

合浦珠母贝和长耳珠母贝的生化遗传变异

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摘要 用淀粉凝胶电泳测定了养殖合浦珠母贝以及野生合浦珠母贝和长耳珠母贝的8-13个蛋白和同工酶座位的遗传变异。合浦珠母贝每个座位观察到的平均等位基因数为2.63,而长耳珠母贝为2.15。它们多型座位(P小于等于99)的比例则分别为0.750和0.692,由野生贝经人工育苗繁育出来的养殖合浦珠母贝的平均杂合度比野生合浦珠母贝的高近一倍(0.223和0.113),而野生合浦珠母贝和野生长耳珠母贝的平均杂合度水平相近(0.113和0.157)。两个合浦珠母贝群体相比较遗传相似度(I)和遗传距(D)为0.992和0.008,野生合浦珠母贝和野生长耳珠母贝相比较为0.252和1.379。

关键词

分类号

Biochemical Genetic Variation in the Pearl Oysters, *Pinctada fucata* and *P. chemnitzii*

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Abstract

P. fucata (Gould) and *P. chemnitzii* (Philippi) are two major species of pearl oysters. And Hepu, Guangxi Province, has been the producing area of world famous pearls - "Nanzhu" since ancient times. With the objective of genetic improvement and selective breeding of the pearl oysters, genetic variation has been assayed by starch gel electrophoresis at 8-13 loci in the wild population of *P. fucata* and *P. chemnitzii* sampled from the Hepu coast, the Gulf of Beibu, as well as the cultured population of *P. fucata* at a pearl culture ground. The latter one was produced by artificial hatchery for wild individuals. The average number of alleles observed per locus in *P. fucata* was 1.63 and in *P. chemnitzii* 2.15. The frequency of polymorphic loci ($P \leq 0.99$) was 0.750 and 0.692 respectively. The average heterozygosity (0.223) of cultured *P. fucata* was nearly twice as high as that (0.113) of wild *P. fucata* which was closely similar to that (0.157) of wild *P. chemnitzii*. The genetic identity and genetic distance between wild and cultured *P. fucata* was 0.992 and 0.008, whereas those between wild *P. fucata* and wild *P. chemnitzii* was 0.252 and 1.379 respectively. The deficits of heterozygotes were observed in these three samples of the two species studied. It is suggested that natural selection and Wahlund effect could account for these deficits.

Key words

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