

研究论文

不同生态环境下玉米产量性状QTL分析

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摘要 以玉米 (*Zea mays* L.) 自交系黄早四和Mo17为亲本得到的191个F2单株为作图群体, 衍生的184个F2 : 3家系作为性状评价群体, 分析了单株穗数、穗行数、行粒数、百粒重和单株籽粒产量在北京和新疆2个生态环境下的表现和数量性状基因位点的定位结果。QTL检测结果表明, 2个环境共检测出47个QTL, 分布于除第10染色体以外的9条染色体, 其中与单株穗数相关的QTL共10个, 可解释的表型变异为5.3%~25.6%; 与穗行数相关的QTL共13个, 可解释的表型变异为4.5%~23.2%; 与行粒数相关的QTL有9个, 解释的表型变异为5.4%~13.7%; 与百粒重相关的QTL达10个, 可解释的表型变异为4.9%~13.3%; 与单株籽粒产量相关的QTL有5个, 可解释的表型变异为6.1%~35.8%。大部分产量QTL只在单一环境下被检测到, 说明产量相关QTL与环境之间存在明显的互作。表型相关显著的产量性状, 它们的QTL容易在相同或相邻标记区间检测到。研究还发现了若干个QTL富集区域, 可能是发掘通用QTL的候选位点。

关键词 [玉米](#) [产量性状](#) [环境](#) [数量性状位点](#)

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QTL Analysis of Yield Components in Maize under Different Environments

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Abstract Maize (*Zea mays* L.) is one of the crops studied widely by QTL mapping. There are a lot of reports about QTL for important traits, including yield components, plant height, grain moisture and growth data and so on. Thereinto, grain yield is a very complicated quantitative trait, existing interactions not only with gene by gene, but also gene by environment. Studying the relationship of the interaction between genes and environments and finding the yield QTL expressed in given environment are of importance in practice for cultivating new varieties adapting to some area. If consensus QTL of yield and its adjacent marker can be found, it will provide possibility for molecular breeding by marker assisted selection (MAS). The objective of this experiment was to analysis the expression character of QTL controlling yield, and to detect common genetic loci of yield, as well as adjacent marker, in different environment, which could provide technical basis for fine mapping of yield QTL and MAS. One hundred and ninety-one F2 individuals derived from the cross, Mo17 × Huangzao4, were genotyped by SSR and AFLP markers to construct the genetic linkage map, and 184 corresponding F2 : 3 families were phenotyped for maize yield components in Beijing and Xinjiang. The performance and correlations among 5 yield components including ears per plant (EPP), row number per ear (RN), kernel number per row (KR), 100-kernel weight (KW) and grain yield per plant (GY) were evaluated, and the quantitative trait loci (QTL) were characterized. Totally, 47 QTLs were identified for 5 traits, locating on 9 chromosomes with exception of the chromosome 10. 10, 13, 9, 10 and 5 QTLs were detected for EPP, RN, KR, KW and GY, respectively. Each of these QTLs could explain 5.3% to 25.6% phenotypic variation of EPP, 4.5% to 23.2% of RN, 5.4% to 13.7% of KR, 4.9% to 13.3% of KW and 6.1% to 35.8% of GY. Most of the QTLs are detected in single environment, indicating the significant interactions between QTL and environments. Different QTLs relevant to the yield components which are correlated each other can be identified easily in the same or adjacent chromosome regions. Several regions with clustered QTLs relevant to multiple yield components identified in the study may provide the genetic loci of the universal yield QTLs.

Key words [Zea mays L.](#) [Yield components](#) [Environment](#) [Quantitative trait loci](#)

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