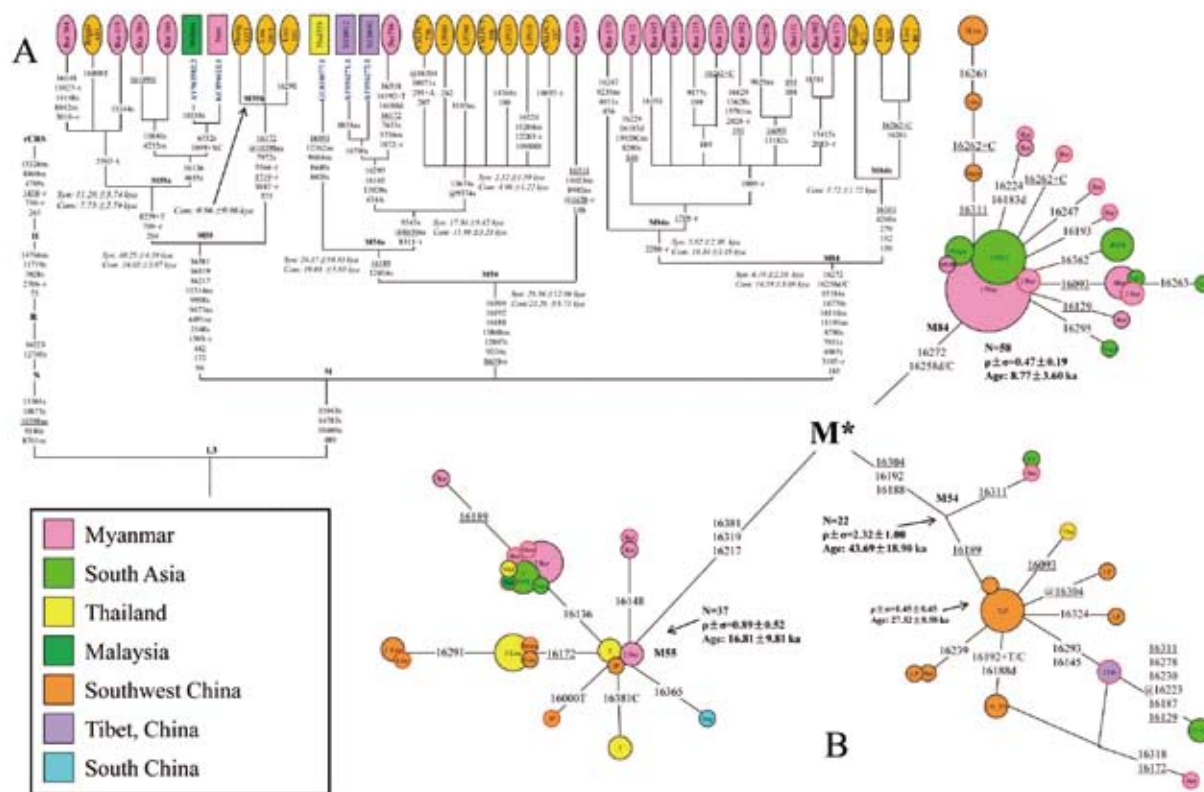


New Genetic Evidence Supports Initial Migration of Settlers into Eastern Asia via Myanmar

Precisely how humans came to initially populate Asia is a matter of some contention. After migrating out of Africa, it is generally agreed upon that humans moved along the coastline, and settled along the way, eventually pushing inland. Another hypothesis posits that humans passed through the mountainous regions by following waterways. Asia is home to several great waterways,

including the Mekong, Salween, and Irrawaddy, and all three could have created hospitable environments and pathways for migration. Indeed, if humans did move inland following the river systems, Myanmar probably served as the corridor. Unfortunately, testing the latter hypothesis is no easy task due to little archaeological research and a general scarcity of genetic information



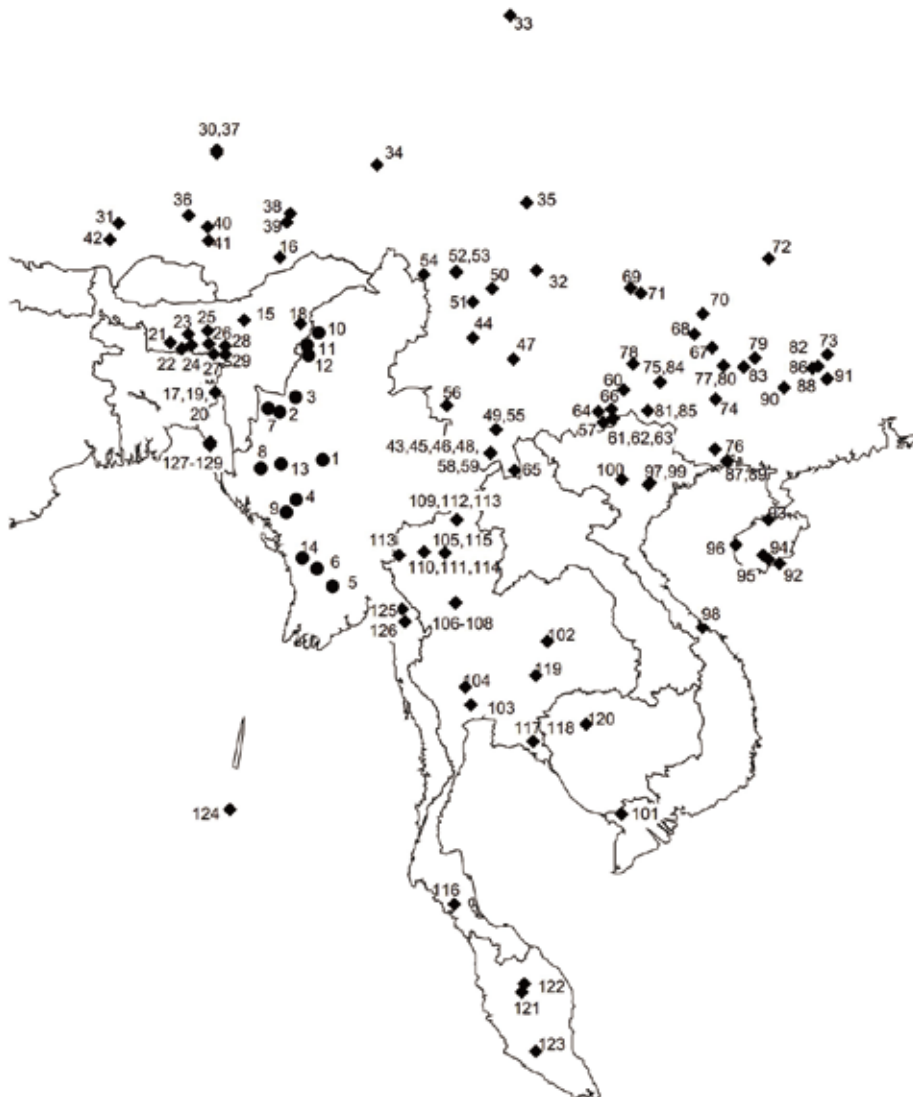
Phylogenetic trees and median networks of haplogroups M54, M55 and M84. Nucleotide position numbers are consistent with the revised Cambridge reference sequence. (a) Phylogenetic trees of haplogroups M54, M55 and M84. The newly sequenced samples in this study were marked in ellipses, while mtDNAs from the published literature were displayed in rectangles. Suffixes A, C and T refer to transversions, “d” means a deletion, and “+” indicates an insertion; recurrent mutations are underlined; “@” means a reverse mutation; “H” means heterogeneity. The C stretch length polymorphism in regions 303–315, AC indels at 515–522, 16182C, 16183C, 16193.1C(C) and 16519 were disregarded for the tree reconstruction. s, synonymous replacements; ns, nonsynonymous replacements; t, change in transfer RNA; r, change in ribosomal RNA gene; nc, mutations at the intergenic noncoding regions in segments 577–16023. Com: coalescent age calculated based on complete genome substitutions; syn: coalescent age calculated based on coding region synonymous substitutions. The geographic origin of samples was shown by different colors. (b) Median networks of haplogroups M54, M55 and M84 based mainly on HVS data. The suffixes have the same meaning with those in the phylogenetic trees. The circles with red frame represent the complete sequenced individuals.

that could provide support for the hypothesis.

Recently, Dr. ZHANG Yaping and Dr. KONG Qingpeng of the Kunming Institute of Zoology, Chinese Academy of Sciences began investigating the Myanmar hypothesis by gathering genetic samples from several Burmese populations. After collecting more than 845 samples from 14 different Burmese populations, analysis of Mitochondrial DNA (mtDNA) along with 5,907 previously published samples found that somewhere between 50 and 20,000 years ago, there was an enrichment in the basal lineage of the mtDNA. This

enrichment suggests that Myanmar was an important of differentiation when human arrived in south-east Asia.

Further analysis of the basal lineages reveal several shared haplogroups dated to around 200 BCE, which was likely due either to population expansion or trade. Other shared haplogroups date even further back, to somewhere between 20,000 and 10,000 years ago. In sum, genetic evidence of both recent gene flow and ancient migration provides strong support for the hypothesis that humans migrated along waterways, as well as along the coast. (By Andrew Willden from the Kunming Institute of Zoology)



Geographic locations of 129 populations analyzed in the present study. The 14 Myanmar populations collected in this study are indicated by solid circles, whereas the rest populations are indicated by diamonds. The map was created by Surfer 8.0 package.