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基于RIL群体的玉米纹枯病抗性QTL分析

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摘要：

利用包含339个家系的重组自交系(RIL)群体为定位群体,构建包含133个SSR标记的遗传连锁图谱,覆盖玉米基因组1658cM,标记平均距离为12.56cM。分别于2008年四川雅安和2009年四川雅安、绵阳和重庆3地,采用麦粒嵌入法人工接菌,于接菌后15d调查以上4点各个家系的病斑高和穗位高,接菌后40天对重庆和绵阳再进行第2次调查,并计算相应各时间段和各地点的病情指数。研究结果共检测到基于病斑高的抗性相关QTL 7个,分别位于6、8、9和10染色体上,平均加性效应和贡献率分别为1.61%和4.52%;检测到基于病情指数的抗性相关QTL 11个,分别位于2、4、5、8和9染色体上,加性效应和可解释表型方差大小分别在0.0165~0.0545和2.81%~7.29%之间。其中,利用病情指数和病斑高在标记区间bnlg1583-dupssr06和bnlg1714-umc2343共同检测到了抗性相关QTL。以上结果为今后开展玉米抗纹枯病的精细定位和分子标记辅助育种奠定了一定的理论和材料基础。

关键词： 玉米　纹枯病　SSR标记　QTL定位

QTL Analysis of Resistance to Banded Leaf and Sheath Blight Based on Maize RIL Population

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Abstract:

Banded leaf and sheath blight (BLSB) is one of the most serious disease around the world, and it is also a disaster disease in southwest of China because of high temperature and humidity, which cause great loss to corn yield and quality. A set of 339 maize recombinant inbred lines (RIL) derived from the cross R15(resistance) by ye478(susceptible) were planted, and the lesion height and ear height were evaluated at the following four enviroments, 2008 in Yaan, 2009 in Yaan, Mianyang and Chongqing of China. The data came from twice investigations which the first one was carried out at the fifteenth day after inoculation through wheat seeds in the fore four environments, and the second investigation at the fortieth day only in the later two environments. A genetic linkage map comprising 133 SSR markers were constructed through the software MAPMAKER version 3.0b based on the recombination, it covered 1658 cM on the 10 maize chromosomes, the average distance between two near markers were 12.56 cM. Compared with the SSR bin map, all markers on 10 chromosomes were arranged in the same order. Using the composite interval mapping method, 7 QTLs related to resistance to BLSB were detected based on lesion height, they were distributed on chromosome 6, 8, 9, and 10, the average value of additive effects and contributions to phenotypic variances were 1.61% and 4.52% respectively; Based on disease index, 11 QTLs relevant to BLSB resistance were mapped on chromosome 2, 4, 5, 8 and 9 through the same method, the range of additive effects and contributions to phenotypic variances were 0.0165~0.0545 and 2.81%~7.29% respectively. Especially, based both on lesion height and disease index, the two intervals bnlg1583-dupssr06 and bnlg1714-umc2343 were identified with resistant QTLs, and this were consistent with the previous results of our team, these intervals may point to potential targets for marker aided selection and fine mapping in maize.

Keywords: Maize　Bande leaf and sheath blight　SSR marker　QTL

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