

五种绢丝昆虫随机扩增多态性DNA分析 The Study on Molecular Phylogenetic and Molecular Marker of Species in Silk Insects

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摘要 本文对家蚕、野桑蚕、蓖麻蚕、柞蚕和天蚕等5种绢丝昆虫进行了随机扩增多态DNA(RAPD)分析。40个引物中有27个引物能扩增出536个清晰且重复性强的条带, 其中可变条带数为520个, 单个引物扩增的条带数在11~28之间, 平均为19.9, 各片段分子量大小在0.29~2.67kb之间。每个样本都能找出其独特的分子标记。家蚕与野桑蚕的遗传距离(D)最小, 为0.3760; 家蚕与蓖麻蚕的遗传距离(D)最大, 为0.7488。根据遗传距离, 用UPGMA聚类分析方法构建了它们的分子树。

Abstract: Five species of silk insects including *Bombyx mori*, *B. manolarina*, *Philosamia cynthia*, *Autheraea pernyi* and *A. yamamai* were analyzed by RAPD method using 40 arbitrary primers. In these primers, 27 of them could amplify clear and repeating bands. 536 fragments were obtained and the variable bands were 520. Each primer gave 11~28 bands and the average was 19.9. The length of the fragments is 0.29~2.67 kb. Some distinctive bands were found in every species. The genetic distance(D) between *bombyx mori* and *B. manolarina* is 0.3760, which is the lowest. The highest D value is 0.7488, which between *Bombyx mori* and *Philosamia cynhia*. The D value was then used to construct a dendrogram by unweighted pair-group method with arithmetical averages(UPGMA).

关键词 [蚕丝昆虫](#) [RAPD](#) [多态性](#) **Keywords** [silk insect](#) [RAPD](#) [polymorphism](#)

分类号

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