

用4个微卫星标记分析7个绵羊群体之间的遗传关系Genetic Relationships Among Seven Sheep Populations Using Four Microsatellite Markers

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收稿日期 修回日期 网络版发布日期 接受日期

摘要

分析了4个微卫星基因座BM143、OarHH35、OarAE101、BMS2508在7个绵羊群体（小尾寒羊、湖羊、乌珠穆沁羊、萨福克羊、多赛特羊、夏洛来羊、多赛特公羊×小尾寒羊母羊F1代杂种羊）286只绵羊中的遗传多态性。结果表明，这4个微卫星标记在7个绵羊群体中的等位基因数分别为9、11、14和9，其多态信息含量/有效等位基因数/杂合度分别为0.7073/3.7231/0.7314、0.8267/6.4399/0.8447、0.5743/2.5178/0.6028、0.6172/3.0712/0.6744，其中OarHH35的遗传变异最大，OarAE101最小。7个绵羊群体中小尾寒羊的遗传变异最大，湖羊的最小。基于Nei氏DA距离和DS标准遗传距离，采用UPGMA方法构建了系统发生树。该发生树将中国地方品种（小尾寒羊、乌珠穆沁羊、湖羊）和法国的夏洛来羊归为一类，将F1杂种羊、英国品种（萨福克羊和多赛特羊）归为另一类。绵羊微卫星基因分型技术为检查品种（群体）之间的遗传关系提供了一个有用的工具。

Abstract: The genetic polymorphisms of four microsatellite loci BM143, OarHH35, OarAE101, and BMS2508 were analyzed in 286 sheep of seven sheep populations (Small Tail Han sheep, Hu sheep, Ujumqin sheep, Suffolk sheep, Dorset sheep, Charolais sheep, F1 of Dorset ♂ × Small Tail Han sheep ♀). The numbers of alleles for BM143, OarHH35, OarAE101, and BMS2508 are 9, 11, 14 and 9 in seven sheep populations, respectively. The polymorphism information content/number of effective alleles/heterozygosity of BM143, OarHH35, OarAE101 and BMS2508 were 0.7073/3.7231/0.7314, 0.8267/6.4399/0.8447, 0.5743/2.5178/0.6028, 0.6172/3.0712/0.6744 in 286 sheep, respectively. The results revealed the greatest genetic variation at OarHH35 locus and the lowest at OarAE101, the greatest genetic variation in Small Tail Han sheep and the lowest in Hu sheep among seven sheep populations. In the unweighted pair group method with arithmetic mean (UPGMA) dendrograms based on Nei's DA distance and Nei's DS standard genetic distance, the Chinese native breeds (Small Tail Han sheep, Ujumqin sheep, Hu sheep) were grouped together, then with Charolais sheep. The F1 crossbred sheep, and the two British native sheep (Suffolk sheep, Dorset sheep) also clustered together. Microsatellite genotyping in sheep provided a useful tool for examining the genetic relationships among breeds (populations).

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·	WANG Ai-Guo
·	LI Ning

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Key words

DOI:

通讯作者