

太湖新银鱼线粒体DNA物理图谱及分析 Physical Map and Analysis of Mitochondrial DNA from *Neosalanx taihuensis* Chen

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摘要 采用改进的碱裂解法制备太湖新银鱼线粒体DNA, 构建其Pvu II、BamHI、XhoI、SalI、EcoRI和PstI等6种限制性内切酶的物理图谱。比较了鲑形目3种鱼的线粒体DNA物理图谱, 根据限制性位点差异法计算它们之间的遗传距离, 利用UPGMA聚类分析法构建分子聚类图, 结果表明: 红点鲑属与大西洋鲑先聚在一起, 再与太湖新银鱼相聚, 前两者间遗传距离为12.33%, 亲缘关系较近, 太湖新银鱼与这两者间的遗传距离为21.36%, 亲缘关系较远, 表明银鱼科与鲑科分离较早。

Abstract: The mitochondrial DNA (mtDNA) from *Neosalanx taihuensis* Chen was prepared by the improved alkaline lysis procedure. The cleavage sites map of six kinds of restriction endonucleases (PvuII, BamHI, XhoI, EcoRI and PstI) was determined. The physical maps of mtDNAs from *N. taihuensis* Chen, *Salvelinus taxa* and *Salmo salar* were analyzed. Genetic distances between mtDNAs were calculated by the formula of Nei and Li (1979). Phylogenetic reconstruction method, UPGMA, was used to analyze the genetic relationships and the molecular dendrogram was established and revealed: the genetic distance between *Salvelinus taxa* and *Salmo salar* is 12.23% and that between *N. taihuensis* Chen and *Salvelinus taxa*-*S. salar* is 21.36%. This indicates that *Salangidae* diverged from *Salmoninae* earlier.

关键词 [太湖新银鱼](#) [线粒体DNA](#) [物理图谱](#) **Key words** [Neosalanx taihuensis Chen](#) [Mitochondrial DNA](#) [Physical map](#)

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