

大白菜抽薹开花时间与SSR和InDel标记的关联分析

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Association Analysis of Bolting and Flowering Time with SSR and InDel Markers in Chinese Cabbage

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摘要 利用57个SSR和InDel标记,对80份大白菜自交系及110份F₁杂交种材料的基因组DNA进行扩增。通过群体遗传结构分析,将供试材料分为3个亚群体,亚群体的划分与群体遗传关系和性状相关联;采用TASSEL软件的GLM (general linear model)方法进行标记与抽薹时间和开花时间的关联作图分析,发现13个标记的17个位点与抽薹时间和开花时间相关,其中15个与抽薹时间相关,12个与开花时间相关。10个位点同时与两个性状相关联。

关键词: 大白菜 分子标记 群体结构 关联分析

Abstract: Fifty-seven markers of SSR (simple sequence repeat) and InDel (insertion-deletion) were used to amplify the genome DNA of 80 inbred lines and 110 F₁ hybrids of Chinese cabbage. Population genetic structure analysis showed that 190 Chinese cabbage accessions are composed of 3 subpopulations. The classification of subpopulations is associated with their genetic relationships and phenotypic traits. The association analysis of markers and bolting time, markers and flowering time were performed using GLM (general linear model) method of software TASSEL. A total of 17 alleles from 13 primers were identified as significant associations with bolting and flowering time, of which 15 alleles were associated with bolting time and 12 alleles were associated with flowering time. Furthermore, we found that 10 alleles were associated with two observed traits simultaneously.

Keywords:

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