

埃及品系尼罗罗非鱼不同选育世代mtDNA D-loop区 遗传多样性分析

肖炜¹, 王腾², 李大宇¹, 邹芝英¹, 祝璟琳¹, 韩珏¹, 杨弘¹

1. 中国水产科学研究院淡水渔业研究中心, 农业部淡水鱼类遗传育种和养殖生物学重点开放实验室, 江苏 无锡 214081; 2. 南京农业大学无锡渔业学院, 江苏 无锡 214081

Genetic variation of mitochondrial DNA D-loop region in different generations of Egyptian strain of *Oreochromis niloticus*XIAO Wei¹, WANG Teng², LI Dayu¹, ZOU Zhiying¹, ZHU Jinglin¹, HAN Jue¹, YANG Hong^{1,2}

1. Key Lab. of Freshwater Fisheries and Germplasm Resources Utilization, Ministry of Agriculture; Freshwater Fisheries Research Center, Chinese Academy of Fishery Sciences, Wuxi 214081, China; 2. Wuxi Fisheries College, Nanjing Agricultural University, Wuxi 214081, China

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摘要

为评价现有选育方式下的遗传结构现状及选育潜力, 采用mtDNA D-loop序列差异分析技术, 对埃及品系尼罗罗非鱼 (*Oreochromis niloticus*) 的3个选育世代群体共80尾鱼开展世代间遗传结构变异分析。结果显示: 1) 3个世代群体中个体序列长度为552~555 bp, 包括52个变异位点、12个单倍型, 平均单倍型多样性 (H) 为0.569; 2) 3个世代群体的核苷酸多态性 (P_i) 分别为0.021 9、0.040 3和0.039 7, 各世代具备较高的多态性; 3) 3个世代中, F_1 具有5个单倍型, F_2 和 F_3 均具有7个单倍型, F_1 、 F_2 和 F_3 共享2个单倍型, F_1 与 F_2 共享1个单倍型, 3个选育世代群体的单倍型在NJ系统树上相互交叉, 无独立的进化枝。表明在目前选育方式下埃及品系尼罗罗非鱼世代间遗传信息较为稳定, 选育并没有对罗非鱼选育群体的遗传结构造成大影响。

关键词: 埃及品系尼罗罗非鱼, 选育世代, mtDNA s-LOOP, 遗传结构变异**Abstract :**

To evaluate the effect of the present breeding ways on genetic structure and breeding potential of Egyptian strain of *Oreochromis niloticus*, we analyzed the variation of mitochondrial DNA D-loop region in their three generations (80 individuals). The results show that: 1) The length of the region sequences was 552~555 bp; 52 variable sites and 12 haplotypes were detected. The average haplotype diversity was 0.569. 2) The nucleotide polymorphisms (P_i) of three generations were 0.021 9, 0.040 3 and 0.039 7, respectively, each generation showing high polymorphism in the mitochondrial genetic diversity. 3) F_1 generation contained five haplotypes; F_2 generation contained seven haplotypes; F_3 generation contained seven haplotypes. The three generations shared two haplotypes, and F_1 and F_2 generations shared a haplotype. The haplotypes of three generations crossed each other in the NJ tree and no unique clade of haplotype existed in each generation. It is concluded that there was no significant variation in genetic structure at the control region sequence in the three generations. The genetic information among three generations of *O. niloticus* was stable by the present breeding ways.

Key words: Egyptian strain of *Oreochromis niloticus* selected genetiions mitochondrial DNA D-loop genctic structure variation

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通信作者: 杨弘 (1966-), 男, 研究员, 从事鱼类遗传育种研究。E-mail: yangh@ffrc.cn**作者简介**: 肖炜 (1982-), 男, 硕士, 助理研究员, 从事罗非鱼遗传育种研究。E-mail: xiaow@ffrc.cn**引用本文:**肖炜 王腾 李大宇 邹芝英 祝璟琳 韩珏 杨弘. 埃及品系尼罗罗非鱼不同选育世代mtDNA D-loop区 遗传多样性分析[J]. 南方水产科学, 2015, 11(3): 29-34. XIAO Wei, WANG Teng, LI Dayu, ZOU Zhiying, ZHU Jinglin, HAN Jue, YANG Hong. Genetic variation of mitochondrial DNA D-loop region in different generations of Egyptian strain of *Oreochromis niloticus*. South China Fisheries Science, 2015, 11(3): 29-34.**链接本文:**<http://www.schinafish.cn/CN/10.3969/j.issn.2095-0780.2015.03.005> 或 <http://www.schinafish.cn/CN/Y2015/V11/I3/29>

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