研究论文

利用重组自交系进行陆地棉产量及产量构成因子性状的QTL定位

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摘要

以高产陆地棉栽培品种中棉所12和8891的杂交组合湘杂棉2号为材料，采用单粒传法构建了含有180个家系的重组自交系(RILs)群体。本研究的目的是分析产量及其构成因子的相互关系并进行相应的QTL定位。重组自交系群体、两亲本和F1于2002年、2003年分别种植于南京农业大学江浦实验农场和江苏省灌云棉花基地。收获每行中间五株的籽棉并考察产量及产量构成因子性状。调查的产量及产量构成因子性状包括单株籽棉产量、单株皮棉产量、单株铃数、铃重、衣分、衣指和籽指。筛选了4,106对SSR引物和384个AFLP引物组合，分别得到127和18个多态位点；此外，2个RAPD引物、1个SRAP引物组合以及来自亲本8891的显性黄花药基因P1也被用来作为标记检测群体基因型。最终共获得149个多态位点，其中132个位点分布于26个染色体/连锁群，覆盖865.20 cM，约占棉花基因组的18.57%，标记间平均距离6.55 cM。利用此遗传图谱结合重组自交系群体3个环境下的产量及产量构成因子性状，应用QTL Cartographer 2.0的复合区间作图法进行单位点QTL定位。对各环境资料的分离分析共定位出34个QTL，而利用三环境平均值的联合分析定位出15个QTL。本研究定位的QTL可为棉花产量育种提供信息，其中衣分QTLqLP-A10-1在联合分析及分离分析下的两个环境都能检测到，可能对标记辅助选择有实际应用价值。通径分析结果表明，各产量构成因子中，铃数对皮棉产量贡献最大，这与产量构成因素性状在F1的杂种优势表现一致；因此，在棉花育种上，可优先考虑单株铃数并结合其它产量构成因素进行品种选育和杂交组合选配。

关键词　数量性状基因定位；产量及产量构成因子；重组自交系；棉花育种
分类号

QTL Mapping of Yield and Yield Components for Elite Hybrid Derived-RILs in Upland Cotton

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Abstract

<P>A population of 180 recombinant inbred lines (RILs) was developed by single seed descended from the cross of high yield Upland cotton (Gossypium hirsutum L.) varieties Zhongmiansuo12 (ZMS12) and 8891, the two parents of Xiangzamian2 (XZM2). A genetic linkage map consisting of 132 loci and covering 865.20 cM was constructed using the RIL population chiefly with SSR markers. Yield and yield components were investigated for RILs in three environments in China. The purpose of the present research was to analyze the relationship between yield and its components and to map QTL for yield and yield components in cotton. QTL were tagged with data

sets from single environment (separate analysis) and a set of data from means of the three environments (joint analysis). A total of 34 QTL for yield and yield components were independently detected in three environments, whereas fifteen QTL were found in joint analysis. Notably, a stable lint percentage QTL qLP-A10-1 was detected both in joint analysis and in two environments of separate analysis, which might be of special value for marker-assisted selection. The QTL detected in the present study provide new information on improving yield and yield components. Results of path analysis showed that bolls/plant had the largest contribution to lint yield, which is consistent with the mid-parent heterosis value in F1. Accordingly, in cotton breeding, bolls/plant can be considered first and other yield components measured as a whole to implement variety enhancement and hybrid selection of cotton.</P>

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