锘
作物学报 2009, 35(2) 246-254 DOI: 10.3724/SP.J.1006.2009.00246 ISSN: 0496-3490
CN: 11-1809/S

论文

花生栽培种EST-SSRs分布特征及应用研究

梁炫强;洪彦彬;陈小平;刘海燕;周桂元;李少雄;温世杰

广东省农业科学院作物研究所，广东广州510640

摘要：

利用自行开发的20 160条花生栽培种荚果EST, 通过序列拼接, 获得8 289条无冗余EST。经搜索, 共检测出740个SSR位点, 分布于651条EST中, 发生频率为7.8%, 平均每6.8 kb EST序列含一个SSR位点。功能注释结果表明具生物过程、分子功能和细胞组分的EST分别为73、111和56条。在花生荚果EST-SSR中, 三核苷酸重复类型出现频率最高, 占总SSR的62.8%, 其次是二核苷酸重复类型, 占总SSR的33.6%。在出现的26类重复基序中, AG/TC重复基序出现频率最高, AAG/TTC次之。利用Primer premier 5从651条含有SSR的EST中共设计引物233对, 从中随机选取100对引物检测EST-SSR在花生栽培种中的多态性及在野生种中的可转移性。结果表明, 有86对引物在供试的22个花生栽培品种中得到有效扩增, 其中10对在栽培种中具有多态性, 每对引物检测出的等位基因数2~3个, 平均2.2个。可扩增引物在野生种中的可转移率为12.5%~100%，平均96%。在野生种间检测出多态性的引物76对，每对引物检测出等位基因2~9个, 平均4.06个。

关键词： 花生栽培种 EST SSR 开发

Characterization and Application of EST-SSRs in Peanut(*Arachis hypogaea* L.)

Crops Research Institute, Guangdong Academy of Agricultural Sciences, Guangzhou 510640,Guangdong,China

Crops Research Institute, Guangdong Academy of Agricultural Sciences, Guangzhou 510640,Guangdong,China

Abstract:

Peanut (*Arachis hypogaea* L.) is one of the most important oilseed crops in China. Although there is a great difference in growth habit, growth stage, and agronomic traits for peanuts, there is little polymorphism on the molecular level of RFLP, RAPD and AFLP. With development of peanut EST, a vast amount of available EST sequence has been documented. The objective of this study was to investigate distribution characteristics of EST-SSRs. Developed with a total of 20 160 EST from cDNA library of two peanut cultivars, There were 651 SSR-containing EST identified, on average, one SSR had 6.8 kb of EST sequence with tri-nucleotide motif (62.8%) as the most abundant motif types followed by di- (33.6%), tetra- (1.9%), hexa- (0.8%) and penta-nucleotide (0.8%). The top six motif types with high frequency included AG/TC (25.8%), AAG/TTC (19.1%), AAT/TTA (10.1%), ACC/TGG (7.4%), ACT/TGA (7.0%) and AT/TA (6.1%). Based on the 651 SSR-EST, a total of 233 primer pairs were successfully designed and a subset (100 pairs) were synthesized to test the amplification and polymorphism in 22 peanut cultivars, and to assess the transferability among 16 different wild species. The results showed that 86 primer pairs were amplified effectively in peanut cultivars, 10 primer pairs of which exhibited polymorphism with 2–3 alleles, with an average of 2.2 alleles, were detected. The cross-transferability of cultivated peanut EST-SSR markers to peanut wild species was very high, ranging from 12.5 to 100% with an average of 96%. Seventy-six markers exhibited polymorphism in wild species with 2–9 alleles, and an average of 4.06 alleles. The results indicated that peanut EST could be a resource for developing SSR. The high level of transferability to wild species also implied that EST-SSR is a potentially useful marker for genetic studies in wild species.

Keywords: Peanut(Arachis hypogaea :.) EST mining SSR

收稿日期 2008-04-21 修回日期 2008-09-11 网络版发布日期 2008-12-10

DOI: 10.3724/SP.J.1006.2009.00246

基金项目:

本研究由国家高技术研究发展计划（863计划）项目（2006AA10Z156），广东省自然科学基金项目（06025389，07117967）资助

通讯作者:

作者简介:

参考文献：

本刊中的类似文章

文章评论 (请注意:本站实行文责自负, 请不要发表与学术无关的内容!评论内容不代表本站观点.)

HTTP Status 404 - /zwxb/CN/comment/listCommentInfo.jsp

type Status report