

短串联重复序列D7S2201基因座的群体遗传学研究 Population Genetic Study of the STR Locus D7S2201 in Chinese and Thai Populations

黄代新, 张林, 吴梅筠, 陈国弟, 陈于波 HUANG Dai-xin, ZHANG Lin, WU Mei-yun, CHEN Guo-di, CHEN Yu-bo

华西医科大学法医学院法医物证教研室, 四川成都 610041 Department of Forensic Biology, West China University of Medical Sciences, Chengdu 610041, China

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摘要 用扩增片段长度多态性技术分析短串联重复序列D7S2201基因座的遗传多态性, 在262个中国成都地区汉族无关个体及119个泰国曼谷地区泰人无关个体中分别发现7个和5个等位基因, 首次获得该基因座在两群体中的频率分布, 其等位基因片段大小范围为100~124bp。两群体的基因型频率分布均符合Hardy Weinberg平衡。该基因座在两群体中的个人识别能力 (PD)、杂合度 (H)、多态性信息含量 (CPI) 及非父排除率 (PE) 分别为0.7038、0.5992、0.4789、0.2900和0.7351、0.5882、0.5012、0.2770。家系调查证实了等位基因的传递遵循孟德尔遗传规律。 χ^2 检验表明两群体间等位基因频率分布无显著性差异。

Abstract: The polymorphism of a new short tandem repeat (STR) locus D7S2201 was analyzed by using AmpFLP. Seven alleles were observed in 262 unrelated Chinese individuals living in Chengdu and five alleles in 119 unrelated Thai individuals living in Bangkok, the ranges of fragment size were 100~124bp. The genotypes distributions of D7S2201 locus in the two populations were in accordance with Hardy Weinberg equilibrium. The discriminating power (PD), observed heterozygosity (H), polymorphism information content (CPI) and power of exclusion (PE) were 0.7038, 0.5992, 0.4789, 0.2900 in Chinese population and 0.7351, 0.5882, 0.5012, 0.2770 in Thai population respectively. Family studies confirmed Mendelian inheritance of alleles. No significant difference was observed between the two populations.

关键词 [短串联重复序列](#) [聚合酶链反应](#) [D7S2201基因座](#) [多态性](#) **Keywords** [short tandem repeat](#) [polymerase chain reaction](#) [D7S2201 locus](#) [polymorphism](#)

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