

研究论文

小麦赤霉病抗性QTL分析

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摘要 以小麦赤霉病抗源望水白与感病品种Alondra杂交产生的104个重组自交系为材料, 采用JoinMap@3.0软件构建了含有2个RAPD、109个SSR和105个AFLP标记共25个连锁群的遗传连锁图, 其中24个连锁群可以确定为相应的染色体; 采用自然发病和土表接种方法, 对该重组自交系群体在建阳和苏州进行了连续两年赤霉病抗性鉴定, 结果表明: 小麦赤霉病抗性由多基因控制, 存在主基因效应, 抗病基因表达受环境条件影响较大。用MapQTL@4.0软件进行了赤霉病抗性QTL分析, 共检测到位于染色体2A、3B、4A、4D、5A、5B、6A、6B和7A的10个QTL, 其中8个由抗病亲本望水白提供, 2个由感病亲本Alondra提供, 分别可以解释8.3%~23.6%的赤霉病抗性。与赤霉病抗性QTL紧密连锁的两侧分子标记可以为小麦抗赤霉病分子辅助育种提供帮助。

关键词 [小麦](#) [赤霉病](#) [QTL](#)

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Analysis of QTL for Fusarium Head Blight Resistance in Wheat

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Abstract With the population of 104 F7-derived recombinant inbred (RI) lines from Wangshuibai (resistance to Fusarium head blight) and Alondra (Susceptible) as mapping population, the wheat genetic map consisting of 2 RAPDs, 109 SSRs and 105 AFLPs markers was constructed by JoinMap@3.0 software. Up to 24 of the 25 identified linkage groups were identified to the chromosome. The FHB resistance of RI lines was evaluated by natural infection and soil surface inoculation in Jianyang and Suzhou for two years. The results showed that resistance to FHB was inherited in a quantitative manner and controlled by few genes with major effects, but the expression of these resistance genes were strongly affected by environment. 10 QTLs, 8 derived from Wangshuibai and 2 from Alondra, associated with FHB resistance were detected using MapQTL@4.0 software. They were located on the chromosomes 2A, 3B, 4A, 4D, 5A, 5B, 6A, 6B, 7A and explained 8.3%—23.6% of the phenotypic variance for FHB resistance respectively. It is suggested that the flanking markers of QTL may be used in the breeding for resistance to FHB by marker-assisted selection.

Key words [Wheat](#) [Fusarium head blight](#) [QTL](#)

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