

线粒体基因组揭示我国福寿螺的种群遗传结构及扩散路径

樊佳乐¹ 邹红菲^{1*} 兰天明^{2*}

1. 东北林业大学野生动物与自然保护地学院
2. 东北林业大学华大生命科学研究院联合研究中心

摘要:【目的】福寿螺(*Pomacea spp.*)是我国第一批外来入侵物种之一,自入侵以来已广泛分布于我国南方多地,野外入侵种类多达三种,并且存在向北扩散趋势。本研究旨在探究其具有向北分布趋势的主要种类及可能的入侵事件。本研究以全球范围为研究尺度,以我国目前主要入侵福寿螺种群为研究对象,通过线粒体氧化色素酶 I 基因(*COI*)的单倍型分析、系统发育学分析及遗传多样性分析阐明我国福寿螺遗传结构,并推断其入侵来源及路线。【方法】本研究采集来自 10 个省市地区共 119 个样本,并基于全基因组测序数据进行线粒体全基因组组装,成功获取 113 个福寿螺个体的线粒体全序列。同时,本研究在 NCBI 数据库收集了 1602 条福寿螺线粒体 COI 数据,与现有数据共同进行系统发育、遗传结构及单倍型网络分析。【结果】(1) 1715 条序列长度为 523bp 的 COI 序列共计 111 个单倍型,其中 Hap107 是本研究发现的特有单倍型。基于序列相似性对 111 个单倍型进行聚类,最终所有单倍型分为 3 组,基于 ML 与 BI 构建的单倍型系统发育树显示出一致的拓扑结构。对本研究所采集样本的 13 个蛋白质编码基因建立无根树显示小管福寿螺、斑点福寿螺及隐秘福寿螺明显聚为三支,且斑点福寿螺及隐秘福寿螺具有更近的亲缘关系,而小管福寿螺存在地域差异性。(2) 遗传多样性分析表明,小管福寿螺种群遗传多样性最为丰富,斑点福寿螺与隐秘福寿螺相比,前者具有更高的核苷酸多样性,后者具有更高的单倍型多样性。(3) 单倍型网络图显示,小管福寿螺呈现多中心辐射状分布;斑点福寿螺中,巴西国家呈明显网状分布,北美及亚洲地区开始呈现中心辐射状分布(源于南美,传入北美,传至亚洲);隐秘福寿螺呈单一中心辐射状分布。(4) 中性检验分析结果显示,隐秘福寿螺 Tajima' D 值为-2.09681, $P < 0.05$, Fu and Li's 值为-7.394,可能存在种群扩张。【结论】补充了现有福寿螺的分布数据,提供了其在北方分布的直接证据;明确了我国目前三种主要分布福寿螺的遗传结构;探讨了小管福寿螺及斑点福寿螺与各国之间可能的扩散路径;推断隐秘福寿螺可能存在近期的种群扩张,并发现其有一新的单倍型分布。

关键词: 福寿螺; 入侵路径; 线粒体; *COI*; 种群结构

Mitochondrial genome reveals the population genetic structure and diffusion path of Chinese Golden apple snails

Jiale Fan¹ Hongfei Zou^{1*} Tianming Lan^{2*}

1. College of Wildlife and Protected Area, Northeast Forestry University
2. BGI Life Science Joint Research Center, Northeast Forestry University

Abstract

Objective: *Pomacea spp.* is one of the first invasive alien species in China. Since its invasion, it has been widely distributed in many places in southern China. There are as many as three invasive species in the wild, and there is a trend of spreading northward. This study aims to explore its main species with a northward distribution trend and possible invasion events. This study takes a global scale as the research scale and takes the main invasive apple snail populations in China as the research object. Through haplotype analysis, phylogenetic analysis and genetic diversity of the mitochondrial oxidative chromase I gene (COI), the genetic structure of Chinese apple snails was analyzed, and infer its invasion source and route.

Methods: This study collected a total of 119 samples from 10 regions, and assembled the complete mitochondrial genome based on whole-genome sequencing data, successfully obtaining the complete mitochondrial sequences of 113 apple snail individuals. At the same time, this study collected 1,602 apple snail mitochondrial COI data in the NCBI database, and conducted phylogenetic, genetic structure and haplotype network analysis together with existing data.

Results: (1) There are 1715 COI sequences with a sequence length of 523 bp, totaling 111 haplotypes, among which Hap107 is the unique haplotype discovered in this study. 111 haplotypes were clustered based on sequence similarity, and finally all haplotypes were divided into 3 groups. The haplotype phylogenetic tree constructed based on ML and BI showed a consistent topology. The establishment of an unrooted tree for the 13 protein-coding genes of the samples collected in this study showed that the *Pomacea canaliculata*, the *Pomacea maculata*, and the *Pomacea occulta* are obviously clustered into three branches, and the *Pomacea maculata* and the *Pomacea occulta* have a closer genetic relationship, while the *Pomacea canaliculata* have regional differences. . (2) Genetic diversity analysis showed that the genetic diversity of the *Pomacea canaliculata* population is the richest. The *Pomacea maculata* has higher nucleotide diversity and the *Pomacea occulta* has higher haplotype diversity. (3) The haplotype network diagram shows that the *Pomacea canaliculata* show a multi-center radial distribution; among the *Pomacea*

maculata, Brazil has an obvious network distribution, and North America and Asia have begun to show a center-radial distribution (originating from South America, introduced to North America, spread to Asia); the *Pamacea occulta* is distributed in a single center and radial pattern. (4) The results of the neutrality test analysis showed that the Tajima's D value of the *Pamacea occulta* was -2.09681, $P < 0.05$, and the Fu and Li's value was -7.394, indicating that there may be population expansion.

Conclusions: It supplements the existing distribution data of golden apple snail and provides direct evidence of its distribution in the north; The genetic structure of three main species of apple snails currently distributed in China has been clarified; The possible diffusion paths between *Pomacea canaliculata* and *Pomacea maculata* and various countries were discussed; It was inferred that there may be recent population expansion of the cryptic apple snail, and a new haplotype distribution was found.

Key words: apple snail; invasion pathway; mitochondria; *COI*; population structure