

研究论文

## 玉米抗丝黑穗病QTL分析

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**摘要** 以Mo17(抗)×黄早四(感)的F2分离群体(191个单株)为作图群体, 构建了含有84个SSR位点和48个AFLP位点的遗传连锁图谱, 全长1 542.9 cM, 平均图距11.7 cM。在吉林省公主岭和黑龙江省哈尔滨2个地点通过人工接种方法对184个相应的F3家系(缺失7个)进行抗病鉴定。采用复合区间作图法对抗丝黑穗病数量性状位点(QTL)进行定位及遗传效应分析。在吉林公主岭地区检测到5个QTL, 分别位于第1、2、3、8、9染色体上, 解释的表型方差为10.0%~16.3%。在黑龙江哈尔滨地区也检测到5个QTL, 分别位于第1、2、3、4、7染色体上, 解释的表型方差为4.6%~13.4%。比较分析发现, 两地一致在第2、3染色体上各检测到1个QTL, 其中第2染色体上的表现为超显性效应, 第3染色体上的表现为加性效应。研究结果为玉米抗丝黑穗病种质改良提供了重要信息。

**关键词** [玉米](#) [玉米丝黑穗病](#) [抗性遗传](#) [数量性状位点](#) [分子标记](#)

分类号 [S513](#)

## QTL Identification of Resistance to Head Smut in Maize

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**Abstract** Head smut of maize (*Zea mays* L.) caused by *Sporisorium reilianum* is an important fungal disease in China. Development of varieties resistant to this disease is one of the effective approaches to control the disease. In this study, we mapped and characterized quantitative trait loci (QTL) conferring resistance to head smut. A genetic linkage map with 84 SSR and 48 AFLP marker loci were constructed based on a maize (*Zea mays* L.) population consisting of 191 F2 individuals from the cross Mo17×Huangzao4. The linkage map spans maize genome 1 542.9 cM with average interval of 11.7 cM between adjacent markers. The corresponding 184 F3 families (7 missed) were evaluated for head smut resistance with two replications in Gongzhuling, Jilin province and Harbin, Heilongjiang province under artificial inoculation with chlamydospore, respectively. Quantitative trait loci (QTL) were detected using composite interval mapping. In Gongzhuling, 5 putative QTL conferring resistance to head smut were detected on chromosomes 1, 2, 3, 8 and 9, respectively, accounting for 10.0% to 16.3% of the phenotypic variance. In Harbin, 5 putative QTL for resistance to head smut were found on chromosomes 1, 2, 3, 4 and 7, respectively, accounting for 4.6% to 13.4% of the phenotypic variance. The QTL with high LR values could be consistently identified on chromosomes 2 and 3 over two environments, displaying over-dominant and additive effects, respectively. These results provided important information for germplasm improvement of head smut resistance in maize.

**Key words** [Zea mays L.](#) [Head smut](#) [Resistance inheritance](#) [Quantitative trait loci](#) [Molecular marker](#)

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