

基于CO I 和Cyt b基因序列的凤蝶科六属分子系统学研究

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Molecular systematics of six genera of Papilionidae (Lepidoptera) based on mitochondrial cytochrome oxidase I and Cyt b gene sequences

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- 摘要
- 参考文献
- 相关文章

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摘要

对凤蝶科6属25种的CO I 基因和20种Cyt b基因的部分序列进行测定和分析, 探讨它们之间的系统发育关系; 以茶小卷叶蛾*Adoxophyes honmai*为外群, 用邻接法(neighbor-joining, NJ)、最大简约法(maximum parsimony, MP)和贝叶斯法(Bayesian inference, BI)重建了凤蝶科6属的分子系统树。结果表明: CO I 基因部分序列长度为661 bp, 其中保守位点417个, 可变位点244个, 简约信息位点191个; A+T的平均含量为70.3%, 明显高于C+G的平均含量29.6%。Cyt b基因部分序列长度为433 bp, 其中保守位点239个, 可变位点194个, 简约信息位点135个; A+T的平均含量为74.2%, 明显高于C+G的平均含量25.7%。分子系统树表明, 凤蝶属*Papilio*、斑凤蝶属*Chilasa*、尾凤蝶属*Bhutanitis*、珠凤蝶属*Pachliopta*和喙凤蝶属*Teinopalpus*为单系性, 与传统形态分类结果相一致。但青凤蝶属*Graphium*单系性不够明确, 需要进一步探讨。研究结果为我国凤蝶科分子系统学研究积累了资料。

关键词:

Abstract:

Partial sequences of CO I genes of 25 species and Cyt b genes of 20 species in six genera of Papilionoidea were sequenced and analyzed for exploring their phylogenetic relationships. *Adoxophyes honmai* was used as outgroup to reconstruct the phylogenetic trees of six genera with neighbor-joining (NJ), maximum parsimony (MP) and Bayesian inference (BI) methods. The results indicated that CO I genes are 661 bp in length by alignment, including 417 conserved, 244 variable and 191 parsimonious/informative sites, and the average percentage of A+T is 70.3%, much higher than that of C+G (29.6%). The Cytb genes are 433 bp in length by alignment, including 239 conserved, 194 variable and 135 parsimonious/informative sites; and the average percentage of A+T is 74.2%, much higher than that of C+G (25.7%). The molecular phylogenetic trees showed that the genera *Papilio*, *Chilasa*, *Bhutanitis*, *Pachliopta* and *Teinopalpus* are all monophyletic clades and separated from each other in the molecular phylogenetic trees. The results correspond with the classification based on traditional morphological characters. However, the monophyletic position of the genus *Graphium* is not certain and needs further study. The results accumulated data for the molecular systematic study of the family Papilionidae in China.

Key words:

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