

研究论文

虾夷扇贝 (*Patinopecten yessoensis*) 5个群体的遗传多样性

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摘要 虾夷扇贝为20世纪80年代初从日本引入我国并逐渐开展养殖的双壳贝类, 目前已在我国北方地区大面积养殖。实验采用微卫星分子遗传标记技术对大连獐子岛底播增殖放流群体(CC)、黄海北部海区采集的野生群体(HQ)、日本青森养殖群体(JX)、俄罗斯远东日本海沿岸养殖群体(RX)及大连大长山岛养殖上壳白化群体(ZB)等5个虾夷扇贝群体的遗传多样性进行研究。其中HQ群体为本课题组2005年在黄海北部采集的野生群体, 本研究筛选出一个该群体的特异性遗传标记。用8个微卫星位点进行扩增, 共获得45个等位基因, 每个位点的等位基因数处于3~9之间, 大小为100~340bp, 平均有效等位基因数为3.1535, 基因型数为3~21个, PIC (Polymorphism Information Content) 值处于0.0322~0.5944之间。5个群体的平均观测杂合度分别为0.3292、0.3048、0.3167、0.2708、0.3042, 平均期望杂合度分别为0.4595、0.4002、0.3838、0.3620、0.3885, 群体间的多态性差异不显著。根据群体间遗传相似性系数、遗传距离及UPGMA聚类分析发现, CC和HQ群体亲缘关系最近, JX和RX群体的亲缘关系较近, ZB群体与JX和RX群体的亲缘关系较近。通过Hardy-Weinberg平衡及F-检验发现, 5个群体都不同程度的偏离平衡, 表明各群体基因频率和基因型频率的稳定性较低, 且5个群体均处于不同程度的杂合子缺失状态, 群体间的遗传分化程度较高, 但遗传变异主要来自群体内的个体间。

关键词 虾夷扇贝 微卫星 遗传多样性

分类号 Q14

Genetic diversity in five scallop populations of the Japanese scallop (*Patinopecten yessoensis*)

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Abstract The Japanese scallop (*Patinopecten yessoensis*) was introduced from Japan to Dalian in the 1980s. It has been cultured on large scale in this area. In this study genetic diversity of 5 cultured and natural populations of Japanese scallop were investigated by microsatellites. The 5 populations were the population in Zhangzidao island (CC), the natural population in north area of the Yellow Sea (HQ), Japanese cultured population (JX), Russian population (RX) and albino population collected in Dachangshan island (ZB). HQ is a natural population which has been collected in north area of Yellow Sea in 2005. A specific genetic marker was found in this population. Thirty individuals from each population were analyzed. Amplifications were performed in a PCR reactor with 8 microsatellite loci, tested by agarose gel electrophoresis and analyzed by gel analysis software. In this study 45 alleles were obtained. The number of alleles of each locus ranged from 3 to 9, and allele size ranged from 100 to 340bp. The mean number of effective alleles (a_e) was 3.1535 and the number of genotypes ranged from 3 to 21 in each locus. PIC (Polymorphism Information Content) per locus ranged from 0.0322 to 0.5944. The average observed heterozygosity (H_o) for the five populations was 0.3292, 0.3048, 0.3167, 0.2708 and 0.3042, respectively. The average expected heterozygosity (H_e) for the 5 populations was 0.4595, 0.4002, 0.3838, 0.3620 and 0.3885, respectively. The difference in genetic diversity among the 5 populations is not significant. According to their genetic similarity (I) and genetic distance (D), we found that the genetic distance between CC and HQ was the least, followed by that of JX and RX. The distance between ZB to JX and RX were both closer than those of CC and HQ. The P value test o

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f Hardy-Weinberg equilibrium showed that the populations departed from Hardy-Weinberg equilibrium in some loci. All 5 populations showed the absence of heterozygosity. The results of the F-test suggested high genetic differentiations among the 5 populations, and mainly due to individual difference.

Key words _ *Patinopecten yessoensis* _ microsatellites _ genetic diversity

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