

太湖日本沼虾野生群体遗传结构的微卫星分析

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Genetic structure of wild *Macrobrachium nipponense* populations in Taihu Lake based on microsatellite analysis.FENG Jian-bin¹, WU Chun-lin¹, MA Ke-yi¹, DING Huai-yu², HUA Xue-ming¹, LI Jia-le^{1,3}

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摘要 利用8个高度多态性的微卫星位点分析了太湖日本沼虾野生群体的遗传结构.结果表明: 在15个群体中至少有3个位点经Bonferroni校正后显示杂合不足,显著偏离了Hardy-Weinberg平衡; 15个群体中观测杂合度均大于0.683,显示出较高的遗传多样性水平,但其波动明显,如太湖东、南部的渡口和陆巷等群体的遗传多样性高于西、北部的华庄和洋渚等群体; 突变-漂移平衡分析结果显示, 15个群体中部分位点杂合显著过剩,偏离了突变-漂移平衡,且近期曾经历过瓶颈效应,群体数量曾经下降; 群体间AMOVA分析表明,太湖日本沼虾群体间遗传分化程度较低($F_{ST}=0.011$), 98.9%的遗传变异来自群体内, 1.1%来自群体间,并没有形成显著的遗传结构,在种质资源保护和管理上可视为一个单元; 华庄与吴塘门群体间 D_A 遗传距离达到0.206,已接近种间分类界限,故太湖日本沼虾种质资源可持续利用工作仍须深入的研究.

关键词: 日本沼虾 太湖 微卫星 遗传结构

Abstract: By using eight highly polymorphic microsatellite DNA loci, this paper analyzed the genetic structure of wild *Macrobrachium nipponense* populations in Taihu Lake. For the 15 *M. nipponense* populations in the Lake, there were at least three of the loci presenting heterozygosity deficiency and obvious deviation from Hardy-Weinberg equilibrium after Bonferroni correction. The observed heterozygosity values of the 15 populations were all above 0.683, displaying a high genetic diversity, but the diversity varied obviously with site. For example, the genetic diversity of the eastern and southern populations at Dukou and Luxiang was higher than that of the western and northern populations at Huazhuang and Yangzhu. For the 15 populations, parts of the loci showed heterozygote excess and departure from mutation-drift equilibrium, suggesting that the population structure had experienced bottleneck effect and the population amount had declined. The AMOVA analysis across all the populations and loci showed that the genetic divergence among the 15 populations was at a lower level ($F_{ST}=0.011$). 98.9% of the genetic variation came from intra-population, and 1.1% came from inter-population, suggesting that all the *M. nipponense* populations in the Lake could be protected and managed as a single unit in genetic resource. However, the genetic distance between Huazhuang and Wutangmen populations reached 0.206, being close to the delimitation of species identification. Further studies would be needed for the sustainable utilization of the genetic resource of *M. nipponense* in Taihu Lake.

Key words: *Macrobrachium nipponense* Taihu Lake microsatellite genetic structure

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