

宽皮柑橘单核苷酸多态性的高分辨率熔解曲线分型

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Genotyping Single Nucleotide Polymorphisms in Mandarin Cultivars Using High Resolution Melting Analysis

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摘要 高分辨率熔解曲线分析 (High resolution melting analysis, HRM) 可以检测单碱基改变引起的DNA双链熔解温度 (T_m) 值变化, 从而可以对样本在单核苷酸多态性分子标记 (Single nucleotide polymorphism, SNP) 上进行基因分型。通过分析NCBI数据库中宽皮柑橘的表达序列标签 (Expressed sequence tag, EST) 数据鉴别SNP位点, 并用小片段扩增法高分辨率熔解曲线分型技术 (High resolution melting analysis of small amplicons) 分析11个宽皮柑橘 (*Citrus reticulata*) 品种以及柳橙 (*Citrus sinensis* Osbeck var. 'Liucheng') 的5个SNP位点的基因型。结果显示, 小片段扩增法高分辨率熔解曲线分型可以快速、清楚地分辨纯合与杂合基因型, 在校正温度差异后也可以很好地分辨同一个SNP位点不同的纯合型。统计分析表明样本在所有SNP位点上均存在多态性, 5个SNP位点的平均多态性信息含量 (PIC) 为0.3190, 显示样本在这组SNP位点上具有较高的杂合率。

关键词: 宽皮柑橘 高分辨率熔解曲线 单核苷酸多态性 基因分型

Abstract: High resolution melting analysis (HRM) is capable of detecting changes in melting temperature (T_m) of double strand DNA sequences caused by single nucleotide changes, and is suitable to genotype genetic samples using known single nucleotide polymorphic sites (SNPs). *Citrus reticulata* ESTs from NCBI EST database were searched for SNPs, and 5 SNPs were selected to genotype 11 mandarin and 1 sweet orange cultivars using HRM genotyping of small amplicons. The results showed that, at a given SNP site, a heterozygous genotype could be easily and clearly distinguished from a homozygous genotype by HRM, and 2 different homozygous genotypes could also be easily identified when temperature was calibrated. All 5 SNPs were found polymorphic in analyzed citrus samples, with an average polymorphic information content (PIC) value of 0.3190, indicating that these samples are highly heterozygous at these SNP sites.

Keywords: mandarin, high resolution melting, single nucleotide polymorphism, genotyping

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[1] 殷豪; 王彩虹; 田义钊; 李节法; 王然; 戴洪义. 利用高分辨率熔解曲线 (HRM) 分析梨微卫星标记[J]. 园艺学报, 2011, 38(8): 1601-1606

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