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Population Genetic Structure of Northern Thai Indigenous Pigs and their Utilisation as Genetic Resources

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Abstract

The study of genetic information in indigenous and wild animals has recently become a topic of highest importance worldwide. The aim of this study was to investigate the population genetic structure of Thai indigenous pigs and Thai wild boars. The complete mitochondrial DNA control region was sequenced using 72 Thai indigenous pigs and 11 Thai wild boars collected at twelve locations in five provinces in Northern Thailand. To assess the population genetic structure, Thai indigenous pigs were grouped into five population zones defined by the sampling areas (zone-I to zone-V). Thai wild boars were grouped into one population. In total, 24 different mtDNA haplotypes have been described in the Thai pigs. The distribution of individuals/haplotypes showed 6/2, 20/9, 14/2, 11/5, 21/9 and 11/4 respectively per group. Median joining network analysis revealed similarities between Thai indigenous and Thai wild boar haplotypes. A high haplotype (mean \pm SD; $H = 0.938 \pm 0.011$) and nucleotide diversity ($\pi = 0.007 \pm 0.003$) of Thai pig populations was observed. Published D-loop sequences of other Asian and European haplotypes assessed from GenBank were used to compare their genetic relationships with our data. The average pairwise difference within populations (PiX) ranged from 1.828 to 6.207 in Thai pigs. Moreover, the average pairwise difference between populations ($PiXY$) ranged from 5.362 to 9.481 among Thai pigs and other Asian pigs, and ranged from 21.312 to 27.261 among Thai pigs and European pigs. The population demographic parameters such as Tajima's D-values and Fu's F_s test revealed negative values ($p < 0.05$) between Asian and European pigs and suggested a population expansion occurred in the past. This investigation proposes that Thai indigenous pigs are closely related with Thai wild boars and may eventually go back to the common Asian ancestor, whereas Thai and other Asian pigs are distinctly different from European pigs. Our study describes the first approach to apply mtDNA sequence information for population structure analysis in Thai indigenous pigs and Thai wild boars, and it will be a benefit for the conservation and utilisation of indigenous pigs as an important genetic resource in the future.

Keywords: Genetic resources, mitochondrial DNA, Northern Thailand, population structure, Thai indigenous pigs