

与白菜霜霉病抗性主效QTL连锁的分子标记开发

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摘要 霜霉病是危害大白菜的三大病害之一, 该病的发生会严重影响大白菜的产量及品质, 因而研究与霜霉病抗性QTL紧密连锁的分子标记对大白菜抗病新品种培育具有重要意义。该研究在前期工作的基础上, 选用高感霜霉病株系91-112、高抗霜霉病株系T12-19以及由二者为双亲构建的DH群体为实验材料, 针对大白菜霜霉病抗性主效QTL——*BrDW*所在的标记区间, 利用已有的大白菜基因组信息发展与抗性QTL紧密连锁的分子标记, 通过Blast和IMap分析, 将与*BrDW*连锁的RAPD标记K14-1030定位于大白菜KBrB058M10上(位于Contig214上), 根据KBrB058M10附近的BAC及BAC-end序列设计引物, 结合限制性内切酶酶切及HRM分析方法, 筛选得到5个与*BrDW*连锁的分子标记, 包括1个Indel标记Brb062-Indel230, 3个CAPS标记Brb094-Dra I₇₈₇、Brb094-Aat II₆₆₆和Brb043-Bgl II₇₁₅, 1个SNP标记Brh019-SNP₁₃₇; 同时, 通过筛选与目标区域具有同源性的Unigene序列得到了1个与*BrDW*紧密连锁的SSR标记bru1209。标记Brb062-Indel230、Brb094-Dra I₇₈₇、Brb094-Aat II₆₆₆、Brb043-Bgl II₇₁₅、Brh019-SNP₁₃₇和bru1209与RAPD标记K14-1030之间的遗传距离分别为4.3 cM、1.7 cM、5.9 cM、5.9 cM、4.6 cM和0.8 cM, 在对DH群体中的抗性株系选择上准确率分别为69.7%、70.9%、72.4%、72.4%、58.3%和74.2%, 可应用于分子标记辅助选择, 为霜霉病抗性分子育种奠定了良好基础。

关键词: 大白菜 (*Brassica rapa* L. ssp. *pekinensis*) 霜霉病 BAC序列 分子标记

Abstract: Downy mildew, caused by the oomycete *Hyaloperonospora parasitica* Constant. (Pers. ex Fr.), is one of the most severe diseases in Chinese cabbage, leading to reduction of yield and quality of the harvested products. Therefore, identifying molecular markers linked to the major QTL for downy mildew resistance will be helpful in breeding resistant varieties of Chinese cabbage. Here, one highly susceptible line 91-112, one highly resistant line T12-19, and the derived DH population were employed to develop linked molecular markers for the major QTL, *BrDW*, for downy mildew. With BLAST and IMap analysis, the RAPD marker K14-1030 linked to *BrDW* was anchored on KBrB058M10 (on Contig214). On the basis of the BAC and BAC-end sequences around KBrB058M10, a set of PCR primers were designed, and the methods of restriction analysis and HRM analysis were used to develop molecular markers. Finally, five polymorphism markers were developed, containing one Indel marker named Brb062-Indel₂₃₀, three CAPS markers named Brb094-Dra I₇₈₇, Brb094-Aat II₆₆₆ and Brb043-Bgl II₇₁₅, and one SNP marker named Brh019-SNP₁₃₇. In addition, one SSR marker from Unigene sequence homologous with KBrB058M10 (known as bru1209) was developed. The map distances between the six markers and RAPD marker K14-1030 were 4.3 cM, 1.7 cM, 5.9 cM, 5.9 cM, 4.6 cM, and 0.8 cM, respectively. The percentage of accuracy in selecting for downy mildew-resistant lines from the DH population were 69.7%, 70.9%, 72.4%, 72.4%, 58.3%, and 74.2%. These markers could be used in marker assisted selection to improve downy mildew resistance in Chinese cabbage.

Keywords: Chinese cabbage (*Brassica rapa* L. ssp. *pekinensis*), downy mildew, BAC sequence, molecular marker

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