

研究论文

# 利用RAPD-PCR探讨天蓝喇叭虫生物群系分化

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**摘要** 选择天蓝喇叭虫(*Stentor coeruleus*)作为研究对象,对武汉市南湖、月湖、关桥3个水体共5个样点天蓝喇叭虫(*S. coeruleus*)样本的总DNA进行随机扩增多态DNA聚类分析,以检测各个样本的遗传相似性和趋异程度,借以评估样本间的遗传变异度。结果如下:(1)从98条随机引物中筛选12条引物共扩增出89条大小为100~1500bp的清晰条带,平均每条引物扩增出7.4条片段。(2)用Rapdistance 1.04分析显示,不同样点样本之间存在着一定的变异,其遗传距离在0.076~0.416之间。(3)构建的聚类图中,南湖3个样点的遗传距离较近,在聚类图上聚成一枝,应该为同一个种群。本试验将为探讨水体原生动物迁徙能力对生物群系分化的影响积累实例资料,更希望可以促进水体原生动物的研究和种间过渡区本质及物种扩散行为的研究。

**关键词** [天蓝喇叭虫\(\*Stentor coeruleus\*\)](#) [生物群系](#) [RAPD](#); [南湖](#)

分类号

## Applicability of RAPD-PCR pattern to genetic diversity of *Stentor coeruleus*

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**Abstract** *Stentor coeruleus* is widely distributed in many regions of the world. In this paper, we selected five samples of *Stentor coeruleus* from three Lakes (Lake Nanhu, Lake Yuehu, Pond Guanqiao). Genotype data from these five samples were analyzed by Randomly Amplified Polymorphic DNA (RAPD) marker to assess the genetic diversity of the *S. coeruleus* populations. The results were as followed: (1) The 11 primers produced 89 clear bands with an average of 7.4 fragments, ranging from 100-1500bp. (2) Considerable genetic diversity in these populations was suggested using the calculating genetic distance (0.076-0.416) between them. (3) Assessment of differences in populations by the phylogenetic tree erected using Rapdistance 1.04 showed that the three samples from N. Lake clustered into one branch indicating that these samples belong to one biotype. Our results show that RAPD technology is a rapid, precise and sensitive technique for identification of *S. coeruleus* genotypes and provides experimental evidence for the applicability of RAPD on the genetic diversity of *S. coeruleus*. Moreover, it can help in investigations of differences in populations and the mechanism of speciation. However, the phylogenetic relationships within *S. coeruleus*, must be interpreted with caution.

**Key words** [Stentor coeruleus](#) [biotype](#) [RAPD](#) [Lake Nanhu](#)

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