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PCR扩增近交系大鼠微卫星位点DNA多态性的研究 Rat Gene Polymorphism Using PCR-Analyzed Microsatellites

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摘要　本实验选取大鼠7条染色体上的微卫星位点合成了10对引物,利用聚合酶链反应(PCR)扩增技术对国内北京和哈尔滨等4家单位提供的6个品系(SHR、SHRSP、LEW、RCS、WKY和F344)的8个近交系大鼠群体进行了DNA多态性分析的研究.结果表明:9个微卫星位点具有显著多态性;不同品系个体之间具有多态性;同一群体不同个体之间除SHR(哈)的SMST位点和WKY(哈)的AGT位点出现一定的差异外,其他均没有差异;不同地区同一品系的不同个体之间也存在一定的差异.该方法能有效地对近交系与杂交系、品系与品系、品系与亚系加以区分.因此,本实验为开展近交系大鼠遗传作图、基因定位和为实验动物的遗传背景监测提供可靠的信息,为大鼠遗传基因的研究提供了一个快捷简便、特异准确的方法。

Abstract:In the experiment,It were selected that 20 primers were assigned on 7 chromosomes of inbred rat.DNA polymorphism of 8 colonies from 6 inbred rat strains(SHR、SHRSP、WKY、LEW、RCS、F344)were studied in national Beijing and Harbin using PCR-analyzed microsatellites.The results indicated that there were remarkable polymorphism in 9 microsatellite loci;There is a polymorphism among the various rat strains;and no polymorphism in the same rat strains except SMST locus of SHR(Harbin)and AGT locus of WKY(Harbin)and there is a little difference among the same inbred rat strains in different areas.The method of PCR-analyzed microsatellites can be used for distinguishing between inbred and outbred、different strains、strain and substrain.and it provides a lot of information for genetic mapping,gene location and heredity probe of the inbred rat strains,and a speedy、convenient method for genetic research of the inbred rat.

关键词　近交系大鼠　微卫星　DNA多态性　Key words　inbred rat　microsatellites　DNA polymorphism

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