

## 人类Y染色体36个新STR位点的筛选与鉴定

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**摘要** 通过对NCBI数据库中的Y-STR位点和生物信息学预测的新Y-STR位点的分析, 选取了133个位点在48个全球分布的样本中进行检测验证, 获得41个可靠的高频位点, 其中36个为首次发现验证的新Y-STR位点。利用这41个Y-STR位点, 在200个上海随机男性样本中共发现200种单倍型, 实现了人群内个体间100%区分, 并通过对浙江江山一姜氏聚集地的9个5代以内无血缘关系的姜氏个体和7个上海随机人群的姜氏个体的单倍型的分析, 发现6个江山姜氏个体具较近的亲缘关系(彼此差异位点在2~4个之间)。这41个Y-STR位点具备较高的信息度, 能有效区分群体内不同家族来源的个体, 这将有助于群体内个体间近代亲缘关系研究, 并有望在法医学法医个体识别、亲权鉴定, 人类起源、迁徙等研究中发挥重大作用。

**关键词:** Y-STR 多态性 单倍型 区分度 近代亲缘关系

**Abstract:** 133 candidate Y-STR loci were selected from NCBI STS database or by bioinformatics analysis in human Y-chromosome sequence, and were screened among 48 DNA samples around the world. Forty-one Y-STRs with high allelic frequency were validated, 36 of which were first reported. Two hundred haplotypes of the 41 STRs were identified among 200 randomly sampled male individuals in Shanghai, indicating 100% inter-individual discrimination. By network analysis of haplotypes of the 41 STRs among nine Jiang-surname male individuals with no consanguinity within 5 generations from a Jiang-surname individual gathering at Jiangshan, Zhejiang Province, and 7 Jiang-surname male individuals from the random shanghai population, 6 Jiang-surname individuals from Jiangshan were close with only 2-4 STR locus difference. These 41 Y-STR loci provide enough information by which individuals from each other with different early modern family origin can be effectively distinguished. This will promote studies on identification of non-lineal relationship in forensics, ancestry location of oversea Chinese, the surname origin and evolution, origin and migration of modern humans and many other studies of Contemporary Anthropology.

**Keywords:** Y-STR, polymorphism, haplotype, discrimination, early modern genetic relationship

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