

论著

钉螺AFLP分子标记电泳图谱信息数量化数据的分析

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摘要

目的 探讨扩增片段长度多态性(AFLP)分子标记电泳图谱信息数量化数据的分析方法。方法 从现场采集的钉螺中筛选出40只阴性钉螺,随机分为两组,用于基因组DNA模板的制备。再用Glyko BandScan软件将钉螺扩增片段长度多态性电泳图谱信息数量化,使用不同的读带标准读带,得到相应的数据集,然后对这些数据集进行遗传学统计分析 with 描述性总结。结果 不同的标准所得到的遗传变异结果均有所差别,但随着读带标准值的增加,反映钉螺种群遗传多样性指标(如: Shannon's信息指数)也增加,当其增加到一定水平时,又开始下降,而基因流和基因一致度则相反。不同读带标准所得的遗传变异结果均呈明显的正态分布(P>0.05)。以总灰度或以总灰度百分比划分读带标准,所得遗传变异结果的平均值均十分接近。两组钉螺平均基因一致度在总灰度百分比数据中为0.956,在总灰度数据中为0.958;两组间的平均遗传距离在总灰度百分比数据中为0.045,在总灰度数据中为0.043。结论 将电泳图谱信息数量化,再以不同的读带标准去处理与分析数据的模式,是一种较为合理且准确的分析方法。

关键词 [钉螺](#) [扩增片段长度多态性](#) [电泳图谱](#) [数据分析](#)

分类号

Linking Quantitation of Electrophoresis Pattern and Data

Analysis in AFLP for Oncomelania hupensis

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Abstract

Objective To search into a method for analyzing the quantitative data in amplified fragment length polymorphism (AFLP) electrophoresis. Methods Oncomelania snails collected from the field were screened. Forty snails found uninfected with schistosomiasis were divided randomly into two groups and used to isolate genomic DNA. AFLP electrophoresis pattern was first transformed into quantitative data by Glyko BandScan software, and the bands were read according to different standards of band-reading to acquire the corresponding data. These data sets were analyzed by genetic statistics to get an inference set, and the analysis of this inference set was performed to reach a summary description. Results The results of genetic variation from different standards of band-reading were different. With the increase of the standard value of band-reading, the indices indicating the genetic polymorphism of Oncomelania hupensis population (e.g. Shannon's information index) also increased. When the standard value reached at certain level, the values of these indices began to decrease. Compared with the above indices, the change for gene flow turned out contrary to the genetic identity. The distributions of inference results from different standards of band-reading all showed significant normal distribution. The mean value of genetic variation based on total grey was very close to that on the proportion of total grey. The average genetic identity between the "subpopulations" was 0.956 according to proportion of total grey or 0.958 from the total grey with an average genetic distance between the "subpopulations" of 0.045 and 0.043 respectively. Conclusion It seems to be a reasonable and accurate method by quantifying the AFLP electrophoresis pattern followed by analyzing the data through the use of the different standards of band-reading.

Key words [Oncomelania hupensis](#) [AFLP](#) [Electrophoresis pattern](#) [Data analysis](#)

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