

西瓜核心种质枯萎病抗性与SRAP分子标记的关联分析

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Association Analysis of *Fusarium wilt* Resistance of Core Collection of Watermelon Germplasms Based on SRAP Markers

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摘要 对35份西瓜核心种质进行了抗枯萎病鉴定,再采用SRAP分子标记技术对35份核心种质进行多态性分析。从63对引物组合中筛选出46对多态性引物。SRAP扩增共产生445个条带,其中262条为多态性条带,多态率为58.88%。平均每对引物产生9.67个条带。在对供试材料进行群体结构分析的基础上,利用TASSEL软件对多态性标记与枯萎病抗性进行关联分析。群体遗传结构分析将35份西瓜核心种质分为3大群体:1个野生西瓜群体和2个栽培种群体。分析发现在2个栽培种群体中存在基因渗透。聚类分析结果与群体遗传结构分析结果一致,分为4个类群,其中第2类群又细分为5个小类群。聚类分析结果说明具有相同抗性水平的材料倾向于聚在一起。关联分析发现有1个标记位点与枯萎病抗性显著关联($P < 0.01$),该位点对表型性状的解释率为0.2035。本研究结果表明利用SRAP标记可以有效地对西瓜种质资源进行群体结构的划分,且关联分析能够找到与西瓜枯萎病抗性相关联的SRAP标记,为西瓜抗病育种和分子标记辅助选择奠定了基础。

关键词: 西瓜 枯萎病抗性 SRAP 聚类分析 关联分析

Abstract: SRAP technique was applied to analyze the genetic variation and relationships of 35 core collection watermelon germplasms whose *Fusarium wilt* resistance were evaluated. 46 of 63 SRAP primers generated a total of 445 reproducible bands, 262 (58.88%) of which were polymorphic, with an average of 9.67 for each pair of primers. Based on the population structure analysis, the association analysis between SRAP markers and *Fusarium wilt* resistance was performed by using of TASSEL GLM. The population structure analysis showed that 35 watermelon genetic resources were clustered into 3 groups including 1 group of wild-type and 2 groups of cultivar-type. The gene introgression was also discovered in the 2 cultivar-TYPES. The dendrogram result which was constructed by using UPGMA method was consistent with the population structure analysis, with 4 clusters and 5 classes in cluster 2. The dendrogram result indicated that the genetic resources of watermelon with similar resistant level tend to gather together. 1 SRAP loci associated with *Fusarium wilt* resistance character ($P < 0.01$) was found based on the association analysis, and the explanation rate was 0.2035. The research indicated that SRAP markers was effective to differentiate the population structure of watermelon germplasms, and SRAP loci association with *Fusarium wilt* resistance could be identified by associated analysis. The outcomes of this study will help us to accelerate the watermelon breeding for disease resistance and molecular marker-assisted breeding.

Keywords: Watermelon, *Fusarium wilt* resistance, SRAP, cluster analysis, association analysis

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