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三峡库区浮游生物群落结构与DNA多态性比较分析

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摘要: 以三峡库区所设A、B、C、D、E、F和G等7个站点为研究区域, 利用RAPD技术就其浮游生物群落遗传多样性与物种多样性的关系进行了探索性研究. 共鉴定出浮游生物41种, 其中藻类4种, 原生动物10种, 轮虫类19种, 枝角类4种, 桡足类4种. 物种组成相似性最高的是B站和C站, 最低的是A站和F站. 而站点间浮游生物群落遗传距离分析表明: 相距最近的是C站与D站, 最远的为D站与F站. 树状聚类图也显示: 各站点物种组成聚为一类; 而DNA多态性RAPD最先聚在一起的是B与F, 它们的对应枝由A、C、D、E构成, G单独成为一枝. 研究表明, 所发现的物种组成与所揭示的遗传多样性并未完全吻合. 这或许是物种信息的缺失(如藻类与细菌), 或许是RAPD技术的缺陷, 或许两者所致. 因此, 本研究积累了三峡库区浮游生物群落遗传多样性的一些背景资料, 而要阐释浮游生物群落遗传多样性与物种多样性之间的相互关系则有赖于应用灵敏的、重复性好的, 且能分别分析原核和真核生物的DNA分子标记技术.

关键词: 三峡库区; 浮游生物; RAPD; 遗传多样性; 物种多样性

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