研究论文

玉米抗穗粒腐病QTL定位

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用已构建的包括88个AFLP标记和151个SSR标记的遗传图谱和230个F2植株用于抗病QTL定位研究,在四 川雅安、绵阳对F2株系进行抗病性鉴定,采用复合区间定位法进行抗病QTL检测。在雅安检测到位于第2、3、 4、6和9染色体上的抗病QTL 6个,解释表型变异的8.3%~25.7%;在绵阳检测到位于第1、6、7和9染色体上的抗病 QTL 4个,解释表型变异的11.3%~26.4%。在10个抗病QTL中,位于第6和第9染色体上的2个同时在两点被检测 到,贡献率均超过15%,表明玉米穗粒腐病确实存在遗传抗病性。利用2个环境抗病指数的平均值进行抗性 QTL 检 测,共检测到位于第1、6和7连锁群上的3个抗性QTL,单个QTL的贡献率在8.9%~17.2%之间。结果有助于了解玉 米穗粒腐病的抗性机制,并为分子标记辅助选择提供理论支撑。

穗粒腐病 SSR AFLP QTL定位 玉米 关键词 分类号

Molecular Mapping of QTL for Resistance to Maize Ear Rot Caused by Fus arium moniliforme

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Abstract Maize ear rot, mainly caused by Fusarium moniliforme, is one of the most destructive diseases of maize in the w orld. Infected maize is lower yielding and contains toxins that are dangerous to livestock and human. The aims of this study were to identify quantitative trait loci (QTL) associated with genetic resistance to F. moniliforme, their positions and effect s in the maize genome; investigate the consistency of QTL across two environments and their utilization in a marker-assiste d selection programme. A previous genetic map containing 88 AFLP and 151 microsatellite markers and 230 F2 plants were used for QTL mapping in Maize. QTL analysis was performed using joint composite interval mapping. In Ya' an, six QT L conferring Fusarium moniliforme ear rot resistance on chromosomes 2, 3, 4, 6, and 9 were detected and explained 8.3% – 25.7 % of the phenotypic variance; while in Mianyang, four QTL were identified on chromosomes 1, 6, 7, and 9 that accou nted for 11.3% - 26.4% of the total phenotypic variance. Two QTLs on chromosomes 6 and 9 were identified consistently in both environments, which revealed that resistance to F. moniliforme was determined by genetic factors. Three QTLs on c hromosomes 1, 6 and 7 that accounted for 8.9% - 17.2% of the total phenotypic variance were detected using the mean resi

stant disease index of two locations. QTL mapping results will be helpful to further understand genetic basis of ear rot resis

Key words Maize (Zea mays L.) Ear rot SSR AFLP QTL mapping

tance in maize and lay a basis for marker-assisted selection for the resistance species.

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