

研究论文

小麦白粉病抗性QTL分析

霍纳新, 周荣华, 张丽芳, 贾继增

中国农科院品种资源研究所/农业部作物种质资源与生物技术重点实验室, 北京100081

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摘要 本研究以国际小麦作图组织提供的(W7984×Opata85)重组近交群体为材料, 2001—2002年对其亲本和114个株系进行了人工接种条件下的抗白粉病鉴定, 并利用基于混合线性模型的复合区间作图软件QTLMAPER, 进行了抗白粉病QTL分析, 共检测到3个与小麦白粉病抗性相关的加性QTL, 分别位于3B、5D、7D染色体上, 可以解释42.8%的表型变异。其中位于7D染色体的QTL贡献最大, 可解释抗性变异的29.6%。另有2对互作基因可以解释12.0%的表型变异。

关键词 [小麦](#) [白粉病](#) [QTL](#)

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Mapping Quantitative Trait Loci for Powdery Mildew Resistance in Wheat

HUO Na-Xin, ZHOU Rong-Hua, ZHANG Li-Fang, JIA Ji-Zeng

Key Laboratory of Crop Germplasm & Biotechnology, Ministry of Agriculture; Institute of Crop Germplasm Resources, Chinese Academy of Agricultural Sciences, Beijing 100081

Abstract Powdery mildew is one of the serious diseases of wheat in the world. The attempt to control powdery mildew with major resistance genes has not provided a durable resistance. Breeding for quantitative resistance to the disease is more promising, but is difficult to select on a phenotypic basis. Molecular markers linked with QTLs for adult-plant resistance offer the possibility of marker-assisted selection for quantitative resistance. In this study, a population of 114 RIL lines from the cross of (W7984×Opata85) was evaluated for powdery mildew resistance under inoculation condition during 2001—2002. The genetic linkage map was gained based on the 938 segregation markers published online. With the method of mixed-model composite interval mapping, three putative QTLs related to powdery mildew resistance were detected in this population, totally accounted for 42.8% of phenotypic variation. The largest and most consistent powdery mildew resistance locus was identified on the short arm of chromosome 7D, accounted for 29.5% phenotypic variation. The resistant effects derived from Opata 85. The other two minor QTLs located on chromosome 3B and 5D, accounted for 7.3% and 5.9% of phenotypic variation, respectively. Analysis indicated that resistant effects derived from Opata 85 and synthetic line W7984. Two digenic interactions associated with this disease were detected in this population, totally accounted for 11.99% of phenotypic variation.

Key words [Wheat](#) [Powdery mildew](#) [QTL](#)

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通讯作者 贾继增 jzjia@mail.caas.net.cn

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