

## Abstract

---

**Project Code :** TRF5780010

**Project Title :** *In vitro* characterization of novel reassortant pandemic (H1N1) 2009 influenza viruses isolated from experimentally co-infected quail

**Investigator :** Aunyaratana Thontiravong

Faculty of Veterinary Science, Chulalongkorn University

**E-mail Address :** a.thontiravong@gmail.com; Aunyaratana.T@chula.ac.th

**Project Period :** 2 years

**Abstract :**

Quail are considered as one of the intermediate hosts for generation of the novel reassortant influenza A viruses (IAVs). We have showed previously that the novel pandemic H1N1 2009 (pH1N1) reassortant viruses could be easily generated in the respiratory tract of the experimental co-infected quail. However, whether these novel pH1N1 reassortant viruses would be viable for replication in avian and mammalian hosts remain unknown. In this study, we evaluated the replication ability of the three novel dominant pH1N1 reassortant viruses recovered from pH1N1 and duck H3N2 (dkH3N2) co-infected quail in embryonated chicken eggs, mammalian (MDCK) and human lung derived (A549) cells compared with their parental viruses. In addition, the genetic characteristics of HA and NA genes of such reassortant viruses were also analyzed. Our study demonstrated that all of the reassortant viruses tested replicated efficiently in avian and mammalian cells, albeit with slightly lower titers than the parental viruses. Of note, all of the reassortant viruses showed enhanced replication in human lung derived (A549) cells compared to their parental viruses. Interestingly, a P(NA,NS)-DK reassortant virus containing NA and NS genes derived from pH1N1 and the remaining genes from dkH3N2 exhibited the highest replication ability in all *in vitro* models among reassortant viruses tested, indicating a high level of compatibility among gene segments of this reassortant virus. Sequence analysis revealed that all reassortant viruses tested showed a similar mutation (S215P) in the HA protein, while only P(NA,NS)-DK reassortant virus had amino acid mutations in NA protein. Our results highlight the potential role of quail as intermediate hosts for the generation of viable reassortant viruses with ability to replicate efficiently in avian, mammalian, and particularly human lung derived cells. These findings emphasize the need for the continuous

IAV surveillance in quail to prevent the risk of the emergence of novel reassortant viruses with pandemic potential.

**Keywords :** quail, reassortant virus, pandemic H1N1 2009 influenza viruses, *in vitro* characterization