



## Genetic affinities of central China populations

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Genet. Mol. Res. 13 (1): 616-625 (2014)

Received January 10, 2013

Accepted June 6, 2013

Published January 28, 2014

DOI <http://dx.doi.org/10.4238/2014.January.28.7>

**ABSTRACT.** Hunan locates in the south-central part of China, to the south of the middle reaches of the Yangtze River and south of Lake Dongting. According to the historical records, the peopling of Hunan by modern human ancestors can ascend to 40 thousand years ago. Thus, to trace the ancient maternal components can offer further insight into the origin of south-central China. In this study, we investigated the mitochondrial DNA of 114 individuals from Hunan Province (including 34 Han, 40 Tujia and 40 Miao). Hypervariable regions I and II of the mtDNA control region were sequenced, and the relative diagnostic variations in coding region according to the updated worldwide phylogeny tree were selected and typed by restriction fragment length polymorphism analysis or direct sequencing. All individuals were classified into specific (sub)haplogroups. By comparison with the surrounding populations, southern China-prevalent haplogroups were detected with relative higher frequency in the Tujia and Miao ethnic

populations, such as haplogroup B, with more than 20%, lacking in the Han population, which illustrated its southern origin characters. In addition, we also detected northern of East Asia prevalent haplogroups with a relative higher frequency in Tujia populations than in the Miao and Yao ethnic groups, implying a gene flow from Han populations. However, the language-clustering tendency was supported by our principal component analysis and further genetic estimation results. Han and ethnic groups in central China exhibited specific ancestors related to their closer language affinity, although there was extensively genetic admixture between Han and ethnic groups.

**Key words:** mtDNA; Origin; Ethnic group; Hunan