



利用置换系检测棉花第22染色体短臂的产量相关性状QTLs

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Tagging QTLs of Yield-related Traits in Chromosome 22sh of Allotetraploid Cotton Using Substitution Line

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摘要

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摘要 CSB22sh为以陆地棉 (*Gossypium. hirsutum* L.) 遗传标准系TM-1为背景的第22染色体短臂被海岛棉 (*Gossypium. barbadense* L.) Pima3-79置换的海陆置换系。TM-1与CSB22sh杂交, 构建了104个F₂单株的作图群体, 应用6748对SSR引物对亲本进行分子标记筛选, 获得90个多态性标记位点。其中85个标记位点构建了总长85.24 cM的遗传图谱, 标记间平均距离1.0 cM, 覆盖棉花基因组的1.8%。通过复合区间作图法对F_{2:3}和F_{2:4}家系的7个产量相关性状(衣分、铃重、子指、株高、第一果枝节位、单株铃数、单株果枝数)进行QTL检测, 共检出28个不同QTLs, 解释性状表型变异的3.5%~44.8%。仅在一个环境中检测到的QTLs有17个, 2个环境同时检测到的QTLs有8个, 3个环境同时检测到的QTLs有3个。不同的QTL在相同区段的成簇分布表明, 控制不同性状的基因可能紧密连锁或一因多效。检测到的稳定的QTL可以用于相应性状的分子标记辅助选择。

关键词: 置换系 遗传连锁图谱 产量相关性状 QTL 陆地棉 海岛棉

Abstract: The CSB22sh is a substitution line with chromosome 22 short arm substituted for corresponding chromosome arm of Pima 3-79 (*Gossypium. barbadense* L.) in genetic background of TM-1, a genetic standard line of upland cotton (*G. hirsutum* L.). A genetic linkage map with 85 SSR marker loci was constructed using an F₂ population derived from a cross between CSN22sh and TM-1. The map covered a total genetic distance of 85.24 cM with the average distance of 1.0 cM between two markers, covering approximately 1.8% of the recombination length of the cotton genome and about half of chromosome 22. Composite interval mapping was used to identify the quantitative trait loci (QTLs) in F_{2:3} and F_{2:4} family lines. 28 QTLs for 7 yield-related traits, which lint percent, boll weight, seed index, height, boll number, fruit branch number, the first branch node, were identified. These QTLs explained 3.5%~44.8% of the phenotypic variance, respectively. There were 17, 8 and 3 QTLs simultaneously significant in one, two and three environments, respectively. None of QTL was consistently significant in all environments. QTLs affecting different traits were detected within the same chromosomal regions, suggesting close linkage or pleiotropy of QTLs. The molecular markers linked closely to the steady QTLs may be used in marker-assisted selection to improve target agronomic traits.

Keywords: chromosome substitution line genetic linkage map yield-related traits QTL upland cotton island cotton

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