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论文

梨SRAP体系的优化及其在杂交后代中的分离方式

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摘要:

采用正交设计建立并优化了梨的SRAP－PCR分子标记技术体系,在20 μL的反应体系中含有DNA 15 ng／mL ,Primer 0.5 μmol／L,dNTPs 0.1 mmol／L,Mg^{2+} 2 mmol／L, Taq DNA聚合酶1.5 U。应用20对引物组合对SRAP标记在“红巴梨×南果梨”F 1群体的多态性和分离方式进行了研究。结果表明:SRAP标记在该群体中具有较高的多态性,分离位点占总位点数的44 59%。其中,符合孟德尔分离位点110个,占分离位点数的83.33%;偏离孟德尔分离比例位点22个,占分离位点数的16 67%;异常分离位点8个,占总位点数的2.55%。

关键词: 梨 分子标记 SRAP 分离方式

Optimization of Reaction System for SRAP Molecular Marker in Pear and Segregation Patterns in Hybrid Progenies

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Abstract:

By the method of orthogonal design, the reaction system for SRAP-PCR molecular marker in pear was established and optimized, 15 ng／mL DNA, 0.5 μmol/L Primer, 0.1 mmol/L dNTP, 2 mmol/L Mg^{2+}, 1.5 U Taq DNA polymerase in 20 μL reaction system. The polymorphism and the segregation patterns of the SRAP markers in the F 1 progenies from two pear cultivars (Red Bartllet×Nanguo pear) were studied using 20 primer combinations. The results showed that the polymorphism of the SRAP markers in the F 1 population was high, and the frequency of the segregation loci was 44 59%. The segregation patterns included Mendelian, deviation from Mendelian and new segregation loci, and their frequency and number were 83.33%,110;16.67%,22; 2.55%,8 respectively. All the above could provide some theoretical basis for the further work of theconstruction of pear genetic map and relevant study.

Keywords: pear molecular marker SRAP segregation pattern

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