

论著

不同地域阴道毛滴虫分离株的随机扩增多态DNA技术分析

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摘要

目的 分析比较阴道毛滴虫 7个分离株基因组DNA的遗传多态性。方法 应用随机扩增多态DNA技术对阴道毛滴虫北京 1株、北京 2株、承德株、唐山株、九江 1株、九江 2株与九江 3株基因组扩增,并对扩增产物进行聚类分析。结果 7虫株两两间的遗传相似指数为 77.4%~ 94.7%,遗传关系密切。其中:北京 1株和唐山株为 89.2%,九江 1株和九江 2株为 92.1%,北京 2株和九江 3株为 94.7%,亲缘关系较近。而九江 1株和承德株间遗传相似指数为77.4%,同源性相对较低。结论 7株阴道毛滴虫遗传关系密切,但在基因水平上存在种内差异性;地理位置对阴道毛滴虫遗传学特性影响不大。

关键词 [阴道毛滴虫](#) [随机扩增多态DNA技术](#)

分类号

RAPD Analysis on Different Isolates of *Trichomonas vaginalis*

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Abstract

Objective To study genetic polymorphism of DNA on seven isolates of *Trichomonas vaginalis*. Methods The random amplified polymorphic DNA (RAPD) technique was performed to amplify genomic DNA of the seven *T. vaginalis* isolates, including Beijing 1, Beijing 2, Chengde, Tangshan, Jiujiang 1, Jiujiang 2 and Jiujiang 3. The DNA bands detected were analyzed by clustering analysis with SPSS software. Results The percentage of genetic similarity among the seven isolates was from 77.4% to (94.7%,) showing a close genetic relationship among them. The percentages between the isolates of Beijing 1 and Tangshan, Jiujiang 1 and Jiujiang 2, Beijing 2 and Jiujiang 3 were 89.2%, 92.1% and 94.7% respectively, while that of Jiujiang1 and Chengde was 77.4%, indicating a lower homology. Conclusion There are a close genetic relationship and certain gene polymorphism among the seven *T. vaginalis* isolates; geographical origin plays little role to the genetic characteristics.

Key words [Trichomonas vaginalis](#) [random amplified polymorphic DNA technique](#)

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