

### 萝卜EST资源的SSR信息分析及EST-SSRs标记开发

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#### Data Mining for SSRs in EST Resources and EST-SSR Markers Development in Radish

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**摘要** 从NCBI数据库下载了287 349条萝卜EST序列,经预处理后得到无冗余EST序列58 105条,全长38 622.476 kb。利用MISA搜索SSR位点,得到含有SSR位点的EST序列3 523条,共3 718个SSR,平均每10.39 kb就出现1个SSR。分析发现萝卜EST序列中存在265种重复基元类型,其中二、三、六核苷酸重复是主导的重复基元类型,二核苷酸中以比例高达91.34%的AG/CT重复基元为主;三核苷酸中主导的重复基元类型是AAG/CTT,比例为35.86%;六核苷酸中,存在两种主要的重复基元,分别为AAGGAG/CCTCTT和AAGAGG/CCTTCT,所占比例为12.78%。这些结果表明,萝卜EST-SSRs出现频率较高,类型丰富,具有良好的多态性潜能和开发利用价值。使用primer3.0批量设计,并以不同主导重复基元类型初步合成183对EST-SSR引物,以12份典型萝卜种质、1对亲本及其F1的基因组DNA为模板,对其有效性进行验证,筛选出有清晰扩增产物的引物159对,其中多态性引物64对;在试验亲本及其F1中表现多态性的引物30对,共显性引物27对。

**关键词:** 萝卜 EST SSR特征 标记开发

**Abstract:** A total of 287 349 ESTs of radish were downloaded from NCBI database. After preprocessing, 58 105 non-redundant ESTs with the total length of 38 622.476 kb were obtained. By using the MISA program, a total of 3 718 SSRs were observed in 3 523 ESTs and the average distance between SSRs was 10.39 kb. 265 types of motifs were found in radish's ESTs and the dominant motifs types are dinucleotide, trinucleotide and exanucleotide repeats. AG/CT was the main motifs type (91.34%) in dinucleotide repeats; AAG/CTT was the main motifs type (35.86%) in trinucleotide; AAGGAG/CCTCTT and AAGAGG/CCTTCT were two main motifs types (total 12.78%) in exanucleotide. Comprehensively analysis indicated that EST-SSRs of radish with high frequency and rich motifs types were potential for the development of polymorphic primers. Using the primer 3.0, 183 primers were designed and synthesized based on different dominant motifs types, and verified with 12 typical radish germplasms for polymorphism and one pair of parents and their F1 for codominance. The results showed that the products of 159 primers are clear and effective, 64 pairs were polymorphic among the germplasms and 27 were codominant between the parents and their hybrids.

**Keywords:** radish, EST, SSR characteristics, markers development

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