

## 福建畲族群体17个Y-STR基因座单倍型及遗传关系

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**摘要** 应用Y-filer<sup>TM</sup>试剂盒及基因分型技术, 检测152份福建畲族无关男性个体17个Y-STR基因座的多态性分布, 计算等位基因频率及单倍型多样性, 并结合已公开发表的其他11个群体相应基因座的单倍型资料, 分析福建畲族群体遗传距离和聚类关系。福建畲族DYS385a/b基因座检出50种单倍型, 其余15个Y-STR基因座分别检出3~11个等位基因, 基因多样性GD值在0.4037(DYS391)~0.9725(DYS385a/b); 观察到DYS19和DYS390基因座双等位基因和DYS385a/b基因座三等位基因, 以及DYS448等部分基因座出现的“off-ladder”等位基因现象。17个Y-STR基因座共同构成的单倍型144种, 其中138种单倍型出现1次, 5种出现2次, 1种出现4次, 累计GD值为0.9990。从遗传距离分析发现, 福建畲族与浙江汉族之间的遗传距离最近(0.0042), 与青海藏族(0.2378)之间的遗传距离相对较远。福建畲族最靠近由台湾群体、浙江汉族、南方汉族等典型南方汉族群体聚成的分支区域。结果表明该17个Y-STR基因座在福建畲族群体中具有丰富的遗传多态性, 对建立Y染色体STR数据库, 研究群体遗传学和进行法医学应用有重要意义。

**关键词:** Y染色体 短串联重复序列 单倍型 遗传距离 福建畲族

**Abstract:** To investigate the genetic polymorphisms of 17 Y-chromosomal short tandem repeats(Y-STR) loci in She ethnic population from Fujian province, and to evaluate their forensic application values and genetic relationship with other 11 populations, 152 unrelated male individuals of She ethnic population in Fujian were used to determine the distribution of allele frequencies and haplotypes by using Y-filer<sup>TM</sup> System. Cluster analysis and phylogenetic trees were applied to show the genetic distance among the populations. As a result, 50 haplotypes were found in *DYS385a/b* loci, and 3~11 alleles were found in the rest 15 Y-STR loci. The GD value was from 0.4037(*DYS391*) to 0.9725(*DYS385a/b*). This study has also revealed “off-ladder” alleles at several Y-loci, namely *DYS448*, *DYS393*, *DYS458* and *DYS635*, and several occurrences of duplications at the *DYS385a/b*, *DYS19* and *DYS390* loci. One hundred and forty-four haplotypes were found in 17 Y-STR loci, of which 138 were unique, 5 were found in 2 individuals, 1 was found in 4 individuals, and the observed haplotypes diversity value was 0.9990. Comparing with 11 populations, the genetic distance between She ethnic and Han population in Zhejiang was the smallest (0.0042), while it was the largest between She ethnic and Tibet ethnic population (0.2380). Cluster analysis and phylogenetic tree both demonstrated that genetic distance between She ethnic and several south Han populations is closer than between She ethnic and non-Han populations. Multiplex detection of the 17 Y-STR loci revealed a highly polymorphic genetic distribution, which would be very powerful for establishing a Y-STR database, for population genetics and forensic practice.

**Keywords:** Y-chromosome, short tandem repeats, haplotype, genetic distance, She ethnic population in Fujian

收稿日期: 2012-02-02; 出版日期: 2012-08-25

基金资助:

教育部长江学者和创新团队发展计划资助项目(证据科学研究与应用)(编号: IRT0956), 国家自然科学基金面上项目(编号: 81172902), 北京市科技新星计划(编号: 2010B073)和中国政法大学青年教师学术创新团队资助项目

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引用本文:

百茹峰, 杨利海, 袁丽, 梁权赠, 鲁涤, 杨雪, 石美森. 福建畲族群体17个Y-STR基因座单倍型及遗传关系. 遗传, 2012, 34(8): 1020-1030.

BAI Ru-Feng, YANG Li-Hai, YUAN Li, LIANG Quan-Zeng, LU Di, YANG Xue, SHI Mei-Sen. Polymorphism of 17 Y-STR loci in She ethnic population in Fujian and genetic relationship with 11 populations. HEREDITAS, 2012, V34(8): 1020-1030.










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