

研究报告

玉米雄穗分枝数与主轴长的QTL鉴定

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收稿日期 2006-11-27 修回日期 2007-1-12 网络版发布日期 2007-7-23 接受日期

摘要

在包含103个SSR标记的连锁图谱基础上, 运用复合区间作图法检测玉米组合(N87-1×9526)F3家系在正常与干旱胁迫环境下的雄穗分枝数与主轴长性状QTL。雄穗分枝数在正常环境下被检测到2个QTL座位, 分别位于第5和7连锁群上; 在胁迫环境下被检测到4个QTL座位分别位于 2、5、7和10连锁群上, 其中位于第5和7连锁群上的QTL不仅具有一致性而且与本作图群体中曾检测到的耐旱相关性状QTL存在连锁。雄穗主轴长在正常环境下被检测到2个QTL位于第2和第6连锁群上, 在干旱胁迫环境下被检测到了3个QTL分别于第2、4和10连锁群上, 其中位于第2染色体上的QTL是两种环境下所共同检测到的QTL。分析QTL的遗传作用方式表明, 雄穗分枝数以部分加性效应为主, 而雄穗主轴长全部表现为显性和超显性。

关键词 [玉米](#) [雄穗分枝数](#) [雄穗主轴长](#) [数量性状座位](#)

分类号

Identification of QTL associated with tassel branch number and total tassel length in maize

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Abstract

<P>On the basis of 103 SSR linkage map, QTLs associated with tassel branch number (TBN) and total tassel length (TTL) were studied by composite interval mapping with F3 families, which were developed from the cross N87-1 × 9526 and surveyed for phenotype under normal condition (CK) and drought-stress environment (DS). Four QTLs on chromosomes 2, 5, 7, and 10, respectively, were associated with TBN under DS, two of which were not only repeatedly detected on chromosomes 5 and 7 under the CK but also were linked to some QTLs related to drought tolerance that had already been reported in the same mapping population. The two QTLs controlling TTL were identified on chromosomes 2 and 6 under CK, while three QTLs for TTL were detected on chromosomes 2, 4, and 10 under DS. The QTL on chromosome 2 for TTL was consistent under two environments. Most of QTLs for TBN were partial additive while QTLs for TTL were dominant and over-dominant in terms of gene action.</P>

Key words [maize \(Zea mays L.\)](#) [tassel branch number](#) [total tassel length](#) [quantitative trait loci](#)

DOI:

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