

2个尼罗罗非鱼群体GHSR基因5'侧翼序列的多态性及其遗传多样性分析

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Sequence polymorphism of 5'-flanking regions of *GHSR* gene and genetic diversity of two populations of Nile tilapia (*Oreochromis niloticus*)WANG Chunxiao^{1,2}, GAO Fengying¹, LU Maixin¹, LIU Zhigang¹, ZHU Huaping¹, YE Xing¹

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摘要

该试验以快长尼罗罗非鱼 (*Oreochromis niloticus*) 和普通尼罗罗非鱼2个群体为研究对象, 通过PCR扩增与测序, 获得GHSR基因5'侧翼区序列77条, 片段大小为1 217 bp。共检测出变异位点57个, 包括12个插入/缺失位点和45个多态性位点。共发现16种单倍型, 其中Hap2可能为原始单倍型。16种单倍型在进化树中聚为A和B 2支, A支中有11种单倍型, 在普通群体和快长群体中均有分布, 但快长群体中所占比例较高; B支中有5种单倍型, 均分布于普通群体中。遗传多样性参数显示普通尼罗罗非鱼群体的核苷酸多样性 (P_i)、单倍型多样性 (H_d) 和平均核苷酸差异数 (K) 都高于快长尼罗罗非鱼群体。AMOVA分析结果显示快长和普通尼罗罗非鱼2个群体之间的 F_{ST} 为-0.200 0 ($P>0.1$), 表明2个群体间遗传分化不明显, 且2个群体的遗传差异主要来自群体内 (120%)。

关键词: 尼罗罗非鱼, GHSR基因, 5'侧翼区, 多态性, 遗传多样性

Abstract:

We obtained 77 sequences of 5'-flanking regions of *GHSR* genes from two populations (fast-growth group and normal-growth group) of Nile tilapia (*Oreochromis niloticus*) by PCR amplification and sequencing method, and detected 57 variation sites (12 inserting or deleting sites and 45 polymorphic sites) and 16 kinds of haplotypes. Hap2 might be the original haplotype. There were two branches (A and B) in the phylogenetic tree of 16 kinds of haplotypes. Branch A contained 11 kinds of haplotypes which could be found in both groups but showed higher-frequency distribution in fast-growth group; while Branch B contained five kinds of haplotypes which only distributed in normal-growth group. The nucleotide diversity (P_i), haplotype diversity (H_d) and average number of nucleotide differences (K) in fast-growth group were higher than those in normal-growth group. The F_{ST} value (-0.200 0, $P>0.1$) and genetic difference (120%, mainly from intragroup) between the two groups suggest that no genetic differentiation exist between the two groups.

Key words: *Oreochromis niloticus*, *GHSR* gene, 5'-flanking region, polymorphism, genetic diversity

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