

研究论文

镜湖萼花臂尾轮虫 (*Brachionus calyciflorus*) 种群遗传多样性的季节变化

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摘要 运用随机扩增多态DNA (RAPD) 技术研究了于2005年春季和夏季采自芜湖市镜湖的萼花臂尾轮虫 (*Brachionus calyciflorus*) 种群基因组DNA多态性。从44个随机引物中筛选出10个谱带清晰、重复性好的引物。10个引物共检测到76个位点, 其中65个位点显多态性, 多态位点比例 (P) 为85.5%。对RAPD 扩增结果进行聚类分析, 基于遗传距离指数构建了萼花臂尾轮虫的UPGMA和ME系统树。经计算, 各克隆平均遗传距离指数为0.5219, 春季种群内遗传距离指数 (0.4416) 大于夏季种群内遗传距离指数 (0.4304); 两季节种群间遗传距离指数为0.6010, 明显大于季节种群内遗传距离指数。16个克隆分别聚在2个主要簇群中, 在UPGMA系统树中, 春季种群和夏季种群明显分聚在两个主要支系中; 而在ME树中, 除了夏季Su2克隆和春季种群聚到一个支系外, 其它夏季种群则聚在一个独立支系中。上述结果表明, 春季种群和夏季种群在遗传上具有较大的差异; 镜湖萼花臂尾轮虫种群存在着明显的季节更替, 而Su2克隆可能是春季和夏季种群间的过渡。

关键词 萼花臂尾轮虫; 季节种群; DNA多态性; RAPD; 遗传距离

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Seasonal changes in the genetic diversity of *Brachionus calyciflorus* population in Lake Jinghu

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Abstract Genetic diversity of spring and summer populations of *Brachionus calyciflorus* collected from Lake Jinghu in Wuhu City was analyzed using RAPD method. 10 primers that produce repeatable and discernible bands were chosen from 44 random primers. Among the total of 76 loci detected, 65 loci (85.5%) were polymorphic. UPGMA and ME dendrograms of *B. calyciflorus* were constructed by clustering the amplified bands on the basis of the index of genetic distance. The average genetic distance among all samples was 0.5219. The genetic distance within summer population (0.4304) was shorter than that within spring population (0.4416). The genetic distance (0.6010) between the two seasonal populations was longer than that within either seasonal population. The two trees both showed that the sixteen samples were obviously divided into two different clades. In UPGMA trees, the spring and summer populations were divided into two clades. In ME trees, all the summer samples except Su2 were separated as an independent clade. The results indicated that there is an obvious genetic difference between the two seasonal populations and a seasonal alternation in *B. calyciflorus* population collected from Lake Jinghu, and the sample Su2 may be an interim population.

Key words [Brachionus calyciflorus](#) _ [seasonal population](#) _ [DNA polymorphism](#) _ [RAPD](#) _ [genetic distance](#)

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