

山茶属植物ITS的多态性——一个广泛逃离一致性进化的实例

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Polymorphism of the Internal Transcribed Spacer of rDNA in *Camellia*—an Escape from Concerted Evolution

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摘要

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摘要 利用位于45S rDNA内转录间隔区(ITS)的3对SSR引物, 对山茶属(*Camellia* L.)的40个物种进行PCR扩增, 检测3个SSR位点的多态性, 研究物种倍性与多态性之间的关系。实验结果显示, 37个种(占92.5%)的ITS片段存在个体内长度多态性, 在这些种类的个体内至少有2-6类ITS拷贝, 表明山茶属植物的ITS片段存在广泛的非一致性进化; ITS序列上存在易于滑动的SSR位点, 并且其基因组中有较多位于不同染色体上的rDNA位点, 这很可能是山茶属植物ITS片段存在广泛多态性的原因。然而, 研究中没有发现多倍体种类ITS片段的多态性显著高于二倍体种类。山茶属植物ITS片段的多态性提示该属植物的rDNA可能存在更为复杂的进化模式, 在利用ITS片段解决该属植物的系统分类问题时应更为谨慎。

关键词: 山茶属 一致性进化 多态性 rDNA ITS

Abstract: In this study, we used 3 pairs of simple sequence repeat (SSR) markers from the 45S rDNA internal transcribed spacer (ITS) for PCR amplification in 40 species of *Camellia* to detect polymorphism in *Camellia* and the relationship between ploidy and polymorphism of species. In total, 37 species (92.5%) exhibited length polymorphism within individuals. At least 2-6 types of the ITS copies were found in individuals of these species, which indicates that non-concerted evolution is common in the ITS fragments in *Camellia*. Extensive non-concerted evolution may have resulted from SSR loci, which slip easily in the ITS region, and multiple rDNA loci that are located on different chromosomes. However, we did not find a significant difference in polymorphism between polyploidy and diploid. The polymorphism of the ITS region in *Camellia* species shows that there may be a more complex model of evolution in the rDNA of the genus, so the ITS sequences should be used with caution in solving the systematics problems of the genus.

Keywords: *Camellia* concerted evolution polymorphism rDNA ITS

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