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Maternal Genetic History of the Mon in Thailand

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ABSTRACT

Multiple studies based on the archaeology and anthropology of the Mon in Thailand have been reported, but little is known about their genetic history. The present study investigated polymorphisms in the hypervariable region I of mitochondrial DNA (mtDNA) in 112 new Mon samples from central and western Thailand, and then compared them with previous mtDNA data from modern Mon and ancient Mon, or Nyah Kur, from northern and northeastern Thailand. The Mon from western Thailand showed the highest genetic diversity, reflected by the haplotype diversity and number of polymorphic sites. Demographic expansion parameters and the Bayesian sky plot analysis indicated that almost all Mon populations, with the exception of the northeastern Thai Mon, have had constant population sizes or have continuously incremented over time, until reductions around 5,000 to 1,000 y ago. The multidimensional scaling plot and neighbor joining tree revealed the closest genetic relatedness between the central Thai Mon from Ratchaburi province and northeastern Thai Mon, indicating a likely common genetic ancestry. The other Mon populations had diverged genetically, perhaps driven by genetic admixture with different population sources. Interestingly, a genetic distinction between the Mon and Nyah Kur was detected, reflecting different genetic stocks between the modern and ancient Mon. Therefore, future studies of haplogroup lineages from the complete mtDNA genome and Y chromosome could elucidate a deeper and broader picture of the Mon's genetic history.

Keywords: Mon, Mitochondrial DNA, Hypervariable region I, Genetic relationship