated egg yielded a volume of 60 μ l of extracted RNA. Multiplex RT-PCR was carried out in three reaction tubes with combinations of the following primer sets: NA plus PB1 plus NP, HA plus PA plus PB2, or NS plus M. Sequences of these primers are shown in Table 1. The thermocycling was performed in a GeneAmp PCR system 2400 thermal cycler (Perkin Elmer) using a QIAGEN OneStep RT-PCR kit (QIAGEN, Valencia, CA) with standard reaction conditions (a 50 μ l volume containing 1 \times PCR buffer, 5 to 10 μ l of extracted RNA, 400 μ M (each) deoxynucleoside triphosphate, 2.5 mM MgCl₂, 2 μ l enzyme mix, and 2 U RNase inhibitor). The thermocycling profile was 50°C for 30 min, 95°C for 15 min, 35 cycles of 95°C for 45 s, 55°C for 45 s, and 72°C

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TABLE 1. Sequences, concentrations used in the reaction, nucleotide positions, and product sizes of PCR primers for the eight gene segments

Gene	Primer name	Sequence	Concn in PCR (μ M)	Nucleotide positions	Product size (bp)
PB2	SPB2F	GAA TGA ACA AGG GCA GAC G	0.3	237–255	117
	SPB2R	ACT GCA CTT GTC GCC GGC	0.3	336–353	
PB1	SPB1F	AAT GAG AAT CAG AAT CCT AGG	0.4	952–972	377
	SPB1R	GTG GTT TTG GTG TAC CTT TTC	0.4	1308–1328	
PA	SPAF	AAT TGA AAG CAT GAT TGA AGC C	0.3	1797–1818	167
	SPAR	TGA ACA CAG ACT TCG CCA GC	0.3	1944–1963	
HA	HA-H5f	ACT CCA ATG GGG GCG ATA AA	0.6	897–916	352
	HA-H5r	CAA CGG CCT CAA ACT GAG TGT	0.6	1228–1248	
NP	SNPF	GAC AGC TAT CCA CCA GAG GG	0.3	1112–1131	174
	SNPR	CCG AGA AAG TGG GCT GAA CG	0.3	1266–1285	
NA	NA-N1f	CTC ATG CTC CCA CTT GGA	0.6	332–349	515
	TNAr5	CCC TGC ACA CAC ATG TG	0.6	830–846	
M	SMF	TCG CAC TCA GCT ACT CAA CC	0.3	369–388	142
	SMR	TGA GAC CGA TGC TGT GAA TCT	0.3	490–510	
NS	SNSF	GAT AAG GCA CTT AAA ATG CCG	0.4	250–270	253
	SNSR	ACG GTG AGA TTT CTC CCA CG	0.4	483–502	

for 45 s, and a final extension of 72°C for 10 min. The PCR products were visualized by ethidium bromide staining after electrophoresis in a 2% agarose gel.

In our multiplex RT-PCR assay, potential reassortants would show the lack of one or more of the eight amplicons in the case of H5N1 viruses and the presence of one or more amplicons in the case of H1N1 and H3N2 viruses. With the designed primer set, we could initially amplify all eight genomic segments from 105 out of 109 H5N1 viruses. Four viruses initially gave negative amplification results for NA. However, these four viruses yielded positive NA band results

in separated single-gene amplifications, and multiplex reamplification using 1.5- to 2-fold-higher RNA input gave positive amplification results for all genes. Representative results obtained with the multiplex RT-PCR products are shown in Fig. 1. None of the human H3N2, H1N1, or influenza B virus isolates yielded any amplification products by this method (data not shown). In order to verify the lack of reassortment, all human H5N1 viruses and a subset of animal viruses (62 out of 103) were subjected to a full-genome sequencing protocol as previously described (4). Phylogenetic analyses of the sequence data revealed that all viruses contained their respective genomic segments and that no evidence of reassortment was found (data not shown). In addition to detecting human-avian virus reassortants, our assay may also be able to detect some reassortants that acquire genomic segments from some other unrelated avian viruses. However, the assay was not designed to detect reassortment among avian viruses, which are unlikely to play a role in viral adaptation to the human host. The absence of a band in the amplification of H5N1 viruses is not always due to reassortment. Full-genome sequencing is needed for result confirmation. Because the performance of this assay is directly affected by variation in the sequences of circulating H5N1 strains, the primer sequences should be frequently re-evaluated and updated accordingly.

Our multiplex RT-PCR was designed for egg- or MDCK-propagated viruses. Although the assay may be able to detect some of the genes in some clinical specimens, the level of sensitivity is probably not sufficient to reliably detect all the genomic segments simultaneously. This makes our assay less suitable for direct screening using clinical specimens. Nevertheless, the possibility of using a more sensitive version of this assay with clinical specimens should be further explored.

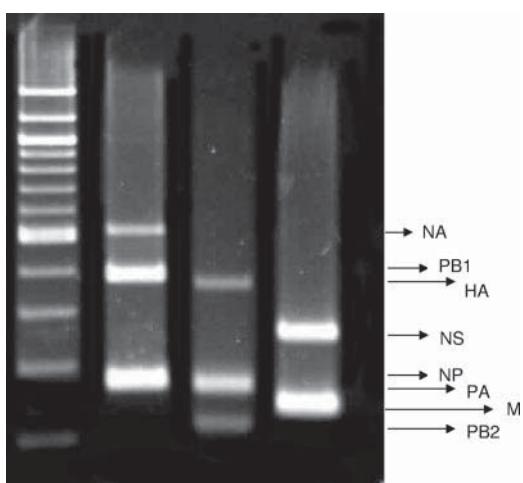


FIG. 1. A representative photograph of multiplex RT-PCR products from an H5N1 virus after electrophoresis in 2% agarose and ethidium bromide staining. Each lane shows products from each tube. The first lane is a 100-bp DNA ladder, and the target gene of each amplification product is labeled on the right.

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Short Article

Seroprevalence of 2009 H1N1 Virus Infection and Self-Reported Infection Control Practices Among Healthcare Professionals Following the First Outbreak in Bangkok, Thailand

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A serologic study with simultaneous self-administered questionnaire regarding infection control (IC) practices and other risks of influenza A (H1N1) pdm09 (2009 H1N1) infection was performed approximately 1 month after the first outbreak among frontline healthcare professionals (HCPs). Of 256 HCPs, 33 (13%) were infected. Self-reported adherence to IC practices in >90% of exposure events was 82·1%, 73·8%, and 53·5% for use of hand hygiene, masks, and gloves, respectively. Visiting crowded public

places during the outbreak was associated with acquiring infection (OR 3·1, $P = 0\cdot019$). Amongst nurses, exposure to HCPs with influenza-like illness during the outbreak without wearing a mask was the only identified risk factor for infection (OR = 2·3, $P = 0\cdot039$).

Keywords 2009 H1N1 pandemic, Thailand, healthcare workers, seroprevalence, hemagglutination assay

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Introduction

The outbreak of influenza A (H1N1) pdm09 (2009 H1N1) pandemic in Thailand started in early June, peaked around July to August, and waned in September.¹ Healthcare professionals (HCPs) are at risk of exposure to infection from the community as well as in the workplace. However, they also have the greatest access to personal protective equipment (PPE) and are likely to receive the annual seasonal vaccine that may provide some protection against 2009 H1N1 infection.² The 2009 H1N1 outbreak was an opportunity to evaluate the effectiveness of infection control (IC) practices in HCPs.

We conducted a serologic study of 2009 H1N1 infection among frontline HCPs who were involved in the care of 2009 H1N1 patients during the first outbreak in two large public hospitals in Bangkok, Thailand. The aim of the study was to understand the magnitude of acquisition of infections among HCPs in relation to self-reported IC

practices and the factors associated with infection during the outbreak. This information may be useful for future outbreak control and vaccination strategies.

Methods

HCPs who worked during the peak of the 2009 H1N1 outbreak (June–August, 2009) on the wards that cared for patients with influenza and at emergency rooms of Siriraj Hospital and Thammasat Hospital, two large public tertiary care centers in Bangkok, were randomly invited to participate in the study. These two hospitals served adults and children patients. The wards at which the HCPs in this study were working were 3 ERs, four pediatric wards, three adult wards, and three intensive care units. Immunocompromised patients were being cared for in some of the wards participating the study. Approximately, a third of HCPs in each of these wards were invited and 97% accepted. The study was conducted from October 1 to 19,

1 2009, approximately 1 month after the end of the outbreak.
 2 An anonymous self-administered questionnaire was administered prior to a single blood draw for assessment of hem-
 3 agglutination inhibition (HI) titer. The questionnaire
 4 consisted of demographic information, medical history,
 5 and factors that may be associated with community-
 6 acquired and occupational-acquired influenza. Adherence
 7 to hand hygiene (alcohol-based hand rub and/or hand
 8 washing with water) and using mask and gloves when in
 9 contact (defined as having activities or procedures that
 10 potentially resulted in contact or droplet transmission) with
 11 patients with suspected 2009 H1N1 were categorized as:
 12 every time or >90–100%, mostly or 70–90%, and <60%,
 13 respectively. The wards were classified as isolation wards
 14 (1–three patients in a room, PPE practice for airborne and
 15 contact precautions when entering the patients' room), semi-open ward (share up to 12 patients in a room, PPE
 16 practice for airborne and contact precaution when entering
 17 patients' area), and open ward or emergency room (large
 18 ward hold up to 24 beds or walk-in patients, PPE practice
 19 for contact and droplet precaution as needed). There
 20 was no verification of the accuracy of responses in the
 21 questionnaire.

22 HI assay was performed using the protocol previously
 23 described.^{3,4} We defined an HI titer ≥ 40 as seropositive
 24 and a marker of acquiring recent infection assuming
 25 that none of the HCPs had been infected with the 2009
 26 H1N1 virus prior to the outbreak and that pre-existing HI
 27 antibody to 2009 H1N1 was uncommon.

31 Statistical analysis

32 Descriptive analysis was performed on the demographic
 33 and other variables associated with risk of influenza infection.
 34 Univariate analysis was performed using a binomial
 35 test. Multiple logistic regression analysis was used for mul-
 36 tivariate analysis of self-reported factors including the IC
 37 practices associated with an HI titer ≥ 40 . Stata (Version
 38 9.2) was used for the data analysis.

41 Results

42 There were 256 HCPs, 93% female, who participated in
 43 this study. The median (range) age was 34 (20–61) years.
 44 The majority (81.3%) were nurses and nurse assistants. Of
 45 the 198 HCPs working in specific wards, 72 (36.4%) were
 46 working in isolation wards, 57 (28.8%) in semi-open
 47 wards, and 69 (34.8%) in open wards or emergency rooms.
 48 The majority (82%) had received seasonal influenza vac-
 49 cines (Southern Hemisphere strain 2008) between April
 50 2008 and May 2009, at least 1–2 months before the out-
 51 break started. Adherence to IC practices in >90% of the
 52 exposure events when in contact with patients with sus-
 53 pected 2009 H1N1 infection was 82.1%, 73.8%, and 53.5%

with hand hygiene, using a mask, and using gloves, respectively. One hundred and twenty (47.1%) HCPs reported a history of respiratory tract infection (RTI) during the outbreak.

30 Thirty-three (13%) HCPs had a serum HI titer ≥ 40 suggesting acquisition of 2009 H1N1 infection during the outbreak. The proportions seropositive in HCPs aged <25, 25–49, and ≥ 50 years were 20.9%, 12.9%, and 2.8%, respectively. HCPs with a history of RTI during the outbreak tended to have a higher proportion seropositive than those who had no history of RTI (16.7% versus 8.9%, $P = 0.06$). The proportions seropositive among nurses and nurse assistants in different patient care areas were not different: 12.5% versus 19.3% versus 11.6% ($P = 0.411$) in isolation, semi-open, and open wards, respectively.

31 The univariate analysis revealed that a younger age (<25 years) and visiting crowded public places during the outbreak were associated with acquiring infection. In multivariate analysis, the only risk factor was visiting crowded public places during the outbreak (odds ratio = 3.1, 95% CI = 1.2–8.1, $P = 0.019$, Table 1). The rates of adherence to IC practices were not associated with acquisition of infection. The HCPs with adherence to hand hygiene and mask use at 70–90% of exposure events had a similar rate of infection to those with adherence >90–100%. In a subgroup analysis of 198 nurses and nurse assistants, there was a weak association between acquisition of 2009 H1N1 infection and close contact with HCPs with influenza-like illness (ILI) during the outbreak without wearing a mask (odds ratio = 2.3, 95% CI 0.9–5.6, $P = 0.039$).

32 Discussion

33 This study revealed a rate of 2009 H1N1 infection among
 34 frontline HCPs of 13%, indicated by a serum HI titer ≥ 40 ,
 35 after the first outbreak in Bangkok. This result was consis-
 36 tent with a previous report of 18% of HCPs in a large hos-
 37 pital in Bangkok who became sick with the 2009 H1N1
 38 infection during the same outbreak,⁵ and higher than the
 39 7% reported among healthy blood donors in Bangkok
 40 around the same period of this study,⁶ suggesting that
 41 HCPs had a higher risk of getting 2009 H1N1 infection
 42 than the general population.

43 A report of the 2009 H1N1 outbreak in England found
 44 that 42%, 20%, and 6% of the general population age 5–14,
 45 15–24, and 25–44 years in London and West Midlands had
 46 an HI titer against 2009 H1N1 of ≥ 32 .⁷ This evidence of
 47 higher prevalence in a younger age group correlated well
 48 with a large study of the 2009 H1N1 outbreak in the US
 49 in which 40% and 35% of the patients were in the age
 50 groups 10–18 and 19–50 years, respectively, and only 5%
 51 occurred at age >50 years.⁸ This age bias was probably due
 52 to the increased number of social or institutional gathering

Table 1. Factors associated with serologic evidence of recent infection defined by hemagglutination inhibition (HI) titer ≥ 40

Characteristics	No. (%)	No. (%) Cases with HI ≥ 40	No. (%) Cases with HI <40	Crude odds ratio (95% CI)	P-value	Adjusted odds ratio (95% CI)	P-value
Age (years)	(n = 256)	(n = 33)	(n = 223)				
<25	43 (16.8)	9 (27.3)	34 (15.2)	9.0 (1.1–405.8)	0.0198*	5.7 (0.7–49.0)	0.111
25–49	178 (69.5)	23 (69.7)	155 (69.5)	5.0 (0.8–213.8)	0.14*	4.3 (0.6–33.6)	0.163
50–64	35 (13.7)	1 (3)	34 (15.3)	1			
Body Mass Index	(n = 254)	(n = 33)	(n = 221)				
≥ 25	44 (17.3)	4 (12.1)	40 (18.1)	0.6 (0.2–1.9)	0.47*		
<25	210 (82.7)	29 (87.9)	181 (81.9)	1			
Career	(n = 256)	(n = 33)	(n = 223)				
Physician	30 (11.7)	3 (9.1)	27 (12.1)	1			
Nurse or nurse assistant	208 (81.3)	28 (84.8)	180 (80.7)	1.4 (0.4–7.7)	0.78*		
Others	18 (7)	2 (6.1)	16 (7.2)	1.1 (0.1–10.9)	1.00*		
Received the seasonal influenza vaccine between April 2008 and May 2009	(n = 250)	(n = 32)	(n = 218)				
Yes	205 (82)	27 (84.4)	178 (81.7)	1.2 (0.4–4.3)	0.71		
No	45 (18)	5 (15.6)	40 (18.3)	1			
Living with children younger than 5 years	(n = 255)	(n = 33)	(n = 222)				
Yes	52 (20.4)	8 (24.2)	44 (19.8)	1.3 (0.5–3.2)	0.56		
No	203 (79.6)	25 (75.8)	178 (80.2)	1			
Living with children age 5–15 years	(n = 253)	(n = 33)	(n = 220)				
Yes	59 (23.3)	4 (12.1)	55 (25.0)	0.4 (0.1–1.3)	0.12*		
No	194 (76.7)	29 (87.9)	165 (75.0)	1			
Having household member sick with respiratory tract infection during the outbreak	(n = 253)	(n = 33)	(n = 220)				
Yes	117 (46.2)	12 (36.4)	105 (47.7)	0.6 (0.3–1.4)	0.22		
No	136 (53.8)	21 (63.6)	115 (52.3)	1			
Visiting crowded public places during the outbreak	(n = 256)	(n = 33)	(n = 223)				
Yes	149 (58.2)	27 (81.8)	122 (54.7)	3.7 (1.4–11.4)	0.0032	3.1 (1.2–8.1)	0.019
No	107 (41.8)	6 (18.2)	101 (45.3)	1			
Mask type used when caring for patients with suspected/confirmed 2009 H1N1	(n = 239)	(n = 30)	(n = 209)				
N95 respirator	142 (59.4)	16 (53.3)	126 (60.3)	1			
Surgical Mask	78 (32.6)	10 (33.3)	68 (32.5)	1.2 (0.4–2.9)	0.73		
Use either mask	19 (8)	4 (13.4)	15 (7.2)	2.1 (0.4–7.7)	0.26*		
Frequency of hand hygiene before and after caring for patients with suspected/confirmed 2009 H1N1	(n = 246)	(n = 32)	(n = 214)				
All the time (>90–100%)	202 (82.1)	27 (84.4)	175 (81.8)	1.2 (0.4–4.1)	0.76		
Most of the time (70–90%)	43 (17.5)	5 (15.6)	38 (17.8)	1			
Sometimes (<60%)	1 (0.4)	0	1 (0.4)	–			
Frequency of mask use when caring for patients with suspected/confirmed 2009 H1N1	(n = 244)	(n = 32)	(n = 212)				
All the time (>90–100%)	180 (73.8)	24 (75.0)	156 (73.6)	0.9 (0.4–2.5)	0.86		
Most of the time (70–90%)	56 (23)	8 (25)	48 (22.6)	1			
Sometimes (<60%)	8	0	8 (3.8)	–			
Frequency of glove use when caring for patients with suspected/confirmed 2009 H1N1	(n = 245)	(n = 32)	(n = 213)				
All the time (>90–100%)	131 (53.5)	19 (59.4)	112 (52.6)	1.4 (0.4–4.9)	0.57		
Most of the time (70–90%)	69 (28.2)	8 (25)	61 (28.6)	1.0 (0.3–4.4)	0.94		
Sometimes (<60%)	45 (18.3)	5 (15.6)	40 (18.8)	1			
Having respiratory tract infection during the outbreak	(n = 255)	(n = 32)	(n = 223)				
Yes	120 (47.1)	20 (62.5)	100 (44.8)	2.1 (0.9–4.8)	0.06	1.8 (0.8–4.0)	0.132
No	135 (52.9)	12 (37.5)	123 (55.2)	1			

*Fisher's exact test.

2 activities and less pre-existing cross-protective antibody in
3 the younger compared with the older participants.⁹ In our
4 study, we also found that having an HI titer ≥ 40 was associated
5 with younger age and visiting crowded public places,
6 suggesting that the outbreak spread more widely in a younger
7 population, probably from gathering in public places.

8 Conducting a serologic study immediately after the first
9 outbreak of 2009 H1N1 infection was a unique opportunity
10 to look at the effectiveness of IC practices. Assuming from
11 a previous study that approximately 11% of the HCPs had
12 an HI antibody titer to 2009 H1N1 ≥ 40 before the outbreak,⁶ we can expect that the serologic evidence reported
13 is primarily due to the acquisition of infection during the
14 outbreak. The HCPs who participated in this study were
15 the frontline personnel at highest risk of exposure to 2009
16 H1N1-infected patients and were well trained in using PPE
17 and IC practices. Ideally, these HCPs should not acquire
18 2009 H1N1 infection from patient care. However, our set-
19 up was not ideal. Aerosol-generating procedures were per-
20 formed in many of the patient care areas and none of the
21 wards had the perfect negative pressure needed to limit aer-
22 osol spread. Moreover, adherence to IC practices was not
23 perfect in real life.

24 A previous report revealed that frontline HCPs were
25 actually less likely to contract 2009 H1N1 than other HCPs,
26 probably because of good adherence to IC practices and
27 use of PPE.¹⁰ However, we found that only about half of
28 our HCPs reported perfect adherence (>90% of exposure
29 events) to wearing of gloves, and around 70–80% perfectly
30 adhered to mask use and hand hygiene. Despite this imper-
31 perfect adherence, it seemed that the HCPs in our study
32 acquired infection from the community rather than from
33 patient care. A report from the US also found acquisition
34 from the community as a major route of infection in
35 HCPs.¹¹ We did not find the levels of adherence to hand
36 hygiene and mask use (70–90% versus 90–100%) to be
37 associated with infection. This is in line with a previous
38 study that revealed a protective effect of >75% adherence
39 to hand hygiene.¹⁰

40 The hospital environment is the setting where HCPs
41 spend much of their time and may be the source of infec-
42 tion, in addition to patient care activities. Environmental
43 contamination in household settings of patients with influ-
44 enza was well documented.¹² A study in Singapore reported
45 that contact with H1N1-infected colleagues was associated
46 with 2009 H1N1 infection in hospital staff.¹³ We found that
47 exposure to HCPs with ILI was associated with 2009 H1N1
48 infection in a subgroup analysis of nurses and nurse assis-
49 tants, but not in the whole cohort analysis. Of note, almost
50 half of the HCPs in this study had an RTI during the
51 outbreak but only 16.7% of these RTI episodes appeared to be
52 associated with HI seroconversion to 2009 H1N1 suggest-
53 ing that other respiratory viruses co-circulated during the

outbreak, and this may have masked the effect of ILI contact in the whole cohort. Hospital policies to monitor ill HCPs and prevent transmission of infection from ill HCPs are needed.

There are several limitations of the study. First of all, our sample size was not large. Inherent self-report survey-based research compared with observer-based research, in particular when reporting hand hygiene and PPE habits, is that over-reporting of the habit cannot be excluded. We do not have verification of the accuracy of the answers to the questionnaire and we did not monitor for adherence to IC practices in our study.

In conclusion, we found that of 2009 H1N1 infection among frontline HCPs was somewhat higher than in the general population. The risk of infection was found to be associated with community exposure risk, particularly in the young, as well as exposure to other HCPs with ILI without protection.

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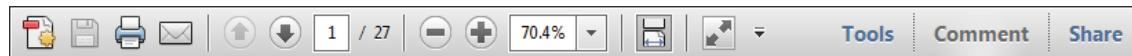
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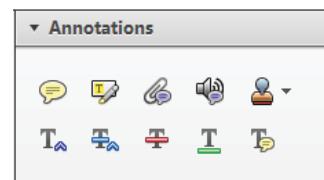
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1. Replace (Ins) Tool – for replacing text.



Strikes a line through text and opens up a text box where replacement text can be entered.

How to use it

- Highlight a word or sentence.
- Click on the [Replace \(Ins\)](#) icon in the Annotations section.
- Type the replacement text into the blue box that appears.

standard framework for the analysis of monetary policy. Nevertheless, it also led to exaggerated claims of strategic coordination. The main problem is that the structure of the economy, which led to the main components of the model, are excluded. In particular, the important works on money by Mankiw and Weil (henceforth) we open the 'black box' of the model to see what is inside. The model is based on the assumption that there is no room for extra profits at the margin. The mark-ups are zero and the number of firms is not determined by the market structure. Blanchard and Kiyotaki (1987), in contrast, argue that perfect competition in general equilibrium models of aggregate demand and supply is not consistent with the classical framework assuming monopolistic competition and an exogenous number of firms.



2. Strikethrough (Del) Tool – for deleting text.



Strikes a red line through text that is to be deleted.

How to use it

- Highlight a word or sentence.
- Click on the [Strikethrough \(Del\)](#) icon in the Annotations section.

there is no room for extra profits at the margin. The mark-ups are zero and the number of firms is not determined by the market structure. Blanchard and Kiyotaki (1987), in contrast, argue that perfect competition in general equilibrium models of aggregate demand and supply is not consistent with the classical framework assuming monopolistic competition and an exogenous number of firms.

3. Add note to text Tool – for highlighting a section to be changed to bold or italic.



Highlights text in yellow and opens up a text box where comments can be entered.

How to use it

- Highlight the relevant section of text.
- Click on the [Add note to text](#) icon in the Annotations section.
- Type instruction on what should be changed regarding the text into the yellow box that appears.

dynamic responses of mark ups to the **VAR** evidence



4. Add sticky note Tool – for making notes at specific points in the text.



Marks a point in the proof where a comment needs to be highlighted.

How to use it

- Click on the [Add sticky note](#) icon in the Annotations section.
- Click at the point in the proof where the comment should be inserted.
- Type the comment into the yellow box that appears.

there is no room for extra profits at the margin. The mark-ups are zero and the number of firms is not determined by the market structure. Blanchard and Kiyotaki (1987), in contrast, argue that perfect competition in general equilibrium models of aggregate demand and supply is not consistent with the classical framework assuming monopolistic competition and an exogenous number of firms.

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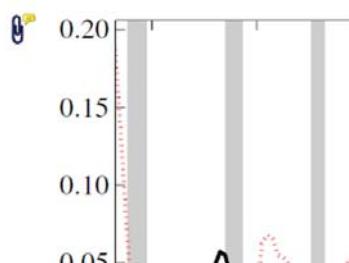
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Inserts an icon linking to the attached file in the appropriate place in the text.

How to use it

- Click on the [Attach File](#) icon in the Annotations section.
- Click on the proof to where you'd like the attached file to be linked.
- Select the file to be attached from your computer or network.
- Select the colour and type of icon that will appear in the proof. Click OK.

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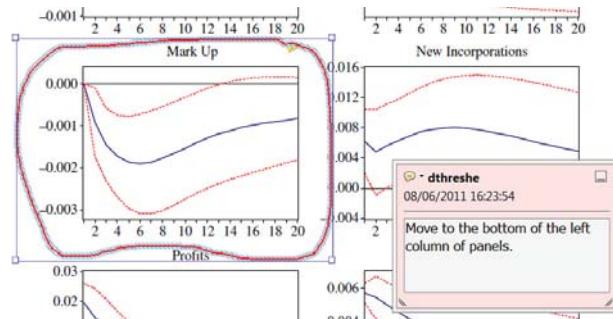
How to use it

- Click on the [Add stamp](#) icon in the Annotations section.
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- Click on the proof where you'd like the stamp to appear. (Where a proof is to be approved as it is, this would normally be on the first page).

or the business cycle, starting with the on perfect competition, constant returns to production. In this environment goods extra profits due to entry in market he model of the New-Keynesian model. F determined by the model. The New-Keynesian model, introduced by A. W. Phillips in 1954, has introduced production function models with nominal and real variables. Most of this literature

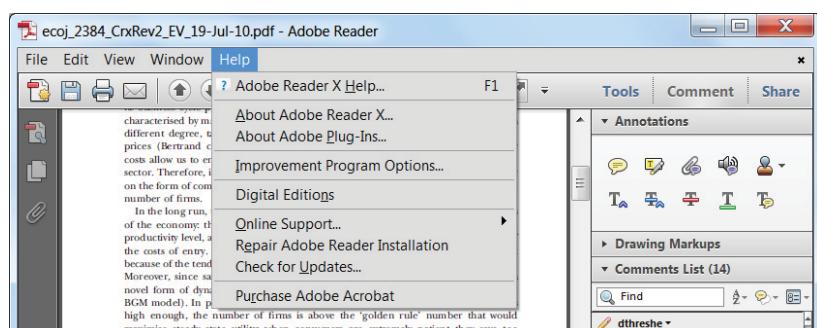
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Viral Immunology: <http://mc.manuscriptcentral.com/viral>

**Biological properties of H5 hemagglutinin expressed by
vaccinia virus vector and its immunological reactivity with
human sera**

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Keyword:	Influenza, Immunity, Antibodies, Animal model

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1 Biological properties of H5 hemagglutinin expressed by vaccinia virus vector and its

2 immunological reactivity with human sera

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1
2
3 26 **Abstract**
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A recombinant vaccinia virus harboring the full length hemagglutinin (*HA*) gene derived from a highly pathogenic avian influenza A/Thailand/1(KAN-1)/2004 (H5N1) virus (rVac-H5 HA virus) was constructed. The immunogenicity of the expressed HA protein was characterized using goat antiserum, mouse monoclonal antibody and human sera. The expressed HA protein localized both in the cytoplasm and on the cytoplasmic membrane of the thymidine kinase negative cells infected with the rVac-H5 HA virus, as determined by immunofluorescence assay. Western blot analysis demonstrated that the rVac-H5 HA protein was post-translationally processed by proteolytic cleavage of the HA0 precursor into HA1 and HA2 domains; and all of these HA forms were immunogenic in BALB/c mice. The molecular weight (MW) of each HA domain was the same as the wild-type H5 HA produced in Madin-Darby canine kidney cells infected with the H5N1 virus, but was higher than that expressed by a baculovirus-insect cell system. Sera from all H5N1 survivors reacted to HA0, HA1 and HA2 domains; whereas sera from H5N1-uninfected subjects reacted to the rVac-H5 HA2 domain only, but not to HA0 or HA1, indicating that some cross-subtypic immunity exists in the general population. There was a lot-to-lot variation of the recombinant HA produced in the baculovirus-insect cell system that might affect the detection rate of antibody directed against certain HA domains.

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3 51 **Introduction**
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Based on hemagglutinin (HA) and neuraminidase (NA), influenza A viruses are classified into 17 HA (H1-17) and 9 NA (N1-9) subtypes, respectively. While influenza A virus subtypes H1-16 are found in aquatic birds (1), H17 was recently discovered in bats in Guatemala by using nucleotide sequence analysis (2). The major influenza A subtypes currently circulating in the human population include H3N2 viruses and H1N1 viruses derived from the 2009 pandemic H1N1 virus (H1N1pdm). The presence of H1N2 viruses are also sporadically reported in many countries such as United Kingdom, Germany, France, Egypt, Singapore, Canada and United States (3-5). Occasionally, avian influenza viruses have crossed species barriers to infect humans (6-7). Among the various subtypes reported, the highly pathogenic avian influenza (HPAI) H5N1 virus is the most virulent. This subtype has spread globally throughout the world by migrating birds and poultry shipments, especially in Asian countries; and its transmission to humans posts a pandemic threat (7).

HA is a type I integral membrane glycoprotein and is a major component of the viral envelope where it exists as noncovalent homotrimers. Initially, it is synthesized as a precursor polypeptide (HA0) that further undergoes post-translational modifications including glycosylation, proteolytic cleavage and signaling peptide removal (8-10). SDS-polyacrylamide gel electrophoresis of purified virus particles has demonstrated that the monomeric HA0 has a molecular weight (MW) of approximately 80 kilodaltons (kDa) and is cleaved into two glycosylated functional subunits, HA1 (MW 56-58 kDa) and HA2 (MW 25-26 kDa) which are connected together by disulfide linkages (11-13). The cleavage of the HA0 precursor into HA1 and HA2 is necessary for viral infectivity (9, 14). The HA1 is a hypervariable domain, which shares only 34-59% amino acid sequence identity between influenza virus subtypes (15). This domain is responsible for binding to host cellular receptors and the antibody against HA1 is relatively strain or subtype specific (13). On the

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3 76 other hand, HA2 mediates fusion between the viral envelope and the endosomal membrane
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5 77 during the uncoating step of the viral replication cycle (13). It is more conserved than HA1,
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7 sharing 51-80% amino acid sequence identity between subtypes and inducing heterosubtypic
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9 79 immunity (15, 16). Neutralizing antibody against HA is the most important correlate of
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11 80 protection against influenza virus infection and is used for assessing vaccine immunogenicity.
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13 81 In addition, Western blot assay for antibody to H5 HA has been recommended by the World
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15 82 Health Organization (WHO) as the confirmatory test for serodiagnosis of patients infected
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17 83 with HPAI H5N1 virus (17).

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21 84 Several protein expression systems have been employed to express the recombinant
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23 85 H5 HA for use as vaccine candidates, in studying host immune responses, and for disease
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25 diagnosis. These expression systems include: the infection of mammalian or avian cells with
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27 recombinant vaccinia viruses (18-22) or pseudotype lentiviral viruses (23), the infection of
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29 insect cells with recombinant baculoviruses (24-26), and the infection of plant cells with
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31 recombinant bacteria (27-28). In addition, the expression of H5 HA in yeast or bacterial cells
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33 transformed with recombinant plasmids have also been reported (29-30). Among these
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35 expression systems, the vaccinia virus vector provides a powerful tool for production of
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37 antigenically and biologically active proteins. Several seasonal influenza proteins including
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39 HA, NA, NP, M, NS, PB1, PB2 and PA have been expressed in the recombinant vaccinia
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41 viruses (31-34) and used to demonstrate influenza subtype-specific and cross-reactive
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43 immune responses (35-36).

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48 96 Even though the rVac-H5 HA has been expressed by several groups of investigators
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50 97 (18-22), their immunobiological activities have only been investigated in animal models and
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52 never with human samples. Herein, we constructed a recombinant vaccinia virus harbouring
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54 the complete influenza *HA* gene derived from an HPAI H5N1 virus. Localization of the
55
56 rVac-H5 HA in the infected cells was visualized by immunofluorescence microscopy; and its
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3 101 antigenicity was determined by Western blot assay using serum samples from H5N1
4 survivors and H5N1-uninfected subjects. The use of rVac-H5 HA as the test antigen was
5 compared with the H5 HA produced from Madin-Darby canine kidney cells (MDCK)
6 infected with wild-type H5N1 virus, and with the recombinant H5 HA expressed in a
7 baculovirus-insect cell system.
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18 107 **Materials and Methods**
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20 108 **Ethical issues**
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23 109 This study has been approved by the Institutional Review Boards of the Faculty of
24 Medicine Siriraj Hospital, Mahidol University.
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28 112 **Human subjects and blood specimen**
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30 113 A total of 20 serum samples employed in this study comprised 11 anonymously
31 archived samples, 3 from HPAI H5N1 survivors, 8 from influenza A/H3N2-infected patients,
32 33
34 115 and 9 serum samples from healthy individuals with informed consent. All patients were
35 diagnosed by real time reverse transcription polymerase chain reaction (real time RT-PCR)
36 using the protocols established by the U.S. Centers for Disease Control and Prevention.
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38 117 Virus isolation and/or serodiagnosis were also performed in most of the patients. The acute
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40 118 and convalescent blood samples were collected from H3N2 patients at approximately 3
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42 119 weeks apart while single blood samples were collected from healthy individuals. Serum and
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44 120 plasma samples were kept frozen at -20°C until used.
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52 123 **Cell lines and viruses**
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54 124 Madin-Darby canine kidney (MDCK) cells were grown in Eagle's minimum essential
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56 medium (EMEM) (Gibco, NY) supplemented with 10% fetal bovine serum (FBS) (Gibco,
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3 126 NY) and antibiotics. Influenza A viruses: A/Thailand/Siriraj-Rama-TT/2004 [A/New
4 Caledonia/20/1999 (H1N1)-like virus], A/Siriraj ICRC/SI-154/2008 [A/Brisbane/10/2007
5 (H3N2)-like virus] and A/Thailand/1(KAN-1)/2004 (H5N1) clade 1 virus (KAN-1 virus)
6
7 128 were propagated in MDCK cell monolayers maintained in EMEM in presence of trypsin-
8 tosylphenylalanyl chloromethyl ketone (trypsin-TPCK) (Sigma-Aldrich, MO) and antibiotics,
9
10 130 and without FBS supplement. The culture supernatants were harvested, centrifuged,
11 and aliquoted and kept as virus stocks.
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13

14 133 TK⁻ (thymidine kinase negative) cells were grown in Dulbecco's modified Eagle
15 medium (DMEM, Gibco) supplemented with 10% FBS and antibiotics. The culture media
16 was replaced with DMEM supplemented with 2% FBS for virus propagation and titration.
17
18 136 Vaccinia virus vaccine strain Lister, kindly provided by the Thai Government Pharmaceutical
19 Organization, was used as the gene vector for construction of the recombinant virus harboring
20
21 137 H5 HA gene insert. The virus infected cell cultures were harvested, frozen and thawed three
22 times, followed by treatment with 0.1 volume of 0.25% trypsin (Gibco) for 15 minutes at
23
24 139 37°C in order to break the aggregates of the viral progenies and facilitating the viral release.
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26 140 Subsequently, a 0.1 volume of FBS was added to terminate the trypsin activity. The cell
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28 141 lysates were centrifuged, aliquoted and kept as the virus stocks.
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43 144 **Construction of recombinant vaccinia virus carrying H5 HA gene insert**
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145 Total RNA was extracted from MDCK cells infected with the KAN-1 virus using a
146 QIAamp[®] viral RNA mini kit (Qiagen GmbH, Hilden, Germany). The complete HA
147 genomic segment was amplified by One-step RT-PCR kit (Qiagen) using universal primers:
148 Bm-HA-1 (5'-TATTCGTCTCAGGGAGCAAAAGCAGGG-3') and Bm-NS-890R (5'-
149 ATATCGTCTCGTATTAGTAGAAACAAGGGTGT-3') (37). The PCR product of
150 1,807 base pairs (bp) in length was purified by using QIAquick[®] gel extraction kit (Qiagen)
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3 151 and cloned into pGEM®-T Easy vector (Promega Corporation, Madison, WI) by using T4
4 DNA ligase (Promega) before transforming into *E. coli* JM109 cells. The *Not*I fragment
5 containing complete *HA* gene with sticky ends derived from the cutting product of the
6 recombinant plasmid was repaired by using klenow DNA polymerase (New England Biolabs
7 Inc., Ipswich, MA) in order to generate blunt end DNA strands. The DNA product was
8 subcloned into a pSC11 expression vector kindly provided by Prof. Bernard Moss, National
9 Institute of Allergy and Infectious Disease, Maryland, USA. This vector contains the *Sma*I
10 insertion site located downstream of vaccinia virus p7.5 promoter together with the *E. coli*
11 *lacZ* gene which encodes for β-galactosidase under a p11 promoter, and is flanked with
12 thymidine kinase sequences (TK_R and TK_L). *E. coli* JM109 cells were transformed with the
13 recombinant pSC11 containing *HA* gene insert (pSC11/*HA*) and plated on LB agar containing
14 5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside (X-gal) (Promega) plus ampicillin as the
15 selective marker. The cloned bacterial colonies were cultured in LB broth and the plasmids
16 were extracted by a QIAprep® Spin mini kit (Qiagen). The purified plasmids were cut by the
17 enzyme *Pst*I in combination with *Xho*I (New England Biolabs) in order to check for the
18 presence of the *HA* gene insert with correct orientation. DNA sequencing was performed in
19 order to determine the in-frame translation of the *HA* insert using a set of 4 sequencing
20 primers comprising pSC11 P7.5F (5'-GCACGGTAAGGAAGTAGAATC-3'), HAH5F (5'-
21 ACTCCAATGGGGCGATAAA-3'), HAH5R (5'-CAACGGCCTCAAACGTGAGTGT-3')
22 and pSC11R (5'-CATCGAGTGCGGCTACTATAAC-3'). A mixture of pSC11/*HA*
23 recombinant plasmids and DMRIE-C transfection reagent (Invitrogen, Carlsbad, CA) in
24 DMEM was transfected into the TK⁻ cells that had been pre-infected with vaccinia vaccine
25 virus at the multiplicity of infection of 0.01 plaque forming unit (pfu)/ml for 2 hours. The
26 HA sequence flanked with TK_R and TK_L was inserted into the parental vaccinia viral genome
27 by homologous recombination with the *tk* gene. As a result, the recombinant virus harboring
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3 176 the *HA* gene insert lost the ability to produce thymidine kinase enzyme (TK⁻ phenotype). The
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5 transfected culture was further incubated for 2 days to allow virus replication. The
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7 recombinant vaccinia virus was distinguished from the parental TK⁺ vaccinia virus by plaque
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9 selection on the TK⁻ cell monolayer in the presence of 5-bromo-2'-deoxyuridine (BrdU)
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11 (Sigma Aldrich, St. Louis, MO) and X-gal in which the plaques produced by cells infected
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13 with the recombinant vaccinia virus appeared blue. Plaque purification of the recombinant
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15 virus was performed three times using low melting point agarose containing BrdU and X-gal.
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17 In parallel, the recombinant vaccinia virus containing pSC11 vector (rVac-pSC11) was
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19 constructed for use as the vaccinia virus control.
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27 186 **Immunofluorescence assay**
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TK⁻ cells infected with recombinant vaccinia viruses containing the *HA* gene insert were investigated for expression and localization of HA protein by immunofluorescence assay (IFA). Goat antiserum against HA from A/Vietnam/1203/04 (H5N1) (VN1203) kindly provided by Prof. Robert G. Webster and Dr. Richard Webby, St. Jude Children's Research Hospital, USA and a mouse monoclonal antibody raised against purified VN1203 HA (US Biological, Swampscott, MA) were used as the primary antibodies. Fluorescein isothiocyanate (FITC) conjugated-rabbit anti-goat Ig (Dako Cytomation, Glostrup, Denmark) or FITC conjugated-goat anti-mouse Ig (Light DiagnosticsTM, Temecula, CA) was used as the secondary antibody. The slides were counterstained with trihydrochloride trihydrate (Hoechst 33342- Invitrogen, Eugene, Oregon) together with 5% Evan blue's dye and examined for the presence of fluorescent cells under laser scanning confocal microscopes (LSM 510 Meta, Zeiss, Jena, Germany).

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2 **201 Western blot (WB) assay for detection of anti-H5 HA antibody**
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45 202 The WB assay was performed for 2 purposes in this study. Firstly, to investigate the
6 expression, MW, and post-translational proteolytic cleavage of HA protein in TK⁻ cells
7 203 infected with either rVac-H5 HA or rVac-pSC11 virus in comparison with the KAN-1 virus
8 204 infected MDCK cells and recombinant HA expressed in a baculovirus-insect cell system.
9 205 Secondly, the assay was used to detect specific and cross-reactive antibodies to HA antigen in
10 206 H5N1 survivors and H5N1-uninfected subjects.
1112 208 The H5 HA antigens used in the WB assay were derived from 3 sources: the lysates of
13 TK⁻ cells infected with rVac-H5 HA virus; the lysates of MDCK cells infected with KAN-1
14 209 virus; and the recombinant H5 HA expressed in baculovirus-insect cell system (rBV-H5
15 210 HA), either purchased from Protein Sciences Corporation, Meriden, CT (lot numbers 45-
16 211 05034RA-2 [designated lot no. 1] and 0880-125 [designated lot no. 2]) or kindly donated by
17 212 BEI Resources through the NIH Biodefense and Emerging Infections Research Resources
18 213 Repository, NIAID, NIH (catalog number NR-660, lot number 59137402 [designated lot
19 214 no.3]). Briefly, infected cell lysates or recombinant antigens were mixed with 4X reducing
20 215 sample buffer (8% SDS, 250 mM Tris Cl pH 6.8, 8% β-mercaptoethanol, 0.4% bromophenol
21 216 blue, 40% glycerol), boiled for 5 minutes and subjected to 10% denaturing (SDS)
22 217 discontinuous polyacrylamide gel electrophoresis (SDS-PAGE- Laemmli method) (38). The
23 218 proteins present in gel were blotted onto a nitrocellulose membrane (Protran[®], Whatman,
24 219 GmbH, Germany) by using Trans-Blot[®] SD semidry transfer cell (Bio-Rad). The blotted
25 220 membrane was blocked with 5% skim milk in Tris-buffer saline plus 0.1% tween-20 (TBS-
26 221 T). Characterization of the rVac-H5 HA protein employed specific antibodies of 3 origins:
27 222 goat antiserum to VN1203 HA (St. Jude Children's Research Hospital), mouse monoclonal
28 223 antibody to VN1203 HA (US Biological), and pooled mouse sera collected from BALB/c
29 224 mice immunized with the recombinant vaccinia virus carrying the *HA* gene of KAN-1 virus
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3 226 (kindly provided by Dr. Molvibha Vongsakul, Faculty of Science, Mahidol University). The
4 227 anti-species specific immunoglobulin: horseradish peroxidase enzyme (HRP) conjugated-
5 228 rabbit anti-goat Ig (Dako Cytomation, Glostrup, Denmark) or goat anti-mouse Ig (Dako) was
6 229 used as the secondary antibody. The antigen blotted on nitrocellulose membrane was
7 230 incubated with the primary test serum overnight at 4°C before washing with TBS-T and
8 231 followed by incubation with the corresponding secondary antibody for 2 hours at room
9 232 temperature. The mixture of 3, 3'-diaminobenzidine (Sigma-Aldrich, St. Louis, MO), 8%
10 233 NiCl₂ and H₂O₂ was used as the chromogenic substrate. The detection of specific or cross
11 234 reactive antibody to H5 HA in H5N1 survivors and H5N1-uninfected subjects employed sera
12 235 at dilution of 1: 100. The HRP conjugated-goat anti-human IgG (Invitrogen) at dilution of 1:
13 236 1000 was used as the secondary antibody.
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238 **Microneutralization (microNT) assay**

239 The protocol of ELISA-based microNT assay for detection of neutralizing (NT)
240 antibodies was conducted according to that described in the WHO manual (39) and
241 Lerdsamran, *et al* (40). The test serum was heat inactivated at 56°C for 30 minutes before
242 making a serial two-fold dilution starting from the dilution of 1: 5 and proceeding to 1: 2560.
243 The assay was performed by mixing 60 microliters (μl) of the diluted serum with 60 μl of the
244 virus suspension at a concentration of 200 tissue culture infective dose 50 (TCID50) and
245 incubated at 37°C for 2 hours. One hundred microliters of the serum-virus mixture were
246 transferred onto an MDCK cell monolayer and further incubated for 24 hours. In order to
247 verify the amount of virus inoculum, virus back-titration at concentrations of 0.1, 1, 10 and
248 100 TCID50 was included in every reaction plate in duplicate. The relative amount of
249 influenza viral nucleoprotein in the reaction plates was determined by an ELISA using a
250 mouse-specific monoclonal antibody (Chemicon, Temecula, CA) as the primary antibody.

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2 251 goat anti-mouse Ig conjugated with HRP (Southern Biotechnology, Birmingham, AL) as the
3 252 secondary antibody, and TMB (KPL Inc., Gaithersburg, MD), as the chromogenic substrate.
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5 253 The NT antibody titer was defined as the reciprocal of the highest serum dilution that reduces
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7 254 ≥50% of the amount of viral nucleoprotein in the reaction wells as compared to the virus
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9 255 control wells.
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18 257 **Results**
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20 258 **Characterization of rVac-H5 HA**
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22 259 Recombinant baculovirus H5 HA protein (rBV-H5 HA) of known molecular weights
23 260 (72 kDa for HA0, 45 kDa for HA1 and 25 kDa for HA2 domains as indicated in the product
24
25 261 brochure) was used to characterize specificity of a goat antiserum and mouse monoclonal
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27 262 antibody against H5 HA by WB assay. Collective results from 3 lots of rBV-H5 HA
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29 263 demonstrated that the goat antiserum was reactive against HA0, HA1 and HA2 domains;
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31 264 whereas mouse monoclonal antibody was reactive only to HA0 and HA1 domains (Figure 1).
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33 265 The goat antiserum and mouse monoclonal antibody were further used to characterize our
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35 266 rVac-H5 HA. Lysates of TK⁻ cells infected with rVac-H5 HA virus were analyzed on their
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37 267 mobility in SDS-PAGE and WB assay in parallel with those of TK⁻ cells infected with rVac-
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39 268 pSC11 as the negative control. Three bands of proteins at MW of approximately 75, 55 and
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41 269 27 kDa corresponding to the uncleaved HA0 precursor and its HA1 and HA2 cleavage
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43 270 products, respectively were observed as analyzed with goat anti-H5 HA antiserum (Figure
44
45 271 1A). On the other hand, 2 bands corresponding to HA0 and HA1 polypeptides were observed
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47 272 when anti-H5 HA monoclonal antibody was employed (Figure 1B). Notably, the MWs of
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49 273 HA1 and HA2 derived from the recombinant baculovirus virus were clearly lower than those
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51 274 derived from the recombinant vaccinia virus. The discrepancy in MW between our system
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2 275 and the baculovirus system may be due to differences in the glycosylation pattern of HA
3 276 produced in insect cells compared to vertebrate cells, as discussed below.
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7 278 **Expression and localization of rVac-H5 HA protein expressed in the infected TK⁻ cells**
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9 279 Localization of rVac-H5 HA in the infected TK⁻ cells was determined by indirect
10 280 immunofluorescence assay using a goat anti-H5 HA antiserum and mouse anti-H5 HA
11 281 monoclonal antibody. The rVac-pSC11 virus infected TK⁻ cells were used as the negative
12 282 control. The result showed that the fluorescent rVac-H5 HA protein localized both in the
13 283 cytoplasm and on the cytoplasmic membrane of the infected cells; no fluorescent signal was
14 284 observed in the rVac-pSC11 infected TK⁻ cell control as visualized under a confocal
15 285 fluorescence microscope (Figure 2). It was noted that our recombinant H5 HA could be
16 286 recognized by antibodies raised against wild-type HA derived from strain VN1203 which
17 287 belongs to the same clade.
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34 289 **Comparison between rVac-H5 HA and wild-type H5 HA**
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36 290 The recombinant H5 HA protein expressed in TK⁻ cells infected with rVac-H5 HA
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38 291 virus was compared with the wild-type HA protein synthesized in MDCK cells infected with
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40 292 KAN-1 virus. The results showed that HA proteins produced in both virus-cell systems were
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42 293 similar in size and number of the cleavage products (Figure 3).
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47 295 **Immunogenicity and antigenicity of rVac-H5 HA**
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49 296 The immunogenicity of our rVac-H5 HA in the induction of antibody response was
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51 297 investigated in a mouse model. Serum samples collected from BALB/c mice immunized
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53 298 with rVac-H5 HA virus (gift from Dr. Molvibha Vongsakul) were reactive with rVac-H5 HA
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55 299 protein and demonstrated reactivity against HA0, HA1 and HA2 domains (Figure 4), while
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3 300 serum samples from non-immunized mice, or the mice immunized with rVac-pSC11 virus
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5 301 were non-reactive by WB assay (data not shown). Furthermore, the mouse anti-H5 HA
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7 302 antiserum recognized the HA0, HA1 and HA2 domains present either in the recombinant H5
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9 303 HA expressed in the baculovirus-insect cell system or in the wild-type H5 HA synthesized in
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11 304 MDCK cells infected KAN-1 virus.
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18 306 **Reactivity of human sera to rVac-H5 HA protein**
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307 Human sera from various groups of subjects were assayed for the presence of anti-H5
308 antibody by WB assay using crude cell lysates containing rVac-H5 HA and the recombinant
309 H5 HA expressed in insect cells (rBV-H5 HA lot nos. 1 and 3) as the test antigens. The
310 result showed that sera from all 3 H5N1 survivors contained antibodies to HA0, HA1 and
311 HA2 domains, while the H5N1-uninfected subjects contained antibody to HA2 domain only
312 (Figure 5 and Table 1). We further investigated these sera for presence of NT antibody
313 against various influenza virus subtypes. All 3 H5N1 survivors contained high titers of anti-
314 H5N1 NT antibody, whereas none of the H5N1-uninfected subjects including 8 H3N2-
315 infected patients and 9 healthy individuals did so. Interestingly, these H5N1-uninfected
316 subjects had NT antibody to seasonal H1N1 and H3N2 viruses. Therefore, it is plausible that
317 the heterosubtypic antibodies cross-reacted with the H5 HA2 domain in the WB assay.
318 Nevertheless, the frequency of antibody against the HA2 domain in H5N1-uninfected
319 subjects varied according to sources of the recombinant protein antigen used. The
320 recombinant H5 HA antigen from BEI Resources yielded the strongest reactivity with
321 antibody to HA2, whereas our rVac-H5 HA virus expressed a lower amount of HA2 protein
322 as demonstrated by a weaker reaction with antibody to HA2 antigen.
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3 325 **Discussion**
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326 In the present study, the rVac-H5 HA virus was constructed and its immunogenicity
327 was characterized in comparison to wild-type H5 HA produced in MDCK cells infected with
328 KAN-1 virus and to recombinant H5 HA produced in a baculovirus-insect cell system using a
329 goat antiserum and a mouse monoclonal antibody against H5 HA protein. The MW of
330 approximately 75, 55 and 27 kDa of HA0, HA1 and HA2 as expressed by our rVac-H5 HA
331 virus were comparable to those derived from the KAN-1 virus infected MDCK cells. The
332 results demonstrated that the expressed rVac-H5 HA protein was localized in the cytoplasm
333 and on the cytoplasmic membrane of the TK⁻ cells infected with rVac-H5 HA virus; and this
334 expression was stable after serial propagation of the recombinant virus in TK⁻ cells (data not
335 shown). This is the first documentation of H5 HA expression in TK⁻ cells which is a human
336 cell line in origin, however, our recombinant virus had been previously shown to infect and
337 express the H5 HA protein in U937 cells, a human monocyte cell line (41).

338 The TK⁻ cells infected with our rVac-H5 HA virus expressed 3 forms of HA: the HA0
339 polyprotein precursor and its HA1 and HA2 cleavage products, suggesting post-translational
340 proteolytic cleavage of the precursor protein. All these forms of HA were immunogenic, as
341 sera from mice immunized with crude lysates of rVac-H5 HA virus infected cells revealed 3
342 bands of the appropriate size for HA0, HA1 and HA2 against the recombinant H5 HA
343 expressed in insect cells or wild-type H5 HA produced in MDCK cells infected with KAN-1
344 virus in a WB assay. Additionally, we have also investigated for the presence of specific
345 neutralizing antibody in sera from BALB/c mice immunized with our rVac-H5 HA virus by
346 the CPE-based NT assay using the highly pathogenic H5N1 (KAN-1) parental virus as the
347 test virus. We found that the mouse sera contained the neutralizing antibody at titers between
348 80 and 640.

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3 349 The proteolytic cleavage of HA0 precursor into HA1 and HA2 domains is required for
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5 350 the viral infectivity (9, 14). The HA protein of HPAI viruses which contain multiple basic
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7 351 amino acids at cleavage site will be cleaved intracellularly by ubiquitous subtilisin-like
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9 352 proteases, while the HA that contains single arginine at the cleavage site (as found in
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11 353 nonpathogenic viruses) is cleaved extracellularly by trypsin-like proteases (9, 14). Our rVac-
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13 354 H5 HA virus carries the full length HA coding sequence with multiple basic amino acids
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15 355 PQRERRRKRG at cleavage site (GenBank accession number AY555150). This explains
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17 356 why the expressed HA was found in the cleaved forms (HA1 and HA2) together with residue
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19 357 of the uncleaved form (HA0). Other investigators who work on the expression of HA of
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21 358 influenza viruses that contain a monobasic amino acid at the cleavage site had incorporated
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23 359 trypsin into the virus growth medium in order to achieve post-translational proteolytic
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25 360 cleavage of the HA product (42).

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30 361 The MW of approximately 75, 55 and 27 kDa for HA0, HA1 and HA2, respectively
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32 as expressed by our rVac-H5 HA virus were comparable not only to the wild-type H5 HA
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34 derived from the KAN-1 virus infected MDCK cells, but also to that reported by other
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36 investigators using DF-1 cell line infected with modified vaccinia Ankara containing H5 HA
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38 from the VN1203 virus (18). However, the MW of these domains were higher than those of
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40 the recombinant H5 HA expressed by the recombinant baculovirus, i.e., 72, 45 and 25 kDa
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42 for HA0, HA1 and HA2, respectively as shown in this study and also indicated in the product
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44 brochure. However, the MW of 70 kDa for HA0 and 50 kDa for HA1 were previously
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46 reported by the other group of investigators (43). Several published data demonstrated that
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48 the glycosylation of HA in insect cells was significantly retarded and less efficient than in
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50 vertebrate cells; the reduction in carbohydrate contents and truncated oligosaccharides was
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52 also observed (45-46). Moreover, the HA produced in different types of insect cells
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3 373 (*Spodoptera frugiperda* cells and *Estigmene acrea* cells) was different in glycosylation
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5 374 patterns (47).

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7 375 The MW of deglycosylated forms of HA0, HA1 and HA2 is 64.5, 37.6 and 25.1 kDa,
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9 376 respectively according to our prediction by using 2 web-based tools: Compute pI/Mw tool
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11 377 (http://web.expasy.org/compute_pi/) and protein molecular weight calculator
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13 378 (<http://www.sciencegateway.org/tools/proteinmw.htm>). We have also determined the
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15 379 potential sites of glycosylation in the *HA* sequences of H5N1 (KAN-1) and VN1203 viruses
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17 380 using CountGS application in BioEdit program. Both viruses have 8 potential glycosylation
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19 381 sites, 2 within the HA1 globular domain and 6 in the HA2 fusion domain. Therefore, it is
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21 382 conceivable that the recombinant H5 HA expressed in vertebrates (TK⁻ cells from human;
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23 383 MDCK from dog; and DF1 from chicken) had a higher MW than those expressed in insect
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25 384 cells due to the difference in glycosylated moieties of the HA molecule which varies among
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27 385 different influenza strains and subtypes and host of origin (18, 44).

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29 386 Our rVac-H5 HA virus at the concentration of 6×10^6 pfu/50 μ l reaction did not
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31 387 agglutinate goose erythrocytes and the infected TK⁻ cells did not exhibit a hemadsorption
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33 388 property (data not shown). This is in contrast to recombinant vaccinia viruses expressing the
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35 389 HA protein of H1N1 or H3N2 viruses, constructed by Itamura *et al* (34), which had
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37 390 hemagglutination, hemadsorption and cell fusion activities. We have found out that the H5
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39 391 HA sequence of the recombinant vaccinia virus in this study is different from its parental HA
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41 392 sequence originally reported by our group for the wild type KAN-1 virus (GenBank
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43 393 accession number AY555150) by 2 positions (R139G and K218E, H5 numbering). These 2
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45 394 positions were responsible for recognizing the sialic acid receptor present on the host cell
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47 395 membrane according to those previously reported for the HPAI H5N1 virus (48-50). It might
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49 396 be possible that the inability to recognize the cell receptor caused the loss of
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51 397 hemagglutinating activity of our recombinant virus. There are 5 antigenic sites on HA1

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3 398 domains for seasonal and 2009 pandemic A(H1N1) (sites Sa, Sb, Ca1, Ca2, Cb) and H3N2
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5 399 viruses (sites A-E), which are not related to the receptor binding site (51-52). The
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7 400 antigenicity-associated sites corresponding to the sites A-E have been reported for H5N1
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9 401 virus (52). This might be an explanation why our recombinant virus could induce the
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11 402 production of neutralizing antibody in BALB/c mice despite its inability to agglutinate the
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13 403 goose red blood cells.

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16 404 Our previous work confirmed the presence of antibody directed against different H5
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18 405 HA domains by WB assay using recombinant VN1203 HA expressed in a baculovirus-insect
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20 406 cell system (Protein Sciences) as the test antigen. HA1 and HA2 specific antibodies were
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22 407 detected in all of 4 H5N1 survivors and lasted for years (53). Unfortunately, that lot of
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24 408 recombinant HA did not contain HA0 as characterized by the reference antiserum (53), while
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26 409 the second and the third lots in this study did. Our WB assay demonstrated that H5N1-
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28 410 uninfected subjects contained the antibodies directed to the HA2 domain, but not the HA0 or
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30 411 HA1 domains. However, the number of individuals with HA2 antibodies varied according to
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32 412 the lot of the recombinant proteins used. These H5N1-uninfected subjects had no NT
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34 413 antibody to H5N1 virus, while all had NT antibody to seasonal H1N1 and H3N2 viruses. We
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36 414 can conclude that the subjects who have no experiences of H5N1 infection contained cross-
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38 415 reactive antibodies against H5 HA2 as the result of previous or recent infection with seasonal
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40 416 influenza viruses. Therefore, our study can strengthen the WHO criteria for serodiagnosis of
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42 417 HPAI H5N1 in that the true H5N1 positive case should contain antibodies which directed
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44 418 against both the HA1 domain and the HA2 domain in a WB assay.

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47 419 In terms of vaccine development for preparedness against pandemic influenza, it is
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49 420 difficult to predict which subtype of vaccine should be prepared in advance. Collective
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51 421 information suggests that HA2 peptide might be a good candidate (54). While the antibodies
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53 422 to HA1 is strain specific, the antibodies direct against HA2 are conserved and can cross-
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3 423 neutralize various influenza subtypes including H1, H2, H5, H6, H18, H9, H11, H12, H13
4 424 and H16 (16, 55-56). In addition, it has been shown that B lymphocytes from healthy
5 425 individuals without experience of H5N1 HPAI could generate antibodies to H5 HA2 domain
6 426 that exhibited neutralizing activity across influenza subtypes including the HPAI H5N1 virus
7 427 (55). However, those works have generated the clone of monoclonal antibodies with cross
8 428 reactive neutralizing activity against influenza virus subtypes by phage display technique.
9 429 These monoclonal antibodies should be derived from the selected clones and assayed in
10 430 purified and concentrated form for to exhibit the neutralizing activity. On the other hand, our
11 431 assay for neutralizing antibody against H5N1 virus in the non-H5N1 subjects employed the
12 432 native sera. Even though those native sera could bind H5 HA2 protein as demonstrated by
13 433 WB assay, it is likely that those sera contained undetectable level of the neutralizing antibody
14 434 but higher level of binding antibody against the non-neutralizing epitope. An additional
15 435 advantage is a potential robust booster effect in vaccinees most of whom have experienced
16 436 natural influenza virus infection before. Thus, a high level of anti-HA2 antibodies which
17 437 broadly neutralize across heterologous influenza subtypes might be expected. However, the
18 438 antigenicity and stability of the protein produced is of concern, and especially, the host cell
19 439 species for HA2 protein production.

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11 452 No competing financial interests exist.
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616 TABLE 1. Immunological reactivity of recombinant H5 HA with human sera

Subject no.	Age (years)	Blood collection	Antibody to		NT antibody to									
			rBV-H5 HA		rVac-H5 HA		H5N1							
Lot no. 1 ^a			Lot no. 3 ^b											
H5N1														
survivors														
1	32	1y 6m after disease onset	HA1, HA2	HA0, HA1, HA2	HA0, HA1, HA2	160	ND							
2	29	2y 8m after disease onset	HA1, HA2	HA0, HA1, HA2	HA0, HA1, HA2	160	ND							
3	7	11m after disease onset	HA1, HA2	HA0, HA1, HA2	HA0, HA1, HA2	80	ND							
H3N2														
patients														
1	24	Acute bl. Conv. bl.	HA2 HA2	HA2 HA2	HA2 HA2	<5 <5	160 >2560							
2	24	Acute bl. Conv. bl.	No HA2	HA2 HA2	HA2 HA2	<5 <5	80 320							
3	27	Acute bl. Conv. bl.	No No	HA2 HA2	HA2 HA2	<5 <5	80 320							
4	27	Acute bl. Conv. bl.	No No	HA2 HA2	No No	<5 <5	160 1280							
5	49	Conv. bl.	HA2	HA2	HA2	<5	640							
6	41	Conv. bl.	No	HA2	HA2	<5	640							
7	25	Conv. bl.	No	HA2	No	<5	640							
8	23	Conv. bl.	No	HA2	No	<5	640							
Healthy subjects														
1	56	Single bl.	No	HA2	HA2	<5	1280							
2	41	Single bl.	No	HA2	HA2	<5	20							
3	25	Single bl.	No	HA2	No	<5	1280							
4	24	Single bl.	No	HA2	No	<5	20							
5	39	Single bl.	No	HA2	No	<5	640							
6	27	Single bl.	No	HA2	No	<5	80							
7	27	Single bl.	No	HA2	No	<5	80							
8	28	Single bl.	No	HA2	No	<5	160							
9	25	Single bl.	No	HA2	No	<5	640							

617 ^a, Protein Sciences lot no. 45-05034RA-2 and ^b, BEI Resources lot no. 59137402. ND, not done.

618

619 **Figure legend**

620 FIGURE 1. Specificity of a goat antiserum (A); and a mouse monoclonal antibody (B)
621 against H5 HA as characterized by various lots of recombinant H5 HA expressed in
622 baculovirus-insect cell system (rBV-H5 HA) and by our recombinant H5 HA expressed by
623 vaccinia virus vector (rVac-H5 HA). The WB banding patterns of rBV-H5 HA are variable
624 by lots and sources. Collective results from 3 lots of rBV-H5 HA demonstrate that the goat
625 antiserum is specific to HA0, HA1 and HA2 domains with MW of 72, 45 and 25 kDa,
626 respectively; whereas the mouse monoclonal antibody is specific only to HA0 and HA1
627 domains. Moreover, the MWs of HA proteins expressed by the vaccinia virus vector are
628 higher than those expressed by the baculovirus-insect cell system, i.e., they are 75, 55 and 27
629 kDa for HA0, HA1 and HA2 domains, respectively.

630

631 FIGURE 2. Expression and localization of H5 HA protein in TK⁻ cells infected with
632 recombinant vaccinia virus (rVac-H5 HA) as demonstrated by IFA using goat anti-H5 HA
633 antiserum: TK⁻ cells infected with rVac-pSC11 virus as the negative control (A); and rVac-
634 H5 HA virus infected TK⁻ cells (B).

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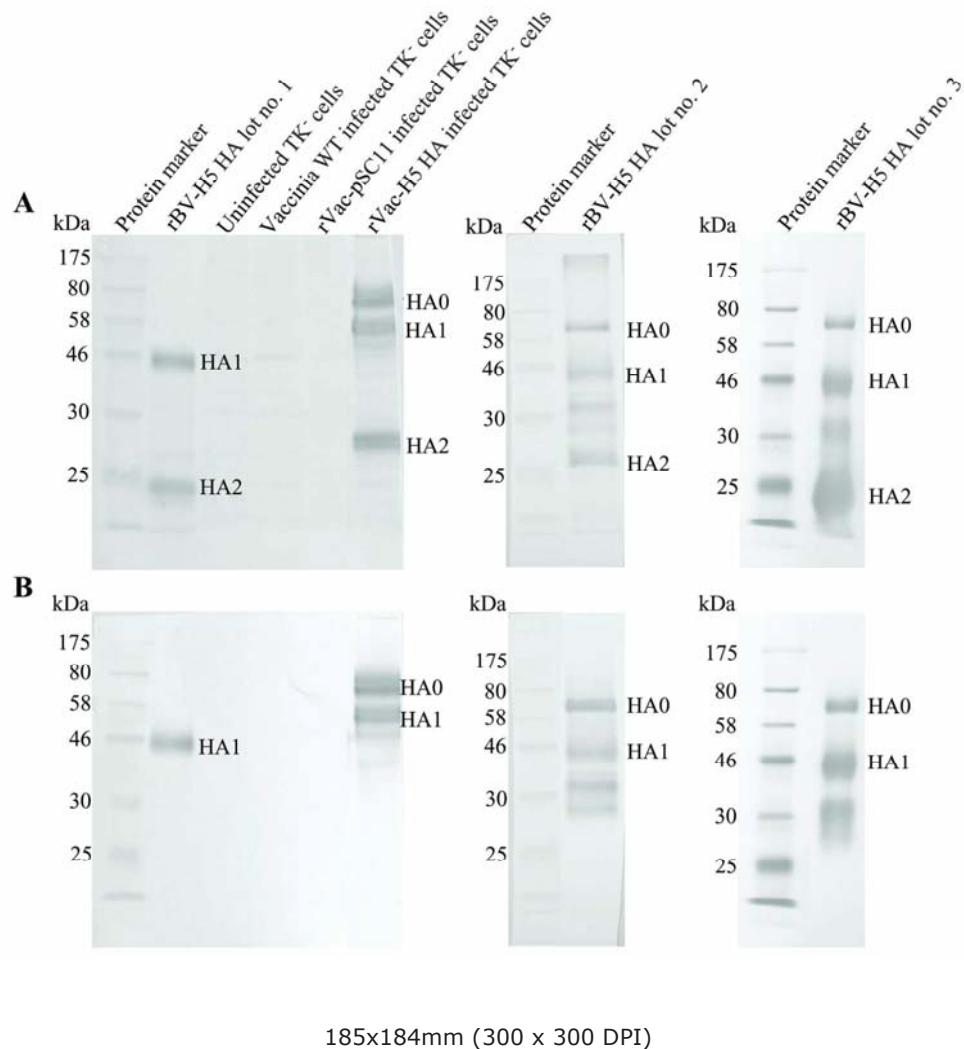
636 FIGURE 3. Comparison on the Western blot banding patterns between the recombinant H5
637 HA protein produced in TK⁻ cells infected with rVac-H5 HA virus and the wild-type H5 HA
638 produced in MDCK cells infected with H5N1 KAN-1 virus. Three bands of the same MWs
639 for HA0, HA1 and HA2 domains are demonstrated by goat anti-H5 antiserum (A); and 2
640 bands for HA0 and HA1 domains are demonstrated by mouse anti-H5 monoclonal antibody
641 (B). The result indicates similar biological processes including glycosylation and proteolytic
642 cleavage in these 2 vertebrate cell sources used for H5 HA protein production.

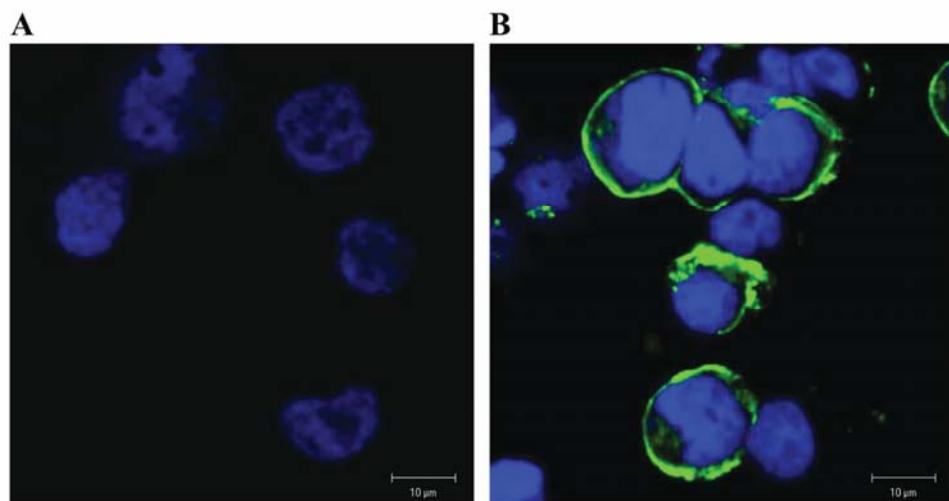
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644 FIGURE 4. Immunogenicity of rVac-H5 HA protein in the induction of antibody response in
645 BALB/c mice. Pooled sera from mice immunized with lysates of TK⁻ cells infected with
646 rVac-H5 HA virus are used to stain the recombinant H5 HA produced in the baculovirus-
647 insect cell system (rBV-H5 HA lot no.3) and the wild-type H5 HA produced in the KAN-1
648 virus infected MDCK cells by WB assay. The result shows that 3 forms of HA proteins:
649 HA0, HA1 and HA2 proteins are expressed and immunogenic in the mouse model.

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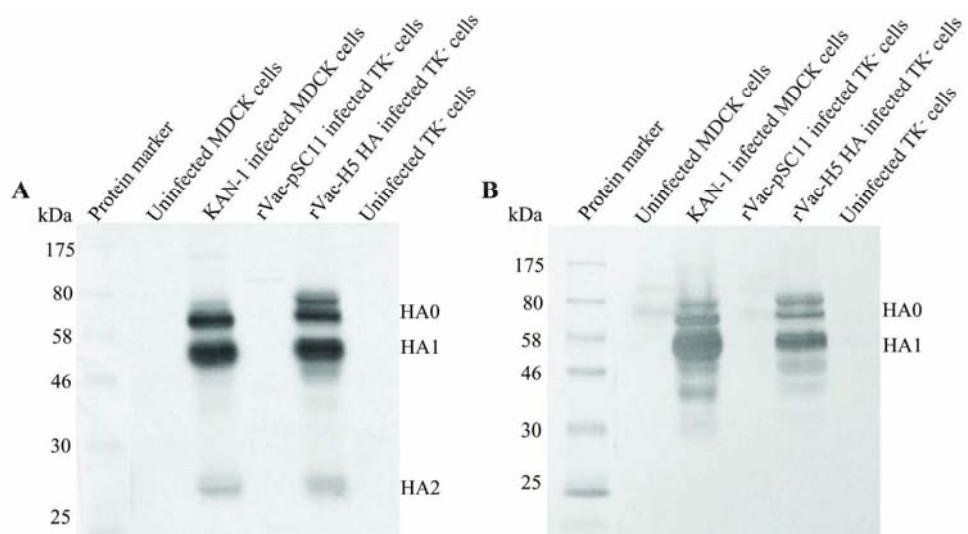
651 FIGURE 5. WB assay for antibody to H5 HA in human sera using the recombinant H5 HA
652 expressed by baculovirus vector (rBV-H5 HA lot no. 1) and vaccinia virus vector as the test
653 antigens. The results demonstrate 3 reactive bands of antibodies directed to HA0, HA1 and
654 HA2 domains in H5N1 survivor (A); and one reactive band of heterosubtypic antibody to
655 HA2 domain in H5N1-uninfected subject (B).



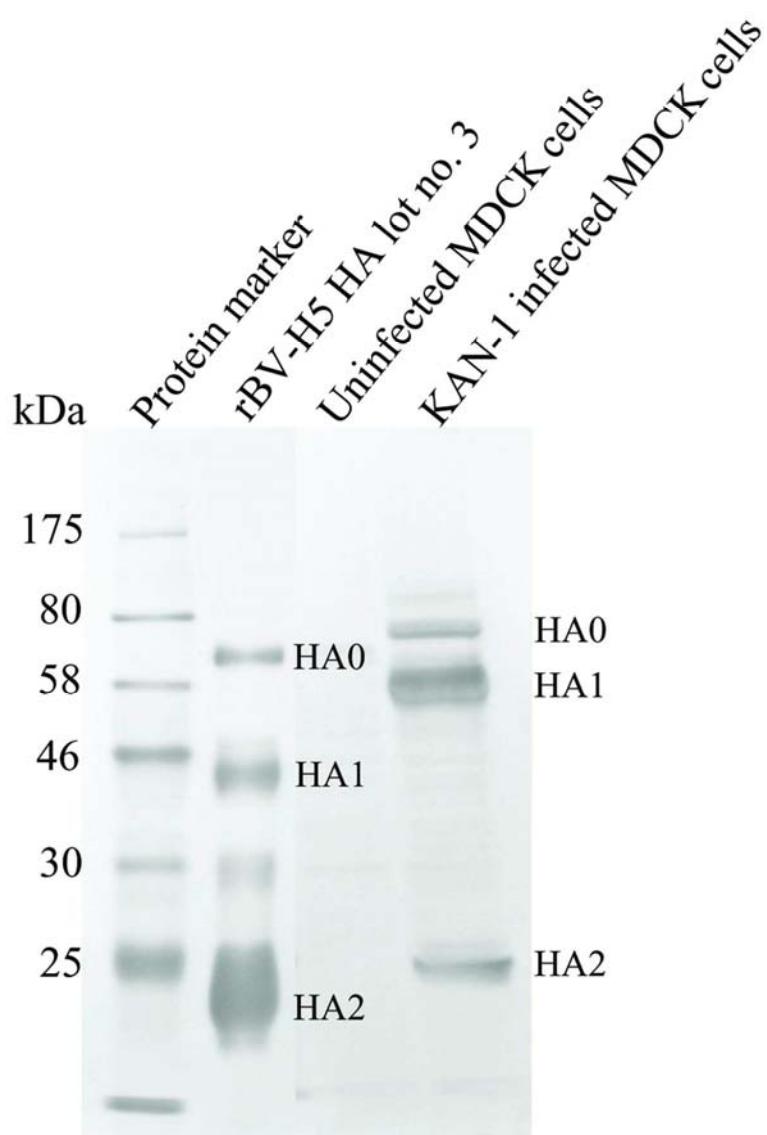


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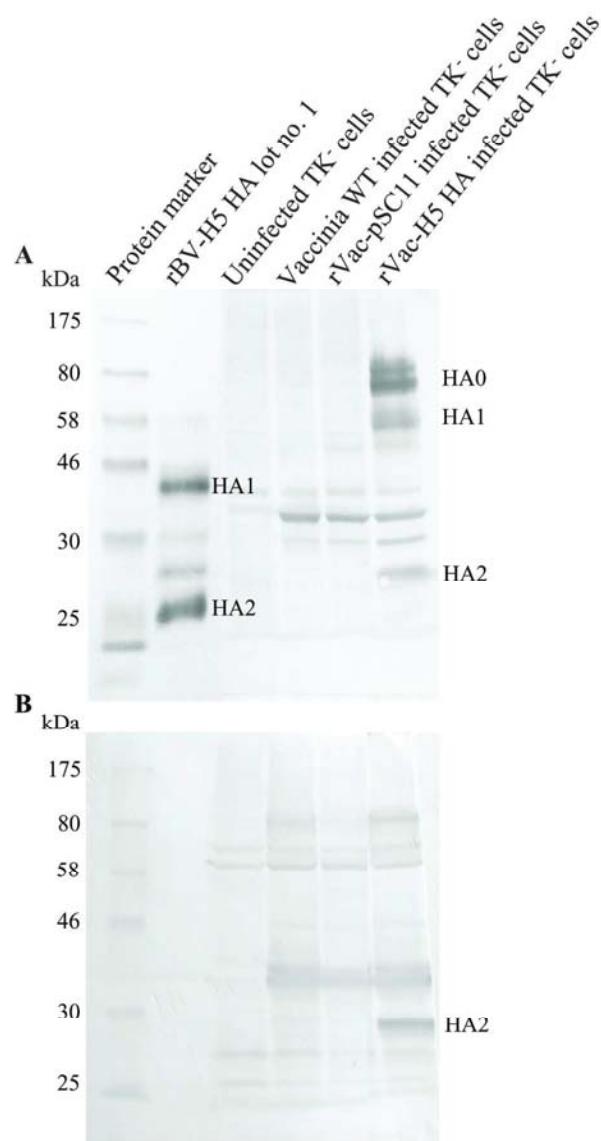
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Electron micrographs of highly and low pathogenic **avian** influenza viruses

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Short running title: Morphology of influenza virus particles

Background: The outbreak of highly pathogenic avian influenza (HPAI) H5N1 virus was first reported in Thailand in 2004. Up to present, electron micrographs demonstrating the morphology of HPAI H5N1 virus particle are quite limited.

Objective: To demonstrate the morphology of free particles of human influenza viruses, HPAI H5N1 viruses and low pathogenic avian influenza (LPAI) viruses as well as the H5N1 structural components in the infected cells. In addition, the amino acid substitutions affecting the virus morphology was also investigated.

Methods: Electron micrographs of the negative stained virus particles and the positive stained thin sections of the HPAI H5N1 virus infected cells were visualized under a transmission electron microscope (TEM). The M1 and M2 amino acid sequences were retrieved from GenBank.

Results: Morphologically, the free influenza virus particles appeared in 3 forms: spherical, regular and irregular rods, and long filamentous particles, were demonstrated. However, spherical form was the most predominant morphological type and took account of more than 80% of the virus populations examined. In addition, the step of viral entry and exit including incomplete particles in the infected MDCK cells were found. mainly spherical.

Conclusion: Of all virus isolates studied, we demonstrated that the spherical particles were the major population observed regardless of virus subtypes, host of origin, virus virulence, passage history and amino acid substitutions in M1 and M2 proteins.

Key words: electron micrographs, virus morphology, influenza virus, highly pathogenic avian influenza H5N1 virus, low pathogenic avian influenza virus

Introduction

Influenza A virus particle comprises a 8 segmented RNA genome surrounded by nucleocapsid and the outermost envelope which is underlined with matrix protein and covered with two kinds of surface glycoprotein projections: hemagglutinin (H) and neuraminidase (N) [1]. Influenza virus particles are pleomorphic and vary in size. The visualized morphology under an electron microscope was classified into three forms: the spherical forms with the diameter at range of 80 to 120 nm, the rod forms at size of 120-300 nm, and the filamentous forms which are normally longer than 300 nm [1-4].

Collective information from previous works suggested that morphology of influenza virus particles were influenced by two factors: type of host in which the viruses were propagated - either cell culture or embryonated egg, and virus passage at investigation - either early or late passage [5-6]. It was reported that the filamentous form predominated among the virus population isolated from chick embryo or cell culture at early passages; alternatively, the laboratory-adapted strains were predominantly spherical [5]. On the other hand, it had been reported that both filamentous and spherical forms appeared simultaneously in tissue culture [2, 6]. Moreover, it had been suggested that spherical form was the final product from segmentation of filamentous particles [5]. Subsequent observation showed that polarized cell type and integrity of the actins microfilament network were important for the formation of filamentous particles [6]. On the other hand, it had been suggested that morphologic features of influenza viruses were under genetic control, not a result of host induced modification [7-11]. It had been suggested that filament forming ability of the viruses was genetically stable under control of multiple genes: *H*, *N*, *M* (matrix) and *NP* (nucleoprotein) genes [8, 12]. Using reverse genetic technique to analyze M1 amino acid sequences, Elleman and Barclay [9] suggested that 3 residues: Ala41, Arg95 and Ala218 might contribute to filamentous morphology; whereas the residues Arg95 and Glu204 were

proposed by Bourmakina et al. [10]. In addition, Rossman et al. [11] suggested that Ser71, Met72 and Arg73 in M2 cytoplasmic tail may contribute to the formation of filamentous morphology.

On the basis of H and N antigens, influenza A viruses are further divided into 17 H and 9 N subtypes [13-16]. The first 16 subtypes have been found in aquatic birds; and most of them are low pathogenic, except for some isolates in H5 and H7 subtypes that are considered to be highly pathogenic avian influenza (HPAI) viruses [1, 13-15]. The 17th subtype was detected in bats by molecular techniques, but the attempts to isolate the virus did not succeed [16]. On the other hand, influenza in human population is attributed only to H1N1, H1N2, H2N2 (which existed from 1957 to 1968) and H3N2 subtypes [17-18]. Nevertheless, a cross species barrier of avian viruses to humans had been documented [19]. Transmission of HPAI H5N1 viruses from poultry to humans were first reported in 1997 and the disease subsided within that year [ref]. The re-emergence of HPAI H5N1 outbreaks since 2003 is even more catastrophic. It globally spreads and involved more human cases with higher fatality rate of about 60% [ref].

Electron micrographs of influenza virus particles had been demonstrated by groups of investigators for longer than 50 years ago, and those studies were mostly confined to human viruses [2-4]. Novel influenza subtypes have been discovered time to time, assuming that morphology of these influenza subtypes are similar to what had been previously shown. Up to present, electron micrographs demonstrating the morphology of avian influenza virus particle, especially HPAI H5N1 viruses are quite limited. Eventually, the viral morphology is one piece of basic information for characterizing a newly virus. With the higher resolution of the electron microscope and the higher quality of reagents and equipment now supported, it is interesting to characterize the morphology of H5N1 virus in terms of: 1) comparative morphology with human influenza viruses and LPAI viruses; 2) the viral structures during

replication in MDCK cells; and 3) the amino acid residues in M1 and M2 proteins that might affect the virus morphology.

Materials and methods

The study viruses

The virus isolates employed in this study were derived from either human or poultry origin. List of the viruses studied comprised 9 HPAI H5N1 isolates (4 from humans and 5 from avian), 4 LPAI isolates and 2 human influenza isolates. These viruses were isolated and propagated in Madin-Darby canine kidney (MDCK) cells or in 9 days-old chick embryonated eggs as shown in **Table 1**. MDCK cells were grown in Eagle's minimal essential medium (EMEM) (Gibco, U.S.A.) containing 10% fetal bovine serum (FBS) (Hyclone, U.S.A.), 200 U/ml penicillin, 20 µg/ml gentamycin and 1 mg/ml fungizone. Upon virus propagation, cells were maintained in EMEM supplemented with antibiotics, fungizone and 1.5 µg/ml trypsin tosyl phenylalanyl chloromethyl ketone (TPCK, Sigma, St. Louis, MO), and no FBS supplement. These virus isolates were stored at -80°C until tested. The experiments on H5N1 viruses were performed in the biosafety laboratory level 3 (BSL-3) in the Faculty of Medicine Siriraj Hospital and the Faculty of Veterinary Science, Mahidol University.

Negative staining of the free virus particles

In order to destroy the viral infectivity, the virus particles in the culture supernatants or allantoic fluids were treated with 2% glutaraldehyde before spinning by high speed centrifugation at 18,000x for 90 minutes. The viral pellets were negatively stained with phosphotungstic acid (PTA), and morphology of the stained virus particles were visualized under a TEM (JEM-1230, JEOL Company, Tokyo, Japan) [20]. Briefly, 10 µl of the virus suspension was absorbed on a grid (SPI supplies, 200 meshes, West Chester, U.S.A.) coated

with formvar-carbon for 1 minute; the excess virus suspension was drained off, followed by UV irradiation of both sides of the grid for 5 minutes. A drop of 1.6% PTA, pH 7.0 is then applied for 1 minute, and the excess fluid was removed prior to examining under a TEM.

Staining of HPAI H5N1 virus infected MDCK cells

MDCK cell monolayer was inoculated with the test virus, A/Thailand/1(KAN-1)/2004 (H5N1), at multiplicity of infection of 1 for 24 hours at 37°C in a CO₂ incubator. The infected cells were pelleted before processing and embedding. Thin sections of the virus infected cells and the uninfected cell control were positively stained and examined under a TEM as previously described [21]. The cell pellets were pre-fixed with 4% glutaraldehyde in PBS for 30 minutes at 4°C, and followed by 3 washes with Millonig's phosphate buffer and post-fixed with 2% phosphate buffered osmium tetroxide for 30 minutes at room temperature, and lastly by two washes in distilled water. Then, the cells were stained with 2% uranyl acetate aqueous solution for 20 minutes at room temperature as described after the protocol for rapid tissue processing [22]. The stained sample was dehydrated in an order of steps as follows: 70% ethyl alcohol for 90 seconds with 2 changes, 80% ethyl alcohol for 90 seconds with 2 changes, 90% ethyl alcohol for 3 minutes with 2 changes, 95% ethyl alcohol for 3 minutes with 3 changes, absolute ethanol for 3 minutes with 3 changes, and, lastly, with propylene oxide for 3 minutes with 3 changes. Then, the stained sample was infiltrated with the 50:50 mixture of propylene oxide and epoxy resin for 30 minutes at 37°C. Subsequently, the mixture solution was replaced with epoxy resin solution and further incubated for 2 hours at 37°C. Finally, the sample was embedded in polypropylene capsules and polymerized in hot air oven at 70°C overnight followed by sectioning with ultra-microtome. The ultra-thin section was mounted onto a copper support grid (SPI supplies, 200 meshes, West Chester, U.S.A.) prior to nuclear staining with uranyl acetate for 30 minutes and followed by

cytoplasmic staining with lead citrate for 15 minutes. The stained grid was examined under a TEM.

Genetic characterization of the study viruses

Our study analyzed the amino acid residues that might affect the virus morphology after those described by Elleman and Barclay [9] and Bourmakina and Garcia-Sastre [10] for M1; and by Rossman et al. for M2 [11]. The M1 and M2 amino acid sequences of our study viruses together with the reference filamentous or spherical type particles were retrieved from the GenBank database (**Table 1**). The amino acid sequences were aligned using the programs BioEdit version 7.0.9.0 [23]. The HPAI H5N1 viruses in this study belong to clade 1, except A/Laos/Nongkhai 1/2007 which belongs to clade 2.3.4.

Result

Electron microscopy of influenza virus particles

Electron micrographs of HPAI H5N1 virus particles originated from humans and avian are demonstrated in **Figures 1** and **2**, respectively; and those of human H1N1 and H3N2 viruses as well as LPAI H3N8, H5N3 and H7N1 viruses are shown in **Figures 3** and **4**, respectively. These virus isolates comprised 3 morphological types of particles: spherical at diameter of 80-120 nm, regular and irregular rods at length between 120-300 nm and filaments at length longer than 300 nm. Nevertheless, majority of them were spherical particles. The multilayered-coil structure suggestive of the helical ribonucleocapsids could be seen inside a virus particle in this study (**Figure 3a**).

Using electron micrographs at magnification of 50,000x and/or 80,000x, numbers of virus particles with different morphological types in a virus isolate was enumerated. In order to avoid an invalid data as too low number of the particles was present in the stained samples,

the results were excluded when the counting number was lower than 80. Therefore, the enumeration was successful with 3 HPAI H5N1 virus isolates and one human H1N1 isolate which demonstrated that approximately 80-90% of the virus populations observed were spherical, and the remaining was the mixed population between rod and filamentous particles (**Table 2**). Unfortunately, numbers of the viral particles for LPAI viruses and human viruses were less than 30 particles; therefore, the counting numbers obtained were excluded from percentage calculation. Nevertheless, it was clearly seen that most of particles were spherical. Collectively, we demonstrated that majority of all influenza viruses in this study were spherical, while filamentous particles were the minority.

Electron microscopy of influenza virus infected MDCK cells

H5N1 virus infected MDCK cells as well as the uninfected cell control was examined using positive staining technique. Morphology of the uninfected MDCK cell surface appendages might be mislead for their appearance as the filamentous like particle (**Figure 5a**). The infected cell with chromatin condense suggesting of cell necrosis (**Figure 5b**), as well as invagination of cell membrane to endocytose a virus particle (**Figure 5c**), budding virus particles (**Figures 5d** and **5e**) and the released virus particles (**Figure 5f**) were visualized. Spherical particle was the predominant form of HPAI H5N1 viruses in all stages of replication in MDCK cells.

Genetic characterization of the study viruses

Our study analyzed the amino acid residues that might influence the formation of filamentous or spherical particle according to previous groups of investigators, i.e., the residues Ala41, Arg95 and Ala218 in M1 for filamentous particle formation and the residues and ... for spherical particle formation were followed after Elleman and Barclay [9]; the

residues Arg95 and Glu204 in M1 for filamentous particle formation were followed after Bourmakina and Garcia-Sastre [10]; and the residues Ala71, Ala72 and Ala73 in M2 cytoplasmic tail for filamentous particle formation were followed after Rossman et al. The analyses demonstrated the presence of all amino acid residues that were suggestive of filamentous morphology in almost of our virus isolates which contained mainly the spherical type particles (**Table 3**). Therefore, our study suggested that there was no amino acid residue unique for certain morphological type of the viral particles.

Discussion

Based on electron microscopy, this study demonstrated 3 morphological types of the virus particles: spherical, rod, and filamentous forms in all of the influenza viruses studied, irrespective of their human or avian host of origin and of their low or high pathogenicity. However, the spherical particles were the predominant population, whereas filamentous particles were the minor populations which took account for approximately 4-16.5%. A previous group of investigator [5] reported that the long filamentous form was predominantly found in early passages of the viruses grown in embryonated eggs; and the filamentous form could turn to be the spherical form after a few to 4-7 sub-passages. Unfortunately, we did not have an opportunity to study the virus isolates at earlier passages due to an inadequate numbers of the virus particles for electron microscopic examination. Nevertheless, almost of our virus isolates were younger than 8 sub-passages. On the other hand, our finding was supported by the electron microscopic study on HPAI H5N1 viruses of the 1997 outbreak in Hong Kong, in which the spherical virions were predominant among the mixed virus population after few subpassages in embryonated eggs, i.e., 65% for the viruses isolated from chicken and 84% for those isolated from humans [24].

Refer to the genetic control of the virus morphology, we analyzed 5 amino acid residues (Ala41, Arg95, Glu204 and Ala218) in M1 and 3 amino acid residues (Ser71, Met72 and Arg73) in M2 cytoplasmic tail that were predictive of filamentous feature together with 4 amino acid residues (Val41 and Lys95) in M1 that were suggestive of spherical morphology based on previous reports [9,... We demonstrated that Ala41, Arg95, Glu204, Thr218, Ser71, Met72 and Arg73 were found in almost of our viruses which contained mainly the spherical particles, irrespective of the virus subtypes, host of origins and the virus virulence. Therefore, our study suggest that the morphology of influenza virus particles is less likely under control of the viral genetics. Unfortunately, we have no opportunity to explore if it is influenced by the number of virus passages.

Bruce et al. [26] demonstrated that TEM failed to demonstrate the morphogenesis of the long filament viruses extruding from the infected cells present in the positively stained thin section, whereas it was successful by the scanning electron microscopy (SEM). In this study, TEM was employed to demonstrate the virion at entry and exit from the infected cells. The multilayered-coil structure of a virus similar to what reported by Clader et al. [27] was visualized. In addition, the appearance of surface pili on the uninfected MDCK cell membrane which some time may be misinterpreted as filamentous particles [3] could be identified by the high resolution and magnification of TEM together with professional experience.

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1U19CI000399-01 from Centers for Disease Control and Prevention. Its contents are solely the responsibility of the authors and do not necessarily represent the official views of CDC. PR was from Srinakharinwirot University. The authors would like to express their sincere thanks to Mekkla Thompson and Steve Durako, Westat, U.S.A. for their kind coordination, and also to Dr. Dianne Gross and Dr. Jacquerine Katz, CDC for their kind supervision of the project. There is no conflict of interest that might influence the outcome of this study.

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Figure legends

Figure 1. Electron micrographs of HPAI H5N1 isolates from humans: A/Thailand/676(NYK)/2005 (a); A/Laos/Nong khai 1/2007 (b); A/Thailand/1(KAN-1)/2004 (c, d); and A/Thailand/NBL 1/2006 (e, f). Note pleomorphic morphology of spherical and filamentous particles.

Figure 2. Electron micrographs of HPAI H5N1 isolates from animals: A/Chicken/Thailand/ICRC-VS143/2007 (a); A/Chicken/Thailand/ICRC-VS195/2008 (b); A/Chicken/Thailand/ICRC-VS213/2007 (c); and A/Duck/Thailand/ICRC-VS629/2008 strains (d).

Figure 3. Electron micrographs of human influenza viruses: A/New Caledonia/20/1999 (H1N1)-like virus (a, b) w; and A/Fujian/411/2002 (H3N2)-like virus (c, d). The multilayered-coil structure of a virus is demonstrated in spherical (a) and rod (d) particles.

Figure 4. Electron micrographs of LPAI isolates from animals: A/Aquatic bird/Hong Kong/D125/2002 (H1N1) (a); A/Duck/Shantou/1883/2001 (H3N8) (b); A/Duck/Jiangxi/6151/2003 (H5N3) (c); and A/Ostrich/Zimbabwe/222/1996 (H7N1) (d).

Figure 5. Electron micrographs of H5N1 infected MDCK cells: MDCK cell control (a); cytopathic change of H5N1 infected cell (b); H5N1 virus [A/Thailand/1(KAN-1)/2004] at entry (c); virus budding from infected cell (d); virus releasing from the infected cells (e); and free virions (f).

Figure 6. Amino acid sequence alignment of influenza M1 protein. The programs BioEdit version 7.0.9.0 were used to produce the alignment. Boxes indicate the positions of amino acid substitution.

Figure 7. Amino acid sequence alignment of influenza M2 protein. The programs BioEdit version 7.0.9.0 were used to produce the alignment. Boxes indicate the positions of amino acid substitution.

Table 1 The study viruses and GenBank accession numbers of influenza M1 and M2 amino acid sequences.

Virus name	Source*	Passage history**	GenBank accession No.	
			M1 protein	M2 protein
H5N1 influenza viruses*				
A/Thailand/1(KAN-1)/2004	MU	LLC-MK2/ MDCK 6	AAV35110	AAV35111
A/Thailand/676(NYK)/2005	MU	MDCK 5	ABC72651	ABC72652
A/Laos/Nong khai 1/2007	MU	MDCK 4	ACA64012	ACA64013
A/Thailand/NBL 1/2006	MU	MDCK 4	ACU46646	ACU46647
A/Chicken/Thailand/ICRC-VS143/2007	MU	MDCK 3/Egg 1	ABW89592	ABW89593
A/Chicken/Thailand/ICRC-VS195/2008	MU	Egg 4	ACE73587	ACE73588
A/Chicken/Thailand/ICRC-VS 213/2007	MU	MDCK 3/Egg 1	ACF36779	ACF36780
A/Duck/Thailand/ICRC-VS629/2008	MU	Egg 3		
A/Chicken/Thailand/ICRC-VS1069/2008	MU	Egg 2		
Human influenza viruses				
A/New Caledonia/20/99 (H1N1)-like virus (Siriraj07/2000)	MU	MDCK 8	ABF21304	ABF21305
A/Fujian/411/02 (H3N2)-like virus (Siriraj 03/2004)	MU	MDCK 8	-	ABB71834
Low pathogenic avian influenza (LPAI) viruses				
A/Aquatic bird/Hong Kong/D125/2002 (H1N1)	SJ	Egg 1/MDCK 3		
A/Duck/Shan tou/1883/2001 (H3N8)	SJ	Egg X/MDCK 2		
A/Duck/Jiangxi/6151/2003 (H5N3)	SJ	Egg 4	ABA12315	ABA12316
A/Ostrich/Zimbabwe/222/1996 (H7N1)	SJ	Egg 2		
Reference strains				
A/Udorn/1972(H3N2)	-	-	ABD79033	ABD79034
A/FW/1/1950(H1N1)	-	-	CAA30888	CAA30889
A/Port Chalmers/1/1973-mouse adapted(H3N2)	-	-	CAA30886	CAA30887

*MU= Mahidol University; SJ =St. Jude Children's Research Hospital

**All H5N1 viruses belong to clade 1 except A/Laos/Nong khai 1/07 which belongs to clade 2; Egg X = unknown passage in egg

Table 2 Morphological types of HPAI H5N1 and H1N1 viruses

Morphological type	Spherical forms	Rod and filamentous forms	Total
A/Thailand/1 (KAN-1) /2004 (H5N1)	79 (90.8%)	8 (9.2%)	87 (100%)
A/Thailand/676(NYK)/2005 (H5N1)	223 (95.7%)	10 (4.3%)	233 (100%)
A/Laos/ Nongkhai/1 /2007 (H5N1)	147 (83.5%)	29 (16.5%)	176 (100%)
A/New Caledonia/20/99 (H1N1)-like virus (Siriraj07/2000)	113 (90.6%)	12 (9.4%)	125 (100%)

Table 3. Panel of amino acid residues that might affect influenza virus morphology in M1 and M2 protein

Virus name*	Amino acid residues in*						
	M1				M2		
	41	95	204	218	71	72	73
A/Udorn/301/1972 (H3N2) [filament]	A	R	E	A/V	S	M	R
A/Victoria/3/1975(H3N2) [filament]	A	R	E	A			
A/WSN/1933 (H1N1) [spherical]	V	K	D	T			
A/PR8/1934 (H1N1)) [spherical]	V	K	E	T			
A/Port Chalmers/1/1973-mouse adapted (H3N2) [spherical]	V	R	E	A	S	M	R
A/Thailand/1(KAN-1)/2004 (H5N1)	A	R	E	T	S	M	R
A/Thailand/676(NYK)/2005 (H5N1)	A	R	E	T	S	M	R
A/Laos/Nong khai 1/2007 (H5N1)	A	R	E	T	S	M	R
A/Thailand/NBL 1/2006 (H5N1)	A	R	E	T	S	M	R
A/Chicken/Thailand/ICRC-VS143/2007 (H5N1)	A	R	E	T	S	M	R
A/Chicken/Thailand/ICRC-VS195/2008 (H5N1)	A	K	E	T	S	M	R
A/Chicken/Thailand/ICRC-VS 213/2007(H5N1)	A	R	E	T	S	M	R
A/New Caledonia/20/99 (H1N1)-like virus (Siriraj07/2000)	A	R	E	A	S	M	R
A/Duck/Jiangxi/6151/2003 (H5N3)	-	-	E	T	S	M	R

*Position of amino acid residues at M1: 41, 95, 218 (Elleman and Barclay. Virol 2004) and 204 (Bourmakina and Garcia-Sastre. J Gen Virol 2003); and at M2: 71,72 and 73 (Rossman JA, et al. J Virol 2010)

**Abbreviations of amino acids: A= Ala; D= Asp; E =Glu; I= Ile; K =Lys; M = Met; R= Arg; S= Ser; T= Thr; V= Val

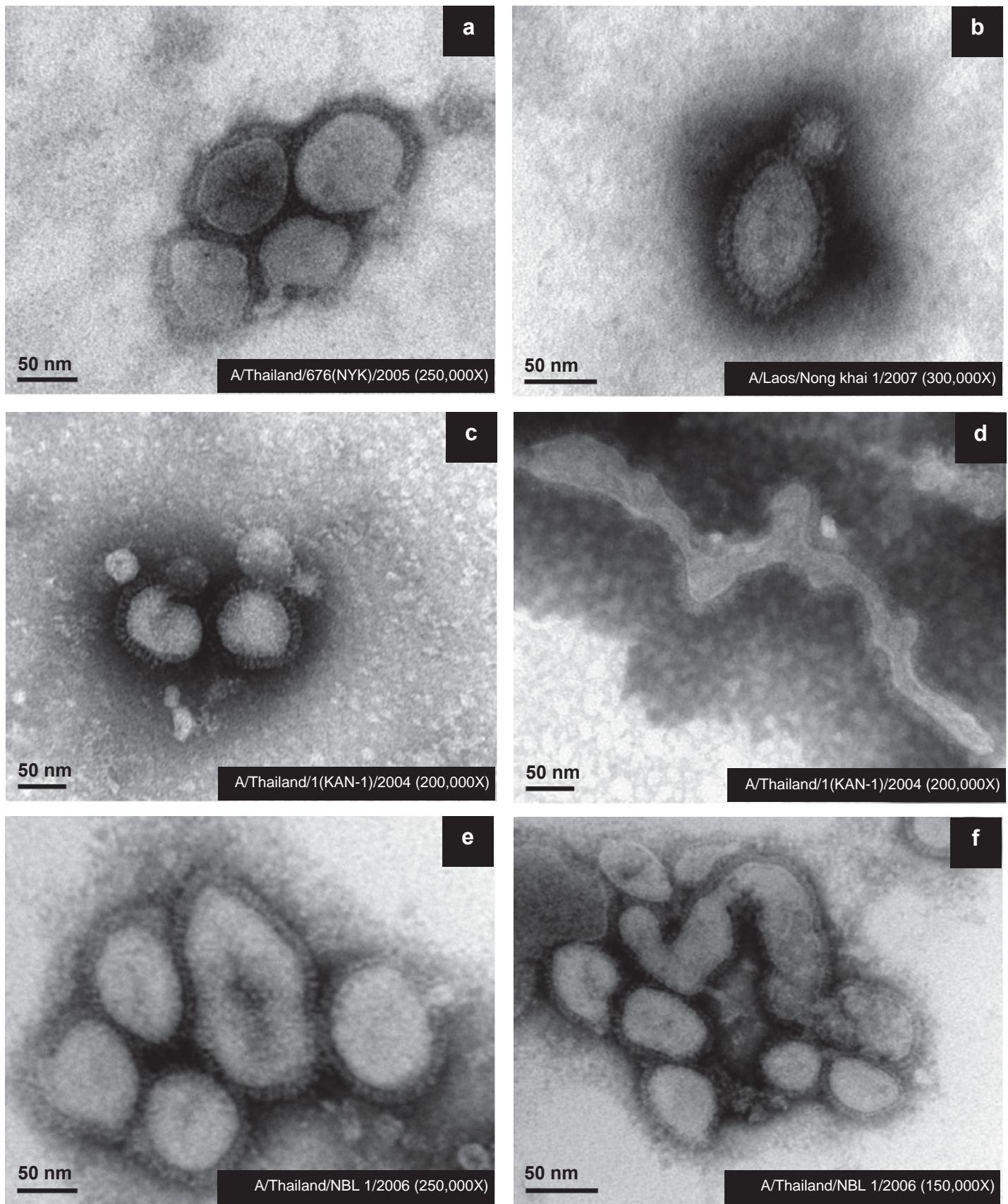


Figure 1.

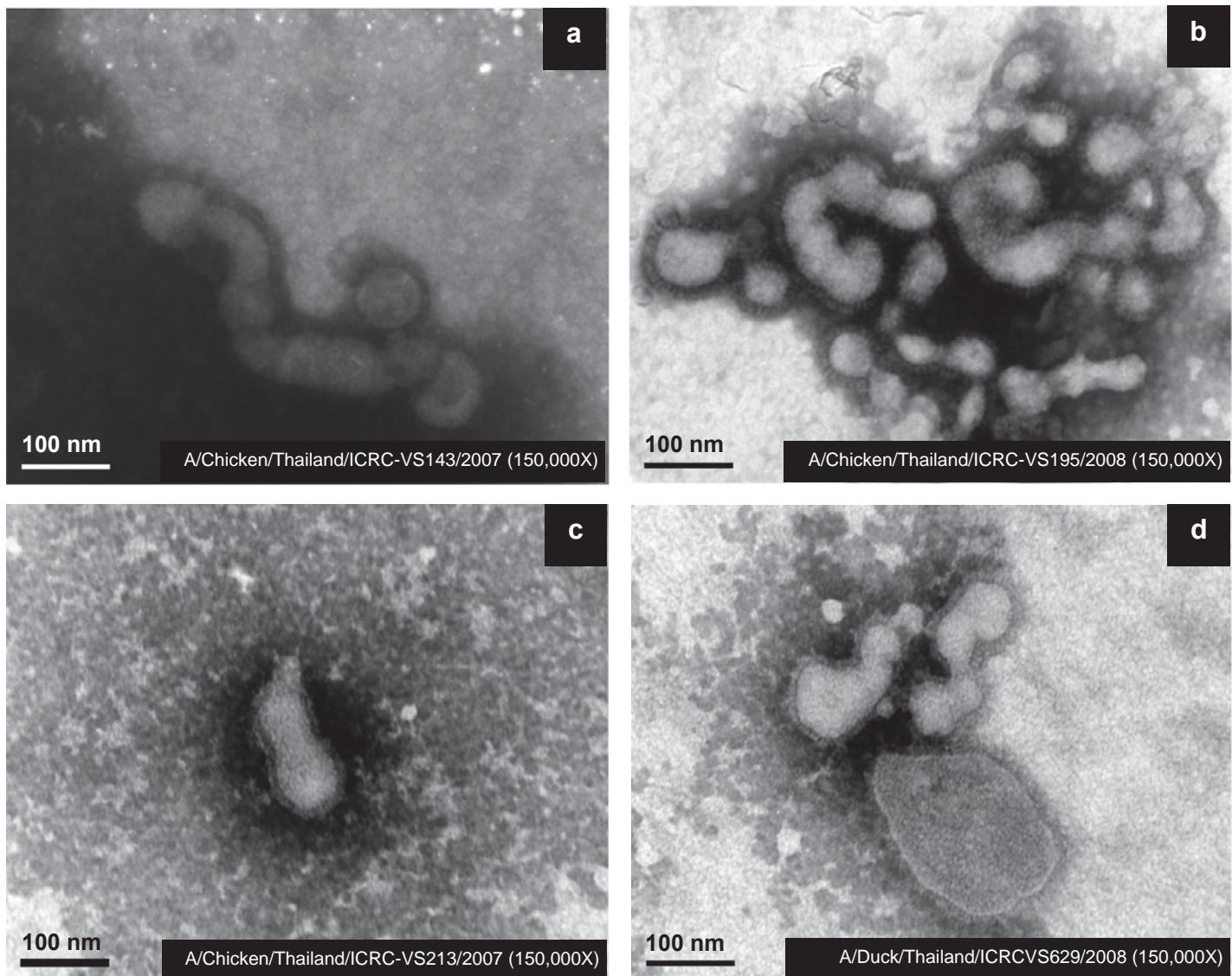


Figure 2.

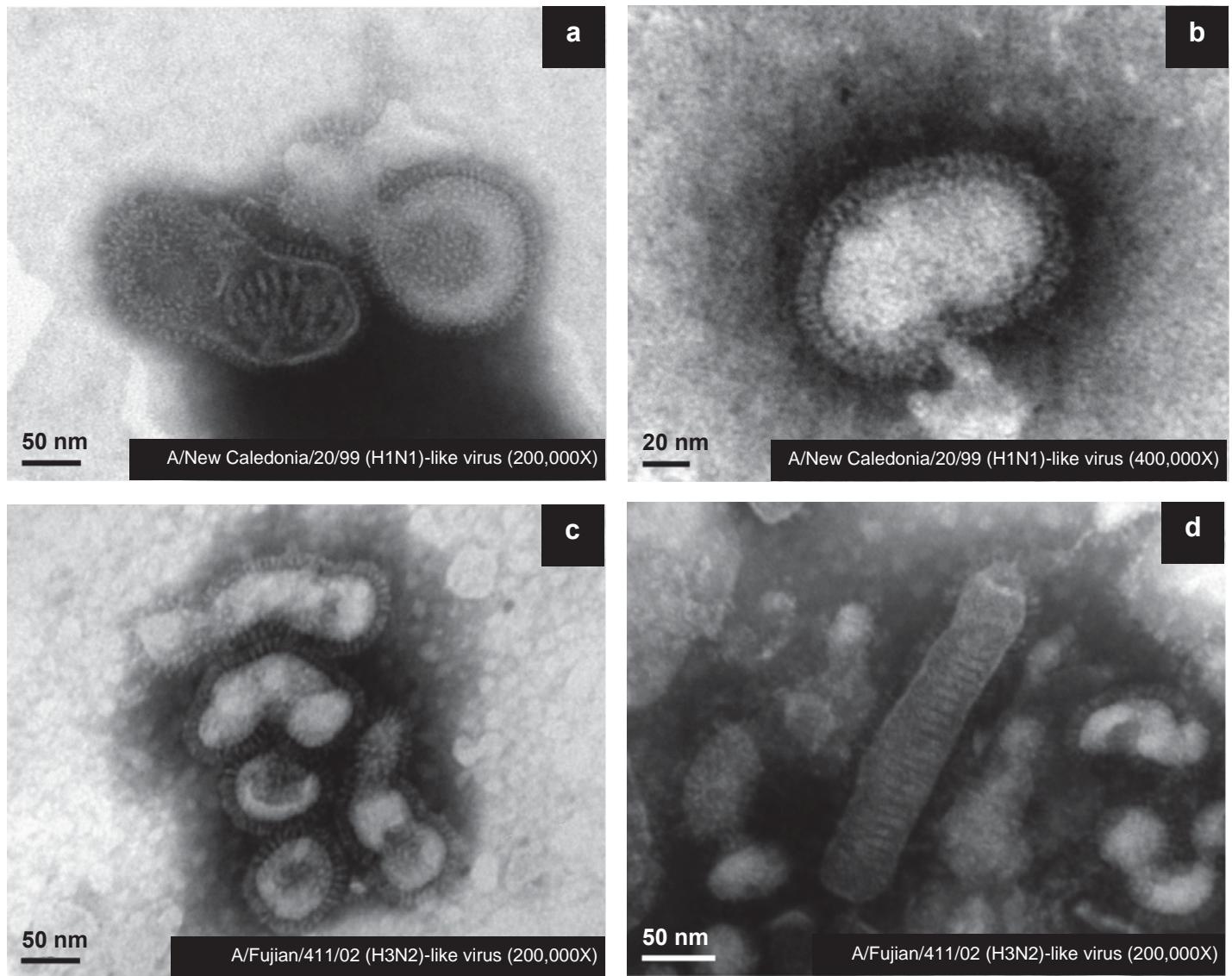


Figure 3.

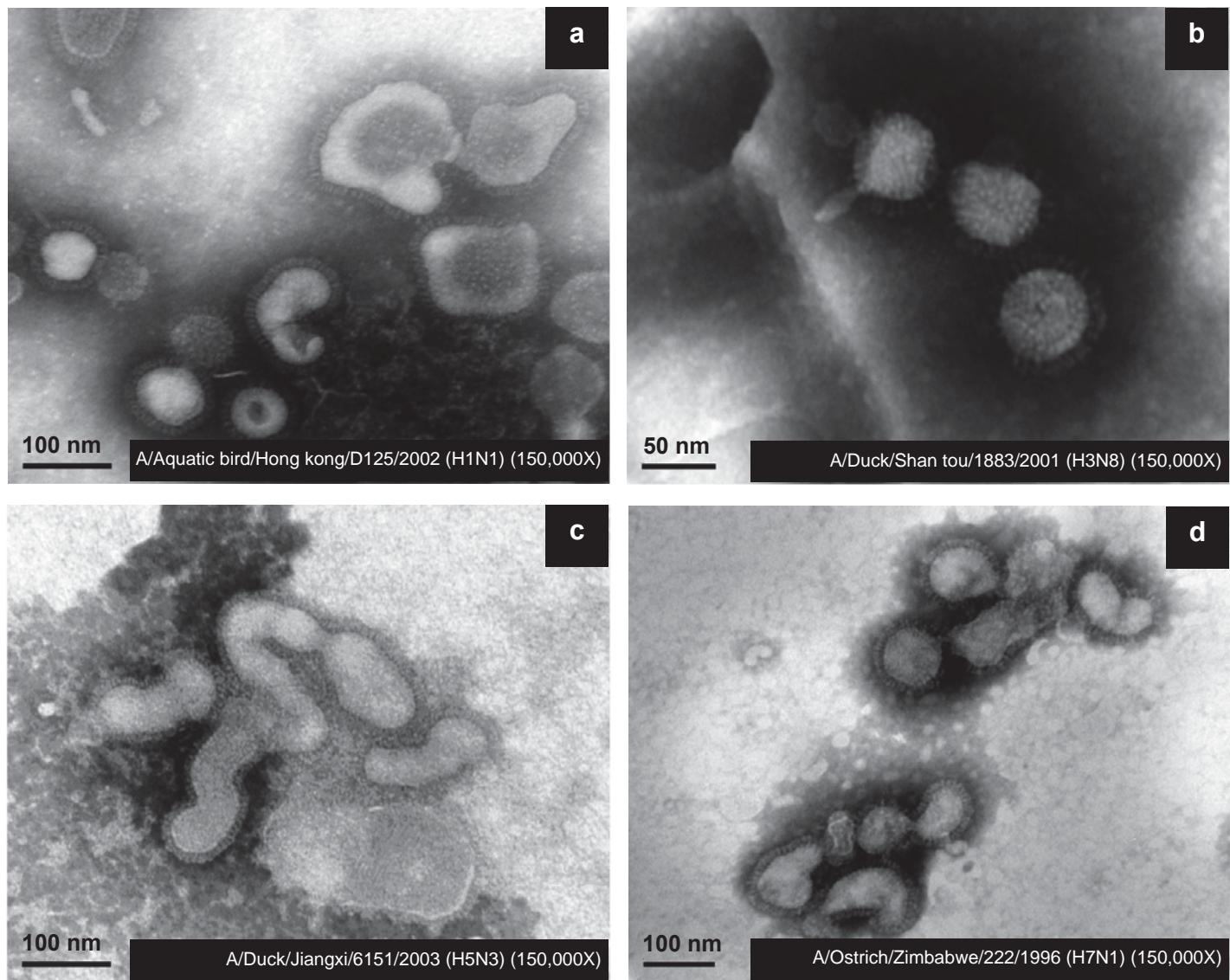


Figure 4.

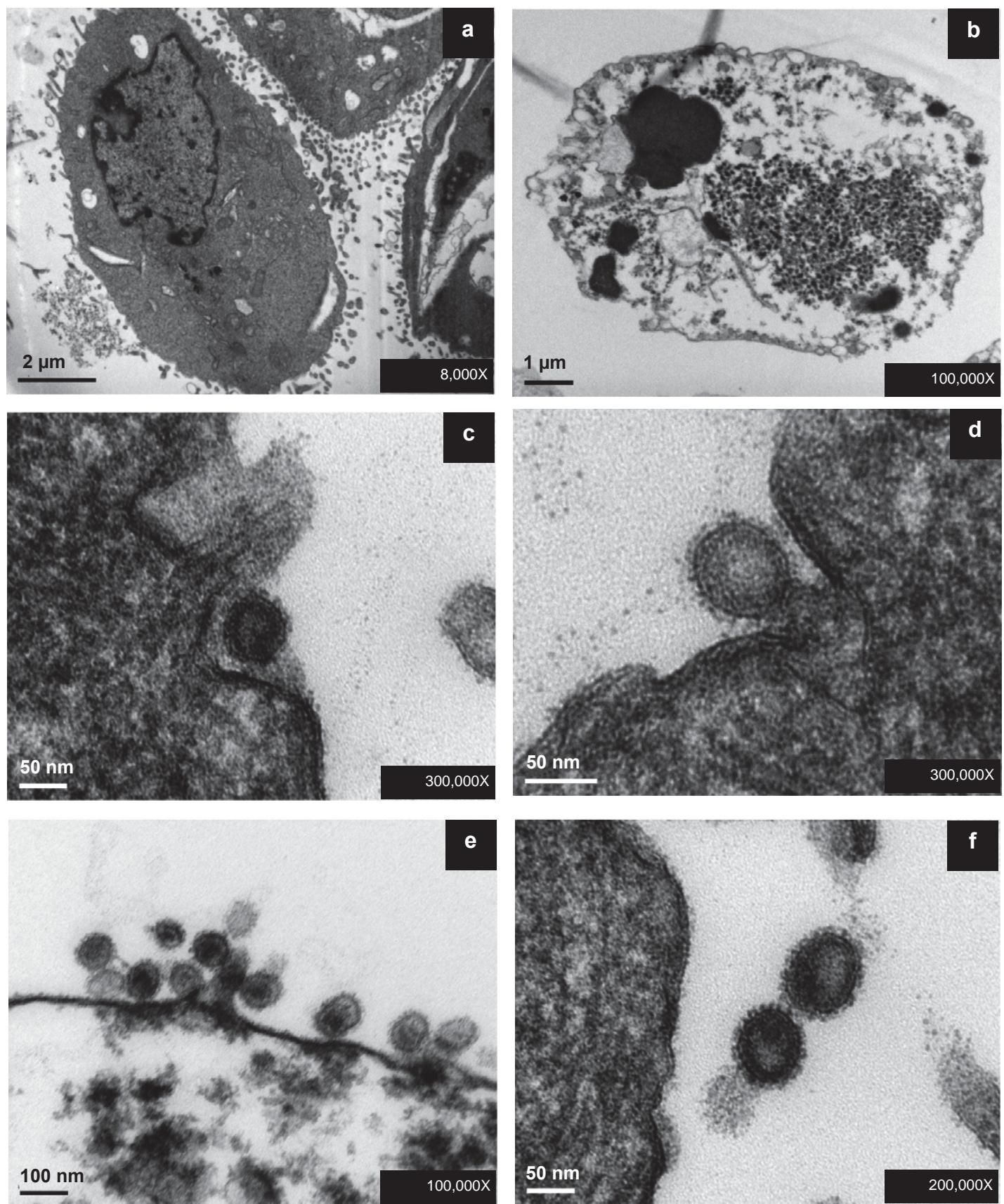
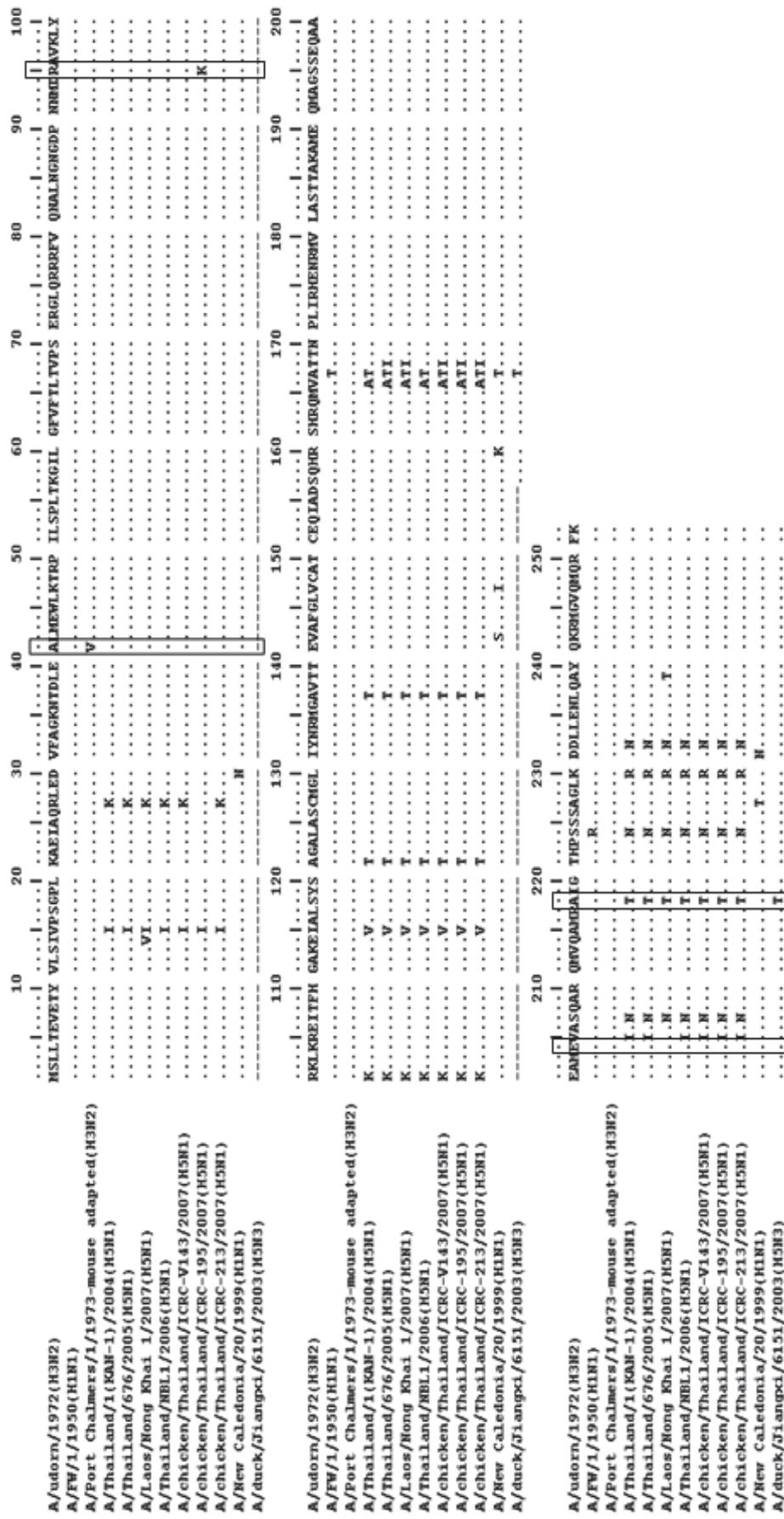
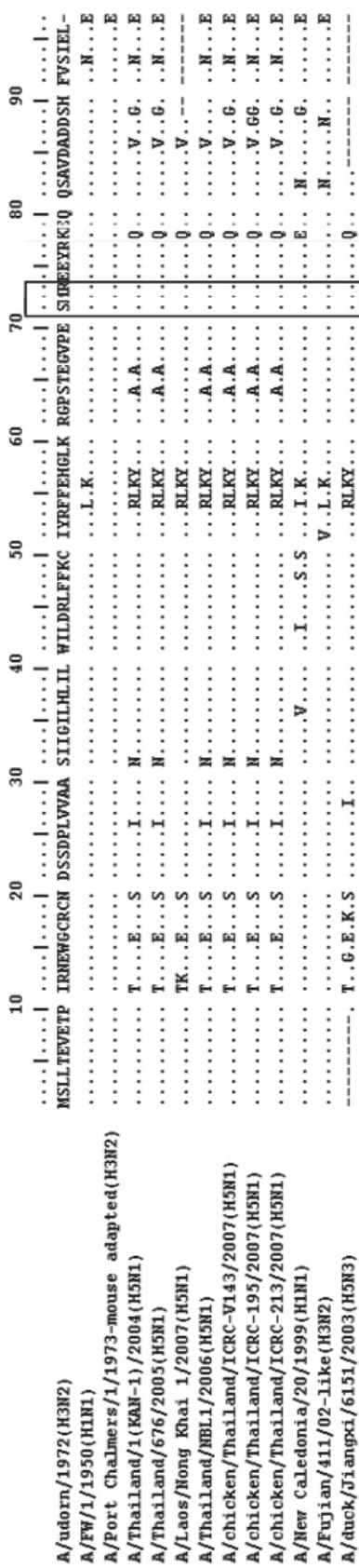


Figure 5.



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PLoS ONE

Satellite tracking on the flyways of Brown-headed gulls and their potential role in the spread of highly pathogenic avian influenza H5N1 virus

--Manuscript Draft--

Manuscript Number:	PONE-D-12-17685
Article Type:	Research Article
Full Title:	Satellite tracking on the flyways of Brown-headed gulls and their potential role in the spread of highly pathogenic avian influenza H5N1 virus
Short Title:	Potential role of Brown-headed gulls on AI spread
Corresponding Author:	Pilaipan Puthavathana Mahidol University Bangkoknoi, Bangkok THAILAND
Keywords:	Highly pathogenic avian influenza H5N1 virus; Brown-headed gulls; satellite telemetry; migratory flyways
Abstract:	Brown-headed gulls (<i>Larus brunnicephalus</i>), winter visitors of Thailand, were tracked by satellite telemetry during 2008-2011 for investigating their roles in the highly pathogenic avian influenza (HPAI) H5N1 virus spread. Eight gulls negative for influenza virus infection were marked with solar-powered satellite platform transmitters, their movements were monitored by the Argos satellite tracking system, and locations were mapped. Five gulls completed their migratory cycles, which spanned 7 countries (China, Bangladesh, India, Myanmar, Thailand, Cambodia, and Vietnam) affected by the HPAI H5N1 virus. Gulls migrated from their breeding grounds in China to stay overwinter in Thailand and Cambodia; while Bangladesh, India, Myanmar, and Vietnam were the places of stopovers during migration. Gulls traveled an average distance of about 2400 km between Thailand and China and spent 1-2 weeks on migration. Although AI surveillance among gulls was conducted at the study site, no AI virus was isolated and no H5N1 viral genome or specific antibody was detected in the 75 gulls tested, but 6.6% of blood samples were positive for pan-influenza A antibody. No AI outbreaks were reported in areas along flyways of gulls in Thailand during the study period. Distance and duration of migration, tolerability of the captive gulls to survive the HPAI H5N1 virus challenge and days at viral shedding after the virus challenging suggested that the Brown-headed gull could be a potential species for AI spread, especially among neighboring countries. This is the only study that demonstrated flyways which links between China and Southeast Asia, the epicenter of H5N1 AI outbreak.
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Cover letter

I would like to submit the article entitled “Satellite tracking on the flyways of Brown-headed gulls and their potential role in the spread of highly pathogenic avian influenza H5N1 virus” for publishing in PLoS ONE. Using satellite telemetry technique, we demonstrated the migratory routes of Brown-headed gulls that encompassed 7 countries affected by H5N1 avian influenza outbreaks: Thailand, Cambodia, Vietnam, Myanmar, India, Bangladesh, and China. It is also the only study that revealed the flyways which linked between China and Southeast Asian countries, the epizootic regions of H5N1 avian influenza. Distance and duration of migration, tolerability of the captive gulls to survive the HPAI H5N1 virus challenge and days at viral shedding after the virus challenging suggested that the Brown-headed gull may be a prime candidate species for AI spread, especially among nearby countries.

We are looking forward for your kind consideration.

Title

Satellite tracking on the flyways of Brown-headed gulls and their potential role in the spread of highly pathogenic avian influenza H5N1 virus

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Abstract

Brown-headed gulls (*Larus brunnicephalus*), winter visitors of Thailand, were tracked by satellite telemetry during 2008-2011 for investigating their roles in the highly pathogenic avian influenza (HPAI) H5N1 virus spread. Eight gulls negative for influenza virus infection were marked with solar-powered satellite platform transmitters, their movements were monitored by the Argos satellite tracking system, and locations were mapped. Five gulls completed their migratory cycles, which spanned 7 countries (China, Bangladesh, India, Myanmar, Thailand, Cambodia, and Vietnam) affected by the HPAI H5N1 virus. Gulls migrated from their breeding grounds in China to stay overwinter in Thailand and Cambodia; while Bangladesh, India, Myanmar, and Vietnam were the places of stopovers during migration. Gulls traveled an average distance of about 2400 km between Thailand and China and spent 1-2 weeks on migration. Although AI surveillance among gulls was conducted at the study site, no AI virus was isolated and no H5N1 viral genome or specific antibody was detected in the 75 gulls tested, but 6.6% of blood samples were positive for pan-influenza A antibody. No AI outbreaks were reported in areas along flyways of gulls in Thailand during the study period. Distance and duration of migration, tolerability of the captive gulls to survive the HPAI H5N1 virus challenge and days at viral shedding after the virus challenging suggested that the Brown-headed gull could be a potential species for AI spread, especially among neighboring countries. This is the only study that demonstrated flyways which links between China and Southeast Asia, the epicenter of H5N1 AI outbreak.

Introduction

To date, 16 hemagglutinin (H) and nine neuraminidase (N) subtypes of influenza A viruses have been identified. All the H and N subtypes have been isolated from wild aquatic birds, particularly from orders *Anseriformes* (ducks, geese, and swans) and *Charadriiformes* (gulls, terns, and shorebirds). Therefore, aquatic birds are widely accepted as the main natural reservoirs of influenza A viruses. Influenza viruses isolated from these birds are the mostly avirulent, low pathogenic avian influenza (LPAI) viruses [1-3].

Only some members of the H5 and H7 subtypes are highly pathogenic [1, 3]. The HPAI H5N1 virus was the first avian virus known to cross the species barriers to infect humans and was recognized as the most virulent subtype. In the first identified occurrence of H5N1 HPAI infection in humans in Hong Kong in 1997, 18 humans were infected and 6 died (fatality rate 33.3%) [4]. The HPAI H5N1 virus re-emerged in Hong Kong in 2001, twice in 2002, and subsequently in 2003. The viruses isolated in Hong Kong before 2002 were pathogenic in gallinaceous birds but not domestic or wild waterfowl. Death of aquatic birds from the HPAI H5N1 virus was first recognized in the 2002 outbreak [5]. The resurging HPAI H5N1 strain is highly virulent in both avian and humans, with a fatality rate of approximately 60% being reported in infected humans [6, 7]. In January 2004, an outbreak of H5N1 HPAI was reported in poultry and humans in Thailand. The virus initially isolated in Thailand belonged to clade 1; while clade 2.3.4 virus was introduced into northeast Thailand in 2006 [8, 9]. However, all of the virus isolates in central Thailand still remained in clade 1. There were 25 cases reported in humans, with 17 deaths (fatality rate 68%). No cases of human infection have occurred since August 2006, but there were some AIV outbreaks in poultry until 2008 [6, 7].

Based on virological data and satellite telemetry studies, many groups of investigators have linked migratory birds with H5N1 HPAI spread [10-17]. The first evidence that supported this claim was an outbreak of genotype z, clade 2 H5N1 viruses that occurred in wild bird populations at Qinghai Lake, western China during late April until June 2005 causing death of more than six thousand birds. The main victim infected were Bar-headed geese (*Anser indicus*) which accounted for more than 50% of the deaths, whereas Brown-headed gulls were the second most species affected [10, 11]. Subsequently, H5N1 HPAI viruses similar to those in the Qinghai area were also isolated in other Asian countries, Europe, the Middle East and some African countries [3]. H5N1 viruses were likely transmitted along the flyways of birds that shared habitats, wintering sites, breeding areas or

1 stopovers [3, 15]. In addition, the results from surveillance for H5N1 HPAI in migratory and
2 wildlife birds in 14 provinces of China from 2004 to 2007 showed that highest infection rates
3 (4.37%) occurred in mallards; while it was 2.39% for Brown-headed gulls [18]. Birds in the
4 Qinghai province had the highest rates of infection, possibly because there are many lake
5 areas in Qinghai, which are natural habitats and breeding ground of numerous bird species
6 [11, 18]. Investigation of the outbreaks and phylogenetic analysis suggested that the
7 migrating birds in Qinghai got infected with H5N1 HPAI viruses through spillover from
8 domestic poultry [11].
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10 Satellite telemetry has been conducted by several groups of investigators to study the
11 potential role of migrants in H5N1 HPAI spread [13-16]. With this technique, flyways of
12 migrants can be illustrated with high accuracy; and the linkage between bird locations and
13 geographical areas of AI outbreaks can be determined. Spatial analysis of distance of
14 migration, duration of asymptomatic infection and duration of viral shedding strongly
15 supported potential role of migratory birds on H5N1 HPAI spread. However, those satellite
16 telemetry studies explored the flyways which spanned Africa, Europe and East Asia, while
17 none involved flyways to Southeast Asia which was the epicenter of the outbreaks.
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19 The Brown-headed gull (*Larus brunnicephalus*, Family *Laridae*) is the most common
20 bird species to annually visit Thailand, staying from October to May [19-22]. According to
21 the Department of National Parks, Wildlife and Plant Conservation of Thailand, there are 2
22 large flocks of Brown-headed gulls in Thailand. The larger flock consists of approximately
23 5,000 birds foraging around the inner gulf of Thailand mainly at mangrove mudflats in the
24 Bang Poo Rest and Rehabilitation Center of the Royal Thai Army, Samut Prakan province
25 (Figure 1). Our group at the Faculty of Veterinary Science, Mahidol University isolated
26 HPAI H5N1 virus from 4 of 153 (2.6 %) apparently healthy birds in this flock between 2005
27 and 2008 (unpublished data), which indicates that this flock may play a role in the spread of
28 the HPAI virus along its flyways. However, the entire migratory route of Brown headed gulls
29 remains unknown. In order to determine the potential role of this bird species on AI spread
30 along its migratory path, satellite telemetry was employed to track the flyways of Brown-
31 headed gulls during 2008-2011. We searched for linkage between bird locations and
32 occurrence of reported H5N1 HPAI outbreak while the birds overwintered in Thailand. Status
33 of H5N1 HPAI infection in the flock was also determined. Gulls in captivity were challenged
34 with H5N1 HPAI virus in order to determine their tolerability to virus infection. The result
35 demonstrated that the infected gulls with virus shedding survived long enough to spread the
36 virus along their migratory routes.
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Results

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Migratory routes and flight distances of Brown headed gulls

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18 Brown-headed gulls employed in the satellite telemetry study were captured
21 from the flock at the Bang Poo study site, Samut Prakarn province, Thailand (Figure 1).
22 They were of adult age, negative for influenza virus infection (see material and method),
23 physiological healthy and energetic. Tagging the birds with satellite transmitters was
24 performed in two consecutive years. The first Brown-headed gull was tagged in March 2008;
25 and the other 7 gulls were tagged between February and March 2009. Flyways of these gulls
26 were monitored until the satellite signals were lost. Demographic data and duration of
27 tracking of each bird are shown in Table 1. Two gulls (I.Ds. 74795 and 88216) completed
28 one migratory cycle, 3 gulls (I.Ds. 88215, 91416 and 91417) completed 2 cycles (Table 2);
29 while 3 gulls (I.Ds. 88217, 88218 and 91418) were lost in Thailand within one month after
30 tagging (Table 1). Flyways of the 5 marked gulls including their habitats in different
31 countries are as shown in Tables 3, and individual flyway of each gull was described in
32 details in Supplementary data.

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30 The mean flying distance of the tagged gulls during migration was 230 km/day (167-
40 295 km/day at 95% C.I.); whereas the local movements within a given site ranged from 1 to
41 28 km/day (1-12 km/day at 95% C.I.) (Table 2). In general, gulls traveled an estimated
42 migratory distance of 2,400 km between China and Thailand with duration of migration of
43 approximately 12 days in average (7-23 days at 95% C.I.). Although all gulls began their
44 flight from the same study site in Thailand, their destinations in China were different. They
45 also arrived and left Thailand at different time points. These results indicated that these
46 Brown-headed gulls belong to different flocks while they were in China, and just gathered
47 together in the same overwintering site in Thailand. Migratory routes of the 5 tracked gulls
48 spanned 7 countries- Thailand, Myanmar, India, China, Bangladesh, Vietnam and Cambodia
49 (Figure 2). Almost all tracked gulls, except gull I.D. 88216, stayed in Cambodia for
50 approximately 30-40 days in a migratory season; and only the gull I.D. 91417 had traveled
51 further to Vietnam. If seasonal habitat is defined as the places where gulls stayed for longer
52 than 1 month, those places were mainly located in three countries: China, Thailand and
53 Cambodia; while Myanmar, India, Bangladesh and Vietnam were considered to be the
54 stopover countries. Moreover, the stopover places of individual gull in each country were
55 different. They could be West Bengal or Assam in India, the Gulf of Martaban, Ayeyarwaddy
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1 or Rakhine in Myanmar and Kien Giang in Vietnam. In the three gulls that were tracked for
2 over two migratory cycles, the migratory routes were only slightly different between years.
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Ecologically, seasonal habitats were always along the coast, wetlands or inland lakes
(Figure 3). Birds stayed over the cold season for 5-6 months in Thailand and stayed in their
breeding places in China for another 5-6 months. Duration that gulls stayed in each country is
shown in Figure 4. Seasonal habitats in Thailand were mainly in three provinces: Samut
Prakan, Samut Sakhon and Samut Songkhram, all of which were situated along the inner gulf
of Thailand. In China, the breeding habitats were in Tibet, Qinghai and Xinjiang. However,
gulls also spent their times at a third habitat in Siem Reap, Cambodia around Tonle Sap, the
largest fresh water lake in Southeast Asia [23]. Although this flock of gulls stayed through
winter along the inner gulf of Thailand, no AIV outbreak was reported in that area through
the extensive national surveillance system.
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Prevalence of avian influenza virus infection in gulls

A total of 75 birds were captured from the Bang Poo study site during 2008 to 2010.
Throat and cloacal swabs as well as blood samples were collected for the investigation of
influenza virus infection. No influenza virus was isolated and the viral genome was not
detected in cloacal and throat swab samples. The H5N1 antibody was not detected in the HI
and MicroNT assays. However, 6.6% of samples were positive for the pan-influenza A
antibody by ELISA.
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Virus challenge assay

Brown headed gulls kept in captivity were inoculated with HPAI H5N1virus in order
to explore whether the infected birds could survive the infection, and therefore might be able
to carry on migratory activity. Group of 3 gulls was inoculated with the H5N1 virus at the
inoculum dose of 10, 10³ or 10⁴ tissue culture infective dose 50 (TCID50) per head (Table 4).
The result demonstrated that all gulls inoculated with the high inoculum dose of 10³ or 10⁴
TCID50 began shedding the virus in cloacae and trachea after 1-2 days post inoculation (dpi.).
These infected birds developed clinical symptoms, but they could tolerate the infection for 4-
6 days before death. One of the three gulls inoculated with 10 TCID50 could shed the virus at
3 dpi. and died on day 7. The two gulls that survived the infection neither shed the virus nor
developed any clinical symptom, of which one of them underwent seroconversion.
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Discussions

The worldwide resurgence of H5N1 HPAI since 2003 has resulted in massive deaths in poultry and human deaths, especially in East and Southeast Asian countries. The global spread of H5N1 HPAI is likely mediated by migratory birds, trade in poultry, and possibly, trade in wild birds [24]. Integrated data and phylogenetic analyses of virus isolates obtained from different geographical locations suggest that the H5N1 spread throughout Asian and African countries involved both migratory birds and trade in poultry, whereas the spread in European countries involved migratory birds [24]. Human population, duck population (particularly, free grazing ducks) and intensity of the rice crop can increase the risk of propagation of H5N1 HPAI in Southeast Asian countries [25-26]. Density of the duck population can be a major risk factor for virus dispersal, especially when viral shedding is observed in asymptomatic infected ducks [27]. There is a close relationship between the density of free grazing ducks and the double or triple cultivation of rice in Thailand, because the falling rice grains left in the fields after harvesting are the source of low-cost food for ducks. Movements of free grazing ducks to post-harvested rice fields has been suggested as the major source of virus spread in Thailand during the initial waves of HPAI outbreaks. Nevertheless, duck movement has been later on prohibited. Natural infection in the other animal species such as tigers and leopards [28], cats [29], and dog [30] was mainly caused by ingestion of infected carcasses or chicken meat. However, most cases of H5N1 HPAI infection in humans in Thailand were mainly caused by exposure to sick or dead chicken.

It has been very difficult to trace how the H5N1 HPAI virus was introduced into Thailand because of the delay between the initial cases and the subsequent spread of the virus throughout of the country [31]. It has been hypothesized that the virus might have been introduced via migratory birds. HPAI usually occurs during low temperature months (October to February) which coincide with the time of arrival of wintering migratory birds [31]. In our study, Brown-headed gulls seem to be a prime candidate species for spreading avian influenza. They are long distant migrant and their flyways involved 7 countries, all of which had been affected by the H5N1 HPAI. Nevertheless, on the basis of an inhabiting time of 1 month or longer, only China, Thailand and Cambodia, were considered to be the gulls' seasonal habitats, whereas Myanmar, Bangladesh, India and Vietnam were stopover places. In our study, Brown-headed gulls spent their breeding time in the lake areas of Tibet, Qinghai and Xinjiang. All of these breeding sites are cold and high altitude lakes of varying salinity

1 [21]. They migrated to warmer places and stayed overwinter in mudflats along the inner gulf
2 of Thailand and Tonle Sap Lake areas in Cambodia.
3
4 Our study illustrates complete migratory cycles of Brown-headed gulls. Gulls in this
5 flock arrived and left Thailand asynchronously; their destinations on migration to China were
6 different, suggesting that they belonged to different flocks while in China. Gulls from these
7 flocks gathered together during the winter time in Thailand. The first group of gulls reached
8 the Bang Poo study site in October and the last group left in May. The migration distance of
9 about 2400 km between Thailand and China and the migration time at range of 5-23 days in
10 our tracked Brown-headed gulls were more or less similar to those previously reported in
11 wildfowl in which the movements of up to 2,900 km in 5-15 days were within the timeframe
12 that was compatible with the preclinical symptom and virus dispersal [16].
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14 We looked for a linkage between the virus from the Qinghai outbreaks and the H5N1
15 HPAI viruses isolated from Brown-headed gulls in Thailand in 2005 and 2008, but no linkage
16 was found. Phylogenetic analysis showed that the viruses isolated from birds in Qinghai in
17 2005 belonged to clade 2.2 [10, 11], whereas the viruses isolated from gulls in Thailand
18 between 2005 and 2008 belonged to clade 1 (unpublished data). Nevertheless, phylogenetic
19 analysis showed a virological linkage between countries situated in the migratory corridor of
20 this flock of Brown-headed gulls. The viruses causing outbreaks in Bangladesh belonged to
21 the Qinghai like-lineage [32]; and the viruses causing the first epidemic wave in Thailand,
22 Cambodia and Vietnam belonged to clade 1 [8, 33]. The clade 1 virus was originally isolated
23 in Yunnan, southern China in 2002 and 2003, and probably spread to Vietnam by poultry
24 trade across the shared border that is 600 km long [34]. Thereafter, the viruses spread from
25 the North to the South of Vietnam. Interestingly, the H5N1 virus isolates in Thailand are
26 closely related to the isolates in Vietnam [6]. It is also claimed that the clade 1 virus spread
27 from Thailand to Cambodia [34]. Nevertheless, it remains unknown for how the clade 1 virus
28 was introduced into Thailand. The firstly H5N1 HPAI outbreaks in Thailand occurred in
29 central part, not at the border of the country. Interestingly, Vietnam, Thailand and Cambodia
30 reported the first outbreak in the country at about the same period of time in 2004, i.e., on
31 January 23 for Thailand, on January 8 for Vietnam, and January 24 for Cambodia [6].
32 Although there might be a lag time period for outbreak identification and report, it is implied
33 that the H5N1 HPAI outbreaks occurred in these countries more or less about the same time.
34 In addition, the time at occurrence of outbreaks in these 3 countries coincides with the
35 overwintering period of Brown headed gulls.
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1 Our study showed that Brown headed gulls kept in captivity were vulnerable to HPAI
2 H5N1 virus. Nevertheless, gulls infected with the inoculum dose of 10^4 TCID₅₀ could survive
3 for 4 days and those inoculated with 10^3 TCID₅₀ could survive for 5-6 days, and with viral
4 shedding from trachea and cloacae which began after 1 dpi. In addition, a gull infected with
5 the low inoculum dose of 10 TCID₅₀ could survive for 7 days with viral shedding which
6 began at 3 dpi. The results implies that the infected gulls may be able to complete migratory
7 route between China and Thailand, or at least, at a shorter distant between nearby countries
8 with virus spread along their flyways.
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10 Although cross border trade may be the major route of H5N1 HPAI virus spread in
11 Asian countries, it cannot be excluded that migratory birds might also play an additional role
12 in the spread of the virus across countries or domestically along its flyways. In spite of the
13 fact that Brown-headed gulls appear to be an ideal candidate for spreading the virus, no
14 H5N1 virus including other influenza subtypes could be isolated, and no H5N1 antibody
15 could be detected in our flock of Brown-headed gulls during the study period. Only anti-
16 influenza antibody was detected by ELISA, indicating previous infection with some subtype
17 of AIVs in these birds. Besides waterfowl, gulls and shorebirds also maintain an influenza
18 gene pool in their species. Predominant AIV subtypes found in gulls are H13 and H16 [2].
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20 The inability to detect the H5N1 virus, however, may simply be due to our small
21 sample size collected from gulls as all migratory birds in Thailand are protected by law; and
22 it may be also due to the absence of HPAI outbreaks during our investigation period of 2008-
23 2011. There was only one outbreak occurred in poultry in Nakhon Sawan and Phichit
24 provinces (upper part of central Thailand) in January 2008, and one in backyard poultry in
25 Sukhothai province (lower north of the country in November 2008). No AI outbreak has been
26 reported since then [6]. Nevertheless, this study is the only flyway monitoring that
27 encompassed the epicenter of H5N1 HPAI in Southeast Asia to date; and it is also the longest
28 flyway monitoring covering complete migratory seasons which has never been reported
29 before.
30

31 **Methods**

32 **Approvals and permissions**

33 This study was approved by the Animal Care and Use Committee of the Faculty of
34 Veterinary Science, Mahidol University, and compiled with the Statement of Compliance
35 (Assurance) with Standards for Humane Care and Use of Laboratory Animals of the Office of
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1 Laboratory Animal Welfare (OLAW No. A5731-01), U.S. Department of Health and Human
2 Services. The study was carried out with permission of the Department of National Parks,
3 Wildlife and Plant Conservation, Thailand, in accordance with the Wildlife Conservation Act
4 of Thailand.
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9 **Study site**
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11 This study was conducted at Bang Poo, a recreation area located in the Samut Prakan
12 province, Thailand, 37 km east of Bangkok. This 63 km² coastal area owned by the Royal
13 Thai Army is a part of the inner gulf of Thailand and comprised mangrove and large mudflat
14 habitats. Gulls gather together here to feed on an abundance number of clams that embedded
15 in the muddy beaches. Bang Poo is an Important Bird Areas (IBA) with more than 135 water
16 bird species being recorded, including 7 species of ducks, 50 species of waders, and 18
17 species of terns and gulls. Thirteen globally threatened species have been recorded in this
18 area [22]. The Brown-headed gull is an important species in this wetland IBA [19-22].
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29 **Study birds**
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31 The Brown headed gull (*Larus brunnicephalus*) is a waterfowl belonging to the
32 family *Laridae*. The common name for this species comes from the presence of brown color
33 on the head of adult birds. These gulls normally feed on small fishes and crabs; nevertheless,
34 they can adapt to a variety of available foods.
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38 **Bird capture and specimen collection**
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40 All migratory birds in Thailand are protected animals by law. Therefore, bird capture
41 was performed by the authorized persons from the Department of National Park, Wildlife and
42 Plant Conservation. Gulls were attracted by fried pork rind, and captured by a hand net.
43 Approximately 10-20 birds were captured in each trap. Tracheal and cloacal swabs as well as
44 blood samples were collected for laboratory investigations to determine the prevalence of
45 AIV infection. The captured birds were also physically examined for general health
46 conditions (body weight, body size) and the healthy, energetic adults that were negative for
47 influenza viral infection, as screened by rapid antigen detection kit (Rapid H5 AIV Ag Test,
48 Bionote, Inc., Gyeonggi-Do, South Korea) at the study site, were chosen for satellite
49 telemetry tracking. Results of samples negative for the virus infection by antigen detection
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were confirmed at the Virology Laboratory at the Faculty of Veterinary Science, Mahidol University.

Satellite telemetry technique and data analysis

Eight gulls negative for influenza antigen were chosen for the satellite telemetry study. The first gull was marked in March 2008 and the second lot of 7 gulls was marked during February and March 2009. Each bird was tagged with a ring band and fitted with a solar powered satellite platform transmitters (solar PTT-100, Microwave Telemetry, Inc., Columbia, MD) on its back by using Teflon harnesses (Bally Ribbon Mills, Bally, PA). A transmitter weighing 12 g was used for the first gull and transmitters weighing 9.5 g were used for remaining 7 gulls. On average, the transmitter packages weighed approximately 1.98 % of the bird's body weight. After being marked, birds were released, usually within 1 hour, to a place close to the capture sites.

The solar PTT-100 transmitter operates at frequency of 401.650 MHz; and flyway data from birds can be retrieved every 2 days. The standard duty cycle of the solar PTTs was set at 10 hours on and 48 off for recharging the batteries. Signals were processed and the data was provided by Argos CLS (Toulouse, France). Bird locations were analyzed and mapped with Google Earth Program version 5.1(Google, Mountain View, CA, USA) with a precision of <1500 m. When the transmitter signal from any tracked bird was lost, the observation was still going on for at least one more month before concluding its disappearance.

Detection of H5N1 HPAI infection in study birds

Prevalence of influenza virus in this flock of gulls as well as the confirmation of the negative results for influenza antigen detection was determined by real time reverse transcription-polymerase chain reaction (RT-PCR) for viral genome detection and the virus isolation from throat and cloacal swab samples. Serological techniques for detection of H5 antibody were performed by hemagglutination-inhibition (HI) assay and microneutralization (microNT) assay; and that for detection of pan-influenza antibody was performed by ELISA.

Real time RT-PCR: Protocols from the Organization des Epizooties (http://www.oie.int/fr/normes/mmanual/2008/pdf/2.03.04_AI.pdf) and/or those established by the U.S. Centers for Disease Control and Prevention (CDC) were used for viral genome detection and subtype identification. Throat and cloacal swabs from each bird were tested separately.

Virus isolation method: Cloacal and throat swab specimens were separately inoculated in duplicate in embryonated eggs and a Madin Darby canine kidney (MDCK) cell monolayer. Amniotic/allantoic fluid and culture supernatant were screened for presence of influenza virus by hemagglutination with 0.5% goose red blood cells before subjected to subtype identification by real time RT-PCR.

Hemagglutination-inhibition (HI) assay: The protocol for H5N1 antibody detection was based on the method given for avian influenza in the World Health Organization (WHO) manual on animal influenza diagnosis and surveillance [35] in which 0.5% goose erythrocytes were chosen as the indicator as previously described by Louisirirotchanakul et al. [36]. The assay was performed in micro-titer V plate in duplicate wells using replicating A/chicken/Thailand/ICRC-V143/07(H5N1) (accession No. EU233413-EU233420) at a final concentration of 4 hemagglutination units/25 µl as the test antigen. Titer was defined as the highest serum dilution that causes complete hemagglutination of the test erythrocytes.

Microneutralization assay: H5N1 antibody was detected by ELISA based MicroNT assay using the protocols as described in the WHO manual for avian influenza [35], and modified by Louisirirotchanakul et al. [36] in which MDCK cell suspension was replaced with MDCK cell monolayer. The assay was performed in micro-titer plates in duplicate. A/chicken/Thailand/ICRC-V143/07(H5N1) at a final concentration of 100 TCID50 was used as the test virus. Viral nucleoprotein synthesized was detected by a mouse monoclonal antibody (Chemicon International, Inc., Tecumala, CA) as the primary antibody together with horse radish peroxidase-conjugated rabbit anti-mouse Ig (Dako Cytomation, Denmark) as the secondary antibody. Titer was defined as the highest serum dilution that causes a 50% reduction in the amount of viral nucleoprotein synthesized.

ELISA: Sera were assayed for antibody to influenza A viruses (pan-influenza A subtypes), using the type A influenza multi species antibody test kit (AI MSp) (BioChek, London, UK) according to the manufacturer's instructions.

Virus challenge test

To study whether infected birds could survive the infection and still be able to carry on migratory activity, wild birds were trapped and kept in captivity for a week prior to viral inoculation. These gulls were negative for influenza virus infection. Each bird was intranasal inoculated with 100 μ l of A/Brown-head gull/Thailand/vsmu-4/2008(H5N1) (accession No. EU676322-EU67329) at an inoculum dose of 10, 10³ and 10⁴ tissue culture infective dose 50

(TCID₅₀). Inoculated birds were kept in an isolator in an animal biosafety laboratory level 3, Faculty of Veterinary Science, Mahidol University, and observed daily for signs, symptoms and death until one month after inoculation.

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Figure legends

35 **Figure 1. Flock of Brown-headed gulls at the study site, and a gull fitted
36 with satellite transmitter.**

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40 **Figure 2. Migratory routes of all study gulls.** (A) Gull I.D. 74795; (B) Gull I.D.
41 88215; (C) Gull I.D. 88216; (D) Gull I.D. 91416; and (E) Gull I.D. 91417. Data
42 accessed on August 6, 2011, Co-ordinates (Main figure and A-E): 21.98°N
43 95.28°E.
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49 **Figure 3. Ecological characteristics of habitats in each country involving
50 the inland lakes and coastal areas.** Data accessed on August 6, 2011 Co-
51 ordinates: (A) 36.97°N 89.23°E; (B) 35.23°N 91.11°E; (C) 31.10°N 90.85°E; (D)
52 13.58°N 100.45°E; (E) 12.95°N 103.92°E; and (F) 9.56°N 105.18°E.
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57 **Figure 4. Duration of stay of each gull in various countries.**
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4 **Table 1.** Demographic data of the tracked gulls.
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Bird I.D.	Sex	Body weight (g)	Marking date	Time at signal loss from monitoring	Place at signal loss	Tracking period
74795	ND	475	Mar 25, 2008	Dec 2008	Cambodia	9 mos.
88215	Male	650	Mar 26, 2009	Mar 2011	Thailand	2 yrs.
88216	Female	600	Mar 13, 2009	May 2010	Tibet	1 yr, 2 mos.
88217	ND	450	Feb 17, 2009	Mar 2009	Thailand	<1 mo.
88218	Female	500	Mar 26, 2009	Apr 2009	Thailand	<1 mo.
91416	ND	440	Feb 17, 2009	Jan 2011	Cambodia	1 yr, 11 mos.
91417	ND	430	Feb 17, 2009	Nov 2010	Thailand	1 yr, 9 mos.
91418	ND	400	Feb 17, 2009	Mar 2009	Thailand	<1 mo.

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25 ND = Not determined
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Table 2. Flying distances of the tracked gulls.

Bird I.D.	Year	Total distance on migration (km)		Duration of migration (days)			Average distance at habitat per day (km)	
		Thailand to China	China to Thailand	Thailand to China	China to Thailand	Average flying distance on migration per day (km)	China	Thailand
74795	2008	2,419	2,747	7	9	326	26	28
88215	2009	3,167	2,372	12	16	201	2	7
	2010	2,223	2,404	9	21	174	9	6
	2011	Lost						6
88216	2009	2,343	2,014	5	15	310	19	6
	2010	2,074	Lost	7				2
91416	2009	2,255	2,067	12	12	177	1	2
	2010	1,954	1,968	23	12	137	3	3
91417	2009	2,924	2,917	39*	22	152	3	6
	2010	2,403	2,870	22	5	360	10	3
Average distance		2,418	2,420	12	14	230	9	7
95% CI		2,139- 2,698	2,143- 2,697	7-23	10-18	167 - 293	3-16	1-12

CI = Confidence interval

*The migratory route started from Thailand to Cambodia and Vietnam, and it took 39 days from Vietnam to China.

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5 **Table 3.** Habitats of the tracked gulls.
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9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	Length of stay (days)				
Bird I.D.	Location	2008	2009	2010	2011	Average																																
74795	Thailand: Samut Prakan, Samut Sakhon	44	-	-	-	-																																
	China: Qinghai, Xinjiang, Tibet	174	-	-	-	-																																
	Cambodia: Siem Reap	35	-	-	-	-																																
88215	Thailand: Samut Prakan, Samut Songkhram	-	90	119	61	90																																
	China: Xinjiang, Tibet	-	170	180	-	175																																
	Cambodia: Pursat, Siem Reap	-	-	40 (02/12/10 -11/01/11)	-	-																																
88216	Thailand : SamutPrakan, SamutSongkhram, Chachoengsao	-	90	98	-	94																																
	China: Tibet	-	183	-	-	-																																
91416	Thailand :SamutSongkhram	-	64	101	-	82																																
	China: Tibet	-	201	189	-	195																																
	Cambodia: Kampong Thom, Pursat, Siem Reap	-	-	42 (19/11/10 - 10/01/11)	-	-																																
91417	Thailand : Samut Prakan, Samut Songkhram	-	83	78	-	81																																
	China: Qinghai, Xinjiang	-	146	180	-	163																																
	Cambodia: Kampong Thom, Pursat, Siem Reap	-	32 (25/12/09- 25/01/10)	-	-	-																																

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6 **Table 4.** Susceptibility of Brown-headed gulls in captivity to H5N1 virus challenge.
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Inoculum dose (TCID50)	Gull No.	Day of shedding after virus inoculation from		Day at death	NT titer at day after inoculation				
		Trachea	Cloacae		0	5	10	15	20
10^4	1	No shedding	2, 3	4	<20				
	2	2, 3	2	4	<20				
	3	1, 2, 3, 4	3, 4	5	<20				
10^3	4	3, 4	No shedding	5	<20				
	5	1, 2, 3, 4	2, 3, 4	5	<20				
	6	2, 4	3	6	<20	20			
10	7	No shedding	No shedding	Alive	<20	<20	<20	<20	<20
	8	No shedding	No shedding	Alive	<20	<20	160	1280	
	9	4	3	7	<20	<20			

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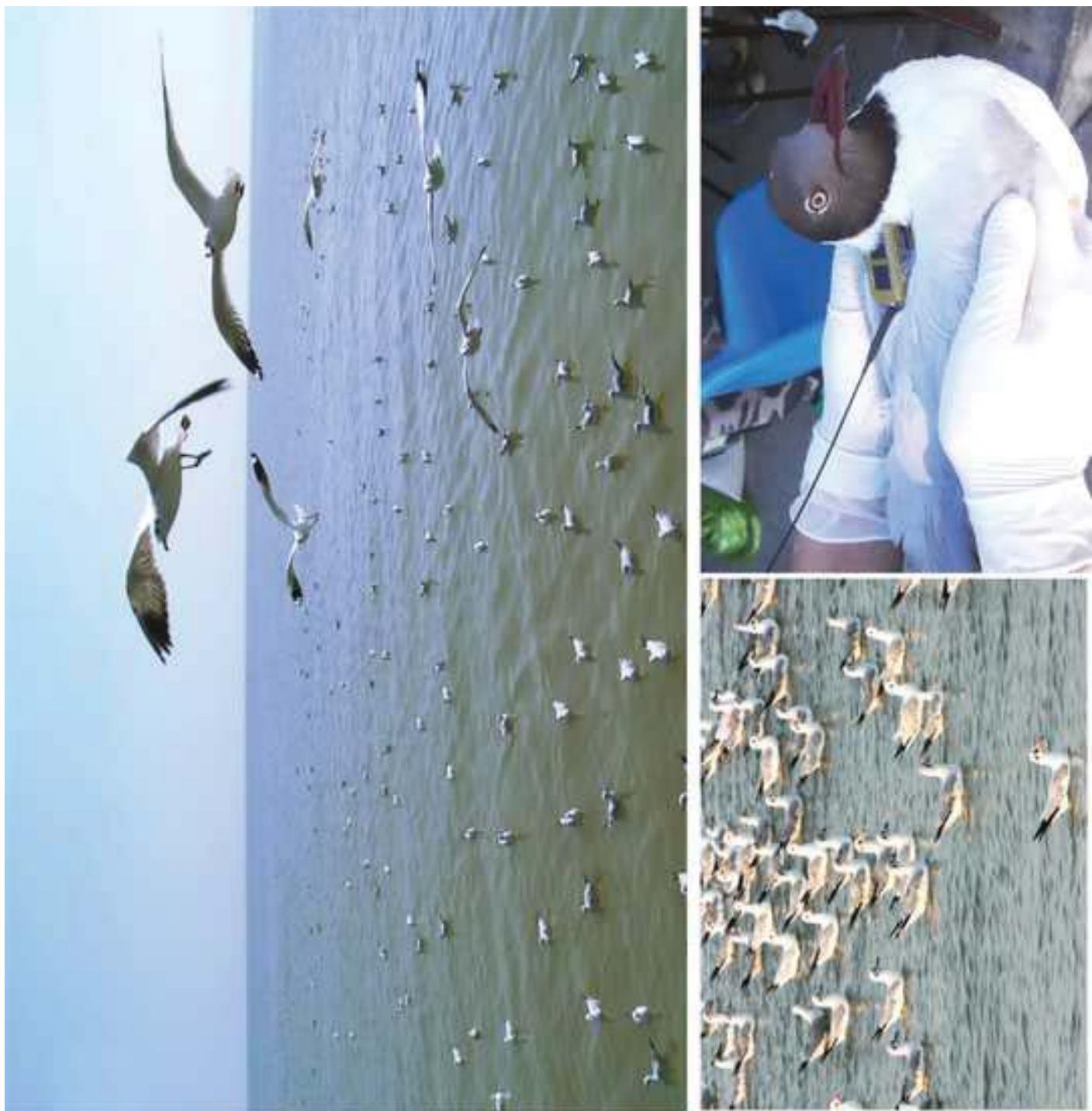


Figure 1
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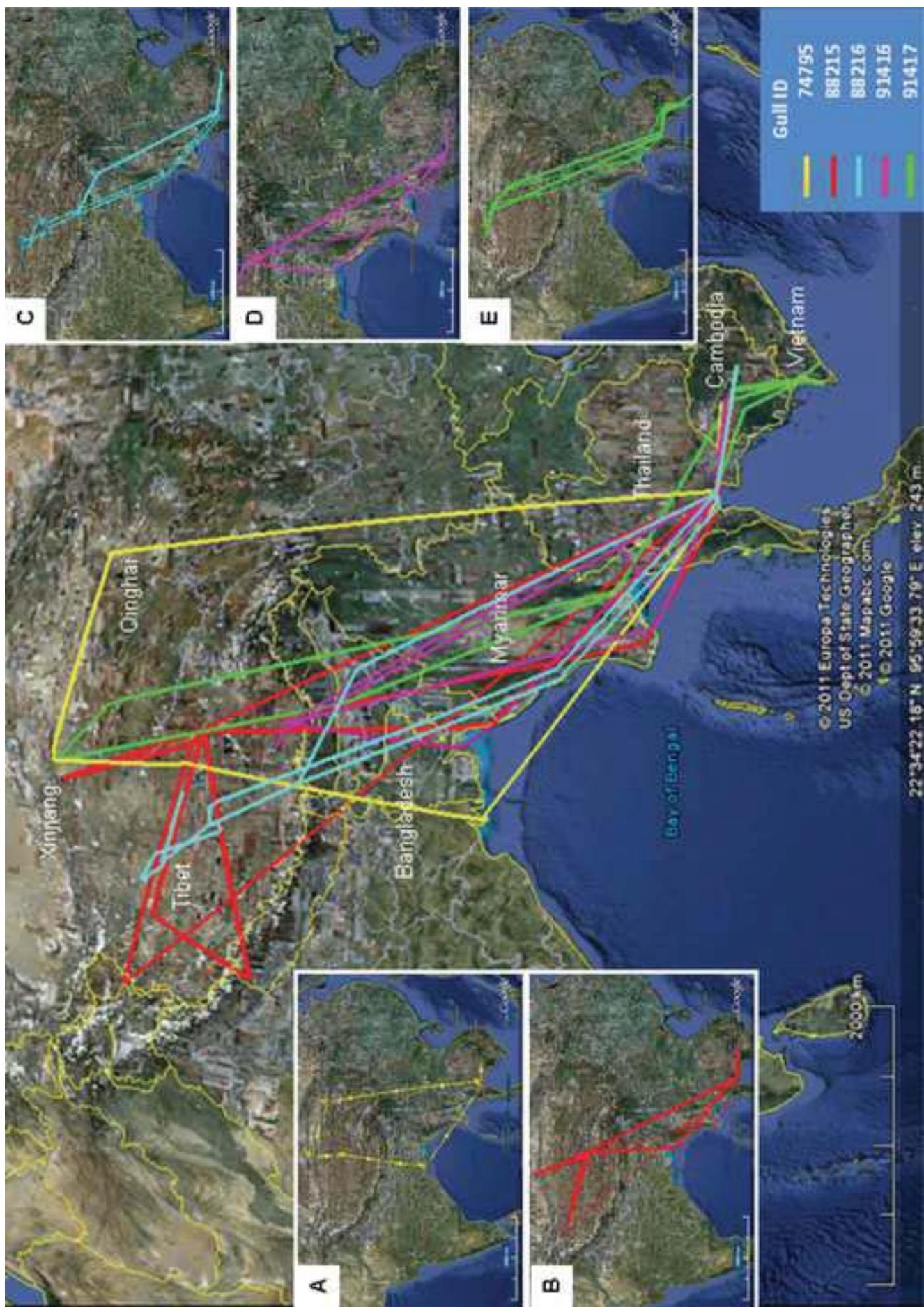


Figure 2
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Figure 3

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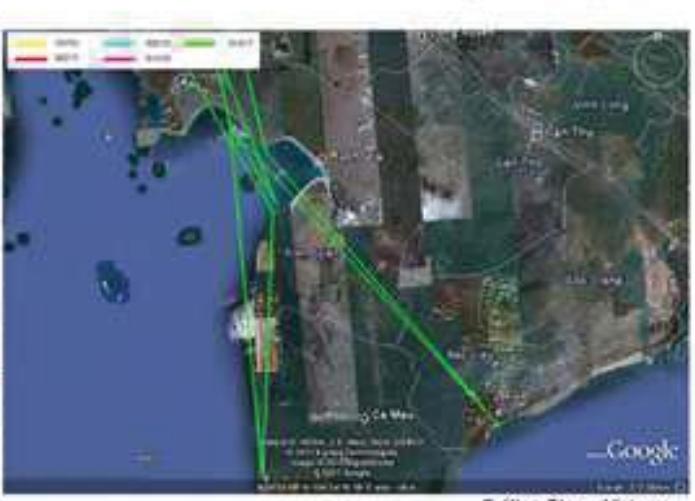
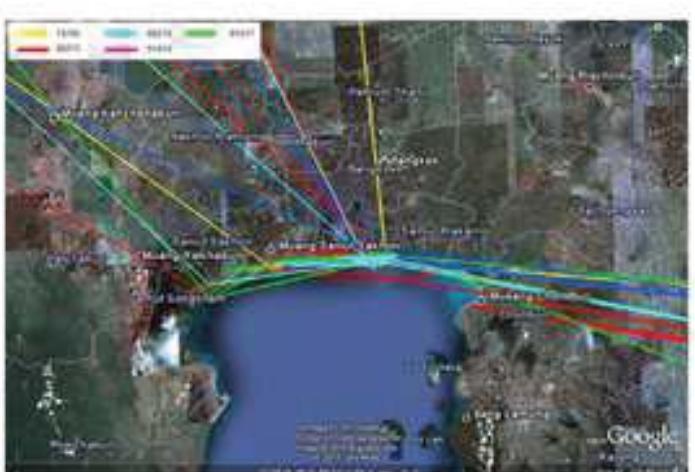
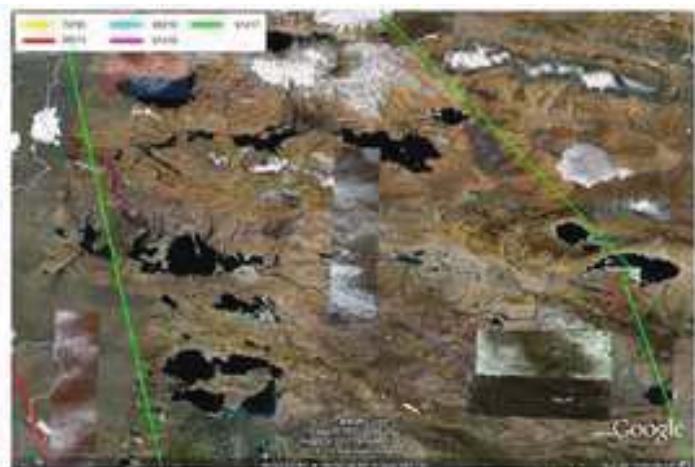
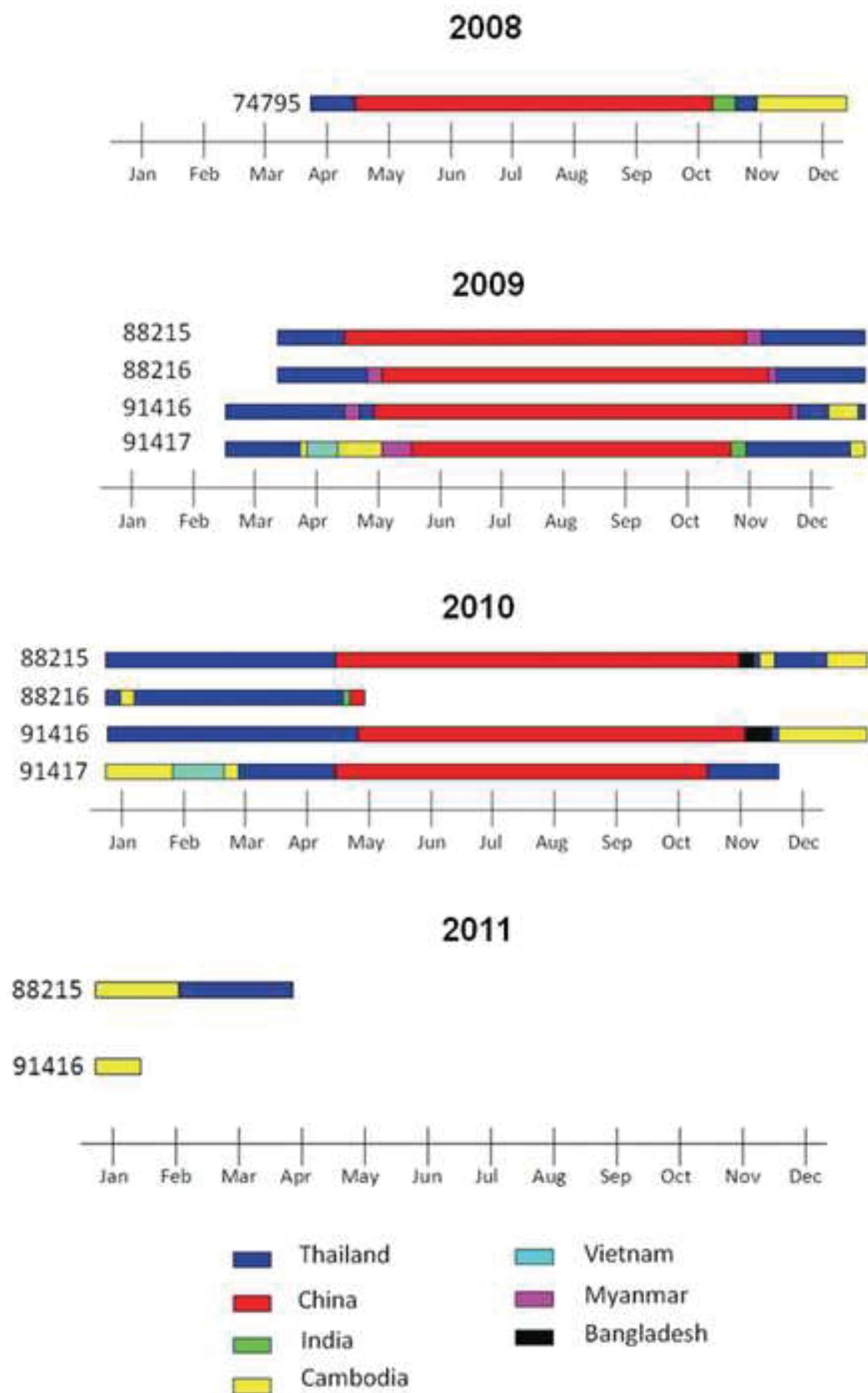


Figure 4

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ปีที่ 41 ฉบับที่ 14 : 16 เมษายน 2553

Volume 41 Number 14 : April 16, 2010

สำนักงานโรคติดต่อ กรมควบคุมโรค กระทรวงสาธารณสุข / Bureau of Epidemiology, Department of Disease Control, Ministry of Public Health

อัตราการติดเชื้อ ระยะเวลาของการขับเชื้อไวรัส และปริมาณเชื้อไวรัส ขณะมีการระบาดของไข้หวัดใหญ่สายพันธุ์ใหม่ 2009



การสอนส่วน
ทางระบบดิจิทัล

ในกลุ่มพหุภาษาเกณฑ์ ศูนย์ฝึกพหุภาษาใหม่แห่งหนึ่ง ประเทศไทย เดือนมิถุนายน พ.ศ. 2552

Infection Rate, Duration of Viral Shedding and Viral Load in an Outbreak of

Novel Influenza A (H1N1) 2009 Infections among Military Conscripts in a Training Center, Thailand, June 2009

 adisorn.ftp@gmail.com

อดิสรณ์ วรรณะศักดิ์ และคณะ

สำนักระบบทดวิทยา กรมควบคุมโรค กระทรวงสาธารณสุข

ความเป็นมา

ต้นเดือนเมษายน 2552 มีรายงานผู้ติดเชื้อไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 (2009 pandemic influenza A (H1N1)) ในประเทศไทยและอเมริกา¹ และเม็กซิโก² ไวรัสได้แพร่กระจายไปยังภูมิภาคอื่นๆ ของโลกอย่างรวดเร็ว และตั้งแต่วันที่ 11 มิถุนายน 2552 องค์การอนามัยโลก (World Health Organization; WHO) ได้ประกาศยกระดับการระบาดของไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 ขึ้น เป็นระดับ 6 ซึ่งเป็นระดับสูงสุด หมายถึงเกิดการระบาดไปทั่วโลก³ ที่เกิดขึ้นภายในเวลาเพียง 6 สัปดาห์ ซึ่งรวดเร็วกว่าการระบาดใหญ่ในอดีตที่ต้องใช้เวลานานกว่า 6 เดือนก่อนแพร่กระจายไปทั่วโลก นับถึงวันที่ 15 มกราคม 2553 องค์การอนามัยโลกได้รับรายงานข้อมูลการระบาดของโรคไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 ใน 208 ประเทศทั่วโลกที่มีผู้ป่วยยืนยันการติดเชื้อและมีผู้เสียชีวิตอย่างน้อย 13,554 ราย⁴ สำหรับในประเทศไทยข้อมูลนับถึงวันที่ 13 มกราคม 2553 มีรายงานผู้ป่วยยืนยันไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 จำนวน 30,852 ราย คิดเป็นอัตราป่วยสะ邵เท่ากับ 48.67 ต่อประชากรแสนคน เสียชีวิตจำนวน 196 ราย การป้องกันการติดต่อกันที่สำคัญที่สุดคือ

คือ การแยกผู้ป่วยออกจากกลุ่มคนเพื่อป้องกันการแพร่กระจายเชื้อไปสู่คนปกติ ดังนั้น ความรู้เกี่ยวกับระยะเวลาขั้นเชื้อไวรัสออกมานในทางเดินหายใจ (Viral shedding) และปริมาณไวรัส (Viral load) ในผู้ป่วยจะมีความสำคัญในการกำหนดมาตรการป้องกันการแพร่ระบาดของโรคไข้หวัดใหญ่สายพันธุ์ใหม่

วันที่ 23 มิถุนายน 2552 สำนักกระบาดวิทยา ได้รับรายงานว่า มีทหารเกลน์ที่ป้ายด้วยอาการ โรคติดเชื้อทางเดินหายใจเฉียบพลัน จำนวนมาก โดยส่วนใหญ่มีอาการไข้ ไอ เสmen ห้าน้ำมูก ปวดศีรษะ เกิดขึ้นภายในสูนย์ฝึกหัดใหม่แห่งหนึ่ง จังหวัดชลบุรี จากการสอบถามโรคเบื้องต้นของทีมเฝ้าระวังส่วนคลื่อนที่เริ่วในพื้นที่ และทีมระบบวิทยาหหารเรื่อ สงสัยว่าเป็นการระบาดของโรคไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 เนื่องจากในอำเภอช้างเคียง คือ อำเภอของ滥มุง จังหวัดชลบุรี มีรายงานการระบาดของไข้หวัดใหญ่สายพันธุ์ใหม่มาประมาณ 1 สัปดาห์ก่อนหน้านี้ สำนักกระบาดวิทยา จึงร่วมกับทีมระบบวิทยากรองทัพเรื่อ ดำเนินการศึกษาระบบวิทยา ของโรคในสูนย์ฯ ตั้งแต่วันที่ 25 มิถุนายน 2552 โดยมีวัตถุประสงค์ เพื่อศึกษาการระบาดของโรค หาสาเหตุการติดเชื้อที่มีผลและไม่มีผลการ



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- วัตถุประสงค์ในการจัดทำ**
รายงานการเฝ้าระวังทางระบาดวิทยาประจำสัปดาห์
1. เพื่อให้หน่วยงานเจ้าของข้อมูลรายงานการเฝ้าระวังทางระบาดวิทยา ได้ตรวจสอบและแก้ไขให้ถูกต้อง ครบถ้วน สมบูรณ์อ่องขึ้น
 2. เพื่อวิเคราะห์และรายงานสถานการณ์โรคที่เป็นปัจจุบัน กั้งใน และต่างประเทศ
 3. เพื่อเป็นสื่อกลางในการนำเสนอผลการสอบสวนโรค หรืองาน ศึกษาวิจัยที่สำคัญและเป็นปัจจุบัน
 4. เพื่อเผยแพร่ความรู้ ตลอดจนแนวทางการดำเนินงานทางระบาดวิทยาและสารานุสุข

คณะที่ปรึกษา

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 กองบรรณาธิการ
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 ลักษณ์ ลิขิตยิ่งรา น.สพ.ธีรศักดิ์ ชักนำ
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 กนกพิพิธ พิพิรัตน์ ประเวศน์ แย้มชื่น
ฝ่ายจัดส่ง : พุนทรพย์ เปี่ยมณี เชิดชัย ดาวาแจ้ง
ฝ่ายศิลป์ : ประมวล ทุมพงษ์
สื่อ宣傳 : บริมาศ ศักดิ์ศรีสัมพันธ์ อมยา พุกชนะนันท์

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 ทักษิรัตน์ เลิศสำราญ⁴ สมกิต คงอยู่⁴ โสกน อุ่ยมศิริถาวร¹
 สำนัก glands วิทยา กรมควบคุมโรค กระทรวงสาธารณสุข
² กองเวชกรรมป้องกัน กรมแพทย์ทหารเรือ กองทัพเรือ
³ โรงพยาบาลอาทิตย์ จังหวัดชลบุรี
⁴ ภาควิชาจุลชีววิทยา คณะแพทยศาสตร์ศิริราชพยาบาล
 มหาวิทยาลัยมหิดล

ระยะเวลาของการขับเชื้อไวรัสและปริมาณของไวรัสในทางเดินหายใจในกลุ่มพหารเกณฑ์ที่มีผลตรวจยืนยันการติดเชื้อไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ 2009

วิธีการศึกษา

การศึกษารั้งนี้ประกอบด้วย 2 ส่วน ได้แก่ 1) การสำรวจอัตราการติดเชื้อไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ด้วย Serological survey และ 2) ศึกษาการขับไวรัส (Viral shedding) และปริมาณไวรัส (Viral load) ในผู้ป่วยรายใหม่ โดยในส่วนของการศึกษา Serological survey ได้สุ่มเลือกพหารเกณฑ์หนึ่งกองร้อยในศูนย์ฝึกพหารใหม่ จ.ชลบุรี เป็นตัวแทนในการศึกษา ทำการเจาะเลือกพหารเกณฑ์ 2 ครั้งห่างกัน 4 สัปดาห์ เป็นตัวอย่างชี้รั้งคู่ (Paired sera) เพื่อส่งตรวจยืนยันการติดเชื้อไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ด้วยวิธี Hemagglutination inhibition (HI) assay

ในส่วนของการศึกษาระยะเวลาของการขับเชื้อไวรัส (Duration of viral shedding) และปริมาณไวรัส (Viral load) คณะผู้ศึกษาได้คัดเลือกจากผู้ป่วยรายใหม่ที่กำลังมีอาการของโรคติดเชื้อทางเดินหายใจเฉียบพลัน (Acute Respiratory Infection; ARI) ด้วยการใช้แบบสอบถามเก็บข้อมูลกลุ่มพหารเกณฑ์กองประจำการ ครูฝึกและข้าราชการในศูนย์ฝึกพหารใหม่ จังหวัดชลบุรี โดยใช้ชื่อผู้ป่วย ได้แก่ ผู้ที่มีอาการอย่างน้อย 2 อาการต่อไปนี้ ได้แก่ ไข้ (อุณหภูมิร่างกาย มากกว่า 37.8 องศาเซลเซียส) ไอ เจ็บคอ และน้ำมูกไหล ระหว่างวันที่ 26 พฤษภาคม - 26 มิถุนายน 2552 และเก็บสารคัดหลังจากคอหอยหลังโพรงจมูก (Nasopharyngeal swab) หรือสารคัดหลังจากคอหอย (Throat swab) นำไปตรวจหาสารพันธุกรรมของเชื้อไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 ทุกวันติดต่อกันเป็นเวลา 12 วัน โดยวิธี Real-time reverse transcriptase polymerase chain reaction (Real-time RT-PCR) ทั้งในเชิงคุณภาพและเชิงปริมาณ โดยส่งตัวอย่างตรวจที่ภาควิชาจุลชีววิทยา คณะแพทยศาสตร์ศิริราชพยาบาล มหาวิทยาลัยมหิดล

ผลการศึกษา

การระบาดของไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 ในพหารเกณฑ์ที่ศูนย์ฝึกพหารใหม่ จังหวัดชลบุรี ที่มีหน่วยพหารจำนวน 4 กองพัน แต่ละกองพันประกอบด้วย 6 กองร้อย แต่ละกองร้อยมีพหารเกณฑ์ประมาณ 150 - 180 คน พบผู้ป่วยรายแรกเริ่มมีอาการตั้งแต่วันที่ 29 พฤษภาคม 2552 หลังจากนั้นพบจำนวนผู้ป่วยเพิ่มขึ้นเรื่อยๆ จนถึงวันที่ 26 มิถุนายน 2552 พบผู้ป่วยทั้งสิ้น 1,231 ราย คิดเป็นอัตราป่วย (Attack rate) ร้อยละ 29.3 ผู้ป่วยไปรับการรักษาที่แผนกแพทย์ศูนย์ฝึกพหารใหม่ โรงพยาบาลอาทิตย์ และโรงพยาบาลจุฬาลงกรณ์ จำนวนเจ้าหน้าที่ 1 ราย อัตราป่วยตาย (Case fatality rate) ร้อยละ 0.08 ทั้งหมดเป็นเพศชาย มีค่ามัธยฐานอายุ 21 ปี พบผู้ป่วยกระจากอายุในทุกกองร้อย พนอัตรา

ป่วยสูงสุดใน กองร้อย 6 กองพัน 1 และ กองร้อย 2 กองพัน 2 เท่ากับร้อยละ 57.9 และ 53.7 ตามลำดับ จำนวนผู้ป่วยรายใหม่เพิ่มมากขึ้น ชัดเจนระหว่างวันที่ 7 - 18 มิถุนายน 2552 (รูปที่ 1) ผู้ป่วยมีอาการไอ มากที่สุด (ร้อยละ 92.4) รองลง ได้แก่ ไข้ มีน้ำมูก ปวดศีรษะ ปวด เมื่อยกล้ามเนื้อ เส็บคอ (รูปที่ 2)

ผลการศึกษาอัตราการติดเชื้อในทหารเกณฑ์ 90 นายที่ถูกสูมเลือกมาจากกองร้อยหนึ่ง เพื่อตรวจหาระดับภูมิคุ้มกันต่อเชื้อไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 พนวจ ไตรเตอร์ $\geq 1:40$ ด้วยวิธี HI จำนวน 61 ราย เท่ากับร้อยละ 67.8 (ตารางที่ 1) ทั้งนี้ ในกลุ่มที่มีผลการตรวจยืนยันว่ามีการติดเชื้อไว้หวัดใหญ่สายพันธุ์ใหม่ 2009 พนวจ เป็นผู้ติดเชื้อที่ไม่มีอาการป่วย (asymptomatic infection) 18 ราย (ร้อยละ 29.5) และเป็นผู้ติดเชื้อที่มีอาการจำนวน 43 ราย (ร้อยละ 70.5)

การศึกษาเกี่ยวกับระยะเวลาของการขับเชื้อไวรัสและปริมาณไวรัส (viral shedding และ viral load) ในกลุ่มทหารเกณฑ์ที่ติดเชื้อไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 ในสิ่งส่งตรวจจากคอหอยหลังโพรงจมูกในผู้ป่วยจำนวน 25 ราย มีอายุ 18 - 26 ปี ค่ามัธยฐานอายุ (Median) เท่ากับ 21 ปี ทั้งหมดเป็นเพศชาย มี 1 รายมีน้ำหนักตัวมาก (102 กิโลกรัม) แต่ไม่มีโรคประจำตัวใดๆ และอีกหนึ่งรายกำลังป่วยเป็นวันโรคปอดอยู่ระหว่างการรักษาด้วยยาต้านเชื้อวัณโรค ผู้ป่วยที่เหลือมีสุขภาพแข็งแรงและไม่มีโรคประจำตัว วันที่เก็บตัวอย่างสารคัดหลังจากหอยหลังโพรงจมูกในผู้ป่วยวันแรกห่างจากวันเริ่มป่วยตั้งแต่ 1 ถึง 9 วัน (ค่ามัธยฐาน 4 วัน) ระยะเวลาของการขับเชื้อไวรัสจากทางเดินหายใจในผู้ป่วยทั้ง 25 รายมีค่ามัธยฐาน 5 วัน โดยระยะเวลาของการขับเชื้อไวรัสออกจากการเดินหายใจสั้นสุด 2 วันและนานสุด 11 วัน (รูปที่ 3) เมื่อพิจารณาข้อมูลรายบุคคล มีผู้ป่วย 3 รายที่สามารถเก็บสิ่งส่งตรวจได้ตั้งแต่วันแรกที่ผู้ป่วยเริ่มมีอาการ และพบเชื้อไวรัสไว้หวัดใหญ่สายพันธุ์ใหม่สามารถที่จะขับทางเดินหายใจได้ตั้งแต่ภายในวันแรกที่ผู้ป่วยเริ่มมีอาการป่วย

ปริมาณไวรัสของผู้ป่วยที่ตรวจพบในการศึกษาครั้งนี้มีจำนวน 2.6×10^2 Copies/ml. ถึง 8.1×10^9 Copies/ml. เฉลี่ย 2.4×10^4 Copies/ml. ปริมาณเชื้อไวรัสที่พบในผู้ป่วยแต่ละราย ส่วนใหญ่จะมีปริมาณมาก สุดในวันที่ 2 ถึงวันที่ 5 หลังจากเริ่มมีอาการป่วย อย่างไรก็ตาม ไม่พบว่ามีความสัมพันธ์ระหว่างปริมาณเชื้อไวรัสกับระยะเวลาของการขับเชื้อไวรัสจากทางเดินหายใจในผู้ป่วยกลุ่มนี้ นอกจากนี้ พนวจระหว่างการขับเชื้อไวรัสในผู้ป่วยที่มีน้ำหนักเกินและเสียชีวิตเท่ากับ 8 วัน และในผู้ป่วยที่กำลังป่วยเป็นวันโรคปอดเท่ากับ 4 วัน

สรุปและวิจารณ์ผลการศึกษา

การระบาดของไวรัสไว้หวัดใหญ่สายพันธุ์ใหม่ 2009 ในทหารเกณฑ์ชายไทยอายุเฉลี่ย 21 ปี มีอัตราป่วยสูงถึงร้อยละ 29.3

และมีผู้ป่วยที่มีน้ำหนักเกินซึ่งจัดเป็นกลุ่มเสี่ยงสูงสุด 1 ราย อาการป่วยที่พบมากสุด ได้แก่ ไอ ไข้ น้ำมูก ปวดศีรษะ ปวดเมื่อยกล้ามเนื้อเจ็บคอ ซึ่งเป็นอาการของโรคติดเชื้อทางเดินหายใจเฉียบพลัน การระบาดเกิดขึ้นรวดเร็วเนื่องจากทหารเกณฑ์มีจำนวนมากและทำกิจกรรมร่วมกันตลอด ประกอบกับอยู่ในสถานที่แออัดซึ่งแพร่กระจายเชื้อต่อเนื่องได้ง่ายเมื่อไม่มีการแยกผู้ป่วยในระยะแรก ๆ ของการระบาดครั้งนี้ นอกจากนี้ยังพบว่าสัดส่วนผู้ติดเชื้อที่ไม่มีอาการป่วยมากถึงร้อยละ 29.5 ของผู้ติดเชื้อทั้งหมด อาจเป็นอีกสาเหตุหนึ่งที่ทำให้มีโอกาสแพร่ระบาดได้เพิ่มขึ้น เนื่องจากทหารกลุ่มนี้ไม่ได้ถูกแยกออกจากผู้ที่ไม่ป่วย ถึงแม้ว่าประชากรกลุ่มนี้จะไม่ไอ ไม่เจ็บ ไม่มีน้ำมูก แต่กิจกรรมการใช้ชีวิตของทหารเกณฑ์มีโอกาสสัมผัสน้ำลายกันได้ง่าย เช่น การดื่มน้ำจากแก้วเดียวกัน หรือใช้ช้อนส้อมร่วมกันในขณะรับประทานอาหาร เป็นต้น

ในขณะมีการติดเชื้อไวรัสไว้หวัดใหญ่ ไวรัสจะถูกขับออกม้าอยู่ในสารคัดหลังบริเวณจมูกและคอหอยหลังห้องป่า และแพร่กระจายเชื้อไวรัสนี้ผ่านทางการไอและจาม⁶ นอกจากนี้มีรายงานการตรวจพบเชื้อไวรัสในอุจจาระ ปัสสาวะ และซีรัม⁷ โดยทั่วไปในผู้ใหญ่ที่แข็งแรง ไม่มีโรคประจำตัว ไม่ได้รับยาด้านไวรัส ที่ป่วยด้วยไว้หวัดใหญ่ตามคุณภาพของเชื้อไวรัสออกมานาน 5-7 วันหลังจากเริ่มมีอาการ^{8,9}

ในส่วนของไว้หวัดใหญ่สายพันธุ์ใหม่ 2009 มีการศึกษาเรื่องระยะเวลาของการขับเชื้อไวรัสออกมานานทางเดินหายใจในต่างประเทศ พบว่าในขณะมีการระบาดของไว้หวัดใหญ่สายพันธุ์ใหม่ ในนักเรียนเตรียมทหารของโรงเรียนนายร้อยอาชีวศึกษาห้วยขลອມวิภาวดีอนุมิถุนายน พ.ศ. 2552 ระยะเวลาของการขับเชื้อไวรัสออกมานานทางเดินหายใจมีค่ามัธยฐาน 5 วัน (พิสัย 1 - 12 วัน) สูงสุดใน 24 - 72 ชั่วโมงหลังเริ่มมีอาการป่วย¹⁰ แสดงถึงการศึกษาในประเทศไทยในการระบาดครั้งนี้ ที่พบว่าระยะเวลาการขับเชื้อไวรัสไว้หวัดใหญ่สายพันธุ์ใหม่ 2009 ในทหารเกณฑ์มีระยะเวลานานเฉลี่ย 5 วัน หลังเริ่มแสดงอาการ แต่สามารถตรวจพบได้ตั้งแต่วันแรกที่เริ่มป่วยจนถึง 11 วัน ซึ่งนับว่าใกล้เคียงกันมาก ซึ่งน่าจะอธิบายได้จากการที่เป็นประชากรอายุใกล้เคียงกันและเป็นการติดเชื้อไวรัสไว้หวัดใหญ่สายพันธุ์ใหม่ในระยะต้นของการระบาด ใหญ่ ที่ยังมีสารพันธุ์กรรมใกล้เคียงกัน โดยปริมาณเชื้อไวรัสสูงสุดอยู่ระหว่างวันที่ 2 ถึงวันที่ 5 หลังจากเริ่มมีอาการ จึงเป็นระยะเวลาที่ต้องมีมาตรการป้องกันการแพร่เชื้อที่เข้มงวด และต้องป้องกันต่อเนื่องตลอดระยะเวลาที่มีการระบาดเพราผู้ป่วยบางรายอาจจะขับเชื้อได้นานกว่า 10 วัน

ในอดีตมีหลายการศึกษา ที่รายงานประสิทธิผลของยาต้านไวรัสชนิด Neuraminidase inhibitor (NAI) เช่น oseltamivir และ zanamivir ว่าสามารถลดระยะเวลาที่มีการขับเชื้อไวรัสออกมานานทางเดินหายใจ

และลดปริมาณไวรัสในผู้ป่วยไข้หวัดใหญ่ต่ำถูกถูกตัด ถ้าหากได้รับยาภายใน 4 วันแรกนับจากเริ่มมีอาการ^{11,12} ซึ่งในกรณีของไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่นี้ ผู้ป่วยที่ได้รับยา oseltamivir มีระยะเวลาของการขับเชื้อไวรัสที่สั้นลง เช่น กัน¹³ อย่างไรก็ตามในการระบาดครั้งนี้มีทั่วโลกที่ติดเชื้อไวรัส 2 รายที่ได้รับยา oseltamivir จึงควรมีการศึกษาเพิ่มเติมถึงประสิทธิผลของยาต้านไวรัสในผู้ป่วยไทยต่อไป

การเก็บตัวอย่างสารคัดหลังจากคอหอยหลังโพรงจมูก (Nasopharyngeal swab) มีโอกาสได้ผลบวกสูง โดยการศึกษานี้พบปริมาณเชื้อไวรัสเนลลี่ข 2.4X10⁴ Copies/ml. และปริมาณสูงสุดระหว่างวันที่ 2 - 5 หลังจากเริ่มมีอาการป่วย ดังนั้น การเก็บตัวอย่างวินิจฉัยมีเหตุการณ์ทำโดยบุคลากรที่มีประสบการณ์และใช้เทคนิคที่ถูกต้องเพาะเป็นการเก็บตัวอย่างจากจุดที่พบเชื้อไวรัสไข้หวัดใหญ่อย่างปริมาณมาก

ข้อจำกัดในการศึกษา

การศึกษานี้ ดำเนินการในสูนย์ฝึกหัดใหม่ ซึ่งผู้ป่วยเป็นหัดเงินที่มีสุขภาพร่างกายแข็งแรงก่อนหน้าการป่วย ทั้งหมดมีอายุไม่เกินสิบห้าปี และมีภาระทางกายภาพต่ำๆ คล้ายกัน และเกือบทุกรายไม่ได้รับยาต้านไวรัส ทำให้ยากต่อการระบุปัจจัยที่มีผลทำให้ระยะเวลาของการขับ เชื้อไวรัสออกมากจากทางเดินหายใจแตกต่างกัน ในส่วนของคุณภาพการหายใจและนำส่งตัวอย่างอาจจะมีความแตกต่างกันในแต่ละวัน เนื่องจากการเก็บตัวอย่างสารคัดหลั่งจากผู้ป่วยกระทำโดยพยาบาลในหอผู้ป่วย ซึ่งผลดีเปลี่ยนกันไปตามเรื่องพยาบาล อาจเป็นสาเหตุทำให้ได้จำนวนเชื้อไวรัสต่ำไม่แน่นอน เนื่องจากทักษะที่แตกต่างกันระหว่างผู้เก็บตัวอย่างแพทย์คน 따라서การป้ายเชื้อที่ก่อให้หลัง โพรงจมูกของผู้ป่วยขึ้นอยู่กับหลักปัจจัย เช่น ตำแหน่งที่ป้ายและความเที่ยงของมือผู้เก็บตัวอย่าง นอกจากนี้ การขนส่งตัวอย่างจากจังหวัดชลบุรีมาตรวจที่ห้องปฏิบัติการในกรุงเทพมหานครยังมีปัจจัยด้านระยะเวลา และคุณภาพการเก็บรักษาตัวอย่างที่ส่งผลต่อคุณภาพตัวอย่างและการตรวจพบปริมาณเชื้อไวรัสได้

กิตติกรรมประกาศ

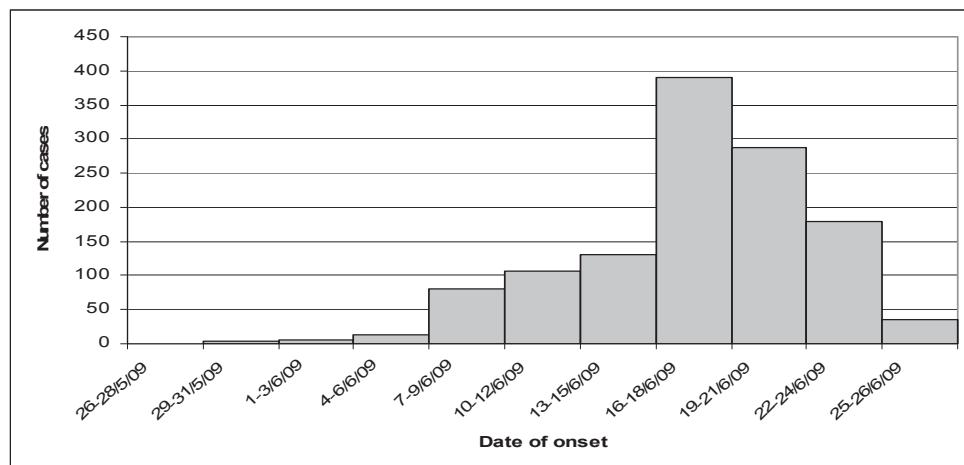
ขอขอบคุณบุคลากรและหน่วยงานที่ให้การสนับสนุน
การศึกษาครั้งนี้ ได้แก่ กรมแพทย์ทหารเรือ ผู้อำนวยการโรงพยาบาล
สมเด็จพระนางเจ้าสิริกิติ์ ผู้อำนวยการโรงพยาบาลภารกิจสืบสานประวัติศาสตร์
วงศ์ ผู้บัญชาการศูนย์ฝึกทหารใหม่ ฐานทัพเรือสัตหีบ สำนักงาน-
สาธารณสุขจังหวัดชลบุรี สำนักงานป้องกันควบคุมโรคที่ 3 ชลบุรี
ที่มีเด่นเด่น วังสอบสวนเกลื่อนที่เริ่วआगोสต์ หิน จังหวัดชลบุรี
ภาควิชาจุลชีววิทยา คณะแพทยศาสตร์ศิริราชพยาบาล
มหาวิทยาลัยมหิดล และสำนักงานกองทุนสนับสนุนการวิจัย (The Thailand Research Fund for Senior Research Scholar) โดยผ่าน
ศาสตราจารย์ ดร.พิไลพันธ์ พุธวัฒน์

เอกสารอ้างอิง

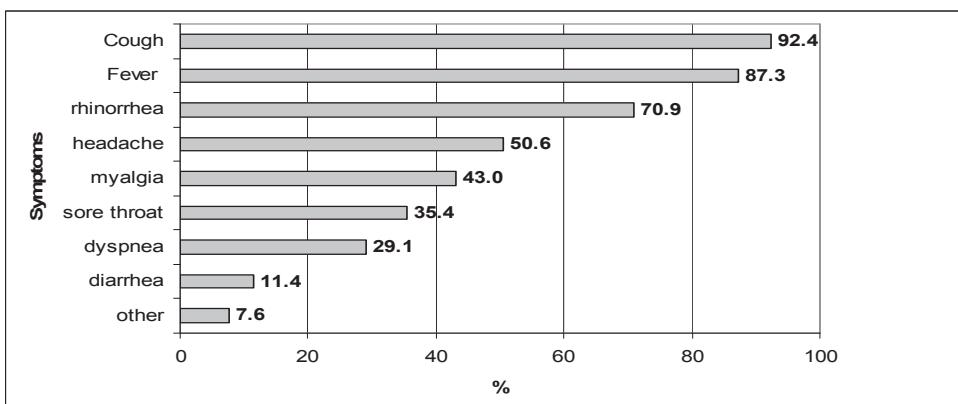
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ตารางที่ 1 แสดงร้อยละของการติดเชื้อไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 และร้อยละของผู้ติดเชื้อที่มีอาการและไม่มีอาการ ในพิพารเกณฑ์ของศูนย์พิเศษใหม่ ที่ได้รับการสุ่มตรวจ วันที่ 9 มิถุนายน 2552 (N = 90)

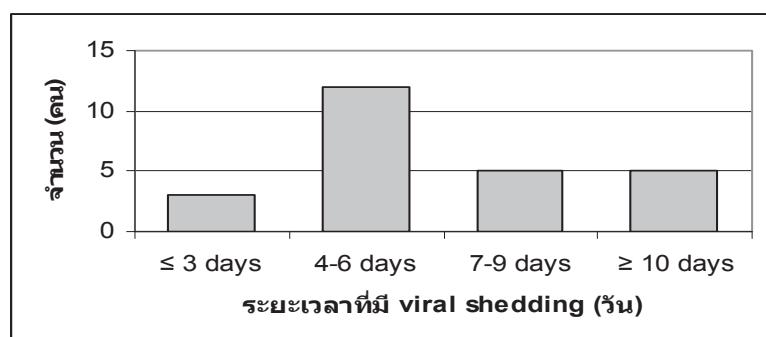
ผลการตรวจ	จำนวน	ร้อยละ	อาการป่วย	จำนวน	ร้อยละ
ติดเชื้อ	61	67.8	มีอาการ	43	70.5
			ไม่มีอาการ	18	29.5
ไม่ติดเชื้อ	29	32.2			
รวม	90	100.0			



รูปที่ 1 แสดงจำนวนผู้ป่วยสงสัยไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 จำแนกตามวันเริ่มป่วย ในพิพารเกณฑ์ศูนย์พิเศษใหม่แห่งหนึ่ง จังหวัดชลบุรี ระหว่างวันที่ 26 พฤษภาคม – 26 มิถุนายน 2552 (N = 1,231)



รูปที่ 2 แสดงร้อยละของอาการและอาการแสดงในผู้ป่วยสงสัยไข้หวัดใหญ่สายพันธุ์ใหม่ 2009 ในพิพารเกณฑ์ศูนย์พิเศษใหม่แห่งหนึ่ง ระหว่างวันที่ 1–26 มิถุนายน 2552 (N = 77)



รูปที่ 3 แสดงจำนวนผู้ป่วยจำแนกตามระยะเวลา (วัน) ที่ติดเชื้อไวรัสไข้หวัดใหญ่สายพันธุ์ใหม่ในพิพารเกณฑ์ศูนย์พิเศษใหม่ จังหวัดชลบุรี ระหว่างวันที่ 27 มิถุนายน - 8 กรกฎาคม 2552 (N=25 คน)

KEYSTONE SYMPOSIA

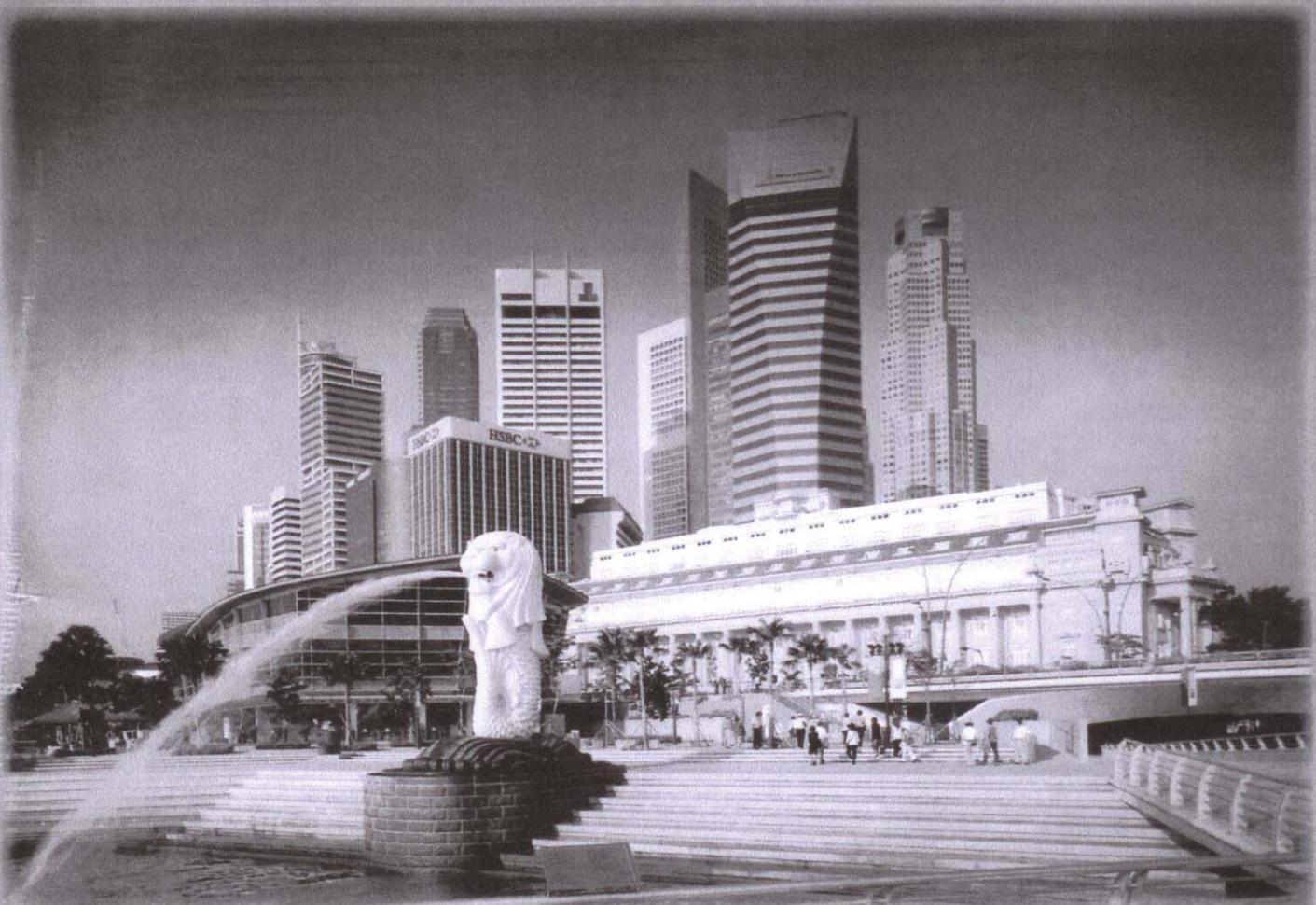
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2006 ABSTRACT BOOK

Respiratory Viruses of Animals Causing Disease in Humans

Stanley A. Plotkin, Albert D.M.E. Osterhaus and Martin L. Hibberd

In collaboration with A*STAR
(Agency for Science, Technology and Research), Singapore



Images courtesy of the Singapore Tourism Board

December 10 - 15, 2006
Swissotel The Stamford/Biopolis • Singapore

Tuesday, December 12: Poster Session 2 Poster Abstracts

221 Pathogen Detection Microarray – from Lab to Bedside

Christopher W. Wong, Charlie Lee Wah Heng, Leong Wan Yee, Shirlena Soh, Martin L. Hibberd, Ken W-K Sung, Lance D. Miller. Microarray and Expression Genomics Laboratory, Genome Institute of Singapore, Republic of Singapore.

Background

Testing for infectious agents in clinical specimens has historically been a hypothesis driven process. While DNA microarrays have recently been used to identify pathogens in a more unbiased fashion, their routine use has been hampered by technical constraints that limit detection sensitivity and specificity.

Methods and Findings

To address these problems, we created an oligonucleotide microarray containing 390k probes spanning the genomes of 35 RNA viruses. By empirically determining signal detection thresholds related to probe-target sequence similarity, and studying the relationship between primer design and PCR-based amplification bias, we have defined novel criteria for selecting probes for the optimal detection of pathogens by microarray. With the *in silico* generation of optimized pathogen "recognition signatures" and the development of algorithms for predicting PCR bias and analyzing probe signal distributions, we were able to identify the presence of pathogens in clinical specimens at the species, genus, or family level. Using this approach, we tested 35 nasal wash samples from 35 children with lower respiratory infections that had been previously tested for respiratory syncytial virus, human metapneumovirus and rhinovirus by real-time PCR and identified pathogens with 94% diagnostic accuracy (75% sensitivity and 100% specificity).

Conclusion

Our findings show that microarrays can be used for the robust and accurate identification of pathogens in patient specimens, and further substantiate the use of microarray technology in clinical diagnostics. This study was supported by funding from Singapore's Agency for Science, Technology and Research (A*STAR).

223 Chinese herbs inhibited the entry of SARS-CoV in vitro

Min Zhuang^{1,2}, Hong Jiang³, Rika Furuta⁴, Peng Xiao¹, Lian-feng Zhang³, Chuan Qin³, and Toshio Hattori^{1*}
 1 Division of Infectious and Respiratory Diseases, Department of internal medicine, Tohoku University, Sendai, Japan, 980-8574; 2 Department of Microbiology, Harbin Medical University, Harbin, China, 150086; 3 Chinese Academy of Medical sciences, Institute of laboratory Animal Science, Beijing, China, 100021; 4 Department of Microbiology, Kansai Medical University, Osaka, Japan 570-8506;

The water extracts of seven Chinese herbs and five Kampo medicines which were used for the treatment of SARS patients, were examined to determine if they could inhibit the SARS viral replication. A human immunodeficiency virus (HIV)/SARS-CoV S pseudotyped virus, containing HIV lentiviral vectors encoding a reporter gene and S protein of SARS-CoV, was used for the screening.

Only Cinnamomi Cortex extract (CCE) and Caryophylli Flos extract (CFE) showed inhibitory activities against HIV/SARS-CoV S pseudovirus with a 50% effective concentration (EC₅₀) of 0.03 mg/ml for the former and 0.058 mg/ml for the latter. Both drugs also inhibited cell membrane fusion between 293T cells and Hela cells expressing either S protein or ACE2 protein almost completely at the concentrations of 0.3 mg/ml. Finally we confirmed that both fractions inhibited wild-type infection in the plaque reduction assay at the selective indices (SIs) of CCE and CFE were 9 and 3.6, respectively. We further examined four fractionated samples from Cinnamomi Cortex (CC) by HIV/SARS-CoV S pseudovirus and found that two fractions (Ethanol extract and Butanol fraction) had inhibitory activities with SI of 2.38 and 5.0, respectively. In cell fusion assay both fractions completely inhibited below 0.3mg/ml. In wild type infection, again both fractions showed inhibitory activities with SI of 18 for Ethanol Fr. and 23 for Butanol Fr.

The results strongly indicated that CC and Caryophylli Flos (CF) contain a potent new inhibitor of SARS-CoV entry, and Butanol fraction of CC showed the strongest inhibitory activities.

This work was supported by Grants-in-Aid from the Ministry of Education, Science, Sports, and Culture of Japan and the Scientific Research Expenses for Health and Welfare Program from the Ministry of Health and Welfare, Japan.

222 Genetic Characterization of an Avian Influenza Virus, subtype H5N2, isolated from ducks imported into Singapore

Dawn Su-Yin Yeo¹, Ley-Moy Ng², Elizabeth Ai-Sim Lim¹, Shirley Gek-Kheng Sean¹, Chin-Wen Liaw¹, Lynn Lay-Hoon Tang¹, Gary Yuk-Fai Lau¹, Wai-Kwan Wong³, Chee-Wee Lim³, Richard Sugrue^{1,2}, Boon-Huan Tan¹, 1DMERI @DSO National Laboratories, 27 Medical Drive, Singapore 117510; 2Nanyang Technological University, Nanyang Avenue, Singapore 639798; ³Agri-food and Veterinary Authority, 6 Perahu Road, Singapore 718827

The avian influenza viruses (AIVs) subtype H5N2 have been reported to mutate from low pathogenic (LPAI) to high pathogenic AIVs (HPAI) in Pennsylvania (1983), Mexico (1994), Italy (1997) and Texas (2004). In addition, avian to human transmission of influenza viruses of both subtypes, H5N1 and H5N2, have been documented.

In 2004, the Defence Medical & Environmental Research Institute received 2 AIVs, (F118 and F189), from the Agri-food and Veterinary Authority of Singapore for diagnostic testing. These samples were isolated from ducks imported into Singapore and suspected to be of the HPAI subtype 'H5N1'. We used real-time polymerase chain reaction (PCR) for diagnostic testing, targeting the hemagglutinin (HA) and neuraminidase (NA) genes. The PCR amplicons were subjected to nucleotide sequencing. Our preliminary results confirmed the AIV samples to be of the virus subtype H5N2, but of low pathogenicity. In this presentation, we fully sequenced the HA and NA genes, and the 6 internal gene segments of isolate F118. Analysis of the cleavage site of the F118-HA protein showed the absence of basic amino acid (aa) residues associated with HPAI. However, the phylogenetic analysis of the F118-HA gene showed a distinct clustering with the Asian HPAI of the subtype H5N1, rather than with the American LPAI of the subtype H5N2. The F118-NA gene showed no deletion in the stalk sequence, which was reported in American viruses of subtype H5N2 isolated in chickens. Phylogenetic analysis of the NA genes further clustered F118-NA closely with subtypes H9N2, H1N2, and H7N2. Examination of the internal proteins of F118 revealed avian-specific aa signatures in the M1, M2, PB1, PB2, PA and NP proteins. No residues associated with amantadine resistance (M2) nor virulence was observed (PB2 and NS1 proteins). Phylogenetic analyses further suggest that the internal genes of the F118 isolate were derived from different influenza A virus subtypes, originating from the Asia-Europe regions. Interestingly, the F118-PA gene clustered more closely with the Asian viruses subtype H5N1, than with any of the AIVs subtype H5N2.

The sequence and phylogenetic data collected in this work will be useful in future molecular and epidemiological studies of the dynamics and evolution of circulating avian influenza viruses, in particular in this region of South-East Asia.

224 Hemagglutinin activity of avian influenza H5N1 viruses

Lerdsamran H, Louisirirotchanakul S, Wiriayrat W, Sangsiriwut K, Pooruk P, Kijphati R, Chaichoune K, Sawanpanyalert P, Pittayawonganon C, Ungchusak K, Auewarakul P, Puthavathana P. Microbiology, Fac. Medicine Siriraj Hospital, Mahidol Univ., Bangkok, Thailand

Horse hemagglutination inhibition (HI) test is recommended by WHO as an adjunct to micro-neutralization test for H5N1 antibody. As horse RBC can not be obtainable easily in most of Southeast Asian countries, the present study searched for an alternative species of RBC which provided as good result as that employing horse RBC in Hemagglutination (HA) and HI assays.

HA activity of 13 H5N1 viruses (5 human isolates and 8 animal isolates) was tested against 5 species of RBC: 1% horse, 0.5% goose, 0.5% chicken, 0.75% guinea pig and 0.75% human group O. Titration of a virus solution as using goose RBC yielded the highest titer, followed by chicken, guinea pig, human group O and horse RBC (Friedman test: $p<0.05$). The results were reproducible upon testing with 3 RBC donors from each species. HI antibody to two human H5N1 isolates was investigated in 15 sera from patients and survivors with the same 5 species of RBC donors. Using A/Thailand/1(KAN-1)/04 virus antigen, horse RBC gave significant higher antibody titer than the other 4 RBC species ($p<0.001$, Wilcoxon's signed-rank test, Bonferroni's adjustment). However, goose RBC yielded the highest titer when A/Thailand/676/05 virus was used as the antigen. These demonstrated that HI antibody activity was dependent on both the virus antigen and RBC species.

We also conducted complete HA genomic sequencing of all 15 H5N1 virus isolates. There were no difference in receptor binding site of these Thailand isolates as compared to Hong Kong 1997 and Vietnam 2005 viruses, except a mutational change of A138V of A/Thailand/676/05 virus. Our study proposes goose RBC as an alternative donor for HA assay and for virus recognition in the virus isolation method, and also as the indicator for HI assay.

This study was granted by BIOTEC and Thailand Research Fund.

Poster Abstracts

Tuesday, December 12: Poster Session 2

225 Adenoviral vector-based pandemic influenza vaccine against antigenically distinct H5N1 strains

Hoelscher², M.A., Garg², S., Bangari¹, D.S., Belser², J.A., Jayashankar², L., Lu², X., Stephenson², I., Bright², R.A., Singh¹, N., Pandey¹, A., Sharma¹, A., Matsuoka², Y., Donis², R.O., Katz², J.M., Sambhara^{2,*}, S., Mittal^{1,*}, S.K.¹ Department of Veterinary Pathobiology, Purdue University, West Lafayette, IN, USA and ²Influenza Branch, Division of Rickettsial and Viral Diseases, Centers for Disease Control and Prevention, Atlanta, GA 30333, USA. *, Equal contributors.

Avian H5N1 influenza viruses currently circulating in Asia, Europe, the Middle East and Africa could potentially cause the next pandemic. However, currently licensed human vaccines are subtype-specific and do not protect against these H5N1 viruses. We aimed to develop an egg-independent strategy to combat the H5N1 influenza virus, because the virus is highly lethal to chickens and the maintenance of a constant supply of embryonated eggs could be difficult in a pandemic.

We constructed a replication-incompetent, human adenoviral vector (HAd-H5HA) that expressed subtype 5 hemagglutinin. Immunization of mice with HAd-H5HA induced both humoral and cell-mediated immune responses significantly better than that of a traditional subunit vaccine when tested against H5N1 viruses isolated from people. Vaccinated mice were effectively protected from H5N1 disease, death, and primary viral replication when challenged with antigenically distinct H5N1 strains. These findings highlight the potential of an adenoviral vector-based delivery system, which is both egg-independent and adjuvant-independent and offers stockpiling options for the development of a pandemic influenza vaccine.

Data from our ongoing pre-clinical studies with new vaccine strategies involving human or nonhuman adenoviral vectors aimed at providing broader protection against pandemic influenza will also be presented.

The work is supported by NIH-AI-059374 and NVPO grants.

227 Use of conserved influenza antigens linked to immunostimulatory DNA (ISS) to generate broad immunity to divergent and potentially pandemic virus strains

Gary Van Nest¹, Tracy dela Cruz¹, Gary Ott¹, Emily Damon¹, Innocent Mbawuike², Brian Livingston¹, and Debbie Higgins¹
¹Dynavax Technologies Corporation, Berkeley, CA 94553 and ²Baylor College of Medicine, Houston TX 77030

Standard trivalent inactivated influenza vaccines (TIVs) have several key limitations. Because TIVs induce immunity to strain-specific HA and NA antigens, they offer limited efficacy against drift virus strains and no expected efficacy against shift virus strains that can lead to pandemics. In addition, TIVs demonstrate only modest immunogenicity in high risk groups such as the elderly. To address these deficiencies, we have conjugated the conserved influenza antigens nucleoprotein (NP) and matrix protein 2, extracellular domain (M2e) to immunostimulatory DNA sequences (ISS) to generate highly immunogenic conserved antigens that can be administered alone or in combination with TIV to induce potent, broadly reactive immunity.

NP-ISS induces strong Th1 and CTL responses that reduce viral replication and provide protection against shift and drift strains in mouse challenge systems. Co-delivery of NP-ISS with TIV enhances the antibody responses to HA in both mouse and primate models. M2e-ISS induces strong IgG2a antibody responses in mice without requiring complex M2e formulations. Similar to NP-ISS, co-delivery of M2e-ISS with TIV enhances the antibody response to HA in mice.

NP-ISS and M2e-ISS represent unique vaccine components that can provide strong, cross-strain protective immunity and can be used with TIV to enhance immunogenicity and possibly provide dose sparing of the TIV components. The NP-ISS/M2e-ISS vaccine represents a promising approach to a broadly reactive, universal influenza vaccine.

Research funding provided by NIAID grant 5U01 AI56447-4.

226 Oseltamivir sensitivity of H5N1 influenza isolates, Thailand

Puthavathana¹, Pooruk P, Sangsiriwit K, Nateerom K, Prasertsopon J, Chaichoune K, Wiriyarat W, Korkusol A, Auewarakul P, Chokephabulkit K, Ungchusak K, Sawanpanyal P, Ratanakorn P. Microbiology, Fac. Medicine Siriraj Hospital, Mahidol Univ., Bangkok, Thailand

Surveillance for oseltamivir sensitivity was conducted in 17 H5N1 viruses (6 isolates from humans, 9 from domestic and wild birds and 2 from tigers) isolated in Thailand during 2004-2006. Plaque inhibition assay using virus at concentration of 50 pfu/well was firstly employed with good success; however it is a laborious and difficult technique to be performed on large sample size. Additionally, some influenza isolates do not form plaque which made the drug sensitivity assay by plaque inhibition impossible. Therefore, the present study established drug sensitivity assay by using ELISA nucleoprotein reduction based method.

H5N1 viruses at concentration of 100, 25 and 5 TCID50/100µl/well were tested with oseltamivir carboxylate at concentration of 800, 200, 50, 12.5, ... and 0.000003 µM in triplicate in MDCK cell monolayer. Inhibitory concentration 50 (IC50) of each virus concentration was established from the dose response curve. With the three virus concentrations tested, IC50 of the 6 human isolates varied from 0.091-36.1 (mean= 12.63), 0.006-1.68 (mean = 0.413), and 0.004-0.43 (mean= 0.134) µM; whereas those of the animal isolates varied from 0.19- >800 (mean= undetermined), 0.031- >800 (mean= undetermined), 0.0007-6.92 (mean= 0.978) µM, respectively. According to dose response curve, oseltamivir resistant virus has not been detected in our study, even though, there were at least 2 human viruses that were isolated from dead cases which had received full course of treatment before. Too high virus inoculum of 100 and 25 TCID50 in two animal isolates may explain the undetermined IC50 of the drug.

Sequencing of all viruses studied did not show mutational change at amino acid positions 119, 274, 292 and 294 in neuraminidase gene.

The present study demonstrated a wide range of IC50 of oseltamivir against human and animal H5N1 isolates. Nevertheless, oseltamivir is still the drug of choice for H5N1 patients. Failure of the treatment should be explained by other factors such as time at drug administration, the drug regimen including mixed infection with other pathogen.

We are grateful to Thailand Research Fund for advanced research scholar; BIOTEC, Thailand; and Roche Company.

228 Acquisition and enhancement of fusogenicity by single amino acid substitutions in the spike protein are essential for adaptability and infectivity of coronavirus in cultured cells

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The cross-species transmission in coronavirus (CoV), such as SARS-CoV and human CoV-OC43, underlies the importance of studying the mechanisms of CoV host adaptation and interspecies transmission. Here we report studies on the adaptation of the Beaudette strain of infectious bronchitis virus (IBV) from chicken embryo to Vero cells and the underlying mechanisms. Following adaptation to Vero cells, a total of 49 amino acid mutations has taken place in the IBV genome, and 26 substitutions (53.06%) are located in the spike (S) protein.

Expression of S protein derived from the Vero cell-adapted strains (primary-adapted, p7; and secondary-adapted, p65) showed cell-cell fusion and syncytial formation. However, S protein obtained from the chicken embryo-adapted strain (EP3) could not cause cell-cell fusion. Construction of chimeric S genes and site-directed mutagenesis studies identified L857-F mutation in the heptad repeat 1 (HR1) is essential for the cell-cell fusion. In addition, G405-D mutation in the S1 domain enhances the fusogenicity of S protein and is responsible for the secondary adaptation. Introduction of F857-L into the S gene of the recombinant IBV virus based on the Vero cell-adapted IBV showed that the recovered virus do contain this mutation. However, only viruses with compensatory mutations at other positions of the S protein (Q523-L and I769-V; P327-S, Q523-L and I769-V) are infectious. Expression and mutagenesis studies confirmed that either Q523-L or I769-V mutation could compensate the F857-L mutation and restore the fusogenicity of the S protein. This study reveals that acquisition of fusogenicity by single amino acid substitutions in the S protein is essential for adaptation of a coronavirus from avian to mammalian species.



Hemagglutinin activity of avian influenza H5N1 viruses



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Horse hemagglutination inhibition (HI) antibody is one WHO notification for the H5N1 confirmed case. Unfortunately, horse erythrocytes can not be accessed easily in Asia countries.

Objective

To investigate the efficiency of avian influenza (H5N1) influenza viruses on erythrocytes receptor from five different species: horse, goose, chicken, guinea pig and human group O for using in both Hemagglutination (HA) and HI tests.

Materials and Methods

- Viruses : 14 human and animal H5N1 influenza viruses
- Serum samples : 15 human sera from 7 cases
- Erythrocytes from 5 species

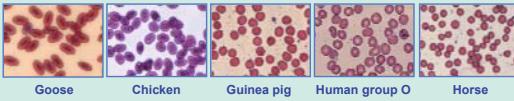


Table 1 : Condition of Hemagglutination test and Hemagglutination inhibition test

Concentration (%)	Guinea pig	Human gr O	Horse	chicken	goose
	0.75	0.75	1	0.5	0.5
Microtiter plate	U	U	U	V	V
Incubation time 4°C, min	60	60	60	30	30

(Stephenson, 2003 and WHO,2002)

Results

Titration of a virus solution as using goose erythrocyte yielded the highest geometric mean titer, followed by chicken, guinea pig, human group O and horse erythrocyte (Friedman test; p<0.05)

Table 2. Hemagglutination titer of influenza A viruses as assayed with erythrocytes from different species

H5N1 Influenza A viruses	Passage history	* HA titer based on erythrocytes of				
		Goose	Chicken	Guinea pig	Human gr.O	Horse
A/Thailand/1(KAN-1)/04	MK2, MDCK8	512	512	128	128	128
A/Thailand/2(SP-33)/04	MDCK8	64	64	32	16	
A/Thailand/3(SP-83)/04	MDCK8	64	64	16	32	16
A/Thailand/5(KK-494)/04	MDCK4	128	64	32	64	32
A/Thailand/676(NYK)/05	MDCK9	256	256	512	256	32
A/Tiger/Thailand/VSMU-11-SPB/2004	Egg I	512	512	256	256	256
A/Clouded Leopard/Thailand/VSKU-6-CB/2004	Egg I	512	512	256	256	<2
A/Great Barbet/Thailand/VSMU-2-CB/2005	MDCK2	128	128	64	64	32
A/Green Peafowl/Thailand/VSMU-3-CB/2005	MDCK2	256	128	64	64	64
A/Crane/Thailand/VSMU-4-CB/2005	MDCK2	512	256	128	128	128
A/Tree sparrow/Thailand/VSMU-16-RBR/2005	MDCK4	64	64	32	32	16
A/Golden Pheasant/Thailand/VSMU-21-SPB/2005	MDCK1	128	64	32	16	32
A/Pigeon/Thailand/VSMU-25-BKK/2005	MDCK3	64	64	32	16	16
A/Chicken/Thailand/(SPB)137/2005	MDCK4	512	512	64	64	128
Geometric Mean titer		190.21	156.03	74.25	67.25	33.62

* Only HA titer obtained from one out of three erythrocyte donors is presented

Table 3. H5N1 HI antibody titers as tested against different erythrocyte species

Serum Code (sequential blood)	A/Thailand/1(KAN-1)/04(H5N1)					A/Thailand/676(NYK)/05(H5N1)					NT Ab titer
	Goose	Chicken	Guinea pig	Human	Horse	Goose	Chicken	Guinea pig	Human	Horse	
CB KAN-1 (1)	20	<20	20	<20	20	<5	20	<20	<20	20	-
CB KAN-1 (2)	640	640	640	640	1280	1280	1280	1280	1280	640	-
TN	20	<20	20	20	40	80	160	80	80	80	40
SJ	20	<20	20	20	40	160	160	80	80	80	80
PT (1)	20	<20	<20	20	20	<5	-	-	-	-	-
PT (2)	20	<20	20	<20	20	5	20	-	-	20	-
PT (3)	40	20	20	40	80	160	320	160	80	320	-
PT (4)	40	20	20	40	80	160	160	80	160	160	80
MY 676 (1)	<20	<20	<20	<20	<20	<5	20	20	<20	<20	-
MY 676 (2)	<20	<20	<20	<20	<20	<5	20	<20	<20	<20	-
RB (1)	<20	<20	<20	<20	<20	5	<20	<20	<20	<20	-
RB (2)	320	160	160	160	640	1280	1280	1280	1280	1280	-
RB (3)	160	80	80	160	320	640	1280	640	640	640	-
RB (4)	20	20	20	40	80	160	80	80	40	40	80
BB	80	40	80	160	320	640	640	320	320	640	-
Geometric Mean antibody titer		36.47	22.97	28.95	33.25	57.89					
											118.9 116.19 80 84.38 92.81

Table 4. Statistical values from the analyses on difference in HI antibody titers as assayed against different viruses

Viruses	Geometric mean antibody titer as using erythrocyte from:				
	Goose	Chicken	Guinea pig	Human	Horse
A/Thailand/1(KAN-1)/04	36.47	22.97	28.95	33.25	57.89
A/Thailand/676(NYK)/05	118.9	116.19	80	84.38	92.81
2-sided exact p-value (Wilcoxon's signed-rank test)	0.001	0.002	0.004	0.004	0.102

Conclusions

- Goose erythrocyte is the most sensitive for virus recognition for influenza A virus, whereas horse erythrocyte can recognize only avian influenza virus.
- Not all H5N1 isolate can agglutinate horse erythrocyte.
- Regarding to HI antibody detection, horse erythrocyte can not demonstrate in clear cut for its advantage over goose as it is depend upon the virus strain.
- Our study proposes that goose erythrocyte confers higher advantage than horse in the determination for both presence of H5N1 virus or HI influenza antibody

Acknowledgments

This study was granted by BIOTEC and Thailand Research Fund.

References

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Respiratory Viruses Associated with Severe Pneumonia

Introduction

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Abstract

Conventional multiplex RT-PCR using Seeplex kit and indirect immunofluorescence (IFA) assay had been used to investigate for viral agents associated with severe pneumonia. Seeplex can diagnose 12 viruses, while IFA can do so for 6 viruses. Seeplex was statistically compared with IFA by agreement over chance in the investigation of 101 patients with severe pneumonia; the index of > 0.9 was found when both tests were used to diagnose respiratory syncytial virus (RSV) infection only. When Seeplex was compared with the gold standard real time RT-PCR in the diagnosis of influenza in 110 patients, its sensitivity was 66.7% for influenza A virus (fluA) and 85.71% for influenza B virus (fluB), while its specificity was 100%. Validation of Seeplex in the diagnosis of other viral agents should be further explored. With combination of all tests, RSV was the most common virus found (19.8%), and followed in order by human metapneumovirus (13.9%), parainfluenza virus type 1 (PIV 1) (11.9%) and adenovirus (11.9%). Seeplex could detect mixed viral infections in 11 (10.9%) cases; of which adenovirus, the most common mixed agent, was found in 8 cases.

The majority of acute upper and lower respiratory tract infections in human, especially pediatric patients, are caused by respiratory viruses such as RSV, PIV1, PIV3, adenoviruses, and influenza viruses. Laboratory assays including IFA, viral isolation, serodiagnosis, and molecular technique for viral genome detection were used for disease diagnosis. Recently, multiplex PCR using multiple primer pairs in single reaction is commercially available in order to investigate multiple agents simultaneously.

Objective

To investigate respiratory viruses associated with severe pneumonia by using multiplex RT-PCR (Seeplex) in comparison to real time RT-PCR and IFA

Materials and methods

Real-time TaqMan RT-PCR: This test was used as the gold standard for diagnosis of fluA and B viruses. **IFA:** Exfoliated cells present in NPA were used for detection of viral antigens by indirect IFA using Respiratory Panel IFA kit, Chemicon, USA. This method can diagnose the following viruses: RSV, PIV1, PIV2, PIV3, influenza A and B viruses, and adenovirus

Results

Multiplex RT-PCR for respiratory viruses (RV): RNA extracts (automated Biorobot EZ1 extraction, QIAGEN, USA) from NPA samples were reverse transcribed with random hexamer primers using Superscript III reverse transcriptase (Invitrogen, USA). Subsequently, cDNA was subjected to Seeplex RV12 ACE Detection (Seegene, Korea). This test kit includes 2 panels (RV1A and RV1B) of primer pairs specific to 12 RV: adenovirus, human metapneumovirus, coronavirus (229E), PIV1, PIV2, PIV3 in RV1A, and Flu A, Flu B, RSV B, Rhinovirus A, and coronavirus (OC43) in RV1B.

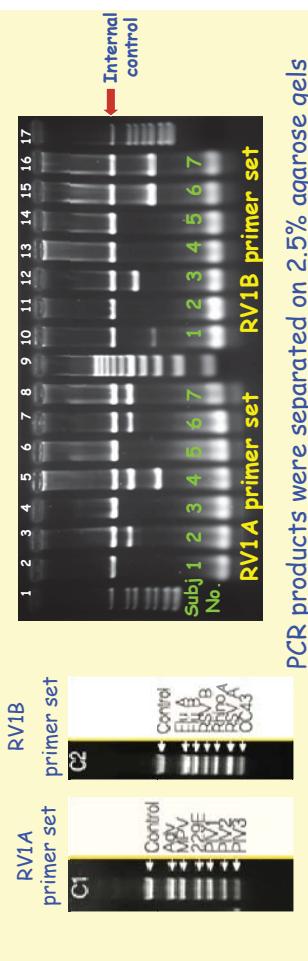
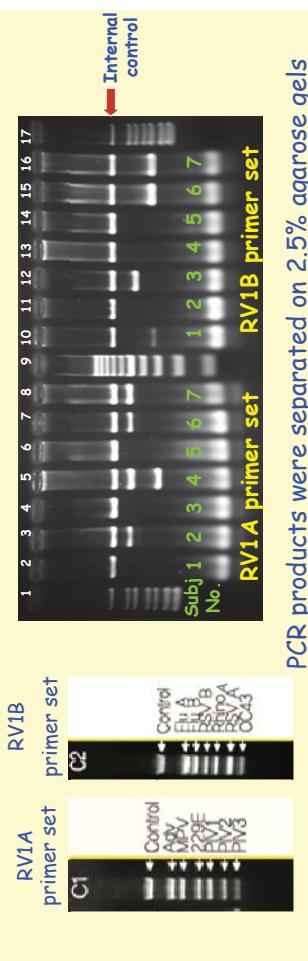
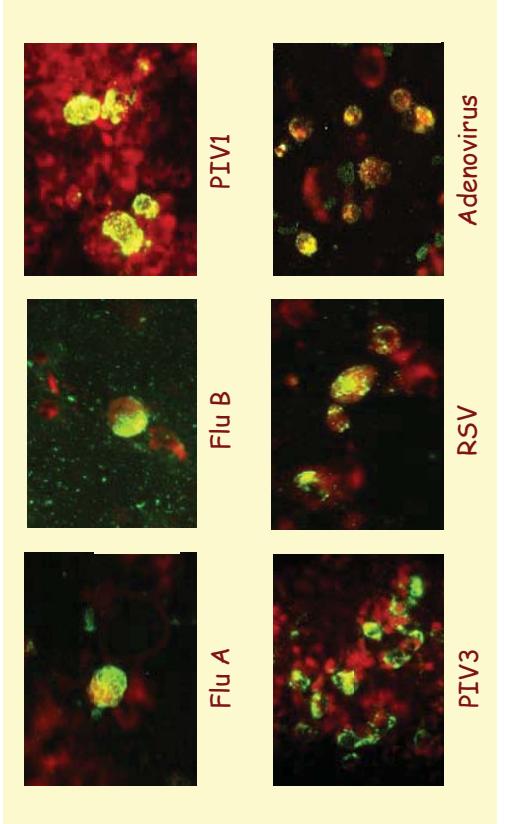


Fig 1. Immunofluorescence staining of virus infected cells in NPA. Positive cells exhibit an apple green color under fluorescence microscope.



PCR products were separated on 2.5% agarose gels

Table 1. Viral agents associated with severe pneumonia

Virus	No. of samples positive by	
	Seeplex method	IFA method
RSV A and B	17 (16.8%)	20 (19.8%)
Metapneumovirus	14 (13.9%)	Not Applicable
Parainfluenza type 1	12 (11.9%)	6 (5.9%)
Adenovirus	12 (11.9%)	5 (5.0%)
Rhino A virus	8 (7.9%)	Not Applicable
Influenza B	6 (5.9%)	5 (5.0%)
Influenza A	4 (4.0%)	5 (5.0%)
Coronavirus 229E and OC43	3 (3.0%)	Not Applicable
Parainfluenza type 3	2 (2.0%)	3 (2.97%)
Parainfluenza type 2	0 (0%)	0 (0%)
Total (n=101 cases)	78 viruses in 67 (66.3%)cases	44 viruses in 43(42.6%) cases

Table 2. Sensitivity and specificity of Seeplex and IFA for the detection of influenza virus *

Test	Virus	Sensitivity (%)	Specificity (%)	Predictive value	
				Pos	Neg
Seeplex	influenza A (n=4)	66.67	100	100	97.94
	influenza B (n=6)	85.71	100	100	98.94
IFA	influenza A (n=5)	71.43	100	100	98.10
	influenza B (n=5)	71.43	100	100	98.10

* real time RT-PCR was used as the gold standard

Among 101 cases investigated, 13 flu cases were diagnosed by real time RT PCR, while Seeplex can diagnose 10 cases

Among 110 cases investigated, 14 flu cases were diagnosed by real time RT PCR, while IFA can diagnose 10 cases

Table 3. Determination for agreement over chance index between Seeplex and IFA on the detection of respiratory viral agents

Virus	Agreement over chance index
RSV	0.96
Influenza A	0.88
Influenza B	0.71
Parainfluenza type 1	0.63
Parainfluenza type 3	0.38
Adenovirus	0.55

Index value between 0.9-1.0 indicates real agreement between two assays

Conclusion

An acute viral respiratory disease can be caused by several respiratory viruses leading to need of tools that can diagnose multiple agents simultaneously, and at the same time, require small amount of respiratory specimens. IFA, with limited supply of specific antibodies, can diagnose 7 viruses; while Seeplex can diagnose 12 viruses. Therefore, Seeplex should be superior to IFA in term of number of agents it can diagnose; and it is also less subjective and requires less experience to run multiplex PCR. However, accuracy of Seeplex has never been demonstrated. When Seeplex and IFA were statistically compared by agreement over chance, good agreement of >0.9 was obtained with RSV diagnosis only. Moreover, when Seeplex was compared with the gold standard RT-PCR for influenza diagnosis, Seeplex could detect only 10 of 13 of cases. Other tools to validate Seeplex on its capability to diagnose other viral agents are needed.

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Respiratory Viruses Associated with Severe Pneumonia

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Abstract

Conventional multiplex RT-PCR using Seeplex kit and indirect immunofluorescence (IFA) assay were used to investigate for viral agents associated with severe pneumonia in Thai patients. Our result demonstrated that > 80% of pediatric cases were associated with viral infection; and 60% of them were two years old. RSV was the most common virus found (23.6%), and followed in order by adenovirus (14.3%), Flu A (8.7%), and HuMV (8.2%). Viral infections were found only in 30% of adult cases. Seeplex could detect mixed viral infections in 14 (7.2%) cases: of which adenovirus was the most common mixed agent. Seeplex was statistically compared with IFA by agreement over chance and it was found that the agreement over 0.80 was found with RSV, flu A and flu B only.

Objective

To investigate respiratory viruses associated with severe pneumonia by using multiplex RT-PCR (Seeplex RV detection kit, Seegene, Korea) and IFA.

Materials and Methods

Subjects: This study comprised 195 severe pneumonia patients: 163 children and 32 adults from 4 hospitals in Thailand. 99 (60.7%) pediatric cases were under two years old. Adult cases had age-range between 27 and 81, of which (71.9%) were older than 50.

Immunofluorescence assay (IFA): Exfoliated cells present in NPA were used for detection of viral antigens by indirect IFA using Respiratory Panel IFA kit, Chemicon, USA.

Multiplex RT-PCR for respiratory viruses (RV): RNA extracts from NPA samples were reverse transcribed with random hexamer primers. Subsequently, cDNA was subjected to Seeplex RV Detection (Seegene, Korea). This test kit includes 2 panels (RV1A and RV1B) of primer pairs specific to 12 RV: adenovirus, human metapneumovirus, coronavirus (229E), PIV1, PIV2, PIV3 in RV1A, and Flu A, Flu B, RSV B, Rhinovirus A, RSV A, and coronavirus (OC43) in RV1B.

Results

Fig 1. Immunofluorescence staining of virus infected cells in NPA. Positive cells exhibit an apple green color under fluorescence microscope.

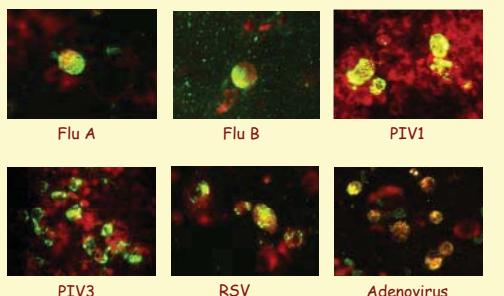
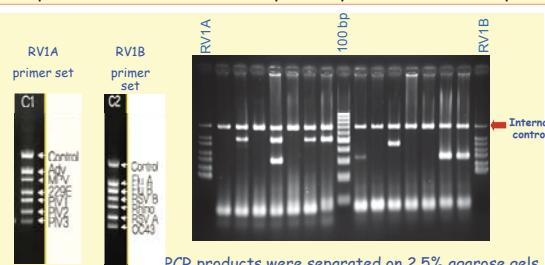


Fig 2. Seeplex® RV detection of respiratory viruses in NPA specimens.



Acknowledgements

This study was supported by Thailand Research Fund for Senior Research Scholar, Mahidol University Research Grant, and South East Asia Infectious Disease Clinical Research Network (SEAICRN).

Table 1. Viral agents associated with severe pneumonia

Virus	Positive by						
	IFA			Seeplex			
Adult	Pediatric	Total	Adult	Pediatric	Total	Grand total	
Flu A	1	15	16	1	14	15	17 (8.7%)
Flu B	0	8	8	1	7	8	9 (4.6%)
PIV 1	1	6	7	1	11	12	12 (6.1%)
PIV 2	0	1	1	0	1	1	1 (0.5%)
PIV 3	1	4	5	1	4	5	6 (3.0%)
RSV	0	43	43	0	41	41	46 (23.6%)
Adenovirus	1	12	13	1	26	27	28 (14.3%)
HuMV	NA	NA	NA	2	14	16	16 (8.2%)
Rhino A virus	NA	NA	NA	1	15	16	16 (8.2%)
Coronavirus	NA	NA	NA	1	2	3	3 (1.5%)
Total viruses	4	89	93	9	135	144	154 (78.9%)

Total positive pediatric cases = 130/163 (79.7%)

Total positive adult cases = 10/32 (31.2%)

Table 2. Investigation for viral agents by IFA and Seeplex

	IFA	Seeplex			Seeplex			Seeplex						
		(+)	(-)	Total	(+)	(-)	Total	(+)	(-)	Total				
IFA	(+) Flu A	14	2	16	IFA	(+) Flu B	7	1	8	IFA	(+) RSV	38	5	43
	(-) Flu A	1	178	179		(-) Flu B	1	186	187		(-) RSV	3	149	152
	Total	15	180	195		Total	8	187	195		Total	41	154	195
	IFA	Seeplex			Seeplex			Seeplex						
	IFA	(+)	(-)	Total	(+)	(-)	Total	(+)	(-)	Total				
	IFA	(+) Adeno	12	1	13	IFA	(+) PIV 1	7	0	7				
		(-) Adeno	15	167	182		(-) PIV 1	5	183	188				
		Total	27	168	195		Total	12	183	195				
	IFA	Seeplex			Seeplex			Seeplex						
	IFA	(+)	(-)	Total	(+)	(-)	Total	(+)	(-)	Total				
	IFA	(+) PIV 2	1	0	1	IFA	(+) PIV 3	4	1	5				
		(-) PIV 2	0	194	194		(-) PIV 3	1	189	190				
		Total	1	194	195		Total	5	190	195				

Table 3. Determination for agreement over chance index between Seeplex and IFA on the detection of respiratory viral agents

Virus	Agreement over chance index
PIV 2	1.00
Flu A	0.89
RSV	0.88
Flu B	0.87
PIV 3	0.79
PIV 1	0.72
Adenovirus	0.56

Index value between 0.9-1.0 indicates real agreement between two assays

Conclusions

An acute viral respiratory disease can be caused by several respiratory viruses leading to need of tools that can diagnose multiple agents simultaneously, and at the same time, require small amount of respiratory specimens. Seeplex should be superior to IFA in term of number of agents it can diagnose; and it is also less subjective and requires less experience to run multiplex PCR. However, accuracy of Seeplex has never been demonstrated.



Human Influenza Virus-Specific T Cells Mediated Cross Reactive Immune Response to Nucleoprotein (NP) Derived from Avian Influenza H5N1 Virus

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Background:

Protection against influenza A virus by specific antibody is relatively strain specific; meanwhile, broader immunity may be conferred by cell mediated immune response (CMIR) (1). Therefore, development of universal influenza vaccine that can confront seasonal influenza viruses as well as avian influenza H5N1 viruses of multiple clades, is desirable. Previous studies had shown that immunity induced by old influenza isolates could alleviate the severity of disease caused by novel strains or subtypes. It is suggested that this cross immunity is mediated by the heterosubtypic T-cell response. In this context, induction of cross-reactive CD4⁺ and CD8⁺ cytotoxic T lymphocytes (CTL) that recognize conserved epitopes in internal protein of influenza virus are of interest (2,3). This prompted us to identify and characterize a set of T cell conserved epitopes that would contribute to broad immune response across influenza virus subtypes. This study measured cross cell-mediated immunity to H5N1 virus in healthy subjects by ELISpot and flow cytometry assays using overlapping peptides derived from nucleoprotein (NP) as the test antigen.

Materials and Methods:

A total of 30 subjects included 23 healthy individuals in which 18 had history of receiving seasonal influenza vaccine at least once, and 7 subjects who had history of influenza infection one month ago. Peripheral blood mononuclear cells (PBMCs) from these subjects were kept frozen until used. A panel of 20 mer peptides with 10 mers overlapping, were synthesized based on amino acid sequence derived from NP of A/Thailand/1(KAN-1)/2004 (H5N1) virus (KAN-1 virus) (accession number AAV 35112). Totally, this panel comprised 49 peptides. Memory T cells that cross-reacted to these NP overlapping peptides were measured by the *ex vivo* IFN- γ enzyme-linked immunospot (ELISpot) assay. Flow cytometry employing intracellular cytokine staining (ICS) was used for immunophenotyping of the peptide restricted T cells. Microneutralization (MicroNT) assay to KAN-1 virus was performed to determine status of previous H5N1 virus infection.

A) >g1|54610029|pb|ANV35112.1| nucleocapsid protein [Influenza A virus (A/Thailand/1(KAN-1)/2004[H5N1])

MASQKTTSYEQMTEGGERNATEIIRASVWRMVGSIQRFVPIQMCTELKLDYEGRLQLNSITTEIRWMLSA

FDEERNRVYLEHHHSAGKDPKPKTGGPQYIYRRDGKWRLELLYKEEIRIRWQGANNEDATAGLTHLM191
SNLNDATYQTRALVVRTMDPRMCSLMQGSTLFRSGAAAGAVKGVQTMVMEMLRKG192INDRNPWRQD
NGRGRVIAYERMGMLKQPKTQAGAQRANRQKRSRSPGNAFQAEIDLFLVQVQVQVQVQVQVQVQVQVQVQVQ
KQVQ
RUVFQKQVQ
ERATIMAPFTQNTPTQPTQPTQPTQPTQPTQPTQPTQPTQPTQPTQPTQPTQPTQPTQPTQPTQPTQ
DNAEAYDN

B) I(Met) 498(Asn)

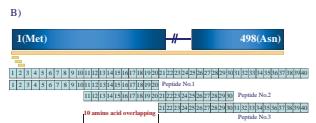


Fig. 1 Amino acid sequence of NP of KAN-1 virus (A); NP overlapping peptides were synthesized by Sigma-Genosys (Sigma-Aldrich, Singapore) in the PEPscreen[®] custom peptide libraries panel. A total of 49 peptides are overlapped by 10 amino acid residues (B); Peptides were pooled in a 2-dimensional matrix system (C).

Results:

All 30 subjects had no antibody to H5N1 virus as tested by microNT assay. However, 13 (43%) subjects exhibited cross-reactive specific T cell response by ELISpot. Altogether, these subjects recognized only 4 of 49 peptides tested (Fig. 3A). The average magnitudes of *ex vivo* ELISpot IFN- γ were 63 SFU/10⁶ PBMCs, and the frequency of responsiveness was 1 to 2 peptides/subject (Fig. 3B). CD4⁺ T cells were mainly responsible for peptide recognition as they were present in all 13 responders; while CD8⁺ T cells were found only in one responder. Examples are shown in Fig. 4. There was only one responder who had both peptide specific CD4⁺ and CD8⁺ T cells, but both types of cells recognized different epitopes. In addition, there was one peptide that can stimulate both CD4⁺ and CD8⁺ T cell response (Table 1).

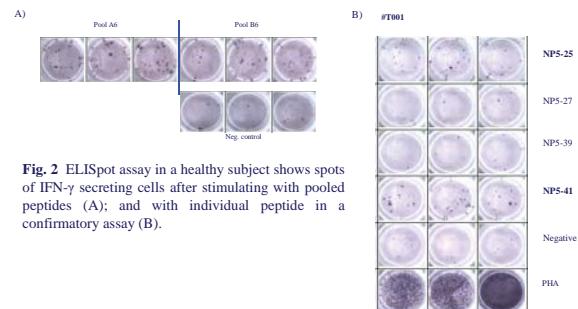


Fig. 2 ELISpot assay in a healthy subject shows spots of IFN- γ secreting cells after stimulating with pooled peptides (A); and with individual peptide in a confirmatory assay (B).

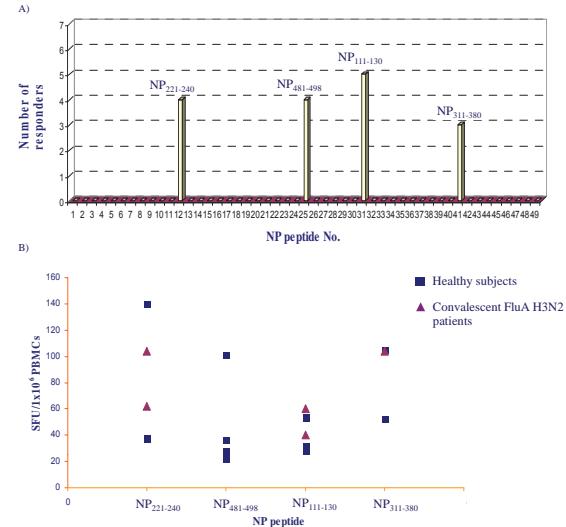


Fig. 3 Peptide recognition and frequency of responsiveness, NP₂₂₁₋₂₄₀ (RMCNLIKGFQTAQRAQMD) denotes NP₅₁₋₅₂, NP₄₈₁₋₄₉₈ (MNNEGSYFFGDNAEYDN) denotes NP₁₁₁₋₁₃₀ (YDKEEIRRIWRQANNGEDAT) denotes NP₅₋₃₁, and NP₃₁₁₋₃₈₀ (QVFSLIRPNENPAHKSQLVW) denotes NP₅₋₄₁ in the 2 dimensional matrix system (A); magnitudes of ELISpot response in 13 responders (B).

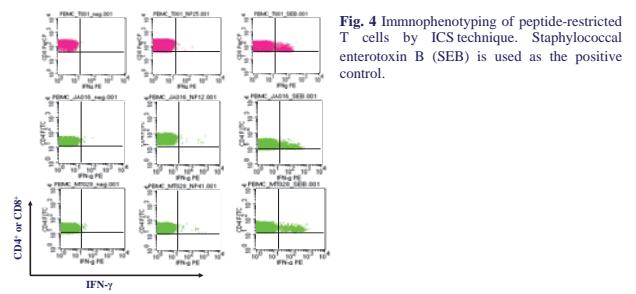


Fig. 4 Immunophenotyping of peptide-restricted T cells by ICS technique. Staphylococcal enterotoxin B (SEB) is used as the positive control.

Table 1. Frequency of NP peptides recognition by CD4⁺ or CD8⁺ T cells from 13 responders

Responders	NP peptide recognized by T cells							
	NP5-12(NP ₂₂₁₋₂₄₀)		NP5-25(NP ₄₈₁₋₄₉₈)		NP5-31(NP ₁₁₁₋₁₃₀)		NP5-41(NP ₃₁₁₋₃₈₀)	
	CD4 ⁺ T cells	CD8 ⁺ T cells	CD4 ⁺ T cells	CD8 ⁺ T cells	CD4 ⁺ T cells	CD8 ⁺ T cells	CD4 ⁺ T cells	CD8 ⁺ T cells
Healthy (n=9)	2	-	3	1	3	-	2	-
Convalescent Flu A patients (n=4)	2	-	-	-	2	-	1	-

Conclusions:

Healthy individuals who had never been infected with H5N1 virus may exhibit cross cellular immunity against this virus as assayed by ELISpot and flow cytometry using overlapping peptides derived from H5N1 NP. Four NP immunodominants were identified. Our study may be useful in the vaccine design and understanding of natural T cell immunity.

Acknowledgement:

This study was supported by the Thailand Research Fund for Senior Research Scholar, and the National Science and Technology Development Agency.

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Electron micrographs of H5N1 virus and its replication in MDCK cells

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Background: Since 2003, re-emergence of highly pathogenic avian influenza (HPAI) H5N1 virus has swept across continents and causes poultry die-off including severe pneumonia in humans. Morphology of this influenza virus subtype has never been characterized. In this study, we demonstrated electron micrographs of HPAI H5N1 particles together with low pathogenic avian influenza (LPAI) viruses. In addition, localization of H5N1 viruses in MDCK infected cells was shown under a transmission electron microscope (TEM).

Materials and methods: The viruses employed in this study included 9 HPAI H5N1 (4 from human and 5 from avian); 4 LPAI virus subtypes H1N1, H3N2, H5N3 and H7N1; and 2 human isolates of H1N1 and H3N2 subtypes. Human viruses were isolated and propagated in cell culture, whereas avian viruses were isolated and propagated in embryonated eggs. These viruses, except one LPAI virus with uncertain passage history, were sub-cultivation for less than 10 passages. The virus particles were visualized by negative staining with 2% phosphotungstic acid. Meanwhile, thin sections of MDCK cells infected with A/Thailand/1(KAN-1)/04 (H5N1) were positively double stained with uranyl acetate and lead citrate. The grids were examined under a transmission electron microscope (JEOL 1230, Japan).

Results: Influenza virus particles were pleomorphic. Three forms of morphology of different sizes were demonstrated: spherical (diameter 80–120 nm), rod (length 121–300 nm) and filamentous (length >300 nm) (Fig. 1). Regarding virus replication in MDCK cells, we demonstrated ultrastructure of virus inclusions in the cell cytoplasm, including virus particles at entry and the budding out particles at exit (Fig. 2).

Acknowledgements:

We thank the skillful technical assistance of the personnel from Virology Laboratory of Department of Microbiology and Veterinary Science, Mahidol University, for providing human and animal influenza viruses collection. And electron microscope team, Department of Pathology, Faculty of Medicine Siriraj Hospital for assistance with photographs



This study was supported by Thailand Research fund for Senior Research Scholar through Prof. Pilaipan Puthavathana

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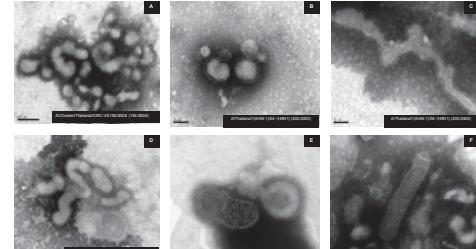


Fig 1. Pleomorphic morphology of influenza A virus from human and avian isolates in culture fluid with negative staining 1) H5N1 HPAI of A/Chicken/Thailand/ICRC-VS195/08 [A] and A/Thailand/1(KAN-1)/04 [B and C]; 2) LPAI of A/Duck/Jiangxi/6151/03 (H5N3) [D]; human influenza A/New Caledonia/20/99 (H1N1) [E] and A/Fujian/411/02 (H3N2) [F] strains.

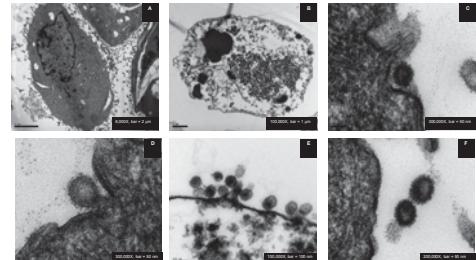


Fig 2. Electron micrograph of H5N1 A/Thailand/1(KAN-1)/04 in MDCK cell culture with positive staining. Negative control [A] and the infected cell [B]. Attachment of the virus onto the cell [C] and budding out from the infected cell [D] and a large number of viruses releasing from the infected cells [E and F].

Conclusions: Electron micrographs of influenza virus particles demonstrated that spherical form was the predominate population among all virus subtypes studied, regardless of host of origin, virus virulence or passage history. Positive staining of uninfected MDCK cells as observed at low magnification showed surface pili which might be miss interpreted as the filamentous form of virus particles. Nevertheless, this appearance could be identified by higher resolution and magnification of the modern electron microscope. Herein, we showed lines of spherical particles budding from the cell surface. Our finding was not different from what had been previously reported with human viruses.

Surveillance for Sensitivity of Influenza A and B Viruses to Neuraminidase Inhibitors



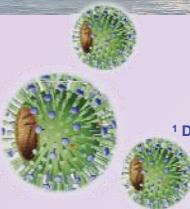
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Background

Oseltamivir and zanamivir are neuraminidase inhibitors against both influenza A and B viruses. Monitoring for neuraminidase inhibitor resistant viruses can be accomplished by phenotypic and genotypic based assays. Our study employed neuraminidase inhibition (NAI) assay together with nucleotide sequence analysis for amino acid substitution in NA gene to determine sensitivity of influenza A and B viruses to oseltamivir and zanamivir.

Materials and Methods

Test viruses:

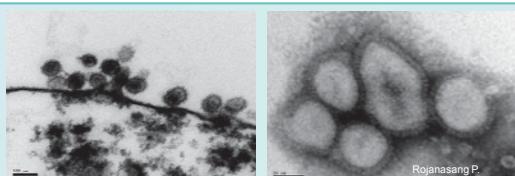
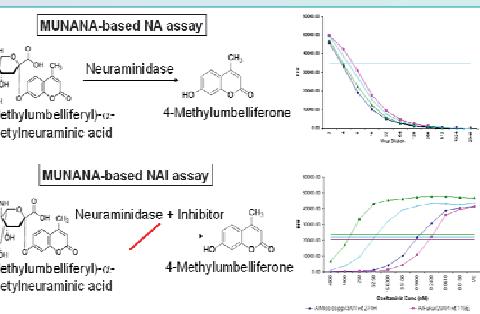
- 38 influenza virus isolates from 2007-2009
- 8 pandemic influenza A/H1N1 isolates
- 6 human influenza A/H1N1 isolates
- 15 human influenza A/H3N2 isolates
- 9 influenza B isolates

Reference viruses:

- A/Mississippi/03/01(H1N1) wild type-274H and its resistant mutant-274Y
- A/Fukui/20/04 (H3N2) wild type (119E)
- A/Fukui/45/04 (H3N2) mutant (119V)

MUNANA-based NAI assay

NA gene sequencing



Acknowledgements

This study was supported by the Thailand Research Fund for Senior Research Scholar, and the South East Asia Infectious Disease Clinical Research Network.

Results

Table. Drug sensitivity and NA molecular marker of influenza A/H1N1, A/H3N2, pandemic influenza A/H1N1/2009 and influenza B viruses

Viruses	IC ₅₀ values (nM)		Resistant markers						
	Oseltamivir	Zanamivir	Oseltamivir			Zanamivir			
			E119V	D198N	H274Y	R292K	E119G/A/D	R152K	R292K
Reference viruses									
A/Mississippi/03/01(H1N1) wildtype-274H	1.53	1.18				H			
A/Mississippi/03/01(H1N1) mutant-274Y	591.66	2.26				Y			
A/Fukui/20/04(H3N2) wildtype-119E	0.31	0.67	E					E	
A/Fukui/45/04(H3N2) mutant-119V	72.63	5.74	V					V	
H1N1 viruses (N=6)									
3043	875.25	3.89	E	D	Y	R	E	R	R
3422	1.27	3.54	E	D	H	R	E	R	R
3461	2.16	2.15	E	D	H	R	E	R	R
3479	391.16	1.53	E	D	Y	R	E	R	R
3509	584.91	2.33	E	D	Y	R	E	R	R
3619	646.77	1.02	E	D	Y	R	E	R	R
Range	1.27-875.25	1.02-3.89							
Median	488.04	2.24							
Mean	416.92	2.41							
H3N2 viruses (N=15)			E	D	H	R	E	R	R
Range	0.29-1.04	0.25-2.64							
Median	0.5	0.62							
Mean	0.54	1.05							
for all isolates									
Pandemic H1N1 viruses (N=8)							Not done		
Range	0.5-1.43	0.27-1.03					Not done		
Median	1.08	0.69					Not done		
Mean	1.10	0.68					Not done		
Influenza B viruses (N=9)									
Range	10.97-45.83	5.26-23.34							
Median	23.93	6.58							
Mean	25.24	10.87							

- Both seasonal and pandemic influenza A/H1N1 together with A/H3N2 isolates were zanamivir sensitive.
- All pandemic A/H1N1 and A/H3N2 isolates were oseltamivir sensitive; whereas, 4 of 6 (66.7%) seasonal A/H1N1 viruses were oseltamivir resistant viruses
- All influenza B isolates showed a decrease in sensitivity to both oseltamivir and zanamivir
- NA sequencing data showed the molecular marker H274Y in seasonal A/H1N1 oseltamivir resistant viruses

Conclusion

Oseltamivir resistant seasonal H1N1 virus is a growing problem worldwide. Nevertheless, influenza B viruses should be closely monitored for emerging of neuraminidase inhibitor resistance as it has been shown to require higher dose for the disease treatment.



Hemagglutinin-Inhibition and Microneutralization Assays for Antibodies to Pandemic Influenza A (H1N1) 2009 Virus



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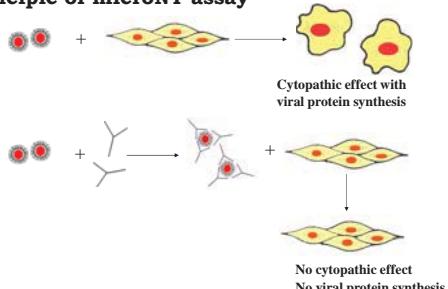
Introduction

Hemagglutinin-inhibition (HI) assay has been established for decades for human influenza diagnosis and evaluation of vaccine immunogenicity. Additionally, on the basis of antigenic drift, HI employing a panel of reference antisera is used for vaccine strain selection by the World Health Organization annually. In contrary, microneutralization (microNT) assay is recommended for detection of antibody to H5N1 and pandemic influenza A (H1N1) 2009 viruses. The present study applied those two assays to determine the cut-off titer for diagnosis of the pandemic influenza A(H1N1) 2009.

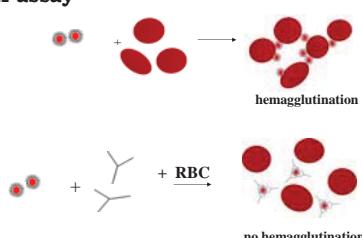
Material and Method

A total of 37 patients (9 children and 28 adults) who were diagnosed pandemic influenza A(H1N1) 2009 by RT-PCR, were enrolled. There were 18 subjects whose first blood samples were collected at ≤ 7 days after disease onset, and later for the remaining cases. Serum samples were assayed for specific antibody by goose erythrocyte HI and ELISA based microNT using A/Thailand 104/09 (H1N1) as the test virus.

Principle of microNT assay



Principle of HI assay



Result:

Rising in antibody titer could be demonstrated mostly in patients whose first blood samples were collected within 7 days and convalescent blood samples were collected between 3 to 5 weeks after onset of disease. Nevertheless, frequency of a four folded rise in HI or microNT titer was low, even in subjects whose first blood samples were collected earlier. This is according to presence of high antibody level in the first blood samples (Table 1 and Figs 1A and 1B).

Table 1. Serodiagnosis of pandemic influenza 2009

Patient	No. cases	Number with a 4-folded rise in antibody titer	
		MicroNT	HI
Adult	28	3	6
Children	9	5	4
Total	37	8 (21.6%)	10 (27.0%)

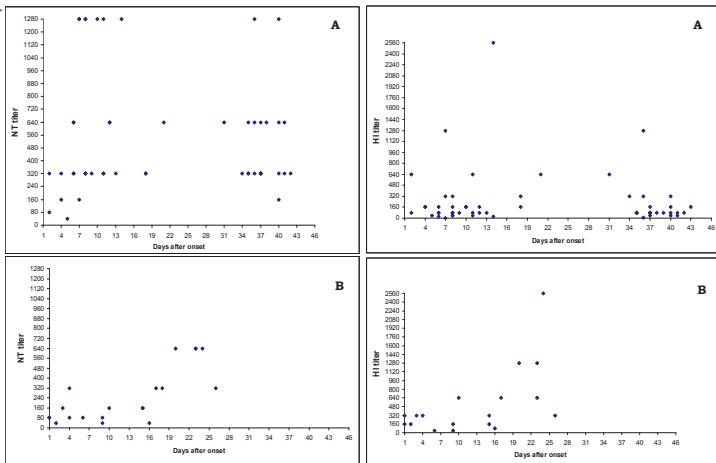


Fig.1 Antibody response in paired blood from adult (A), and pediatric cases (B)

Table 2. Cut-off titers for disease diagnosis

Criteria	Percentages of sensitivity
MicroNT titer ≥ 320	91.9
HI titer ≥ 40	97.3
MicroNT titer ≥ 320 and HI titer ≥ 40	89.2

Conclusion:

Previous seasonal H1N1 infection might boost an anamnestic response, and then, results in a rapid rise in antibody level in acute blood sample such that a marked increase in antibody titer in convalescent blood samples cannot be shown in most of the patients. Therefore, serodiagnosis does not help much in disease diagnosis, but it will be useful for epidemiological study. Our preliminary result proposed the cut-off titers for the diagnosis of pandemic influenza 2009 as shown in Table 2. More data is needed before this criteria is firmly established.

Acknowledgement: This study is supported by the Thailand Research Fund for Senior Research Scholar and the South East Asia Infectious Disease Clinical Research Network (SEAICRN), Thailand.

Viral Load of Pandemic Influenza A (H1N1) 2009 Virus in Various Types of Respiratory Specimens



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Background: Nasopharyngeal aspirate (NPA), nasal swab (NS), and throat swab (TS) are common specimens used for respiratory virus diagnosis by PCR/RT-PCR, antigen detection and viral isolation. However, there is no documented data regarding a type of specimen that yields the best result for viral detection. In this study, real time RT-PCR specific for *M* gene of influenza A virus, was used to determine viral load present in NPA, NS and TS samples collected from the same patient with pandemic A/2009 (H1N1) infection. Copy numbers of *M* genomic segments present in each type of specimen were compared. The results, then, can guide clinicians in making choice of clinical samples for the H1N1 2009 diagnosis.

Materials and methods: A total of 12 patients: 2 adults and 10 pediatric cases, with severe pneumonia caused by pandemic influenza A (H1N1) 2009 virus were enrolled in the study. From each patient, NPA, NS and TS swabs were collected and put into each tube containing 2 ml of viral transport media (VTM). Viral load present in each kind of clinical sample was determined based on copy number of *M* genomic segments. Briefly, known copy numbers of *in vitro* *M* RNA transcripts derived from pandemic influenza A (H1N1) 2009 virus were used as standard RNA, and amplified in parallel with the test sample by real time RT-PCR using CDC protocol version 2009. Alignment of primers/probe against the pandemic 2009 viruses is shown in Fig.1. Standard curve of *M* copy numbers was constructed from the C(t) values of standard RNA transcripts; and then, copy number of *M* segments in the test sample was obtained by extrapolation of its C(t) value against this standard curve (Fig.2).

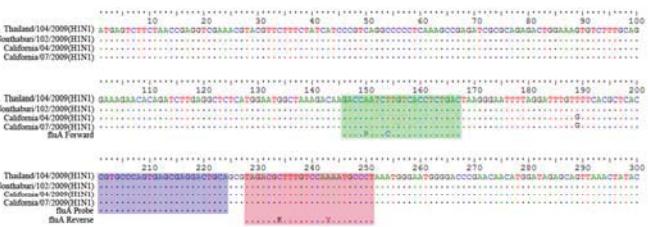


Fig. 1 Sequence alignment of primers/probe set against *M* gene of influenza A (H1N1) 2009 viruses

Results: Of 12 subjects, *M* RNA segments were detected in 12 NPA, 12 NS and 9 TS samples (Table 1). NPA specimens were found to contain the highest amount of influenza viral load, and followed in order by NS and TS samples. Mean copy numbers of viral load in NPA specimens was 1.54×10^8 (range 6.54×10^5 - 8.10×10^8) copies/ml of VTM; and it was 6.53×10^7 (range 5.62×10^2 - 4.93×10^8) copies/ml for NS and 1.05×10^6 (range 0 - 7.38×10^6) copies/ml for TS (Table 2). Examples of real time RT-PCR results are shown in Fig.3.

Table 1 Detection rate of *M* gene in each kind of specimen by real time RT-PCR

Number of subjects	Number of positive cases		
	NPA	NS	TS
12	12 (100%)	12 (100%)	9 (75%)

Table 2 Mean, median and range of copy numbers of viral load in each kind of sample

Virus	Statistics	NPA	NS	TS
H1N1/2009	Mean	1.54×10^8	6.53×10^7	1.05×10^6
	Median	4.02×10^7	8.49×10^6	7.56×10^4
	Range	6.54×10^5 - 8.10×10^8	5.62×10^2 - 4.93×10^8	0 - 7.38×10^6

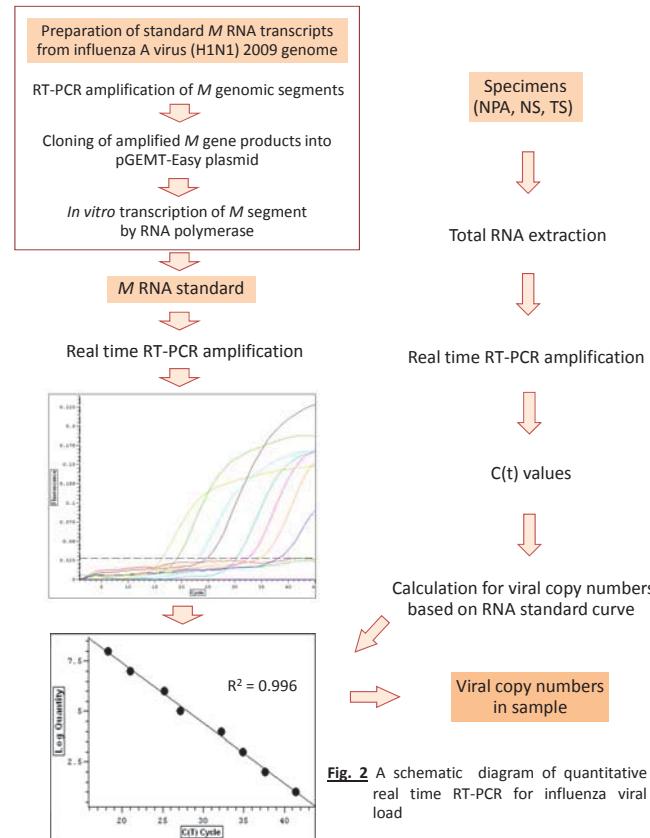


Fig. 2 A schematic diagram of quantitative real time RT-PCR for influenza viral load

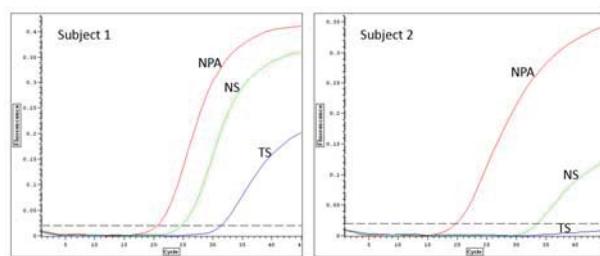


Fig. 3 Examples of real time RT-PCR results

Conclusion: Based on *M* gene copy numbers, we conclude that NPA is the best specimen for detection of pandemic influenza A (H1N1) 2009 virus, and followed in order by NS and TS.

Acknowledgement: This study is supported by Thailand Research Fund for Senior Research Scholar. We thank South East Asia Infectious Disease Clinical Research Network (SEAICRN), Thailand for providing clinical specimens.



Seroprevalence to HPAI H5N1 virus in healthy backyards chickens living in repeated outbreak areas of Thailand

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Background:

Thailand has been affected by several waves of H5N1 HPAI outbreaks since 2004. AI control with biosecurity is strictly implemented in industrial poultry farms. However, this type of control is costly and difficult to implement in villages where flocks of backyard poultry are raised for family consumption. Even though, there has been no human case since August 2006, AI is occasionally reported in free ranging birds in remote areas. Thai native chickens and free ranging ducks are relatively resistant to HPAI H5N1 virus. Some may be infected without developing clinical signs and death. Viruses shed from these infected poultry may contaminate the environment and become sources of viral spread in nature. Therefore, this study conducted serosurveillance to determine H5N1 virus infection rate in backyard, Thai native chickens resided in AI repeated outbreak areas.



Materials and methods:

This study was approved by the Ethical Committee for Animal Health and Welfare, Faculty of Veterinary Science and the Animal Assurance PHS from Office of Laboratory Animal Welfare, USA (OLAW No. A5731-01). The study was carried out during January 2007 to August 2009 in 6 provinces: Nakhonsawan, Lopburi, Sukhothai, Phitsanulok, Kamphaeng Phet and Uttradit. Blood samples were collected from backyards chickens with consent from the owners. ELISA based microneutralization assay in MDCK cell monolayer were conducted in biosafety level-3 containment facilities. The reciprocal antibody titer of 40 was the cut-off level for positive result.



Results:

Among 707 healthy backyards chickens, 12 (1.7%) had H5N1 neutralizing antibody. By location, 6 chickens were in Phitsanulok, 5 in Sukhothai and one in Uttradit provinces.

Table 1. Seroprevalence to HPAI H5N1 virus in healthy backyards chickens

Provinces	No. of positive/ no. of chickens	Seropositive (%)
Nakhonsawan	0/4	0
Kamphaeng Phet	0/6	0
Phitsanulok	6/40	15
Lopburi	0/6	0
Sukhothai	5/588	0.85
Phichit	0/1	0
Uttaradit	1/62	1.61
Total	12/707	1.70

Conclusion:

The study demonstrated that backyards chickens resided in repeated outbreak areas, could survive H5N1 infection. Asymptomatically infected chickens may play role as silent spreaders and maintain the virus in nature. Outbreak may occur when the virus is spread to population of susceptible animals. Our finding lead to the suggestion that HPAI H5N1 virus might has become an endogenous pathogen of Thailand.

Acknowledgement:

This study supported by US. CDC (Cooperative Agreement Number 1U19CI00399-01). The study was also partial supported by Thailand Research Fund for Senior Research Scholar through P.P., the grant PI.



Seroprevalence of HPAI H5N1 Virus in Domestic Dogs and Cats Living in Repeated Outbreak Areas in Thailand

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Background: Highly pathogenic avian influenza (HPAI) H5N1 virus had been documented for its infectivity in several kinds of mammals including tigers and domestic dogs and cats which are the most popular pets of humans. HPAI has been well controlled; and no human cases occurred in human since August 2006. However, small outbreaks occasionally occur in backyard poultry, together with the infection in wild birds and mammal species. Thus, there is a possibility that dogs and cats, especially those living in H5N1 repeated outbreak areas or suspected outbreak areas where abnormal death of poultry were found, have high risk of exposure to H5N1 virus from eating the infected animal carcasses or closed contact with the infected animals. To demonstrate this, we performed serological surveillance in dogs and cats living in 5 provinces where H5N1 HPAI outbreaks or suspected outbreaks were found, by using microneutralization (microNT) assay.

Materials and methods: This study was carried out during January 2007 to August 2009 in dogs and cats living in 5 provinces where H5N1 HPAI outbreaks or suspected outbreaks repeatedly occurred, i.e., Sukhothai, Phichit, Phitsanulok, Uttaradit and Kamphaeng Phet. The study protocol was approved by the Ethical Committee for Animal Health and Welfare, Faculty of Veterinary Science and Animal Assurance PHS from Office of Laboratory Animal Welfare, USA (OLAW No. A5731-01). Blood sample collection was employed under consent from the animal owners. ELISA based microNT assay in MDCK monolayer was performed in biosafety level-3 containment facilities. The reciprocal antibody titer 40 was established as the cut-off level for positive result.



Results: Totally, serum samples from 157 dogs and 42 cats were tested. H5N1 NT antibody was detected in 25 (15.9%) dogs and 2 (4.7%) cats. Highest prevalence was found in animals from Phitsanulok province, and followed in order by Phichit and Sukhothai provinces.

Table 1. Seroprevalence of HPAI H5N1 virus in domestic dogs and cats

Animal	Provinces	No. of positive/ no. of animals	Seropositive (%)
Dog	Nakhonsawan	0/1	0
	Kamphaeng Phet	0/2	0
	Uttaradit	0/3	0
	Phichit	1/3	33.33
	Phitsanulok	8/17	47.06
	Sukhothai	16/131	12.21
Total		25/157	15.92
Cat	Nakhonsawan	0/0	0
	Kamphaeng Phet	0/1	0
	Uttaradit	0/3	0
	Phichit	0/5	0
	Phitsanulok	2/5	40
	Sukhothai	0/28	0
Total		2/42	4.76

Conclusion: We demonstrated that dogs and cats living in the H5N1 outbreak areas could be infected asymptotically or developed only mild symptom. However, time at infection is not known. Dogs and cats can serve as a potential source of HPAI spread in addition to avian species.

Acknowledgement: This study supported by US. CDC (Cooperative Agreement Number 1U19CI00399-01). The study was also partial supported by Thailand Research Fund for Senior Research Scholar through P.P., the grant PI.

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Satellite Telemetry Reveals Migratory Routes of Brown-headed Gulls (*Larus brunnicephalus*) Captured in Thailand.

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Background

A flock of brown headed-gulls (*Larus brunnicephalus*) is seen along the muddy beach at Bang Pu, Samut Prakarn every year during November to March. However, its long distant migratory route has never been reported. Our group could isolate HPAI H5N1 virus from 4 (2.6 %) of 153 birds of this flock in 2005 and 2008. Thus, this flock might play a role in the spread of HPAI virus along its fly ways. The present study conducted satellite telemetry technique to demonstrate the migratory routes of this bird species, including an attempt to isolate H5N1 virus and detect specific antibody by ELISA and microneutralization (microNT) assay.

Methods

Gulls negative for influenza A antigen were tagged with solar powered satellite transmitters (Microwave); and their movements were monitored by Argos satellite tracking system. Most locations, used for analysis and mapping with Google Earth Programme version 4.3, had a precision of <1500 m. Tracheal and cloacal swabs as well as serum samples from birds were collected at convenience, while the flock stayed in Thailand.



Figure 1 : Brown headed-gull (*Larus brunnicephalus*) was being tagged with solar powered satellite transmitters.

Results

We started tracking the first gull in March 2008 and the second group of 7 gulls between February and March 2009. Collective data from the two experiments confirmed that gulls migrated out of Thailand in April. Five of them flew to Xinjiang, Qinhai and Tibet, places of their long stay. The first gull moved from Tibet to West Bengal, India in October before coming back to Thailand. Nevertheless, this bird stayed in Thailand only shortly; then, it flew to Siem Reap, Cambodia in late October and inhabited there until the signals lost in December 2008. Birds could fly at a distance of 330.07 km/day in average. MicroNT assay was performed in 85 birds, and the results were all negative; meanwhile 3.5 % of samples were positive by ELISA for pan-influenza A antibody.

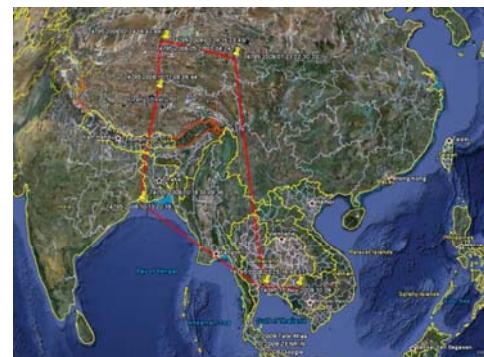


Figure 2 : Migratory route of a Brown headed-gull during March – December 2008.

Conclusions

Brown-headed gulls had migrated across several countries. However, it needs to be further explored that gulls can be infected asymptotically and the infected gulls can migrate that far. Then, role of this species in the spread of H5N1 virus can be concluded.

Acknowledgement

This study supported by US. CDC (Cooperative Agreement Number 1U19CI00399-01). The study was also partially supported by Thailand Research Fund for Senior Research Scholar through P.P. (the grant PI).



Neuraminidase Inhibitor Resistant Seasonal Influenza H1N1 Viruses in Thailand During 2006 to 2009



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Introduction:

Two neuraminidase inhibitors (NAI), oseltamivir and zanamivir, have been used for treatment and prophylaxis of influenza A and B viruses. At present, almost 100% of seasonal influenza H1N1 viruses are resistant to oseltamivir owing to mutational change from histidine to tyrosine at amino acid position 274 (H274Y in N2 numbering) in NA molecule. Nevertheless, the H274Y mutant viruses are still sensitive to zanamivir. The H274Y mutation was seen in N1 in both cell culture passaged viruses and clinical specimens from immunocompetent or immunocompromised patients treated with oseltamivir. Our study conducted a surveillance of oseltamivir and zanamivir resistant seasonal H1N1 viruses prevalent in Bangkok and rural area of Thailand between 2006 and 2009 by using the fluorometric based NA inhibition assay as well as nucleotide sequencing for mutational change in N gene. Our study provided additional data from different geographical sites for both drugs as well as the earlier time period of investigation.

Materials and Methods:

Seasonal influenza H1N1 viruses from 3 provinces of Thailand during 2006 to 2009: 28 virus isolates and 41 respiratory samples.

Neuraminidase (NA) inhibition assay using MUNANA substrate was used to determine 50% inhibitory concentration (IC50) of the virus isolates.

Direct nucleotide sequencing of PCR products derived from amplification of N genomic segments present in clinical samples was performed. The nucleotide sequences were analyzed for amino acid mutation position indicating drug resistance.

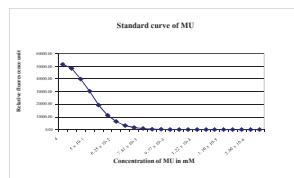


Fig 1. Standard curve of 4-methylumbellifluorone:
The MU solution was serially two fold diluted (4 to 10^{-6} nM), then the RFU (relative fluorescence unit) values obtained were plotted against MU concentrations to generate a standard curve. Therefore, the amount of viruses that yielded RFU value between 20,000 and 40,000 was selected as the standard dose. In general, all tested viruses in our study were assayed at the RFU value about 30,000.

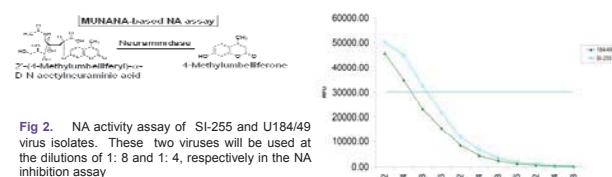


Fig 2. NA activity assay of SI-255 and U184/49 virus isolates. These two viruses will be used at the dilutions of 1: 8 and 1: 4, respectively in the NA inhibition assay

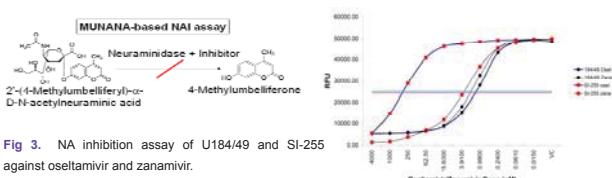


Fig 3. NA inhibition assay of U184/49 and SI-255 against oseltamivir and zanamivir.

U184/49 is sensitive to both drugs (IC50 = 1.46 nM for oseltamivir, and 2.51 nM for zanamivir), while SI-255 is sensitive to zanamivir (IC50=3.31 nM), but resistant to oseltamivir (IC50 = 372.18 nM)



Fig 4. Chromatogram of N1 gene of mutant show changing of amino acid position at position 274

Table 1. Mutation positions indicating NA inhibitor resistance

NA subtype	NA mutation positions (N2 numbering)	
	Oseztamivir	Zanamivir
A/H1N1	H274Y, N294S	Q136K
A/H3N2	E119V, D151E, I222V, R224K, R292K, N294S, R371K, E276D	E119A/D/G, R224K, R292K, R371K, E276D
B	E119A/D/G/V, R152K, D198N, R292K	E119A/D/G, R152K, D198N, R292K

Result:

All 22 influenza isolates investigated in 2006 and 2007 were drug susceptible with mean IC50 of 0.93 and 1.40 nM, respectively for oseltamivir.

The isolates in 2008 and 2009 were oseltamivir resistant with mean IC50 of 437.12 and 709.05 nM, respectively.

All of the 28 isolates tested were zanamivir sensitive, i.e., mean IC50 of 0.42 to 4.89 nM

The resistant mutation H274Y in N gene (N2 numbering) was found in all 6 clinical samples collected in 2008, but none of the 35 samples collected between 2006 and 2007.

All of the 28 isolates tested were zanamivir sensitive, i.e., mean IC50 of 0.42 to 4.89 nM; and no mutational change indicating zanamivir resistance was observed in all clinical samples tested. all of the 28 isolates tested were zanamivir sensitive, i.e., mean IC50 of 0.42 to 4.89 nM; and no mutational change indicating zanamivir resistance was observed in all clinical samples tested.

Table 2. Susceptibility of seasonal influenza H1N1 virus isolates to NA inhibitors

Year	Number tested	Mean, median and range of IC50 in nM	
		Oseztamivir	Zanamivir
2006	18	0.93, 0.94, (0.50-1.42)	1.22, 1.02, (0.42-2.11)
2007	4	1.40, 1.32, (1.02-1.94)	2.04, 1.91, (0.63-3.71)
2008	5	437.12, 428.03, (370.73-495.54)	2.19, 2.13, (1.45-3.30)
2009	1	709.05	4.89

Table 3. Nucleotide sequencing for drug resistant markers in clinical samples from patients with seasonal H1N1 virus infection

Year	Number tested	Amino acid positions on NA gene (N2 numbering)			
		H274	H274Y	N294	N294S
2006	32	32	-	32	-
2007	3	3	-	3	-
2008	6	-	6	6	-

Discussion:

Based on phenotypic and genotypic based assay, our study could not detect any drug resistant seasonal influenza H1N1 virus between 2006 and 2007; meanwhile the high percentages of drug resistance have been discovered in 2008 and 2009.

Regarding zanamivir phenotypic-based sensitivity assay, all of the viruses tested were drug sensitive. Additionally, mutation indicating zanamivir resistant was not found in all clinical samples investigated. Nevertheless, it is interesting to see that the viruses have a trend towards an increasing IC50 values by years; and this point is to be further explored.

Acknowledgement:

This study was supported by the Thailand Research Fund for Senior Research Scholar; and the National Science for Technology Development Agency

Susceptibility of influenza A viruses to neuraminidase inhibitors as determined by phenotypic and genotypic-based assays



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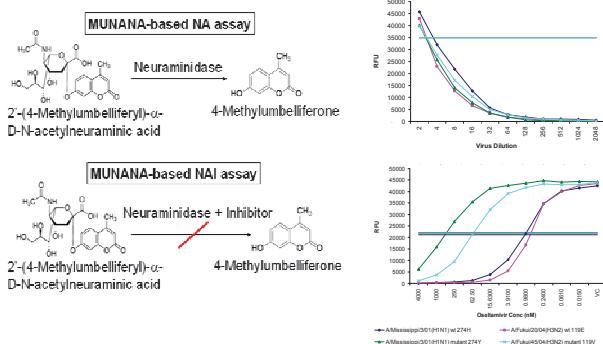
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Introduction

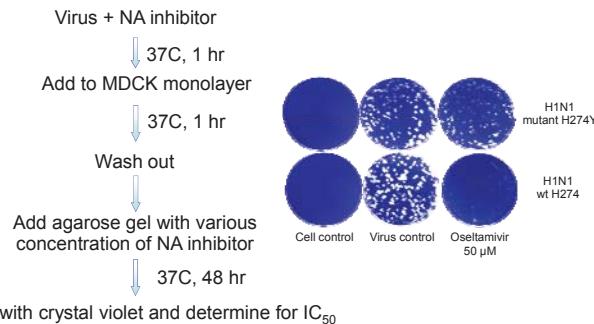
Susceptibility of influenza viruses against anti-viral drugs can be determined by genotypic based assay (such as nucleotide sequencing and RT-PCR) or phenotypic-based assays (such as NAI assay, plaque reduction assay and viral protein reduction assay). The present study proposed that no single assay is adequate for anti-influenza drug resistance surveillance; and at least two assays of different principles should be performed in order to compensate for the disadvantage of another one. Herein, all four assays mentioned above were employed in the detection of oseltamivir and zanamivir resistant influenza viruses.

Phenotypic based assays

MUNANA-based NAI assay



Plaque reduction assay



Results

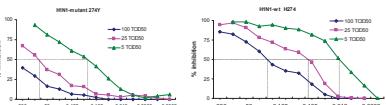
Viruses	Oseltamivir carboxylate			Zanamivir		
	MUNANA-NAI assay (nM)	Plaque reduction assay (μM)	NP reduction assay (μM)	MUNANA-NAI assay (nM)	Plaque reduction assay (μM)	NP reduction assay (μM)
Reference strains						
A/mississippi/03/01(H1N1) wt (274H)	1.799	0.27	0.050	1.28	0.50	0.11
A/mississippi/03/01(H1N1) mutant (274Y)	477.76	43.64	131.12	1.24	0.52	0.331
Seasonal viruses						
A/Brisbane/59/07(H1N1)-like SEA_3043	875.25	104.44	781.49	3.89	0.39	1.659
A/Brisbane/10/07(H1N1)-like SEA_3026	1.21	0.01	0.833	0.64	0.045	2.205
A/Brisbane/10/07/H3N2-like SEA_3613	0.85	0.055	0.166	1.82	0.50	1.331
2009 H1N1 virus						
A/Thailand/104/09(H1N1)	1.02	0.39	1.94	0.60	1.52	4.671
H5N1 viruses						
A/Thailand/1(KAN-1)/04	0.15	1.084	5.68	1.82	14.32	50.282
A/Thailand/3(SP-83)/04	0.19	0.003	0.008	1.02	0.017	0.231
A/Thailand/5(KK-494)/04	0.26	0.031	0.223	2.21	0.885	0.186
A/Thailand/676(NYK)/05	0.17	0.035	0.012	3.12	0.479	0.932
A/Laos/Nong Khai 1/07	8.05	0.528	3.165	1.13	1.104	3.163
A/Thailand/276(NBL)/06	0.86	0.006	0.004	2.04	0.009	0.053
A/Tiger/Thailand/BF154/04	0.13	0.238	0.4395	0.40	0.042	0.099
A/Golden Pheasant/Thailand/BF2743/05	0.18	No plaque formation	>800	0.24	No plaque formation	>800
A/Clouded Leopard/Thailand/VSKU-6/04	0.14	0.003	3.266	0.16	0.038	1.982
A/chicken/Thailand/VS143/07	1.88	0.002	0.007	7.68	0.013	0.14
A/chicken/Thailand/VS195/07	0.53	No plaque formation	560.73	4.9	No plaque formation	259.45

Acknowledgements

This study was supported by the Thailand Research Fund for Senior Research Scholar, the National Science and Technology Development Agency, and the South East Asia Infectious Disease Clinical Research Network. We thank WHO Influenza Reference Laboratory, Melbourne for the reference viruses.

There is no amino acid substitution indicating drug resistance was detected in *N* gene among all of the study isolates. However, based on phenotypic assays, few resistant mutants were detected by infectivity reduction assays but not NAI assay. Our result suggested the novel mutational change that might confer the resistance to NA inhibitors.

Conclusion



20 ปี สหกรณ์ไวรัสวิทยา (ประเทศไทย)



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Normal guinea pig serum mediated inhibitory effects on influenza virus replication

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Abstract

The present study employed normal guinea pig serum as the model to investigate innate immunity against seasonal influenza virus subtypes A(H1N1) and A(H3N2), 2009 pandemic A(H1N1) (H1N1pdm) and highly pathogenic avian influenza A(HPAI) H5N1 viruses. Native guinea pig serum was incubated with 1000 TCID50 of influenza viruses; then, the mixtures were transferred onto MDCK cell monolayers to assay for virus replication. In presence of the serum inhibitors, the viruses were neutralized and resulted in a reduction of the amount of viral nucleoprotein produced in the inoculated cell cultures. The results demonstrated that seasonal influenza A (H3N2) virus was the most sensitive to normal guinea pig serum; meanwhile, seasonal influenza A (H1N1) and H1N1pdm viruses were less sensitive. On the other hand, HPAI H5N1 virus was resistant to guinea pig serum. When guinea pig serum was heat inactivated, the inhibitory effect did not diminish, but decreased by 1.4 to 5.9 folds as compared to those employed the native serum. These results suggested that both heat labile and heat stable inhibitory factors were present in guinea pig serum; and H3N2 subtypes were more sensitive to heat labile factor than H1N1 subtype. The study

also analyzed for correlation between susceptibility to guinea pig serum and number of glycosylation sites present in hemagglutinin (HA) and neuraminidase (NA) molecules. It was found that H3N2 viruses contained highest number of glycosylation sites and followed in order by H1N1 and HPA1 H5N1 viruses. Thus, inversely correlation between sensitivity to guinea pig serum and number of glycosylation sites had been demonstrated. This finding may explain a mechanism to pathogenesis of the virulent H5N1 virus.

Introduction

Host defense against influenza viruses could be mediated by both adaptive and innate immunity. However, the function of specific immunity may be compromised in genetic variants; but function of innate immunity is not affected. In addition to cellular effectors, there are several soluble factors in alveolar secretion and serum of human and animals that possess anti-influenza activity, such as SP-D and SP-A, collectin, mannose-binding lectin (MBL), human mannose binding protein (MBP) and complement (1). Non-specific inhibitors against influenza viruses present in normal sera of various animal species were classified into three types: α -, β -, and γ -inhibitors based on their chemical composition (2). α -inhibitor is not destroyed by inactivation at 56°C for 30 minutes. It is a sialylated glycoprotein which inhibits hemagglutination of influenza type A and B viruses by competitive binding with the cell receptor. However, it can not inhibit infection; and its activity was destroyed by receptor destroying enzyme (RDE). β -inhibitor type is heat labile, Ca^{2+} dependent and not sialylated. β -inhibitor in guinea pig serum had been shown to be MBL which was serologically cross reacted with human MBP (3). β -inhibitors inhibited influenza hemagglutination; and also shown to inhibit

influenza subtype H1 and H3 infections. It is not receptor analogue; therefore, it is not destroyed by RDE. Therefore, hemagglutination inhibiting activity of β -inhibitors was probably mediated through steric hindrance occurring as the result of binding between lectin to carbohydrate side chain on hemagglutinin (HA) molecule, and thus, prevent the viruses from binding with the cell receptor. γ -inhibitor had many properties which were similar to α -inhibitor, but it was alike β -inhibitors on possessing both hemagglutination inhibiting and virus neutralizing activities (4). While β -inhibitors inhibited H1 and H3 subtypes; γ -inhibitor inhibited H2 and H3, but not H1 subtype (5, 6). γ -inhibitor was heat stable, sialylated glycoprotein and inhibited influenza hemagglutination by the mechanism of competitor analogue. Nevertheless, γ -inhibitor was not destroyed by RDE due to unusual sialic acid which was resistant to RDE hydrolysis. In horse and guinea pig serum, γ -inhibitor had been identified as $\alpha2$ -macroglobulin (7).

It is difficult to investigate serum factors that exert innate immunity against influenza viruses in human serum due to interfering effect from specific antibody arose from past infection or vaccination. Guinea pig serum should be a good model to study the serum factors that mediated innate immunity because it is a rich source of complement; moreover, its anti-influenza activity had been well characterized. Guinea pig erythrocytes treated with influenza virus were lysed during incubation in autologous serum at 37°C via an activation of the classical complement pathway (8). Nevertheless, influenza viruses were also reported to activate complement via alternative pathway (9). Guinea-pig serum lacking detectable antiviral antibody efficiently neutralized the infectivity of influenza B virus grown in chick embryos or MDCK cells (10). MBL as well as complement in guinea pig serum exerted lytic activity on influenza

infected BHK-21 cells via classical pathway of complement activation (11).

In the present study, seasonal influenza virus subtypes A/H1N1 and A/H3N2, H1N1pdm and HPAI H5N1 viruses were investigated for their susceptibility to inhibitory factors present in guinea pig serum. We postulated that degree of sensitivity to guinea pig serum may be inversely correlated with pathogenicity of the viruses.

Materials and Methods

Cell lines

MDCK (Madin Darby Canine Kidney) cells were grown in Eagle's Minimal Essential Medium (1X EMEM, GIBCO, N.Y.) supplemented with 10% fetal bovine serum (FBS, GIBCO) plus penicillin, gentamycin and fungizone.

Viruses

A total of 9 influenza virus isolates including seasonal A (H1N1) and A (H3N2), H1N1pdm and HPAI H5N1 viruses of human origins were employed in this study (Table 1). The study viruses were propagated in MDCK cell monolayers maintained in EMEM medium supplemented with 2 μ g/ml trypsin TPCK (Tosyl phenylalanyl chloromethyl ketone, Sigma-Aldrich, MO.) and without FBS supplement. Supernatants of the infected cell cultures were centrifuged, aliquoted and stored at -80 C until used.

Guinea pig serum

Guinea pig serum collected from clotted blood was aliquoted and kept at -80 C.

Complement titration

In order to standardize the amount of guinea pig serum used in each experiment, guinea pig serum was titrated for amount of complement by using hemolysin sensitized sheep red blood cells as the

indicator. Titration was performed prior to its use in every experiment. One hemolytic unit of complement is defined as the highest serum dilution which yields complete hemolysis of the sensitized sheep red blood cell.

Virus titration

Influenza viruses were titrated in MDCK cell monolayer in quadruplicate in a 96 well micro-culture plate using ELISA based viral nucleoprotein assay. Mouse monoclonal antibody to viral nucleoprotein (Chemicon International, Inc., CA.) and goat anti-mouse Ig conjugated horse reddish immunoperoxidase (Southern Biotech) were used as the detector system. The viral titer was calculated by Reed and Munch method and expressed in term of 50% tissue culture infective dose (TCID50).

Influenza virus neutralization by serum factors

Fifty μ l of 1000TCID50 of influenza virus was mixed with 25 μ l of guinea pig serum at concentration 2 hemolytic units and 50 μ l of viral growth media in quadruplicate wells of the micro-titer U-plate. The reaction plate was incubated at 37 C for 45 minutes. Then, the virus-serum mixture was transferred onto MDCK cell monolayers and incubated overnight prior to virus titration. The viruses from the reaction plate was titrated by ELISA based nucleoprotein (NP) production in MDCK cells. High O.D. indicated high viral titer and vice versa. Then, the inhibiting activity of guinea pig serum against the test virus was calculated in compared with the virus control without guinea pig serum.

The assay involved native guinea pig serum was run in parallel with the heat inactivated serum in order to compare their inhibiting activity against the tested influenza strain/subtype.

Result

Influenza nucleoprotein produced in MDCK cell monolayers inoculated with the mixtures of the test viruses and guinea pig serum was assayed by ELISA using mouse specific monoclonal antibody. HPAI H5N1 virus infected cultures yielded highest amount of viral nucleoprotein and followed in order by H1N1 and H3N2 viruses. The percentages of viral NP production as compared to the virus control cultures are as shown in Table 1. The result demonstrated that guinea pig serum contained inhibitory factors that could neutralize influenza virus infectivity, and the degree of inhibition was dependent on the virus subtypes. H3N2 subtype was the most sensitive and H1N1 subtype was intermediate sensitive; meanwhile, H5N1 isolates of both clades were resistant to guinea pig serum. The inhibiting activity was 1.4 to 5.9 folds increased when the native guinea pig serum was heat inactivated (Table 1). Comparison between native serum and heat inactivated serum on the inhibiting activity against H1N1 and H3N2 subtypes are shown in Figs. 1 and 2. Meanwhile, no difference between native serum and heat inactivated serum on inhibiting activity against HPAI H5N1 viruses (data not shown).

Table 1 Viral NP production in MDCK infected cells

Influenza subtypes	Virus name	% production of viral NP in presence of		Fold increase ^e
		Native serum	Heat inactivated serum	
H1N1	A/New caledonia/20/99 A/Brisbane/59/07 A/Fujian/4/11/02 A/Moscow/10/99 A/Sydney/05/97 H1N1 pdm H5N1 clade 1 H5N1 clade 2 H5N1 clade 2.3.4	57.6 38.9 8.8 12.8 15.9 46.8 94.4 93.9 99.2	78.7 64.9 52.1 74.0 61.2 66.4 99.2 92.9 94.7	1.4 1.7 5.9 5.8 3.8 1.4 1.1 1.0 0.9

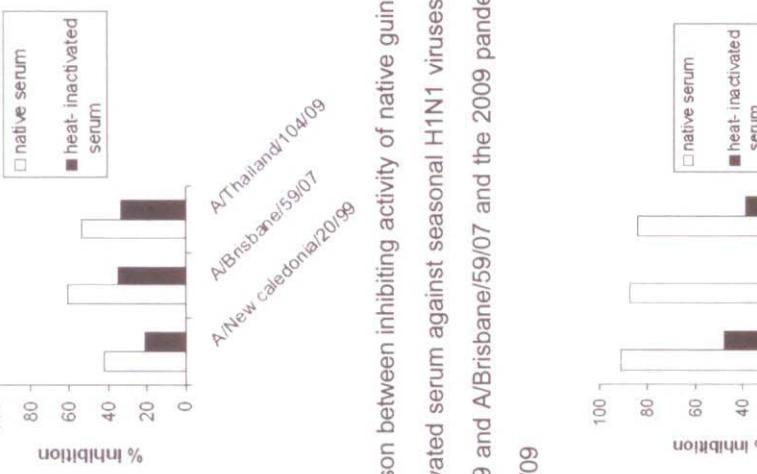


Fig. 1 Comparison between inhibiting activity of native guinea pig serum and heat inactivated serum against seasonal H1N1 viruses: A/New Caledonia/20/99 and A/Brisbane/59/07 and the 2009 pandemic virus: A/Thailand/104/09

version 7.0.4.1. The results in Table 2 shows that H5N1 subtype contained least number of glycosylation sites on both HA and NA proteins.

Table 2 Glycosylation site on HA and NA of influenza viruses

Virus subtype	Number of glycosylation sites on	
	HA	NA
A/New caledonia/20/99 (H1N1)	10	9
A/Brisbane/59/07 (H1N1)	10	9
A/Moscow/10/99 like-virus (H3N2)	11	9
A/Thailand/104/09 (H1N1 pdm)	8	8
A/Thailand/1(KAN-1)/04 (H5N1)	8	3
A/Thailand/676(NYK)/05 (H5N1)	8	4
A/Laos/Nong Khai 1/07 (H5N1)	8	4

Discussion

Serum inhibitory factors which were able to inhibit influenza virus activities had long been demonstrated in different animal species. The present study employed guinea pig serum as the model to study innate immunity against different subtypes and strains of influenza viruses. It was demonstrated that degree of neutralizing activity of guinea pig serum was inversely correlated to number of glycosylation sites present in HA and NA molecules. Nature of the inhibitory factors present in the guinea pig serum was not identified in this study. However, it was demonstrated that there were consisted of at least two components: heat labile and heat stable factors. Based on findings of previous investigators, the heat



Fig. 2 Comparison between inhibiting activity of native guinea pig serum and heat inactivated serum against seasonal H3N2 viruses: A/Fujian/411/02, A/Moscow/10/99, and A/Sydney/05/97

Glycosylation sites on HA and NA molecules of the study viruses

Amino acid sequences of the HA and NA molecules of the study viruses were retrieved from GenBank; and glycosylation sites present on each molecule were predicted by CountGS application in BioEdit program

stable components could be either α - or β -inhibitors or both; and the heat labile component could be both complement and MBL, whose activity was correlated with glycosylation of the influenza viruses.

Activation of the complement system results in virus aggregation, virolysis or opsonization. It can lead to increased vascular permeability and recruitment of phagocytic cells to destroy the pathogens. There are three pathways of complement activation: the classical pathway that occurs when C1q binds to antibody, the alternative pathway in which the pathogen bypasses C1, C4 and C2 binding and initiates the activation pathway by binding with C3, and the lectin binding pathway in which the activation is mediated by binding of MBL with the oligosaccharide present on gram negative bacterial cell wall (12) or glycoprotein on the HIV envelope (13) or mannose glycan on HA of influenza virus (4, 14, 15). Mutations that lead to loss of specific glycosylation gave rise to influenza strains that were resistant to MBL as compared to their MBL sensitive parents (4). MBL is a C-type lectin member in the collectin family, whose molecule contains a collagen like sequence and carbohydrate recognition domain (16). MBL could activate classical pathway of the complement system without antibody binding as well as activate the alternative pathway. In addition, MBL could exert its anti-influenza activity with and without complement involvement (3, 16).

In conclusion, our study suggested that resistance to innate immunity may be an explanation for mechanism to virulence of HPAI H5N1 viruses.

This study was supported by Thailand Research Fund for Senior Research Scholar and Mahidol University Research Grant.

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Immune Complex of HBsAg and anti-HBs in Occult HBV Infection

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Abstract

Since Nucleic acid testing (NAT) was developed to detect low level of hepatitis B virus (HBV) DNA, more information has been revealed on occult hepatitis B virus infection (OBI) with positive HBV DNA but undetectable hepatitis B surface antigen (HBsAg). One of the reasons for the absence of detectable HBsAg may be formation of immune complex with specific antibody. In order to determine the circulating immune complex in occult HBV infection, we investigated 29 plasma samples with occult HBV. HBsAg and immune complex in the samples were precipitated with polyethylene glycol (PEG) method. Subsequently, HBsAg was compared before and after acid dissociation with or without PEG. During the method validation, we found an increase in HBsAg after acid dissociation (p -value<0.05). HBsAg signal became positive in all the occult hepatitis cases after acid dissociation with PEG (p -value<0.05). Immune complex formation might be one of the explanations in the lack of detectable HBsAg in occult hepatitis B infection.

20 ปี สหกรณ์ไวรัสวิทยา (ประเทศไทย)



การประชุมวิชาการประจำปี ครั้งที่ ๒๐

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The 2009 Pandemic Influenza A (H1N1) Virus Infection and Induction of Cytokines and Chemokines in Human Umbilical Vein Endothelial Cells

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Abstract

Three 2009 pandemic A (H1N1) virus isolates: A/Nonthaburi/102/09, A/Thailand/104/09 and A/Thailand/ICRC-1/09, were investigated for their capability to infect and induce cytokine/chemokine production in human umbilical vein endothelial cells (HUEVCs). The infected HUEVC cultures showed degenerative cytopathic effect suggesting of direct cellular damage. However, in term of virus inoculum dose of 1TCID₅₀ per cell with 36 hours incubation, the efficiency of infection was low. Only few percentages of infected cells were detected as determined by immunofluorescence assay using monoclonal antibody specific to influenza A nucleoprotein. Supernatants from the infected cultures were collected at 12, 24 and 36 hours post-infection and titrated for virus titers in MDCK cells as well as assayed for cytokine/chemokine production by ELISA. The result demonstrated successful productive infection with all virus isolates tested. It was noted that the isolates obtained from dead patient (ICRC-1) yielded the highest virus titers and followed in order by the other two isolates obtained from mild cases, Thailand/104 and Nonthaburi/102. IP-10 and IL-8, but not TNF- α and IL-

1 β , were detected in the supernatants of cultures infected by any of the test viruses. Our study suggested that ability to infect endothelial cells and induce cytokine/chemokine production may contribute to mechanism of pathogenesis in severe cases infected with the 2009 pandemic virus.

Introduction

The first pandemic influenza of this century was caused by the 2009 pandemic influenza A (H1N1) virus (H1N1pdm), a reassortant derived from influenza viruses of 4 origins: classical swine, European swine, avian and human influenza viruses (1). There were few differences between H1N1pdm and seasonal H1N1 virus, such as the patients infected with H1N1pdm elicited higher degree of gastrointestinal symptoms (2) the H1N1pdm had higher propensity to infect lower respiratory tract as demonstrated in ferret model, an occurrence which is consistent with the gastrointestinal symptom in patients (3) and the H1N1pdm could infect mouse without prior adaptation, meanwhile, it is needed to adapt seasonal H1N1 virus before mouse infection (4). This finding is suggestive of broader receptor binding activity of the H1N1pdm. The disease produced by H1N1pdm is mild with fatality rate of 1.2% (5). Deaths are usually associated with underlying complications such as cardiopulmonary disease, diabetes, and pregnancy (6,7). Nevertheless, approximately 25-50% of deaths or severe cases occurred in people without predisposing risk factors. Role of cytokine storm as the major pathogenic mechanism of the H1N1pdm is not clearly elucidated. Macrophage cultures infected with H1N1pdm produced lower level of cytokines and chemokines as compared to seasonal H1N1, H3N2 and highly pathogenic avian influenza (HPA) H5N1 virus (8). On the other hand, increased level of cytokines and chemokines was reported in two severe cases infected with the H1N1pdm (9).

It is interesting that pneumonia hemorrhage was the common pathological finding among the 1918 Spanish influenza A (H1N1), HPAI H5N1 virus and the H1N1pdm infected cases (7, 10, 11). Endothelial cells play an important role in regulating vessel permeability and maintaining hemostasis (12). Hemorrhage and edema are the characteristics suggestive of activation or infection of the endothelial cells which consequently lead to loss of tight junction constituents and vascular hyper-permeability, and probably virus dissemination in the body (13). H1N1pdm could infect various cell types such as macrophages (8, 14) and conjunctival cells *in vitro* (15). Moreover, the viruses could be detected in stools and urine of the patients (16). Therefore, it is possible that the H1N1pdm can infect many cell types and disseminate beyond the respiratory tract in the human body. Nevertheless, H1N1pdm infections of endothelial cells have never been reported. The present study explored mechanism of pathogenesis involving H1N1pdm dissemination through investigation on their ability to infect, replicate and induce cytokine and chemokine production in primary endothelial cells derived from human umbilical veins (HUEVCs).

Materials and Methods

Cell cultures

Human umbilical vein endothelial cells

Primary culture of HUEVCs prepared from pool of 8-10 umbilical cords were grown in Medium 199 (M199, GIBCO, N.Y.) plus human endothelial-SFM basal growth medium (GIBCO) supplemented with 10% fetal bovine serum (FBS, GIBCO).

Madin Darby Canine Kidney cells (MDCK)

MDCK cells were grown in Eagle's Minimal Essential Medium supplemented with 10% FBS plus penicillin, gentamycin and fungizone.

Influenza A viruses

The 2009 pandemic influenza A (H1N1) viruses (H1N1pdm) employed in this study were: A/Thailand/102/09, A/Thailand/104/09 and A/Thailand/ICRC-1/09. The first two strains were isolated from mild cases and the third strain was isolated from a dead case with underlying condition of obesity. These viruses were isolated and propagated in MDCK cell cultures in presence of 2 μ g/ml trypsin TPCK (Tosyl phenylalanyl chloromethyl ketone, Sigma-Aldrich, MO.) without FBS supplement. The virus inoculated culture was incubated at 37 C in a CO₂ incubator and daily observed for cytopathic effect (CPE). The supernatants from the virus infected cultures were harvested, aliquoted and kept at -70 C before titration in MDCK cell monolayers.

Virus titration

The test viruses were titrated in MDCK cell monolayers in quadruplicate using ELISA based nucleoprotein assay as the end point measurement for virus infection. The virus titer was calculated by Reed and Muench method and presented as 50% tissue culture infectious dose (TCID₅₀).

Virus infection in HUEVCs

Confluent HUEVC cultures at the 3rd – 4th passage were trypsinized and adjusted to the concentration of 2 \times 10⁵ cells/500 μ l/well of a 24 well culture plate. The plates were incubated at 37 C overnight before replacing with maintenance medium prior to virus inoculation. The cultures were absorbed with the test virus at inoculum dose of 1 TCID₅₀/cell for one hour, then washed once and added with the

maintenance medium supplemented with trypsin TPCK, the culture supernatants were harvested at 12, 24 and 36 hours post infection and titrated for infectious viral titers by TCID₅₀ assay in MDCK cell monolayer as well as quantified for cytokines/chemokines (TNF- α , IL-1 β , IP-10 and IL-8) by ELISA (R&D system, Minneapolis, MN). The infected HUVEC cells were scraped out of the culture plate for detection of viral antigen by immunofluorescence (IF) assay using mouse monoclonal antibody to influenza A nucleoprotein (Chemicon International, Inc., CA.).

Results

H1N1pdm infection in HUVECs

Cytopathic effect (CPE) in HUVECs infected with the test viruses could be clearly recognized after 24 hours of infection. Round and reflection cells were found discretely in the infected cultures. Approximately 2% of HUVECs were positive for viral antigen in nucleus and cytoplasm as measured by IF assay. Successful infection of influenza A virus in HUVECs could be demonstrated by the release of viral progenies in the culture supernatants collected at 12, 24 and 36 hours post infection (hpi.). A/Thailand/ICRC-1/09 yielded the highest virus titers and followed in order by A/Thailand/104/09 and A/Nonthaburi/102/09 (Fig. 1).

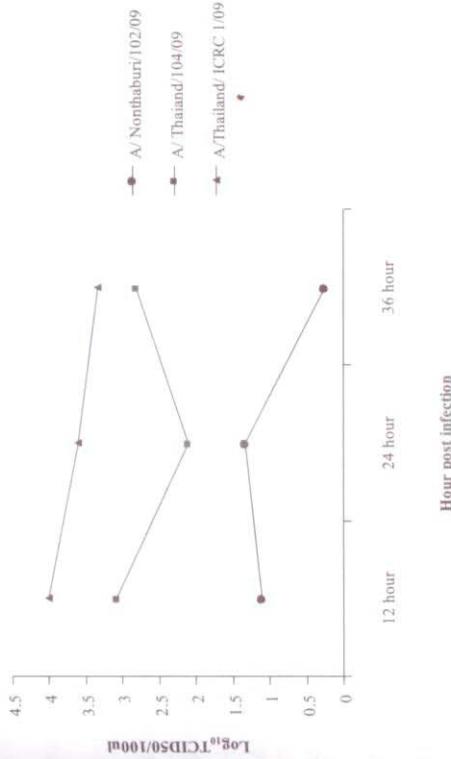


Fig. 1 Titers of H1N1pdm in supernatants of the infected HUVEC culture harvested at different intervals after infection

Cytokines and chemokines produced from viral infected HUVECs

Supernatants collected from the infected HUVECs cultures at 12, 24 and 36 hpi as well as the uninfected cell controls, were investigated for presence of IL-8, IP-10, TNF- α and IL-1 β by ELISA in duplicate wells. Amount of cytokines/chemokines released from the uninfected cells as the background control were subtracted from the test values of the infected cultures to obtain the corrected concentrations. IP-10 and IL-8 were detected in HUVEC cultures infected with any of the test viruses with comparable concentration. On the other hand, TNF- α and IL-1 β were below the detectable level (Table 1).

Table 1. Cytokine/chemokine production from HUVECs infected with H1N1pdm

Cytokine/chemokine		Virus		pg/ml of cytokine/chemokine at		
		12 hpi.	24 hpi.	36 hpi.		
IP-10	A/Nonthaburi/102/09	526	1058	1108		
	A/Thailand/104/09	502	683	1104		
	A/Thailand/ ICRC-1/09	489	1725	1601		
	A/Nonthaburi/102/09	0	112	394		
IL-8	A/Thailand/104/09	69	156	638		
	A/Thailand/ ICRC-1/09	0	143	1219		

Note: hpi = hours post-infection

Discussion

Endothelial cells are abundant in all organs, particularly the lung. They are target and source of cytokines/chemokines (12). Previous investigators reported that human microvascular endothelial cells could be infected at limited extent by seasonal influenza H1N1, but the infection was more pronounced with HPAI H5N1 viruses (17). HPAI H5N1 virus produces severe pneumonia in more than half of the infected cases. Cytokine storm, virus dissemination and multi-organ failure are likely to be the key role to the virus virulence. However, cytokine storm was also linked with human influenza associated neurological complication and encephalopathy (18). In addition, it was reported that HUVEC cells infected with human H1N1 and H3N2 viruses induced the production of a variety of cytokines and chemokines such as IL-6 and TNF- α (19,20). The present study demonstrated that H1N1pdm was able to infect and

induced CPE in HUVECs, suggesting that this virus can cause direct cellular damage even though the extent of infection was low as shown by low number of infected cells by IF assay. In addition, the infected HUVECs secreted IP-10 and IL-8 production. However, we could not detect TNF- α and IL-1 β in our system, meanwhile, these two cytokines could be detected in sera of the H1N1pdm infected patients in the other studies (9, 21). Moreover, one of those two studies also showed elevated serum levels of IFN- γ , IL-1 β , IL-2, IL-4, IL-5, IL-6, IL-8, IL-10, IL-13 and MCP-1 in the patients infected with H1N1pdm (21). Thus, the negative finding in *in vitro* system may not reflect the real situation occurring *in vivo*. In contrast to our result in HUVECs, the others reported low level of cytokine production in macrophages and dendritic cells infected with the H1N1pdm (14). We postulated that different cell types release different kind of cytokines and chemokines.

Nevertheless, in our study, we could detect (unpublished data) IL-8, but not TNF- α , IL-1 β , and IP-10 in culture supernatants of HUVECs infection with seasonal H1N1 and H3N2 viruses. Therefore, we demonstrated that IP-10 synthesis could be induced by H1N1pdm, but not seasonal H1N1 and H3N2 virus; meanwhile, TNF- α , IL-1 β were not found in all.

Collective data demonstrated that H1N1pdm infection could lead to pulmonary hemorrhage in the dead cases (22) and the virus was able to disseminate beyond respiratory tract (16). Thus, our finding suggested that the ability of H1N1pdm to infect HUVECs and induced cytokine/chemokine production may contribute to the pathogenesis and severity of respiratory complications in the patients.

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Normal guinea pig serum mediated inhibitory effects on influenza virus replication

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Abstract

The present study employed normal guinea pig serum as the model to investigate innate immunity against seasonal influenza virus subtypes A(H1N1) and A(H3N2), 2009 pandemic A(H1N1) (H1N1pdm) and highly pathogenic avian influenza A(HPAI) H5N1 viruses. Native guinea pig serum was incubated with 1000 TCID50 of influenza viruses; then, the mixtures were transferred onto MDCK cell monolayers to assay for virus replication. In presence of the serum inhibitors, the viruses were neutralized and resulted in a reduction of the amount of viral nucleoprotein produced in the inoculated cell cultures. The results demonstrated that seasonal influenza A (H3N2) virus was the most sensitive to normal guinea pig serum; meanwhile, seasonal influenza A (H1N1) and H1N1pdm viruses were less sensitive. On the other hand, HPAI H5N1 virus was resistant to guinea pig serum. When guinea pig serum was heat inactivated, the inhibitory effect did not diminish, but decreased by 1.4 to 5.9 folds as compared to those employed the native serum. These results suggested that both heat labile and heat stable inhibitory factors were present in guinea pig serum; and H3N2 subtypes were more sensitive to heat labile factor than H1N1 subtype. The study



Influenza A virus infection and induction of cytokines and chemokines in human umbilical vein endothelial cells

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Abstract

Infection of human endothelial cells may be an explanation for influenza virus dissemination beyond the respiratory tract. Herein, seasonal influenza A(H1N1) and A(H3N2), and H5N1 highly pathogenic avian influenza (HPAI) viruses were determined for their capability to infect and induce cytokine/chemokine production in human umbilical vein endothelial cells (HUVECs). The influenza infected HUVEC cultures showed cytopathic effect (CPE) and expressed viral nucleoprotein as determined by immunofluorescence assay (IFA). Supernatants from the infected cultures were collected at intervals and titrated for virus titers in MDCK cells as well as assayed for cytokine/chemokine production by ELISA. The result showed that most of H5N1 isolates yielded high or moderately high titers of virus progenies; while, only one isolate poorly replicated. On the other hand, seasonal influenza viruses could also replicate in HUVECs, but to a lesser extent. Using commercial ELISA, IL-8 could be detected in supernatants of HUVEC cultures infected with all influenza subtypes; but TNF- α and IL-1 β could not be detected at all. Interestingly, H5N1 HPAI dramatically induced IP-10 production; while H3N2 viruses induced very low level and seasonal H1N1 viruses could not. Our study suggested that an ability to infect and induce cytokine/chemokine production in HUVECs may contribute to mechanism of virulence of H5N1 HPAI viruses in humans.

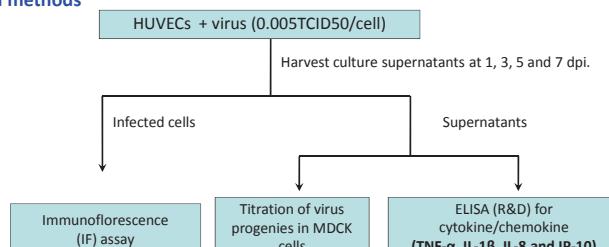
Introduction

With very few exception, an illness produced by human influenza viruses usually confines within the respiratory tract and subsides without sequel in most of the cases. On the other hand, H5N1 HPAI virus is the most virulent influenza subtypes ever reported in human infections. A virulent factor of H5N1 HPAI virus is its ability to disseminate beyond the respiratory tract to distal organs and cause multi-organ failure in most of the patients. Moreover, pneumonia hemorrhage was the common pathological finding in HPAI. Hemorrhage and edema are the characteristics suggestive of activation or infection of the endothelial cells which consequently lead to loss of tight junction constituents and vascular hyper-permeability, and probably virus dissemination in the body. The present study explored mechanism of pathogenesis involving influenza A virus dissemination through investigation on their ability to infect, replicate and induce cytokine and chemokine production in primary endothelial cells derived from pooled HUVECs.

Objectives

- To explore the ability of 15 influenza virus isolates including 9 H5N1 HPAI, 3 seasonal H1N1 and 3 H3N2 viruses to infect HUVECs. Kinetics of their replication was also determined at 1, 3, 5 and 7 days post infection (dpi).
- To study the kinetics of cytokine and chemokine (TNF- α , IL-1 β , IL-8 and IP-10) release in supernatants of the infected HUVEC cultures

Materials and methods



Result

Virus infection in HUVECs

All influenza A subtypes could produce CPE in HUVEC cultures. Nevertheless, CPE produced by H5N1 isolates could be recognized as early as 1 day post infection (Fig.1). The viral antigen was found in nucleus and/or cytoplasm of the infected HUVECs as shown by IFA (Fig.2). Successful productive infection of influenza virus in HUVECs was demonstrated by the release of viral progenies in the culture supernatants collected at 1, 3, 5 and 7 dpi. Among 9 H5N1 isolates, KAN-1, Nong Khai 1 and NBL 1 (feces) viruses replicated efficiently and yielded high virus titers; SP-33, SP-83, 676 NYK, NBL 1 (lung) and NBL 1 (trachea) replicated at moderate efficiency; while, KK-494 poorly replicated in HUVEC cultures. H3N2 viruses could fairly replicate in HUVECs, but least efficiency of replication was noted with Moscow virus. On the other hand, all of the 3 seasonal H1N1 viruses investigated poorly replicated in HUVECs (Fig.3).

Cytokine and chemokine production

All influenza viruses investigated could induce IL-8 in the infected HUVECs as assayed in the culture supernatants collected at different dpi., while none of them induce TNF- α and IL-1 β . Interestingly, H5N1 HPAI viruses was the only subtype that could induce IP-10 production (Fig.4).

Acknowledgements

This study was supported by Thailand Research Fund for Senior Research Scholar and Mahidol University Research Grant.

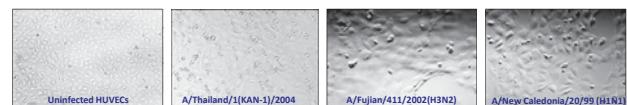


Fig.1 Cytopathic characteristics of HUVECs infected with influenza virus

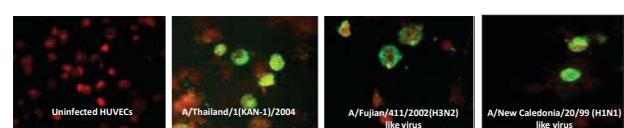


Fig.2 Influenza nucleocapsid antigen in nucleus and/or cytoplasm of the infected HUVECs

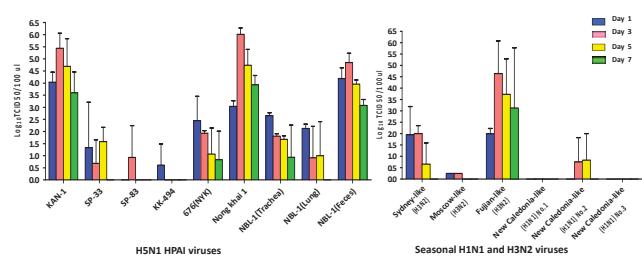


Fig.3 Titers of influenza viruses in supernatants of the infected HUVEC cultures

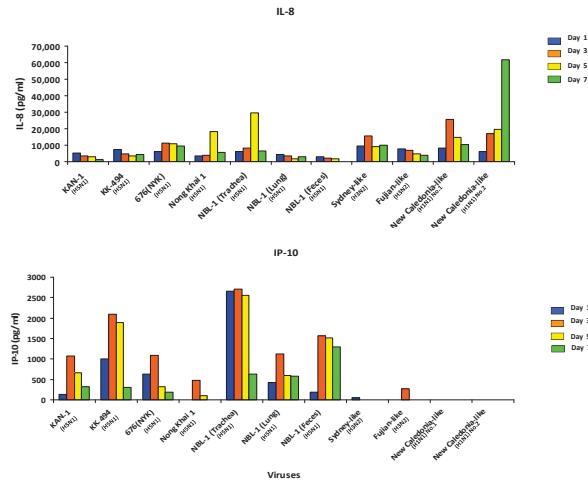


Fig.4 Levels of cytokines and chemokines in supernatants of the infected HUVEC cultures

Conclusion

H5N1 HPAI, seasonal H1N1 and H3N2 viruses could elicit productive infection in HUVECs; and highest efficiency of replication was noted with H5N1 HPAI viruses. IL-8 could be detected in supernatants of HUVEC cultures infected with all influenza subtypes; while TNF- α and IL-1 β could not be detected at all. Moreover, IP-10 induction was typical for H5N1 viruses. Our study suggests that direct cellular damage and induction of high level of IP-10 in the infected HUVECs may contribute to mechanism of pathogenesis in severe H5N1 HPAI patients.



Normal guinea pig serum mediates inhibitory effects on influenza virus infection

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Abstract

Normal guinea pig sera (GPS) were used as the tool to study serum innate immunity against seasonal influenza A(H1N1) and A(H3N2), 2009 pandemic A(H1N1) (H1N1pdm) and H5N1 highly pathogenic avian influenza (HPAI) viruses. GPS was incubated with influenza viruses; and then, the mixtures were transferred onto MDCK cell monolayers to assay for virus infectivity. The results demonstrated that H3N2 virus was the most sensitive to GPS, while seasonal influenza A(H1N1) and H1N1pdm viruses were less sensitive. When GPS was heat inactivated or treated with receptor destroying enzyme (RDE) followed by heat inactivation, the serum inhibitory effect dramatically decreased. Interestingly, all of the H5N1 strains tested were highly resistant to GPS. It was suggested that H or both H and N of H5 viruses may confer this resistance. Two reverse genetic viruses, PR8-H5HA and PR8-H5HN, were tested against GPS in parallel with the reassorted PR8 wild type virus. The result showed that both reverse genetic viruses were resistant, while the reassorted PR-8 wild type was sensitive to GPS. It was found that H3N2 viruses contained highest number of glycosylation sites and followed in order by H1N1 and HPAI H5N1 viruses. Thus, inverse correlation between sensitivity to GPS and number of glycosylation sites had been demonstrated. This finding may explain a mechanism to pathogenesis of H5N1 HPAI virus on its ability to spread beyond the respiratory tract.

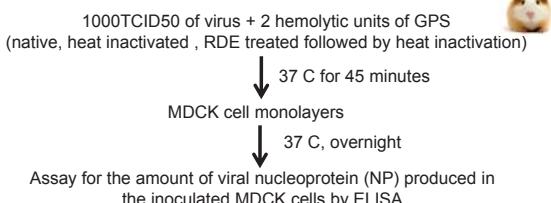
Introduction

Several soluble factors as well as non-specific inhibitors in sera of various animal species possess blocking activity against influenza virus infection. In presence of the serum inhibitors, the viruses were neutralized and resulted in the reduction of the amount of viral nucleoprotein produced in the inoculated cell cultures. It is difficult to study innate immunity against influenza viruses by using human sera due to interference effect from pre-existing specific antibodies arose during past infections or vaccination. Therefore, guinea pigs were chosen as the model in this study.

Objective

- To study seasonal influenza virus subtypes A/H1N1 and A/H3N2, H1N1pdm and HPAI H5N1 viruses on their susceptibility to guinea pig serum inhibitors
- To characterize biological properties of the serum inhibitors
- To determine correlation between glycosylation site on HA and NA and susceptibility to serum inhibitors
- To determine role of HA/NA on susceptibility/resistance to serum inhibitors

Materials and methods



Results

Table 1. Viral NP production in MDCK infected cells

Virus subtype	Virus name	% of NP produced in presence of		
		Native serum	Heat inactivated serum	RDE treated plus heat inactivated serum
H1N1	Reassorted A/PR/8/34	50.1	96.8	96.6
	A/New Caledonia/20/99-like virus	79.1	86.8	98.8
	A/Brisbane/59/07-like virus	69.3	85.1	88.3
H1N1 pdm	A/Thailand/104/09	65.8	85	94.7
	A/Nonthaburi/102/09	16.4	19.4	58.4
	A/California/07/09	11.3	25.5	91.9
H3N2	A/Sydney/97/like virus	19.2	95.3	100
	A/Adelaide/10/99-like virus	0	79.7	100
	A/Fujian/411/02-like virus No.1	3.1	77.8	88
	A/Fujian/411/02-like virus No.2	3.8	51.2	97
H5N1	A/Thailand/1/(KAN-1)/04	92.2	-	-
	A/Thailand/5/(KK-494)/04	89.2	-	-
	A/Thailand/6/76(NYK)/05	94	-	-
	A/Thailand/NBL-1/06 feces	96.5	-	-
	A/Thailand/NBL-1/06 lung	97.8	-	-
	A/Laos/Nong Khai 1/07	99.2	-	-
PR8-H5HA	rgPR8 H5HA (KAN-1)	97.7	98.2	97.8
PR8-H5HN	rgPR8 H5HN (KAN-1)	93.3	94.6	94.5

Note: % of NP produced as compared to that of the virus control

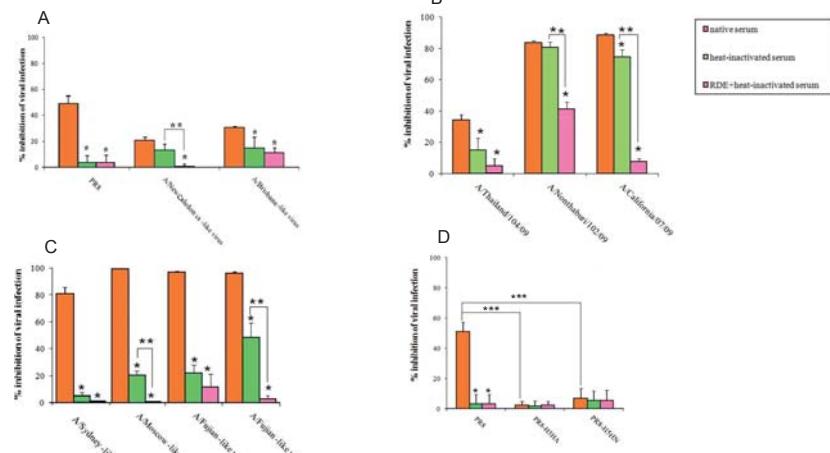


Figure Comparison between inhibiting activity of native, heat inactivated, and RDE treated plus heat inactivated serum against : A. Seasonal H1N1; B. H1N1pdm; C. H3N2 viruses; and D. Reverse genetic viruses

* There was statistically significant difference between the inhibitory activity of native serum and the heat inactivated serum or the RDE + heat treated sera (t -test: $p \leq 0.05$).

** There was statistically significant difference between the inhibitory activities of the heat inactivated serum and the serum treated with RDE + heat inactivation (t -test: $p \leq 0.05$).

*** There was statistically significant difference between the inhibitory activity against rgPR8H5HA or rgPR8H5HN and the PR8 wild type virus (t -test: $p \leq 0.05$).

Conclusion

GPS contained inhibitory factors that could neutralize influenza virus infectivity; and the degree of inhibition was dependent on the virus subtypes and inversely correlated to number of glycosylation sites present in HA or NA molecules. These inhibitory factors were consisted of heat labile, heat stable, RDE resistant, and RDE sensitive factors. Among all virus isolates tested, the inhibitor sensitive H3N2 viruses contained highest number of glycosylation sites. However, the inhibitor sensitive reassorted PR8 and the inhibitor resistant HPAI H5N1 viruses contained the similar least number. Our study has demonstrated a novel mechanism to virulence of H5N1 HPAI viruses, i.e., the resistance to innate serum inhibitors which makes the viruses readily to disseminate beyond the respiratory tract through viremia.

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Serological response to the 2009 influenza A (H1N1) virus strains derived from different epidemic waves in Thailand

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Abstract

Up to the end of 2010, Thailand has encountered 3 epidemic waves of the 2009 pandemic influenza A (H1N1) virus. In order to determine the viral antigenic drift that might occur during these epidemic waves, a total of 105 archival serum samples collected from patients and non-patients in July 2009 were assayed by hemagglutination inhibition (HI) assay using two isolates of the 2009 pandemic viruses derived from each pandemic wave as the test antigens. The result obtained from the two viruses derived from the same epidemic wave (intra-epidemic viruses) showed no significant difference in level of HI titers, i.e., GMT 46.9 and 44.2 for viruses from the first epidemic wave, GMT 55.6 and 51.1 for viruses from the second epidemic wave; and GMT 28.6 and 23.3 for viruses from the third epidemic wave (*t*-test; $p > 0.05$). On the other hand, HI antibody titers obtained from the viruses of the first or second epidemic waves were significantly higher when compared with those titers obtained from viruses of the third epidemic wave (*t*-test; $p < 0.05$). However, HI titers obtained from viruses belonged to the first and the second epidemic waves were not significantly different. Nucleotide sequences derived from HA gene of the six viruses were analyzed; and the result showed that these viruses were grouped into three separate clusters of the phylogenetic tree. The viruses isolated from the same epidemic wave were belonging to the same cluster. Taken together, the results suggested an antigenic change of the 2009 H1N1 viruses to the point that the antibody arose from the first exposure might not be able to protect from the viruses derived from the subsequent epidemic waves. The virus strain incorporated as a component of vaccine in use at present, therefore, might not match with the current strains circulating in the community.

Methodology

- A total of 105 archival serum samples collected in July 2009 from patients and non patients were investigated by HI assay (Figure 1) as described in the WHO manual on animal influenza diagnosis and surveillance. Six virus isolates derived from 3 epidemic waves were used as the test antigens (Table 1).
- Nucleotide sequences derived from complete HA gene of the six viruses were genetically analyzed using BioEdit and MEGA 5 software.

Serum treatment

- serum + RDE at the ratio of 1:3
- 37°C, 16-18 h and 56°C, 30 min
 - + normal saline
 - + goose red blood cells
 - 4°C, 1 h
 - Centrifuge at 1,500 rpm, 10 min

Supernatant of treated serum at working dilution 1:10

Serum, RDE, NSS and 50% RBC are used at the ratio of 1:3:5:1

HI assay

- 25 µL of 10-fold diluted serum + 25 µL of test virus (4 HA units/25 µL)
- RT, 30 min
 - + 50 µL of 0.5% goose red blood cells
 - 4°C, 30 min

Read HI antibody titer as a reciprocal of the last serum dilution that completely inhibits agglutination of RBCs

Figure 1. Hemagglutination inhibition (HI) assay

Table 1. History of virus isolates used in this study

Virus	Month at specimen collection	Epidemic wave No.	Place of origin	Passage history
A/Thailand/104/2009	Apr 2009	1	Imported case from Mexico	MDCK5
A/Thailand/ICRC_CBI_10/2009	June 2009	1	Chonburi, Thailand	MDCK5
A/Thailand/SEA 34002/2010	Feb 2010	2	Bangkok, Thailand	MDCK5
A/Thailand/SEA 34004/2010	Feb 2010	2	Bangkok, Thailand	MDCK4
A/Thailand/ICRC_BKK_1/2010	Aug 2010	3	Bangkok, Thailand	MDCK5
A/Thailand/ICRC_NSN_1/2010	Sep 2010	3	Nakornsawan, Thailand	MDCK6

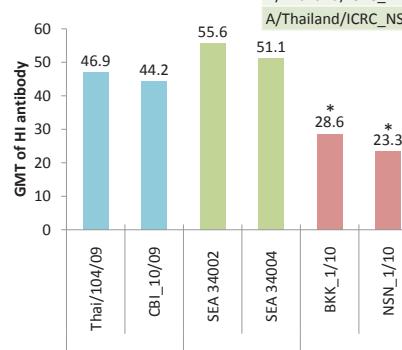


Figure 2. GMT of HI antibodies against each of the six test viruses. * represents statistic different with $p < 0.05$.

Background

Thailand had encountered 3 epidemic waves of the 2009 pandemic influenza A (H1N1) between 2009 and 2010. The first wave lasted between May and October 2009; and followed by the second wave between November 2009 and April 2010, and the third wave between May and October 2010. Based on the RNA nature of influenza virus, genetic drift commonly occurs and subsequently leads to viral antigenic variation such that antibody arose against the virus originated during the first epidemic wave may be not able to protect against those arose during the subsequent epidemic waves.

Objectives

- To determine GMT of antibody in serum samples collected during the first epidemic wave against the 2009 pandemic A (H1N1) (H1N1pdm) viruses derived from the three epidemic waves by hemagglutination inhibition (HI) assay
- To characterize HA gene of the viruses derived from the three epidemics

Results

The test sera harbored various HI antibody titers against each of the test viruses as shown in Table 2. GMT obtained from each of the two viruses derived from the same epidemic wave (intra-epidemic viruses) were not significant different (*t*-test; $p > 0.05$) as shown in Figure 2. And also, GMT obtained from viruses belonged to the first and the second epidemic waves were not significantly different. On the other hand, GMT of HI antibody against the viruses of the third epidemic waves were significantly lower than those against viruses of the first and second waves (*t*-test; $p < 0.05$, *). Nucleotide sequences derived from HA gene of the six viruses were analyzed; and phylogenetic tree demonstrated that viruses derived from the three epidemic waves belonged to different clusters as shown in Figure 3.

Table 2. HI antibody titers against the test viruses

Virus	No. of subjects with HI antibody titer of									GMT
	<10	10	20	40	80	160	320	640	1280	
A/Thailand/104/2009	11	8	6	26	34	16	3	1	-	46.9
A/Thailand/ICRC_CBI_10/2009	13	8	15	19	27	15	5	2	1	44.2
A/Thailand/SEA 34002/2010	11	6	6	24	25	25	6	2	-	55.6
A/Thailand/SEA 34004/2010	10	5	11	26	29	15	7	2	-	51.1
A/Thailand/ICRC_BKK_1/2010	18	11	24	32	16	3	1	-	-	28.6
A/Thailand/ICRC_NSN_1/2010	22	12	21	29	14	6	1	-	-	23.3

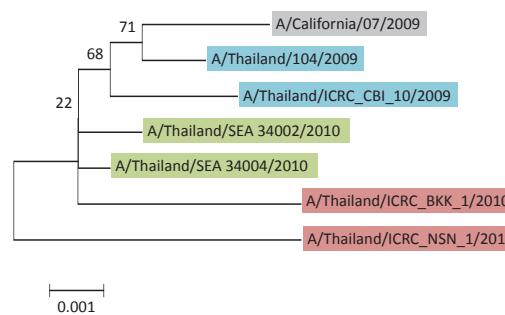


Figure 3. Phylogenetic tree based on HA gene nucleotide sequences

Conclusion

This study demonstrated significant antigenic change of H1N1pdm to the point that the existing antibody arose from the first epidemic wave or vaccination might not be able to protect against the current circulating strains. The virus strain to be incorporated as a component of vaccine, therefore, should be reconsidered to match with the current strains which underwent antigenic change dramatically.

Acknowledgements

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