

陆地棉重组近交系产量及其构成因素的QTL分析

张伟¹, 刘方¹, 黎绍惠¹, 王为^{1,2}, 王春英¹, 张香娣¹, 王玉红¹, 宋国立¹, 王坤波^{1,*}

1 中国农业科学院棉花研究所 / 农业部棉花遗传改良重点实验室, 河南安阳455000; 2 江苏沿海地区农业科学研究所, 江苏盐城224002

QTL Analysis on Yield and Its Components in Upland Cotton RIL

ZHANG Wei¹, LIU Fang¹, LI Shao-Hui¹, WANG Wei^{1,2}, WANG Chun-Ying¹, ZHANG Xiang-Di¹, WANG Yu-Hong¹, SONG Guo-Li¹, WANG Kun-Bo^{1,*}

1 Cotton Research Institute, Chinese Academy of Agricultural Sciences / Key Laboratory of Cotton Genetic Improvement, Ministry of Agriculture, Anyang 455000, China; 2 Agricultural Sciences Research Institute of Coastal Region of Jiangsu, Yancheng 224002, China

摘要

参考文献

相关文章

Download: [PDF \(275KB\)](#) [HTML 1KB](#) Export: [BibTeX](#) or [EndNote \(RIS\)](#) [Supporting Info](#)

摘要 利用爱字棉1517×德州047重组近交系(recombinant inbred lines, RIL)中G6群体构建的SSR遗传连锁图谱及基于混合线性模型的复合区间作图法对QTL进行定位, 并对主效QTL, 加性×加性上位性QTL及与环境互作效应进行分析, 为利用分子聚合方法提高产量提供理论依据。对2006年、2008年以及2009年的产量性状进行分离分析, 检测到24个不同年份的主效QTL, 其中相关于单株籽棉、单株皮棉、衣分、子指以及单株铃数的分别检测到1个不同年份稳定存在的主效QTL; 对3年的产量性状作环境因子联合分析, 检测到14个主效QTL, 其中6个与环境互作, 检测到20对加加上位性QTL, 其中7对与环境互作。不同年份检测的稳定且受环境影响小或不受环境影响的与近处标记紧密连锁的主效QTL可用于分子标记辅助选择, 以提高育种的效率。

关键词: 陆地棉 重组自交系 产量性状 主效QTL 上位性QTL Q×E效应

Abstract: The genetic linkage map of SSR, constructed by mixed linear model composite interval mapping with CRI-G6 (Acala 1517 × Dezhou 047) population was used to detect and localize QTLs, including main-effect QTLs, epistasis QTLs and Q×E interaction effects in order to provide information applicable to cotton MAS (molecular marker assisted selection breeding). In a separate analysis, 24 major QTLs for yield traits were identified in the three different years. Each stable major QTL was detected for seed yield, lint yield, lint percentage, seed index and bolls per plant, respectively. Fourteen main-effect QTLs and 20 pairs of additive-additiveepistasis QTLs were detected by joint analysis in three years, among them six main-effect QTLs and seven pairs of additive-additive epistasis QTLs interacted with environments. These stable main-effect QTLs with a large effect (accounting for over 10% of phenotypic variation), which were scanned in different years and linked closely with markers, can be used for MAS in high-yield breeding program.

Keywords: Upland Cotton Recombinant inbred line Yield trait Main-effect QTL Epitasis QTL QTL × Environment interaction effect

Received 2010-06-18; published 2011-01-17

Fund:

本研究由国家高技术研究发展计划(863计划)(2009AA101104)和国家重点基础研究发展计划(973计划)(2010CB126000)资助。

引用本文:

张伟, 刘方, 黎绍惠, 王为, 王春英, 张香娣, 王玉红, 宋国立, 王坤波. 陆地棉重组近交系产量及其构成因素的QTL分析[J] 作物学报, 2011, V37(03): 433-442

ZHANG Wei, LIU Fang, LI Chao-Hui, WANG Wei, WANG Chun-Yang, ZHANG Xiang-Di, WANG Yu-Gong, SONG Guo-Li, WANG Kun-Bei. QTL Analysis on Yield and Its Components in Upland Cotton RIL[J] Acta Agron Sin, 2011, V37(03): 433-442

链接本文:

<http://211.155.251.148:8080/zwx/CN/10.3724/SP.J.1006.2011.00433> 或 <http://211.155.251.148:8080/zwx/CN/Y2011/V37/I03/433>

Service

- ▶ [把本文推荐给朋友](#)
- ▶ [加入我的书架](#)
- ▶ [加入引用管理器](#)
- ▶ [Email Alert](#)
- ▶ [RSS](#)

作者相关文章

- ▶ [张伟](#)
- ▶ [刘方](#)
- ▶ [黎绍惠](#)
- ▶ [王为](#)
- ▶ [王春英](#)
- ▶ [张香娣](#)
- ▶ [王玉红](#)
- ▶ [宋国立](#)
- ▶ [王坤波](#)