

## MITOCHONDRIAL DNA VARIATION OF INDONESIA WILD BOAR

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### Introduction and Objectives

Wild boars are the ancestors of all domestic pigs. Wild boars are indigenous to Western Europe and Northern Africa, ranging eastwards across the Mediterranean basin through India and South-East Asia (ISEA) to Sri Lanka, Java, Malaysia, Taiwan, Korea and Japan. However, the origin and genetic diversity of many wild boar populations is unclear. ISEA, especially Indonesia, is thought to be the center of pig domestication and origin of the other sister taxa of wild boars, which are identified as three divergent clusters based on mitochondrial DNA (mtDNA) sequences, one the Asian clade and two European groups (Larson *et al.* 2005). To investigate the phylogenetic relationship among *Sus scrofa* from many islands in Indonesia, we determined the nucleotide sequence of the mtDNA.

### Materials and Methods

A total of 125 wild boar (*Sus scrofa*) samples were collected from many islands in Indonesia. The DNA samples were taken from hair, meat and blood. Thirteen wild boars were collected from Sumatera Island (two from Aceh, one from Jambi and ten from Bengkulu). Thirty-seven wild boars were collected from Java Island (six from Bandung, five from Sumedang, one from Garut, two from Cilacap, nine from Purwokerto, eight from Banjarnegara, two from Purbalingga, three from Wonosobo and one from Pacitan). Seventy-five wild boars were collected from Nusa Tenggara Island (forty-eight from Lombok, twelve from Sumbawa, ten from Kupang and five from Flores).

The total DNA was extracted with DNeasy Blood & Tissue Kit (Qiagen®, USA). The amount of DNA was estimated by a spectrophotometer. DNA was amplified with two primers Mt112 (GCG CAC AAA CAT ACA) and Mt106 (AAT ATA CGC GCA CAT GCG TAC) {Okumura *et al.* 1999}. The PCR product was purified with QIAquick PCR Purification Kit (Qiagen®, USA). DNA sequencing was done using BigDye Terminator Cycle Sequencing Kit (Applied

Biosystems, Foster City, CA) and A81 PRISMS 310 Genetic Analyzer. Nucleotide sequences of 574 bp were constructed by connecting 2 or 3 DNA fragments. All mtDNA sequences were aligned using GENETYX-MAC software version 08 (Software Development Co., Tokyo, Japan).

### Results

Total of 574 nucleotide sequences were determined from all samples. Thirty haplotypes were found among 125 samples. Among these, 13 haplotypes (E2, E7, E8, E9, E10, E15, E16, W9, W10, W17, W22, W27, and E22) were independently found from one sample, six haplotypes (E2, E5, W2, W6, W21 and E46) were found from two samples, three haplotypes (E31, E53, and E59) were from three samples, two haplotypes (W19, E26) were from four samples and one haplotypes (W1) was from five samples. Three haplotypes (E4, E11, and W11) were found from seven samples, one haplotype (E23) were found from 15 samples and one haplotype (E45) was found from 40 samples.

The Neighbour-joining (NJ) relationship among 30 Indonesian haplotypes and 87 haplotypes from Asian and European lineages showed three major clusters: the Asian (77% bootstrap value), the European (89% bootstrap value) and the Indonesian (Java and Sumatera islands, 99% bootstrap value) clusters (Fig 1). The Indonesian cluster was divided into two lineages; each with 97% bootstrap value and 74% bootstrap value respectively. The lineages (74% bootstrap value) were furthermore divided into three groups. The haplotypes E59, E53, E7, E4, E31, E26, and E10 were related Vietnamese wild boars.

### Discussion

The Indonesian wild boars from West and Central Java and Sumatra Islands (Bengkulu) take an ancestral position compared with Asian and European groups in NJ tree. Our study strongly indicated that the Indonesian wild boars could be an ancestor of domestic pigs and wild boars distributed both in Asia and Europe.

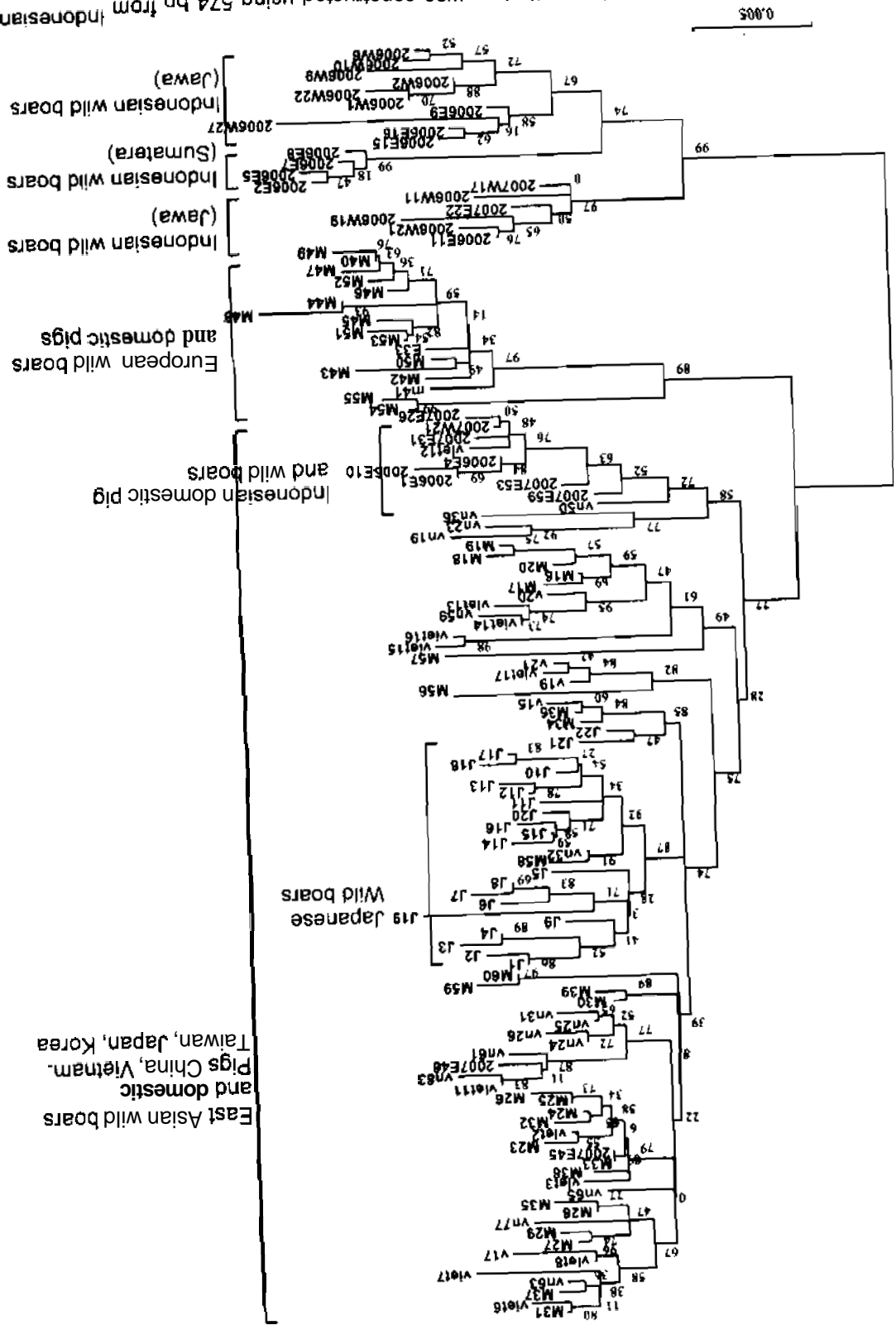


Fig 7. Neighbour-joining phylogenetic tree was constructed using 574 bp from Indonesian wild and domestic boars and other haplotypes.

References

Larson et al. 2005. Science (37): 1618-1621.  
 Okumura et al. 1999. Antropol Sci 107: 213-228.