

研究报告

## 利用RAPD-PCR技术分析东北地区16种小卷蛾的亲缘关系

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收稿日期 2005-6-12 修回日期 2006-2-28 网络版发布日期 接受日期

**摘要** 利用RAPD-PCR技术对东北地区黄卷蛾族的16种小卷蛾的基因组进行随机扩增,构建出系统发育树,对其亲缘关系进行分析.系统树显示褐卷蛾属的3个种、条卷蛾属的两个种和黄卷蛾属的4个种的聚类方式和传统形态分类法基本一致.也发现了一些与传统分类结论不完全一致的现象,如同属的忍冬双斜卷蛾和棉花双斜卷蛾在系统树上没有聚在一起,而和不同属的松褐卷蛾、樱桃铅卷蛾聚在一起等.分析同属和不同属种间的遗传距离,初步得出以下结论,遗传距离0.7可以作为属的分类依据,同一属的种间遗传距离小于0.7,不同属的种间遗传距离大于0.7.

**关键词** [RAPD](#) [小卷蛾](#) [亲缘关系](#)

分类号

## Consanguinity of sixteen olethreutid moth species in northeast China based on RAPD-PCR analysis

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### Abstract

With RAPD-PCR technique,the phylogenetic tree of 16 olethreutid moth species in northeast China was constructed,and their consanguinity was analyzed.The results showed that the clustering of 3 *Pandemis* species,2 *Argyrotaenia* species and 4 *Archips* species on this phylogenetic tree was coincident with their morphological taxonomy,but that of some other species was not.For example,*Clepsis rurinana* and *C.pallidana* were not on the same clade,but on the clade with *Pandemis cinnamomeana* and *Ptycholoma imitator*,respectively.Genetic distance could be an index for genus,and 0.7 was the boundary.The species genetic distance from the same genus was less than 0.7,while that from different genus was more than 0.7.

**Key words** [RAPD](#) [Olethreutid moth](#) [Consanguinity](#)

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