#### 研究报告

# 贵州瑶族3支系Y-DNA及线粒体DNA序列多态性分析

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采用PCR-RFLP技术,通过观察由12个单核苷酸多态位点(SNPs)组成的Y染色体单倍型及由9个多态位点组成的线粒 体DNA单倍型在贵州瑶族中的分布,分析贵州瑶族父系及母系遗传结构,探讨其起源及迁徙。结果显示,97份男性<mark>▶加入引用管理器</mark> 样本分别属于H7、H8、H9、H11 4种Y-DNA单倍型,苗瑶语系特异Y-DNA单倍型H7的平均频率为92.4%;通过对线粒 ▶复制索引 体DNA基因分型,得到8种单倍型,可归入B4、B5、D4、D5和N\*单倍型类群中,Co II/tRNA<sup>Lys</sup>区域间的9bp缺失平均 频率为58.2%。结果提示贵州瑶族父系遗传结构单一,具有典型的苗瑶族群特征,又存在与其他族群的融合。母系 遗传结构相对复杂, 9 bp缺失是贵州瑶族的母系遗传结构特征。

关键词 贵州瑶族; Y-DNA单倍型; mtDNA单倍型类群

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# Analysis of Polymorphisms in Y-DNA Haplotypes and mtDNA Haplogroups. in Yao Ethnic Group from Guizhou

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#### **Abstract**

<DIV>The frequencies of Y-chromosome haplotypes consisting of 12 single nucleotide polymorphisms (SNP) and mitochondrial DNA (mtDNA) haplotypes consisting of 9 SNPs were investigated using PCR-RFLP in 97 Yaos from Guizhou to study the patrilineal and matrilineal genetic structure and the origin of Yao Ethnic Group from Guizhou. Results showed that all 97 samples were classified into 4 Y-DNA haplotypes (H7, H8, H9 and H11). The major haplotype H7 of Hmong-Mien Population was highly prevalent (92.4%) in Yaos from Guizhou. Eight mtDNA haplotypes were identified through mtDNA analysis and all the haplotypes could be classified into 5 haplogroups (B4, B5, D4, D5 and N\*) that were defined previously. The frequency of a 9-bp deletion in the human mtDNA Co II/tRNA<SUP>Lys</SUP> intergenic region was 58.2% in the 97 samples. These data suggest that the patrillineal genetic structure of Yao ethnic group from Guizhou was simple and Yaos from Guizhou had the typical genetic character of the Hmong-Mien Population and some admixture with other populations. The matrilineal genetic structure of Yaos from Guizhou was relatively complex and the 9-bp deletion was a characteristic genetic marker of the matrilineal genetic structure of Yaos from Guizhou.</DIV>

**Key words** Yao ethnic group Y-chromosome haplotype mtDNA haplogroup

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