

基于叶绿体 *trnL-F*, *rbcL* 序列和核核糖体 ITS 序列探讨蓼属 (蓼科) 头状蓼组的系统发育

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摘要

选用叶绿体基因 *trnL-F*, *rbcL* 序列和核核糖体 ITS 序列对蓼属头状蓼组的分类和系统发育进行了分析。以药用大黄为外类群, 用最大简约法对3个片段的单独和联合矩阵分别构建系统发育树。结果表明, 头状蓼组是一个较自然的类群, 与春蓼组、刺蓼组和金线草属的亲缘关系较近; 支持头状蓼组作为一组放在春蓼属, 细茎蓼和蓝药蓼从头状蓼组转移至冰岛蓼属; 不支持将刺蓼组并入头状蓼组; 对于小叶蓼的系统学位置有待于进一步研究。

关键词 [系统发育](#); [trnL-F](#); [rbc-L](#); [ITS](#); [蓼属头状蓼组](#); [蓼科](#)

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Phylogeny of *Polygonum* Sect. *Cephalophilon* (Polygonaceae) Inferred from the Chloroplast *trnL-F*, *rbcL* and Nuclear Ribosomal ITS Sequences

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Abstract

The phylogeny of *Polygonum* sect. *Cephalophilon* was analyzed using the chloroplast genes *trnL-F*, *rbcL* and nuclear ribosomal ITS sequences. Individual and combined analyses of three datasets were performed with maximum parsimony method and the gene trees were constructed with *Rheum officinale* as outgroup. The results show that *Polygonum* sect. *Cephalophilon* is a more natural group which is the most closely related to *Polygonum* sect. *Persicaria*, sect. *Echinocaulon* and the genus *Antenoron*. The results support to put *Polygonum* sect. *Cephalophilon* into the genus *Persicaria* as a section and transfer *P. filicaule* and *P. cyanandrum* from *Polygonum* sect. *Cephalophilon* to the genus *Koenigia*, do not support to attribute *Polygonum* sect. *Echinocaulon* to *Polygonum* sect. *Cephalophilon*. There is strong conflict regarding the systematic position of *Polygonum delicatulum*, which needs further studies.

Key words [Phylogeny](#) [trnL-F](#) [rbc-L](#) [ITS](#) [Polygonum sect. Cephalophilon](#) [Polygonaceae](#)

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