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研究报告

微卫星DNA标记探讨镜鲤的种群结构与遗传变异

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摘要

采用30个微卫星分子标记, 对5个镜鲤群体的观测杂合度(H_o)、期望杂合度(H_e)、多态信息含量(*PIC*)和有效等位基因数(A_e)等进行了遗传检测, 根据基因频率计算遗传相似系数和Nei氏标准遗传距离, 以$\chi 2$检验估计Hardy-Weinberg平衡, 以近交系数(FST)和基因流(Nm)分析群体的遗传分化。同时, 使用PHYLIP3.63软件绘制基于Nei氏标准遗传距离的UPGMA聚类图, 并进行bootstrap自举检验验证进化树的可靠性。在德国镜鲤选育系(*Scattered Cyprinus carpio* L.)和来自4个不同养殖场(松浦、东岗、奉城和辽中)的德国镜鲤群体中共检测到7 083个扩增片段, 长度在102 ~ 446 bp之间, 在群体内扩增出等位基因1~16个不等, 共计356个等位基因。结果表明: (1)5个群体检测的有效等位基因数在1.07~12.30个不等, 平均多态信息含量为0.74、0.74、0.69、0.75和0.75, 无偏期望杂合度的平均值为0.74、0.78、0.70、0.76和0.78, 说明这几个群体属于高度多态, 遗传多样性水平较高。(2)群体间相似系数在0.52以上, 相似性较高。聚类分析显示, 东岗、奉城和辽中3个养殖场的德国镜鲤群体聚类成一个分支, 而德国镜鲤选育系与松浦群体聚类成另一分支。聚类的先后与它们在地理分布上距离远近有一定的相关性。(3)在与功能基因相关的多个微卫星基因座位上, 扩增产物呈现不同程度的缺失现象, 这些无效等位基因的产生可能与结构基因在育种中受到人工选择的影响较大有关。

关键词 微卫星 群体多样性 镜鲤 分子标记

分类号 Q953

Population Genetic Variation and Structure Analysis on Five Popula-tions of Mirror Carp Cyprinus carpio L. Using Microsatellites

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Abstract

<P>In this paper, population genetic variability and genetic structure of five populations of an important cultivation species, mirror carp (<EM>Cyprinus carpio</EM> L.) were analyzed using 30 microsatellite loci. The observed (^{<EM>H</EM>_o}) and expected (^{<EM>H</EM>_e}) heterozygosity values, polymorphic information content (<EM>PIC</EM>) and number of effective alleles ((^{<EM>A</EM>_e})) were all determined. The genetic similarity coefficient and Nei's standard genetic distance were computed based on the allele frequencies. The Hardy-Weinberg equilibrium was checked by <SPAN lang=EN-US style="FONT-SIZE: 10pt; FONT-FAMILY: Symbol; LETTER-SPACING: 0.1pt; mso-fareast-font-family: 宋体; mso-font-kerning: 1.0pt; mso-ansi-language: EN-US; mso-fareast-language: ZH-CN; mso-bidi-language: AR-SA; mso-bidi-font-family: 'Times New Roman'; mso-bidi-font-size: 9.0pt">c</SPAN>2 test. Genetic differentiation and hierarchical partition of genetic

diversity were evaluated by ^{<EM>F</EM>_{ST}} and ^{<EM>H</EM>_m}. A dendrogram was constructed based on UPGMA methods using PHYLIP software package supported by a bootstrap

value of 91.0%. Totally 7 083 fragments were procured. Their lengths were from 102 bp to 446 bp. For each locus, 1—16 alleles were amplified, adding up to 356 alleles in all the 5 populations. We found the genetic variability level was relatively high in all five populations, as shown by ^{<EM>A</EM>_e} = 1.07—2.30, ^{<EM>H</EM>_e}= 0.70—0.78 and <EM>PIC</EM>=0.69—0.75, respectively. The genetic similarity coefficients were all above 0.52, indicating their close genetic relationships. The UPGMA phylogenetic tree showed mirror carps sampled from Donggang, Fengcheng and Liaozhong were clustered into one group and the other two populations, both collected from Songpu, were grouped together. There were obvious relations between genetic distances and geographical distributions of the five populations. No fragments were amplified from some loci of EST-SSRs, which may suggest the loss of these loci in mirror carp genome or sequence divergence at the primer binding sites. These null alleles may result from selection because functional genes are under more selection pressure than non-encoding loci. Overall, population genetic variation is high for each of the five mirror carp, and the differentiations are also significant among populations.
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Key words microsatellite population variety genetic structure mirror carp

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