



鲁棉研15号纤维品质性状QTL定位研究

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QTL Mapping for Fiber Quality Properties in Lumianyan 15

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摘要

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摘要 以陆地棉 (*Gossypium hirsutum* L.) 杂交种鲁棉研15号的F₂群体为作图群体, 利用SSR标记和JoinMap3.0软件构建遗传连锁图谱; 利用复合区间作图法分别对随机组成的3个鲁棉研15号的F_{2:3}家系亚群体进行纤维品质性状QTL定位。构建的遗传连锁图谱包含116个多态位点, 25个连锁群, 全长892.25 cM, 覆盖棉花总基因组的20.05%, 平均每个连锁群4.64个标记, 标记间平均距离7.76 cM; 根据已有图谱的定位结果, 19个连锁群与染色体建立了联系。在3个F_{2:3}家系亚群体中共检测到46个QTL, 其中16个为纤维长度 (FL) QTL、7个为纤维强度 (FS)、12个为麦克隆值 (FM)、6个为伸长率 (FE), 5个为整齐度指数 (FU)。发现在A_n05、A_n08、A_n09、D_n02染色体上QTL有成簇分布的现象, 并在3个亚群体中检测到一些受环境影响较小、稳定遗传的QTL。这些QTL可以在今后应用于分子标记辅助选择。

关键词: 棉花 纤维品质 QTL定位 鲁棉研15号

Abstract: In this study, the F₂ mapping population was assembled using the parents of hybrid Lumianyan 15(613 and R55) to construct a genetic linkage map with SSR markers using JoinMap 3.0 software. The QTLs for fiber quality properties in three F_{2:3} subpopulations were mapped by the composite interval mapping method. A genetic linkage map included 116 SSR loci and 25 linkage groups, covering 892.25 cM and accounting for 20.05% of the cotton genome. The average number of markers per linkage group was 4.64 and the average distance of markers was 7.76 cM. A total of 19 groups were anchored to the chromosomes based on the results of previous studies. Based on data analyses, 46 QTLs were identified in three F_{2:3} subpopulations, including 16 QTLs for fiber length, 7 for fiber strength, 12 for fiber micronaire, 6 for fiber elongation, and 5 for fiber uniformity. Some QTLs were clustered on chromosomes A_n05, A_n08, A_n09, and D_n02. The results revealed that some QTLs could be stably inherited and durable in different environments among the three subpopulations. These QTLs can be used for molecular breeding of fiber quality traits in cotton.

Keywords: upland cotton fiber quality QTL mapping Lumianyan15

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