

研究报告

十字花科植物CYP86MF基因同源序列的克隆与进化分析

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摘要 为了从分子水平阐明十字花科植物间的亲缘进化关系, 给植物种质资源的创建提供理论依据, 试验根据课题组已报道的CYP86MF基因编码的氨基酸保守区域设计特异引物, 运用PCR技术分别从十字花科6个属11个物种中分离克隆到了CYP86MF基因的同源序列, 经比较分析, 结果表明: 这些同源序列的相似性达80%以上, 所推导的氨基酸序列相似性达70%以上, 且两者种间差异分别为1.0% ~ 5.7%和2.6% ~ 7.3%, 属间差异分别是5.6% ~ 22.5%和7.3% ~ 31.2%; 由氨基酸序列构建的分子系统树可知, 在亲缘进化关系上芸薹属与萝卜属较近, 其他依次为蔊菜属、拟南芥属、芥菜属, 而与诸葛菜属最远。因此, CYP86MF基因的核苷酸及其可能编码的氨基酸序列差异属间较种间大, 它可用于属间的分类等级研究, 而难于用于属以下的分类等级研究。

关键词 [十字花科植物](#); [CYP86MF基因](#); [克隆](#); [进化分析](#)

分类号 [Q349+.5](#), [S63](#)

Cloning and Evolutionary Analysis of Homologous Sequences of CYP86MF Gene in Cruciferae

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Abstract

In order to direct the construction of plant germplasms by elucidating the relatives among plants at the level of gene, CYP86MF gene analogues from 11 species of 6 genera in Cuciferae were respectively obtained by PCR strategy using gene specific primers designed from conserved regions of CYP86MF gene reported. Sequence comparison indicated that the similarities among the genes at nucleotide level were over 80%, and the similarities at amino acid level remained above 70%. The differences between the genes at nucleotide and amino acid level between species were 1.0% ~ 5.7% and 2.6% ~ 7.3% respectively, while those between genera 5.6% ~ 22.5% and 7.3% ~ 31.2%, respectively. Phylogenetic analysis showed that Brassica was closely related to Raphanus, followed by Rorippa Scop, Arabidopsis Heynh, Capsella Medic orderly, most distantly related to Orychophrogmus. It was concluded that CYP86MF gene was not applicable to specie and subspecie taxon but genus taxon because the differences of sequences in nucleotides and amino acids were lower between species than genera.

Key words [Cruciferae](#) [CYP86MF gene](#) [cloning](#) [evolutionary analyses](#)

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