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摘要: 从NCBI下载了大豆的EST和GSS序列, 以SSR两侧序列各100 nt的片段作为分析材料, 统计SSR数目、计算侧翼序列碱基组成, 对SSR侧翼序列进行了序列比对和数据库blast搜索。结果表明: 大豆SSR分布频率为1/6.67kb, 侧翼序列GC含量为37.83%, 二核苷重复是SSR的主要类型(65.7%), 同一种重复基元的SSR存在多类型侧翼序列, 同一类型的侧翼序列高度保守, 不同类型的侧翼序列之间相似性较小, 尤其是非SSR区域可以存在与SSR侧翼序列相同的序列。由上述结果推断SSR引物可能扩增出不含SSR的产物, 易位可以产生形成新类型SSR。这一分析结果有助于提高SSR引物设计效率和进一步阐明SSR的形成机理。

Abstract: The soybean EST and GSS sequences were downloaded from NCBI, and the 100 nt SSR flanking sequences were extracted as analyzing material. The number of SSRs and the base composition of the flanking sequences were calculated. Meanwhile, the multiple sequence alignment and the blast scanning were conducted. The results showed distribution frequency of soybean SSRs was 1/6.67kb, GC content of the flanking sequences was 37.83%, and the dinucleotide was major type of the motif. The multiple sequence alignment revealed polymorphic types flanking sequences were in any kind of motif. The same type flanking sequences were highly conserved, but different type flanking sequences had less similarity. Especially, the blast analyzing showed the SSR flanking sequences may exist in no SSR regions. So we claimed no SSR fragments may be amplified by SSR primer pairs, and new type SSR could stem from translocation, which is one kind of chromosomal variations. The analyzing could contribute to efficient design of SSR primers and to further illuminate formative mechanism of simple sequence repeats.

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