

论著

γ拟钉螺等位基因的研究

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收稿日期 修回日期 网络版发布日期 接受日期

摘要

目的: 探讨γ拟钉螺分类演化的遗传学基础。方法: 用微量平面淀粉胶电泳法, 检测浙江省开化及淳安县6个螺群宋氏γ拟钉螺和1个螺群中国γ拟钉螺的24种等位基因酶谱。结果: 共测得29个位点, 宋氏γ拟钉螺多态位点所占比例为6.9%—13.8%; 中国γ拟钉螺全部为单态位点。宋氏γ拟钉螺的种内Nei's遗传距离(Nei's D)小于0.12; 但宋氏γ拟钉螺与中国γ拟钉螺两者种间Nei's D为0.73。结论: 在等位基因水平显示γ拟钉螺种内变异不明显, 种间差异显著。

关键词 [宋氏γ拟钉螺](#), [中国γ拟钉螺](#), [等位基因酶谱](#), [遗传距离](#)

分类号

STUDIES ON ALLOZYME OF GAMMATRICULA

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Abstract

AIM: To furnish molecular genetic evidences for taxonomy of Gammatricula. METHODS: A total of 24 enzymes of 6 populations of Gammatricula songi and 1 population of Gammatricula chinensis collected from Kaihua County and Chunan County of Zhejiang Province were studied using horizontal starch gel electrophoresis. RESULTS: 29 loci were found. The percentages of polymorphic loci of G.songi populations were 6.9%-13.8%. All loci of G.chinensis were monomorphic. The Nei's distance among G.songi populations did not exceed 0.12. The Nei's distance between G.songi and G.chinensis was 0.73. CONCLUSION: The allozyme variations of inter G.songi are limited, but the allozyme variation between G.songi and G.chinensis is significant.

Key words [Gammatricula songi](#) [Gammatricula chinensis](#) [allozyme zymogram](#) [genetic distance](#)

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