新型分子标记——SRAP与TRAP及其应用

http://www.firstlight.cn 2007-12-07

SRAP与TRAP是最近发展的新型分子标记系统，具有简单、高效、高共显性、重复性、易测序等优点，尤其是可检测基因的可译框（ORFs）区域。本文对分别在芸薹属作物与向日葵中开发的SRAP、TRAP标记系统的基本原理与分析程序进行介绍。引物设计是SRAP与TRAP分析的关键，目前已开发出多个SRAP正、反向引物；与SRAP标记技术无须任何序列信息不同，TRAP技术需要基于已知cDNA 或EST序列信息设计固定引物才可进行PCR扩增；二者PCR条件采用复性变温法，前5个循环复性温度为35℃，后30～35个循环为50℃；扩增产物可在聚丙烯酰胺或琼脂糖凝胶上电泳，同位素或银染、EB检测。目前这两种标记系统已开始在多种作物的种质资源鉴定评价、遗传图谱构建(包括转录图谱)、重要性状标记乃至基因分离克隆等方面成功应用。

Abstract：SRAP and TRAP are two kinds of newly developed molecular marker systems with the advantages of simplicity, high throughput, numerous co-dominant makers, highly reproducibility and ready to sequence, especially preferential targeting ORFs. The principle and protocol of SRAP and TRAP，which were developed in Brassica and Helianthus crops firstly, are introduced in the paper. Primer design is a key step for SRAP and TRAP, and some F-and R-primers were developed. Unlike SRAP technique, the TRAP requires cDNA or EST sequence information for fixed primer development. The annealing temperature is 35°C in the first 5 cycles and 50°C in the subsequent 30～35 cycles. The amplicons can be separated by polyacrylamide or agarose gel，and detected by autoradiography，silver or EB staining. SRAP and TRAP are applied in germplasm genetic diversity analysis, genetic map including transcriptome map construction, important trait gene tagging and gene cloning in many crops.

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