

植物生产层

蒺藜苜蓿EST SSRs分布特征及标记的开发

屠德鹏, 魏臻武, 武自念, 雷艳芳, 张栋, 邱伟伟

摘要:

利用蒺藜苜蓿(Medicago truncatula)EST数据库开发新的EST SSRs标记, 分析EST SSRs的分布特征。利用SSRIT软件对NCBI上公布的285 285条蒺藜苜蓿EST序列进行SSR序列的检测, 共检测出6 688个SSR序列, 分布于6 512个EST中, 占整个EST数据库的2.28%。其中二核苷酸重复基元出现的频率最高, 占总EST SSRs的34.4%(2 301条), 其次是三核苷酸重复基元, 占29.6%(1 982条), 4~6核苷酸重复基元所占比例均较小。利用Primer Premier 5.0随机设计100对EST SSRs引物, PCR扩增结果表明, 85对引物在蒺藜苜蓿RIL群体亲本A17和A20上有清晰的扩增条带, 占合成引物总数的85%, 在RIL 8群体中检测到29个EST SSRs引物有多态性, 占可扩增引物的34.1%。本研究开发了85个蒺藜苜蓿EST SSRs新标记。

关键词: 蒺藜苜蓿; EST SSRs; 引物设计; 标记开发

Distribution characteristics and marker exploitation of EST SSRs in *Medicago truncatula*

TU De peng, WEI Zhen wu, WU Zi nian, LEI Yan fang, ZHANG Dong, QIU Wei wei

Abstract:

New EST SSRs markers by EST database of *Medicago truncatula* were developed and the distribution characteristic of EST SSRs was analyzed. 6 688 of 285 285 EST sequences of *M. truncatula* from the National Center for Biotechnology Information (NCBI) were detected by SSRIT software, which accounted for 2.28%. Among them, 2 301 dinucleotide repeat elements, accounting for 34.4%, had the highest frequency and followed by 1 982 trinucleotide repeats, which accounted for 29.6% of the total EST SSRs. The ratio of four to six nucleotide repeat elements was comparatively lower. Selecting 100 primer pairs randomly, 85 primer pairs showed clear amplification belts, accounting for 85% of designed primers and 29 primer pairs showed polymorphisms, accounting for 34.1% of primers available. Besides, 85 new *M. truncatula* EST SSR markers have been developed.

Keywords: *Medicago truncatula* EST SSRs primer design marker exploitation

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作者简介:

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