

Output ที่ได้จากโครงการ

1. การนำเสนอผลงาน poster presentation เรื่อง การวิเคราะห์ลำดับนิวคลีโอไทด์จากไมโทคอนเดรียของ
โครงกระดูกโบราณในแหล่งโบราณคดีที่สูงในปางมะผ้า จังหวัดแม่ฮ่องสอน การประชุมนักวิจัยรุ่นใหม่ พบ
เมธีวิจัยอาวุโส สกว, 9-11 มกราคม 2547 โรงแรมเฟลิทซ์ ริเวอร์แคว จ.กาญจนบุรี

APPENDIX

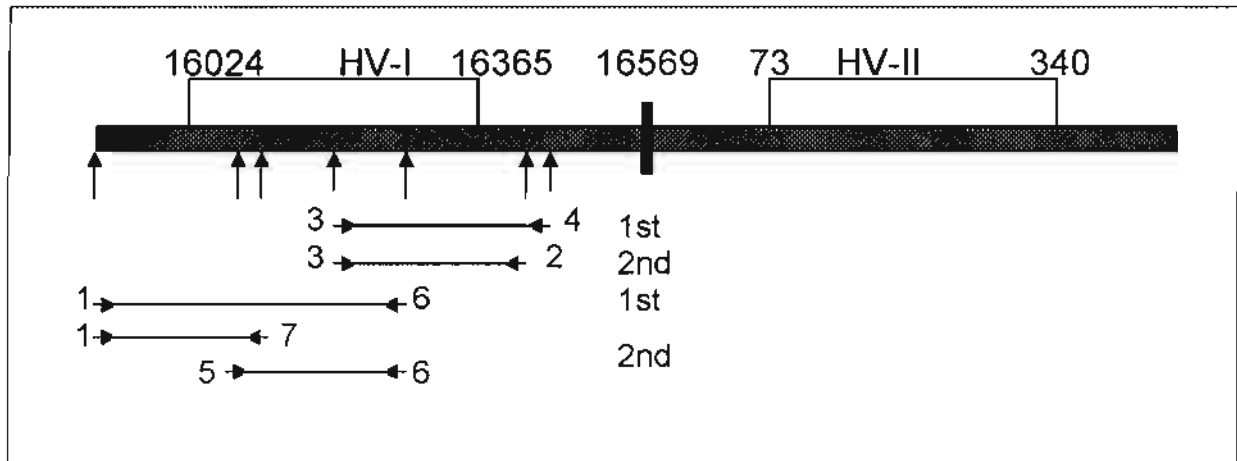


Figure. 1 Schematic diagram of the mtDNA D-loop region containing the hypervariable region-I (HV-I) amplified in mtDNA testing. First and second PCR are indicated. Horizontal arrows indicate forward and reverse primers. Numbers next to the primers are CC primer numbers.

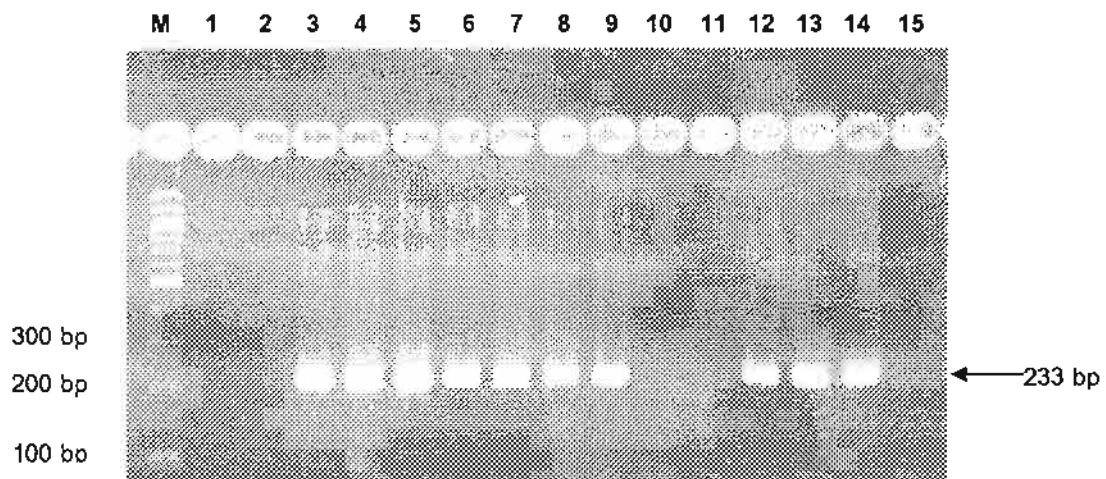


Figure 2 Some of the positive PCR amplification from second PCR reaction using primer CC3/CC2 (lane3 to 15). M: 100 base pair ladder, lane 1: blank control, lane 2: negative control

		111111111122222222223333	
16		226778888902234566690226	
		498291359283462614674172	
ANDERSON.TXT		tqctcaactcgcctcccccttccct	
SAM 161		..T...GT...C.T....C...	1
T126 sam138		..T...T..A.C.T....C...	
T130 sam155		..T...T...C.T....C...	
T145 sam203		C.T....C...	
T161 sam248		C.T....C...	
T166 sam151		C.T....C...	
T110 sam504		..T...T...C.T....C...	
T148 sam211		..T...T...C.T....C...	
T19 sam156		C.T....C...	
T52 sam174		C.T....C...	
T71 sam223		C.T....C...	
T79 sam260		..T...T...C.T....C...	
T92 sam486		C.T....C...	
T8 sam140		G.T..G.T...C.T....C...	
T32 sam158		C.T....C...	
T40 sam160		C.T....C...	
T102 sam502		..T...T...C.T....C...	2
T184 sam493		C.T....C...	
T3 sam175		T....TT.C.TT.	
T24 sam197		T.A.....C	3
T58 sam201		..T.T..T.....A....	4
T90 sam425		T....C...	5
T138 sam196		.A.....CT.T....C...	6
T173 sam245		T....C...	
T180 sam485		T....C...	
T113 sam492		C...	7
T44 sam131		.A.C.....C...	
T66 sam204		C...	

Figure 3 Nucleotide sequence differences in the D-loop region of mtDNA for 28 ancient teeth. A total of at least 24 polymorphic sites are found in comparison with the D-loop region of mtDNA in the reference sequence of Anderson et al. (1981). Only the differences from the reference sequence are shown. T stands for each single clone of the plasmid DNA represent that sample number on the right. Dots(.) represent the same nucleotide as in reference sequence whereas ~ indicates unfinished sequence. Seven clusters of polymorphisms are shown on the right.

OUTPUT from DNASP program

Input Data File: D:\...\ALIGN16209-16390 no anderson.fas

Number of sequences: 28 Number of sequences used: 28

Selected region: 1-182 Number of sites: 182

Total number of sites (excluding sites with gaps / missing data): 182

Pairwise Deletion option:

Sites with alignment gaps or missing data were considered

Analysis in Pairwise Comparisons

Gaps/missing information were excluded ONLY in pairwise comparisons

Number of pairwise comparisons: 378

Average number of sites analyzed: 182.00

Average number of differences: 2.431

Nucleotide diversity, P_i : 0.01336

Analysis at Individual Sites

Number of sites analyzed: 182.00

Number of polymorphic sites, S : 13

Average number of differences: 2.431

Nucleotide diversity, P_i : 0.01336

Theta-W, per sequence: 3.34065

Theta-W, per site: 0.01836

Figure 4 Nucleotide diversity output of the 28 mtDNA sequence from ancient teeth from DNASP program.

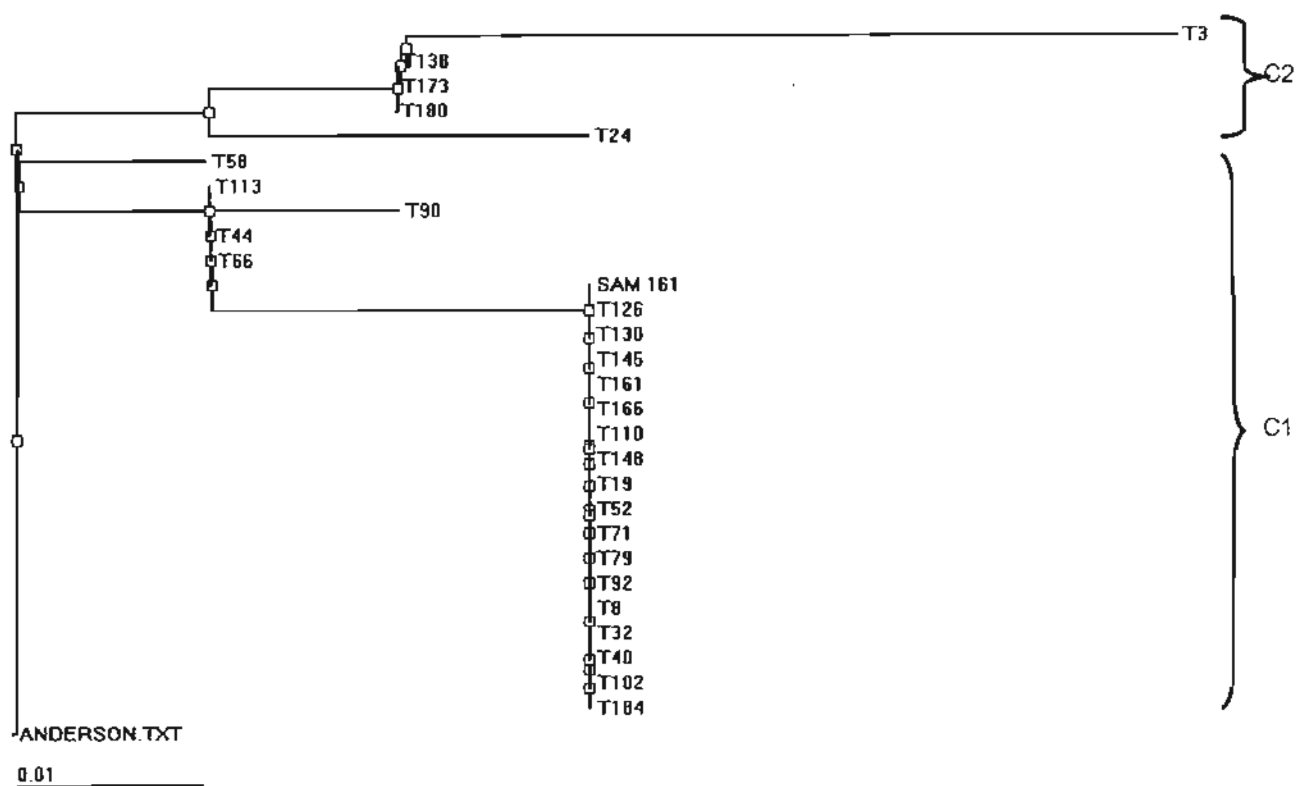


Figure 5 Phylogenetic tree for the 28 mtDNA sequences using Neighbor-Joining/UPGMA method version 3.6a2.1. The two clusters in the tree are indicated by brackets (C1, C2).

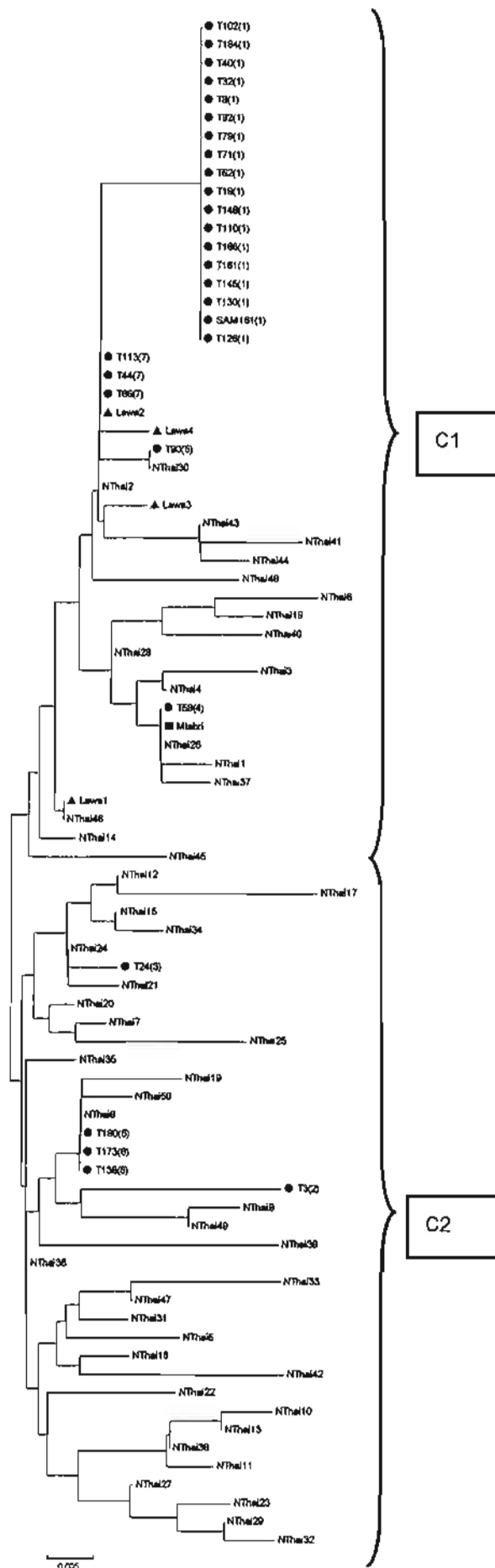


Figure 7 Phylogenetic tree showing 28 ancient mtDNA lineages from Pang Ma Pha and three other populations. The phylogenetic tree was constructed, based on pairwise difference distant method, by the neighbor-joining method. The two clusters are indicated by brackets (C1, C2). The name of ethnic haplotypes (Lawa, Mlabri, and northern Thai or NThai) are indicated at the tips of each branch.

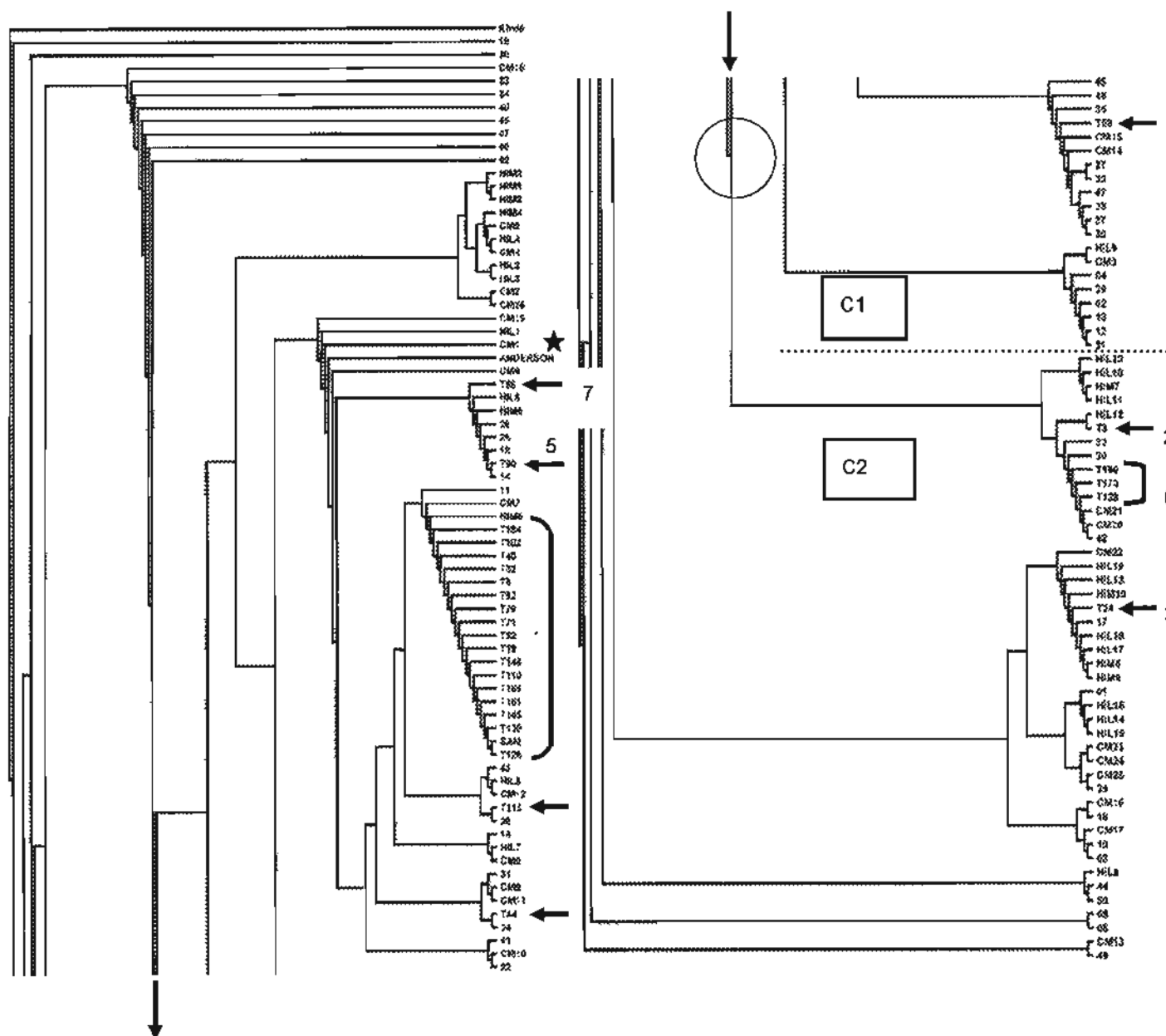


Figure 8 Phylogenetic tree of the 28 ancient DNA comparing with 4 other subpopulations, Lisu (HIL), Mussur (HIM), Thai Chiang Mai (CM) and normal Khon Kaen (number) based on parsimony analysis by the neighbor-joining method. Two main clusters of 2000 year old DNA are observed (C1, C2) diverged at the circle point with the exception of T24 which branches first as shown in the rooted tree.

