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研究论文

秦川母牛群体遗传特性的微卫星标记研究

孙维斌1, 陈宏1,2, 雷初朝1, 雷雪芹 3, 张英汉1

1. 西北农林科技大学动物科技学院，陕西省农业分子生物学重点实验室，杨凌 712100；
2. 徐州师范大学细胞与分子生物学研究所，徐州 221116；
3. 河南科技大学动物科技学院，洛阳 471000

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摘要

为了从DNA分子水平揭示秦川牛群体遗传多态性和群体遗传结构，寻找可用于秦川牛的微卫星标记，本研究选择了12个普通牛（Bos taurus）微卫星标记检测了90头秦川母牛各微卫星位点的遗传变异及多态性。结果表明，在秦川母牛群体中，12个微卫星位点共检测到了247个等位基因，各位点的等位基因数在13（INRA005）～33个(HEL13)之间，平均每个微卫星位点的等位基因数为21个；总有效等位基因数和平均每个位点平均有效等位基因数（Ne）分别分为142.6229和11.8852。各位点平均基因频率取样方差(V（pij）)为2.6036×104。12个微卫星位点平均观察杂合度(Ho)和平均期望杂合度(He)在0.7842（INRA005）～0.9775（BM315）和0.7952（BM315）～0.9446（HEL13）之间。12个位点平均多态信息含量（PIC）在0.7653（INRA005）～0.9420（HEL13）之间，平均为0.8965. 12个微卫星位点均属于高度多态位点，这表明秦川母牛群体中所检测各微卫星位点具有丰富的遗传多态性，具备较大的选择潜力。12个微卫星位点的平均固定指数（F）为-0.0076，即各位点杂合子的缺陷度不高，即偏离Hardy-Weinberg 平衡的程度不大。

关键词 秦川母牛；微卫星DNA；多态性

分类号

Study on Population Genetic Characteristics of Qinchuan Cows Using Microsatellite Markers

Weibin Sun1, Hong Chen1,2, Chuzhao Lei1, Xueqin Lei 1,3, Yinghan Zhang1

1. College of Animal Science and Technology, Northwest A & F University, Shaanxi Key Laboratory of Molecular Biology for Agriculture, Yangling 712100, China;
2. Institute of Cellular and Molecular Biology, Xuzhou Normal University, Xuzhou 221116, China;
3. College of Animal Science and Technology, Henan Sci-tech University, Luoyang 471000, China

Abstract

<P>To evaluate the genetic polymorphisms and to search for available molecular markers for Qinchuan cattle, 90 Qinchuan cows were genotyped with 12 microsatellite markers. A total of 247 alleles were detected, with the number of alleles ranging from 13 (INRA005) to 33 (HEL13), giving a mean number of 21 alleles per locus. The total and mean effective allele number were 142.6229 and 11.8852, respectively. Mean sampling variance of the allele frequency was 2.6036 × 10-4. Allele size ranges of the 12 microsa-tellite loci were different. The observed heterozygosity and expected heterozygosity were from 0.7842 (INRA005) to 0.9775 (BM315) and 0.7952 (BM315) to 0.9446 (HEL13), respectively. Mean observed heterozygosity and mean expected heterozygosity were 0.9117 and 0.9047, respectively. Polymorphism information content values were from 0.7653 (INRA005) to 0.9420 (HEL13), and mean polymorphism information content of the 12 microsatellite loci was 0.8965. All the 12 microsatellite loci were highly polymorphic, which showed that there were rich genetic polymorphisms at these detected microsatellite loci in Qinchuan cows. At the 12 microsatellite loci, the mean fixation index was <I>&#</I>61485;0.0076, reflecting that the degree of heterozygote defect at these loci was not high and deviations from Hardy-Weinberg equilibrium were not significant.</P>

Key words Qinchuan cattle；microsatellite DNA；polymorphism

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通讯作者 陈宏 chenhong1212@263.net