

研究报告

花椰菜遗传图谱的构建及NBS-LRR类抗性同源基因在图谱中的定位

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摘要

利用AFLP和NBS profiling技术, 以花椰菜自交系“AD白花”与高代自交不亲和系“C-8”杂交得到的F1代自交产生的F2代分离群体为材料, 构建了第一个花椰菜遗传连锁图谱。该图谱由234个AFLP标记和21个NBS标记构成了9个连锁群, 总图距为668.4 cM, 标记间平均距离为2.9 cM。每个连锁群包含的位点数从12到47个, 相邻两标记之间的距离范围是0~14.9 cM。NBS标记分布在8个连锁群中, 这些标记大部分聚在一起。本研究为今后的基因定位及重要农艺性状的分析提供框架图。此外, 研究NBS profiling 方法在花椰菜中的稳定性和有效性以及NBS-LRR类RGA在花椰菜基因组中的分布和特点。

关键词 [花椰菜](#) [AFLP](#) [NBS profiling](#) [遗传连锁图谱](#)

分类号

Construction of genetic linkage map and localization of NBS-LRR like resistance gene analogues in cauliflower (*Brassica oleracea* var. *botrytis*)

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Abstract

<P>Nucleotide binding site (NBS) profiling, a new method was used to map resistance gene analogues (RGAs) in cauliflower (*Brassica oleracea* var. *botrytis*). This method allows amplification and the mapping of genetic markers anchored in the conserved NBS encoding domain of plant disease resistance genes. AFLP was also performed to construct the cauliflower intervarietal genetic map. The aim of constructing genetic map was to identify potential molecular markers linked to important agronomic traits that would be particularly useful for development and improving the species. Using 17 AFLP primer combinations and two degeneration primer/enzyme combinations, a total of 234 AFLP markers and 21 NBS markers were mapped in the F2 population derived from self-pollinating a single F1 plant of the cross AD White Flower × C-8. The markers were mapped in 9 of major linkage groups spanning 668.4 cM, with an average distance of 2.9 cM between adjacent mapped markers. The AFLP markers were well distributed throughout the linkage groups. The linkage groups contained from 12 to 47 loci each and the distance between two consecutive loci ranged from 0 to 14.9 cM. NBS markers were mapped on 8 of the 9 linkage groups of the genetic map. Most of these markers were organized in clusters. This result demonstrates the feasibility of the NBS-profiling method for generating NBS markers for resistance loci in cauliflower. The clustering of the markers mapped in this study adds to the evidence that most of them could be real RGAs.</P>

Key words [cauliflower](#) [AFLP \(amplified fragment length polymorphism\)](#) [NBS \(nucleotide binding site\) profiling](#) [genetic linkage map](#)

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