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论文

芝麻EST-SSR标记的开发和初步研究

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摘要：

为了加速分子标记在芝麻研究中的应用，利用网上现有的芝麻EST(expressed sequence tags)数据信息，开展了芝麻EST-SSR功能性标记的开发和利用研究。 在所有的3 328条芝麻EST序列中共确认得到1 785条非冗余EST序列。其中，在含有微卫星重复的148条序列中共检测有155个EST-SSR。非冗余EST序列总长为774.266 kb，平均每4.99 kb含有一个EST-SSR。EST-SSR的分布频率和特征分析表明，以AG/TC为重复基元(motif)的SSR出现最多，占总SSR的37.42%。利用这些序列，设计开发了50对EST-SSR引物，并分别选用36个芝麻、2个棉花、2个大豆和2个油葵进行多态性和通用性研究。其中44对引物在供试芝麻材料中扩增出条带，共产生108个位点，平均每对引物产生2.45个位点，多态信息含量(polymorphism information content, PIC)平均值为0.390。根据遗传相似性系数进行聚类，有26个芝麻材料聚类在两个大的亚类(III和IV)中，聚类结果表明芝麻的基因型与地理来源之间没有必然的联系。此外，分别有2对、3对和4对引物可以在棉花、大豆和油葵中进行通用性扩增。本研究证实这种全新开发的芝麻EST-SSR标记在芝麻遗传多样性分析、遗传图谱构建以及比较基因组等研究方面有广阔的利用前景。

关键词： 芝麻 表达序列标签 (EST) 简单重复序列(SSR) 多态信息含量(PIC) 遗传多样性

Development and Utilization of EST-derived Microsatellites in Sesame (*Sesamum indicum* L.)

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Abstract:

The deficiencies of markers in *Sesamum indicum* L. that can be used at home and aboard seriously restrict its studies in molecular field. To accelerate the application of molecular markers in sesame, EST-SSR markers development and utilization using publicly available sesame EST data were performed. A total of 1 785 non-redundant EST sets were assembled among the 3 328 identified sesame EST. 148 microsatellites sequences containing 155 EST-SSR were detected from these EST. The total length of the non-redundant EST sequences was 774.266 kb, on average one EST-SSR each 4.99 kb. The distribution characteristics of the EST-SSR markers was analyzed. Among the SSR, dinucleotide AG/TC was the most abundant (occurring 58 times), with frequency of 37.42%. According to these EST sequences containing SSR, 50 primer pairs were designed and tested on 36 sesame accessions, 2 cotton accessions, 2 soybean accessions and 2 oil sunflower accessions to detect polymorphisms and transferability. With 44 EST-SSR, 108 loci were successfully amplified in sesame, with an average of 2.45 loci per primer pair. Of the 44 amplified primer pairs, 27(61.4%) primer pairs revealed polymorphisms in the 36 sesame accessions. The PIC (polymorphism information content) ranged from 0.105 to 0.844, with an average of 0.390. Based on genetic similarity coefficient, the UPGMA dendrogram grouped 26 of 36 accessions in to two sub-clusters (III and IV), but it revealed no association between genotypes and geographical sources. In addition, 2, 3 and 4 SSR markers could be transferred to the PCR of cotton, soybean and oil sunflower respectively. This study effectively proved that EST-SSR from sesame is valuable for genetic analysis, linkage mapping and transferability study among oil plants.

Keywords: Sesame (*Sesamum indicum* L.) EST SSR PIC Genetic diversity

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