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东北大口鲇2个群体的微卫星DNA多态分析

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摘要

利用磁珠富集法克隆制备的24个大口鲇（Silurus meriaionalis Chen）微卫星标记，对黑龙江野生群体与松花江养殖群体2个东北大口鲇（S. soldatovi）的地理种群的等位基因频率（P）、观测杂合度（Ho）、期望杂合度（He）、多态信息含量（PIC）和有效等位基因数（Ne）等进行了遗传检测，以遗传偏离指数（d）检验Hardy-Weinberg平衡，并以Nei氏遗传分化系数（GST）和AMOVA分析（ΦST）群体遗传变异的来源。同时，使用PHYLIP3.63软件绘制基于Nei氏遗传距离的个体间UPGMA系统树。结果表明：24个微卫星标记在东北大口鲇的2个群体中共扩增出1357条多态性片段，片段长度为102～385 bp，总体平均等位基因8.875个，可以用于东北大口鲇遗传多样性的评估。并发现8个可区分这2个种群的遗传标记；黑龙江群体的P、Ho、He、PIC和Ne依次为0.165、0.435、0.758、0.742和5.019，松花江群体为0.147、0.299、0.847、0.764和5.944，在这些多样性参数上，方差分析也显示2地理种群差异不显著，在大多数位点并无显著差异，仅HLJcf37位点具有显著差异；在多个位点偏离Hardy-Weinberg平衡，2群体呈现不同程度的杂合体过度，纯合体完全缺失现象，其原因有待证实；群体遗传变异分析证实2群体间遗传分化较弱，其98%以上的变异是由群体内个体间的遗传变异引起的，群体间的变异对总变异影响不显著。UPGMA系统树也显示出个体间遗传距离小，亲缘关系很近。结果表明，人工繁殖没有对东北大口鲇的遗传多样性产生影响，该种群遗传分化小，种质资源状况良好。

关键词 东北大口鲇；微卫星DNA；遗传多样性

分类号

Genetic Polymorphism of Microsatellite DNA in Two Populations of Northern Sheatfish (Silurus soldatovi)

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Abstract

<P>In this article, population variations and genetic structures of two populations of northern sheatfish (Silurus soldatovi) were analyzed using 24 microsatellite loci enriched from southern catfish (S. meriaionalis Chen) by magnetic beads. Gene frequency (P), observed heterozygosity (Ho), expected heterozygosity (He), polymorphism information contents (PIC), and number of effective alleles (Ne) were determined. One population was wild, ripe individuals collected from Heilongjiang River (HNS); the other was cultured fry collected from Songhuajiang River (SNS). The Hardy-Weinberg equilibrium (HWE) was tested by the genetic departure index (d). The coefficient of gene differentiation GST and ΦST by AMOVA (Analysis of Molecular Variety) was imputed using Arlequin software in this study. In addition, a phylogenetic tree was constructed by UPGMA method based on the pairwise Nei's standard distances using PHYLIP. A total of 1 357 fragments with sizes ranging between 102 bp and 385 bp were acquired by PCR amplifications. The average number of alleles of the two populations was 8.875. Results indicated that these microsatellite loci were highly polymorphic and could be used as genetic

markers. The mean values of the parameters P, Ho, He, PIC, and Ne were 0.165, 0.435, 0.758, 0.742, and 5.019 for HNS and 0.147, 0.299, 0.847, 0.764, and 5.944 for SNS, respectively. Although there were differences, there were no significant differentiations except for the locus HLJcf37. These populations to a certain extent deviated from HWE, such as excessive and deficient heterozygote numbers. The value of GST was 0.078 and above 98% of the variation were differences among individuals within the population, so the variation between populations was insignificant. Cluster analysis also showed that the relationships among individuals were very close. In conclusion, the microsatellite markers that were developed through this study are useful for genetic analysis and the genetic culture that was proposed in this study has no significant impact on S. soldatovi.</P>

Key words Silurus soldatovi；microsatellite DNA；genetic polymorphism

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