

论文

栽培稻种内rDNA基因IGS序列分析及系统学意义

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摘要:

以普通野生稻为对照, 将rDNA基因间区(IGS)序列用于栽培稻种内不同亚种以及亚种内不同品种的亲缘关系分析。结果表明, 栽培稻种内IGS序列长度为2 130~2 145 bp, G+C含量为74.59%~75.29%, 变异位点229个, 占10.70%, 信息位点76个, 占3.51%。IGS序列中籼亚种和粳亚种之间有38个亚种标志性碱基差异, 主要分布在IGS 5' 端近400 bp的序列中。用IGS序列构建的系统树能将栽培稻的籼亚种和粳亚种分为两大类, 亚种内不同亲缘关系的品种也能区分开。本研究结果支持爪哇稻为栽培稻中一个独立亚种的观点。

关键词: 栽培稻 核糖体 基因间区(IGS) 系统树

Analysis of rDNA Intergenic Spacer (IGS) Sequences in *Oryza sativa* L. and Their Phylogenetic Implications

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Abstract:

In plant unclear genome, the intergenic spacer region (IGS) is located on the region of 18S–28S and is often used in phylogenetic analysis among species, detecting intra-specific polymorphisms. Rice (*Oryza sativa* L.) is differentiated into not only some subspecies but also many ecotypes of these subspecies. Can the IGS region be a useful tool to study the phylogenetic relationships among these cultivars of *Oryza sativa*? In the study, a comparative analysis of the rDNA intergenic spacer entire sequences of thirteen cultivars in *Oryza sativa* L. was carried out with *O. rufipogon* as outgroup. In the cultivars used, there were six for typical *O. sativa* ssp. *japonica*, five for typical *O. sativa* ssp. *indica*, two for *O. sativa* ssp. *javanica*. The result indicated that the length range of IGS sequences was from 2 130 to 2 145 bp, the content of G+C varied from 74.59% to 75.29%, there were 229 variational loci which were 10.70% of entire bases and 76 informative loci which were 3.51% of entire bases in *Oryza sativa*. Thirty-eight *indica* and *japonica* specific loci were found in the IGS sequences of *Oryza sativa*, most of them were covered a about 400 bp segment located in the upstream of IGS sequence. The *indica* and *japonica* subspecies of *Oryza sativa*, as well as some closely related cultivars, can be discriminated clearly based on the phylogenetic tree constructed by IGS sequences. The study supported the opinion that the *O. sativa* ssp. *javanica* is a subspecies of *Oryza sativa*.

Keywords: Rice (*Oryza sativa* L.) Ribosomal DNA (rDNA) Intergenic spacer (IGS) Phylogenetic tree

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