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研究报告

汉族群体23个Y染色体双等位基因标记遗传多态性研究

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摘要 为了筛选在汉族群体中具有多态性的Y染色体双等位基因标记并获取其群体遗传学数据。采用片段长度差异等位基因特异性PCR和PAGE技术对武汉地区160名男性汉族无关个体的23个Y染色体双等位基因标记（M7，M9，M50，M88，M89，M95，M111，M117，M119，M121，M122，M134，M159，M164，M175，M214，LINE1，MSY2，RPS4Y711，SRY＋465，IMS-JST164520，IMS-JST021354和IMS-JST003305）进行分型。除M50、M159和M164外，其余20个标记在武汉汉族群体中均具有遗传多态性，其基因多样性（GD）范围为0.0126～0.4855，共检出35种不同单体群组合（Hg1～35），单体群多样性（HD）为0.9471。表明20个Y染色体双等位基因标记组成的单体群具有较高的遗传多样性，在法医学应用和群体进化研究中具有较高的实用价值。

关键词 Y染色体,双等位基因标记,片段长度差异等位基因特异性PCR,单体群

分类号 Q347

Genetic Polymorphism of 23 Y Chromosome Biallelic Markers in Chinese Han Population

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Abstract

To search polymorphic Y chromosome biallelic markers in Chinese Han population, and obtain their population genetic data. Genotyping of 23 biallelic markers on human Y chromosome (M7, M9, M50, M88, M89, M95, M111, M117, M119, M121, M122, M134, M159, M164, M175, M214, LINE1, MSY2, RPS4Y711, SRY＋465, IMS-JST164520, IMS-JST021354 and IMS-JST003305) were carried out in a sample of 160 unrelated Chinese male individuals living in Wuhan using fragment length discrepant allele specific PCR (FLDAS-PCR) and PAGE technique. In all 23 biallelic markers, genetic polymorphism were identified for 20 loci in Wuhan Han population except for M50, M159 and M164, and the ranges of gene diversity (GD) were 0.0126～0.4855. A total of 35 different haplogroups (Hg1～35) were observed and the haplogroup diversity (HD) was 0.9471. The haplogroups formed by 20 biallelic markers are highly polymorphic, and can be used in forensic science and population evolution studies.

Key words Y chromosome biallelic marker fragment length discrepant allele specific PCR haplogroup

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