植物遗传学

小麦背景中来自华山新麦草的抗条锈病基因的遗传学分析和分子标记

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收稿日期 2004-5-9 修回日期 2004-9-14 网络版发布日期 接受日期

H9020-17-5是一个通过杂交和回交选育的普通小麦-华山新麦草易位系,接种鉴定表明其对抗条锈病具有 优良抗性。遗传学分析证明易位系H9020-17-5的抗条锈性是由单基因控制的显性性状,抗性基因来自于华山新麦 草,暂定名为YrHua。为了标记这个来自华山新麦草的抗条锈病基因,利用H9020-17-5与感病小麦品种铭贤169杂 交,建立了F2分离群体。应用81对AFLP引物对119个经条锈菌生理小种CY30接种鉴定的F2单株进行了分析,结果得 ▶ 复制索引 到两个与YrHua基因连锁的AFLP标记PM14(301)和PM42(249),遗传距离分别为5.4 cM和2.7 cM ,并分别位于 目标基因的两侧。将标记片断克隆、测序后,根据序列信息和酶切位点多态性设计特异性引物,将AFLP标记PM14 (301)转换成了简单的PCR标记。研究结果可为标记辅助育种提供了分子选择工具,同时也为进一步精细定位和 图位克隆YrHua基因奠定基础。

关键词 华山新麦草,小麦,抗条锈病基因,遗传学分析,分子标记,AFLP 分类号

Genetic Analysis and Molecular Markers of a Novel Stripe Rust Resistance Gene YrHua in Wheat Originating from Psathyrostachys huashanica Keng

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Abstract

The H9020-17-5, a common wheat-Psathyrostachys huashanica Keng translocation line, possesses excellent resistance to wheat stripe rust. Genetic analysis of F2 and BC1 populations derived from H9020-17-5 × Mingxian169 indicated that resistance to stripe rust in H9020-17-5 was a dominant character controlling by single gene originating from Ps. huashanica. This resistance gene originated from Ps. huashanica was reported firstly and named as YrHua in the present study. In order to mapping the resistance gene YrHua, AFLP approach was employed to analyze the 119 individuals of H9020-17-5 × Mingxian169 F2 population which were inoculated by stripe rust isolate CY30. As a result, two markers, PM14(301) and PM42(249) were found to be linked to the resistance gene YrHua, and the genetic distances between the markers and target gene were 5.4 cM and 2.7 cM, respectively. For the convenience of marker-assisted selection in wheat breeding, one of the two AFLP markers was converted to PCR marker using a pair of special primers designed based on the DNA sequence of PM14(301) and the polymorphism of restriction site. Our research results provided a useful tool for marker-assisted selection and yet laid the foundation of the fine mapping and map based cloning YrHua gene.

Key words Psathynrostachys huashanica wheat stripe rust resistance gene genetic analysis molecular marker AFLP

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