

研究论文

甘蓝型油菜产量及相关性状的QTL分析

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摘要 高产是甘蓝型油菜育种的重要目标之一, 产量是多基因控制的数量性状。本文通过QTL作图分析了产量及其相关性状的数量性状位点, 以甘蓝型油菜中油821和保604 F1代小孢子培养获得的DH系为作图群体, 构建了由20个连锁群组成的, 包括251个分子标记(2个RFLP标记, 72个RAPD标记, 91个SSR标记, 86个SRAP标记)的遗传连锁图(10个标记没有分配到连锁群中)。图谱的平均图距为6.96 cM, 共覆盖油菜基因组1 746.5 cM。在此图谱基础上采取复合区间作图法, 检测到与油菜产量及其相关性状有关的QTL共17个。其中控制株高的3个分别位于第4、第9和第10连锁群上, 对性状的解释率为9.42%~17.58%; 与分枝部位有关的4个分别位于第4、第6和第7连锁群上, 其中Bp1 和Bp2 均位于第4连锁群, 对性状的解释率为8.13%~15.20%; 与主花序有效长有关的3个分别位于第4、第10和第16连锁群上, 对性状的解释率为7.49%~23.36%; 与一次有效分枝有关的2个分别位于第1、第4连锁群上, 对性状的解释率为15.29%~19.58%; 与角果总数和千粒重有关的分别位于第4连锁群和第9连锁群上, 贡献率分别为17.42%和7.64%; 与单株产量有关的3个分别位于第3、第4和第15连锁群, 共解释26.60%的表型变异。部分性状的QTL在连锁群上成簇分布, 对性状贡献率很大, 表现主效QTLs的特点, 相应的性状之间也呈显著相关, 这表明一因多效或者相关的QTLs之间紧密连锁是性状相关的遗传基础。本研究中与主效QTLs连锁的标记可用于油菜产量性状的分子标记辅助选择。

关键词 油菜 双单倍体群体 分子标记遗传图谱 产量 数量性状位点 (QTL)

分类号 S565

Mapping of Quantitative Trait Loci for Yield and Yield Components in *Brassica napus* L.

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Abstract Although seed yield is one of the most important objectives in *Brassica napus* breeding program, it is poorly understood because of the multigenic and nongenetic influence. Recent advances in molecular marker techniques provide the possibilities to trace gene behavior at individual gene loci, which greatly helps to understand the complex genetics of quantitative traits of seed yield. The objective of our investigation was to acquire the information on the association between molecular markers and seed yield in *Brassica napus* and on the inheritance of these agronomic traits and to facilitate the selection in breeding programs. A double haploid (DH) population derived from a cross between the rapeseed cultivars Zhongyou 821 and Bao 604 was used to identify quantitative trait loci (QTLs) for seed yield and yield components. Eighty-two double haploid lines as well as two parent lines were evaluated in field environments in Wuhan, with two replications, for 7 agronomic traits, including plant height (PH), branch position (BP), length of main raceme (LMR), No. of primary branches (NPB), No. of pod per plant (NPP), 1000-seed weight (SW) and yield per plant (YPP). It was shown that all the seven agronomic traits had continuous phenotypic distributions and were suitable for QTL analysis (Table 2). A total of 261 molecular markers consisting of 2 RFLPs, 72 RAPDs, 91 SSRs and 86 SRAPs were employed to 82 DH lines and to construct the genetic linkage map, two hundred and fifty-one markers were assembled into 20 linkage groups (LG1 - LG20), no linkage was found between the remaining 10 markers and any of the established linkage groups (Fig.1). The total map length was 1 746.5 cM with an average distance of 6.96 cM between adjacent markers. By employing complex interval mapping, a total of 17 putative QTLs were identified to be significant for the seven traits, of which 3 were for yield, 14 for yield components (Table 4). The phenotypic variation was explained by individual QTL ranged from 9.42% - 17.58% for three QTLs of plant height, 8.13% - 15.20% for four QTLs of branch position, 7.49% - 23.36% for three QTLs of length of main raceme, 15.29% - 19.58% for two QTLs of No. of primary branches, 17.42% for one QTL of No. of pod per plant, 7.64% for one QTL of 1000-seed weight and 8.11 - 9.78 for three QTLs of yield per plant. Some QTLs were mapped at the same or similar position in LG4, there were significant correlations between the corresponding traits. It suggested that the pleiotropism or tight linkage of QTLs for different traits might be the important genetic base for trait correlations. The molecular marker linked closely with main QTLs of yield and yield components in this paper could be used for MAS in rapeseed breeding program.

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Key words [Brassica napus](#) [DH \(doubled haploid\)](#) [Molecular linkage map](#) [Yield](#) [QTL \(quantitative trait loci\)](#)

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