

论文

草棉EST-SSRs的遗传评价

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摘要:

根据GenBank中公布的247条草棉EST序列, 搜索SSR并进行引物设计。其中的25条序列含有27个SSR, 1~6碱基重复类型都存在, 二碱基和三碱基重复的频率较高。为了明确在A、D和AD基因组中的可转移性, 依据25条序列共设计25对EST-SSR引物, 其中22对引物扩增出清晰可辨的DNA条带, 产生92个多态性片段, 平均每对引物产生3.64个多态性片段。引物的多态性信息含量(PIC)在0.49~0.91之间, 平均为0.81。6对引物在BC<sub>1</sub>种间作图群体[(鄂棉22 × Pima3-79) × 鄂棉22]中表现多态性, 产生7个多态性位点, 其中5个为共显性, 2个为显性。除HAU230b标记在BC<sub>1</sub>分离群体中不符合孟德尔式分离比例, 其余引物表现正常分离。6个位点被整合到陆地棉和海岛棉种间BC<sub>1</sub>遗传连锁图谱上的6条染色体: 有4个位于A亚基因组的4条染色体上(Chr. 6、10、11和12), 2个位于D亚基因组的2条染色体(Chr. 19和20)。

关键词: 草棉 表达序列标签 简单序列重复 多态性信息含量 遗传作图

Genetic Evaluation of EST-SSRs Derived from *Gossypium herbaceum*

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Abstract:

*Gossypium herbaceum* (A genome) is generally regarded as the most closely relative of the progenitor at subgenomes of allotetraploid cotton, of which the evolution is necessary to study. In order to investigate the contribution of *G. herbaceum* to the tetraploid genome, EST-SSRs were isolated from 247 EST sequences of *G. herbaceum* documented in GenBank. Twenty-seven perfect SSRs were identified from twenty-five unique ESTs. These SSRs contained 1~6 bp nucleotide motifs with high frequency for 2-bp and 3-bp nucleotide motifs. A total of 25 primers were developed and 22 of them could amplify 24 cotton accessions including 7 diploids of A genome, 11 diploids of D genome and 6 allotetraploids of AD genome; only HAU217 could specifically amplified A genome and the other 21 primers could amplified both A and D genomes. The number of polymorphic fragments generated by each primer ranged from 1 to 9 with an average of 3.64. The PIC values ranged from 0.49 to 0.91 with an average of 0.81. Among the 25 EST-SSR primers, six primers revealed polymorphism between Emian 22 and Pima 3-79, and yielded seven polymorphic loci (five were codominant and two dominant) in the BC<sub>1</sub> [(Emian22 × Pima3-79) × Emian22] population. Only HAU230b showed distorted segregation in the BC<sub>1</sub> population. Six polymorphic loci were integrated into six chromosomes of our interspecific BC1 backbone genetic linkage map among which, four loci were mapped on four chromosomes of A sub-genome (Chr. 6, 10, 11, 12), and two loci on two chromosomes of D sub-genome (Chr. 19 and 20).

Keywords: *Gossypium herbaceum* EST SSR Polymorphism information content (PIC) Genetic map

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