

研究论文

利用SSR标记分析栽培种花生多态性及亲缘关系

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摘要 利用11对SSR引物对24个花生栽培品种(包括四大类型)进行PCR扩增分析, 其中4对检测到明显的多态性, 共检测到33个等位基因变异, 每一个位点上检测到的等位变异数为5~13个, 平均为8.25个。根据扩增结果可以将24个品种中的21个相互区分。供试品种间的遗传相似系数值在0.2~1.0之间, 平均为0.4788。根据UPGMA聚类分析结果, 供试品种大多数按亚种聚为两大类群(I、II); 在两大类群下, 大多数品种也基本上按类型分类。本研究结果表明, SSR在分析栽培种花生DNA多态性和遗传关系方面非常有用。

关键词 [SSR](#) [花生](#) [多态性](#) [遗传关系](#)

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Analysis of DNA Polymorphism and Genetic Relationships in Cultivated Peanut(*Arachis hypogaea* L.) Using Microsatellite Markers

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Abstract Eleven SSR primer pairs were used to amplify the genomic DNA isolated from 24 peanut genotypes including all 4 market types. Four primers could detected polymorphism and produced a total of 33 alleles. The average numbers of alleles per locus was 8.25, and up to 13 alleles were found at one locus. The genetic similarity (GS) indexes among 24 cultivated peanut accessions were calculated based on the data from these SSR markers. The value of GS was varied from 0.2 to 1.0, with an average of 0.4788. The results of UPGMA indicated that the majority of 24 accessions could be divided into two groups by subspecies, and most genotypes were clustered by market types. It is no doubt that microsatellites are very useful DNA markers to analyze DNA polymorphism and genetic relationship in cultivated peanut.

Key words [Microsatellites](#) [Peanut](#) [Polymorphism](#) [Genetic relationship](#)

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