



Mapping Human Genetic Diversity in Asia

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Asia harbors substantial cultural and linguistic diversity, but the geographic structure of genetic variation across the continent remains enigmatic. Our group performed a large-scale survey of autosomal variation, focusing on broad continental relationships, for Southeast Asian (SEA) including 13 populations (Hmong, Yao, Karen, Tai Lue, Tai Yong, Tai Kern, Tai Yuan, Mon, Lawa, Mlabri, H'Tin, Plang and Palong) from Thailand, and East Asian (EA) populations by using the Affymetrix GeneChip HumanMapping 50K Xba Array. Stringently quality-controlled genotypes were obtained at 54,794 autosomal single-nucleotide polymorphisms (SNPs) in 1928 individuals representing 73 Asian and two non-Asian HapMap populations. Apart from developing a general description of Asian population structure and its relation to geography, language, and demographic history, we concentrated on uncovering the geographic source(s) of EA and SEA populations. The results show that genetic ancestry is strongly correlated with linguistic affiliations as well as geography. Most populations show relatedness within ethnic/linguistic groups, despite prevalent gene flow among populations. More than 90% of East Asian (EA) haplotypes could be found in either Southeast Asian (SEA) or Central-South Asian (CSA) populations and show clinal structure with haplotype diversity decreasing from south to north. Furthermore, 50% of EA haplotypes were found in SEA only and 5% were found in CSA only, indicating that SEA was a major geographic source of EA populations.