动物·食品科学

7个地方鸡品种间遗传分化和聚类分析 [*]

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摘要　利用29个微卫星标记，通过计算亚群体杂合度（Hs）、总群体杂合度（Ht）、遗传分化系数（Gst）和基因流（Nm），并基于Reynolds遗传距离、Nei遗传距离运用NJ和UPGMA聚类法构建4类聚类图，比较分析国家地方禽种遗传资源基因库保存的7个地方鸡品种（仙居鸡、鹿苑鸡、固始鸡、大骨鸡、河南斗鸡、狼山鸡和萧山鸡）间的遗传分化和亲缘关系。结果表明，7个地方鸡种29个微卫星标记的总群体杂合度和亚群体杂合度的平均值分别为0.642和0.551，平均遗传分化系数为0.142；7个地方鸡品种间，萧山鸡与鹿苑鸡的基因流动最大，为 5.832 7；狼山鸡与固始鸡的基因流动最小，为 0.805 3；基于Reynolds遗传距离运用 NJ 聚类法获得的7个鸡种间的聚类图较为准确地反映了7个地方鸡种间的遗传分化和亲缘关系。

关键词　微卫星；地方鸡种；遗传分化；聚类分析

分类号　S 831.2

Genetic Differentiation and Clustering Analysis of 7 Chinese Indigenous Chicken Breeds

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Abstract

The average gene diversity (Hs) within population, the total gene diversity (Ht), the coefficient of genetic differentiation (Gst), and gene flow (Nm) of 7 chicken breeds, including Xianju chicken(XJ), Luyuan chicken(LY), Gushi chicken(GS), Dagu chicken(DG), Henan Game chicken(HG), Langshan chicken(LS) and Xiaoshan chicken(XS) conserved in State Gene Bank of China Poultry Breeding, were measured by using 29 microsatellite markers. On the basis of Reynolds'genetic distances and Nei's genetic distances, 4 dendrograms of clustering were constructed for the 7 chicken breeds by using neighbor joining (NJ) method and (UPGMA) method. The results showed that the average Hs, Ht and Gst were 0.642, 0.551 and 0.142, respectively. The highest Nm was 5.832 7 between XS and LY, and the lowest was 0.805 3 between LS and GS. The dendrogram on the basis of Reynolds'genetic distances and using neighbor joining (NJ) method correctly indicated the phylogenetic relationships among the 7 chicken breeds.

Key words　microsatellite　indigenous chicken breeds　genetic differentiation　clustering analysis

DOI:

通讯作者