

研究论文

# 利用大麦基因芯片筛选簇毛麦抗白粉病相关基因及其抗病机制的初步研究

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**摘要** 利用大麦基因芯片筛选差异表达基因并结合RT-PCR分析技术, 对簇毛麦的抗白粉病机制进行了初步研究。基因芯片杂交试验获得了抗病簇毛麦非诱导叶片、抗病簇毛麦和感病突变体经白粉菌 (*Blumeria graminis* f. sp. *tritici*) 诱导叶片的基因表达谱。抗病簇毛麦经白粉菌诱导前后的表达谱及RT-PCR分析结果表明, 抗病簇毛麦中乙烯和水杨酸信号途径的部分基因被白粉菌诱导增强表达, 参与了白粉病的抗性过程。另外, 通过比较诱导的抗病簇毛麦与诱导的簇毛麦感病突变体的表达谱并结合RT-PCR分析, 发现感病突变体中乙烯和茉莉酸途径的部分基因被白粉菌诱导表达参与防卫反应, 未观察到水杨酸信号途径参与防卫反应的证据。同时对抗、感簇毛麦经白粉菌诱导不同时间的叶片进行了内源水杨酸含量的测定, 结果表明抗病簇毛麦经白粉菌诱导后水杨酸含量明显上升, 而感病突变体中水杨酸含量始终处于较低水平。由于乙烯信号途径是抗、感簇毛麦中共同的信号途径, 而水杨酸途径只在抗病簇毛麦中参与抗病反应, 所以在簇毛麦的抗病过程中, 水杨酸途径是一种最有效的信号传导途径。还筛选出一批与簇毛麦抗白粉病相关的基因, 包括病程相关蛋白基因、防卫反应基因、转录因子、信号传导因子和抗病基因类似物等。

**关键词** 大麦基因芯片 簇毛麦 信号传导 防卫反应 白粉病

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## Screening Resistant-Related Genes to Powdery Mildew in *Haynaldia villosa* Using Barley Genechip and Studying Its Mechanism of Resistance

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**Abstract** The technologies of genechip microarray combined with RT-PCR were used to investigate the resistance mechanism of *Haynaldia villosa* to the powdery mildew. The transcriptome of uninoculated resistant *H. villosa*, wildtype resistant *H. villosa* and susceptible mutant inoculated with *Blumeria graminis* f. sp. *tritici* were obtained using barley genechip microarray. RT-PCR and comparison of the transcriptome in inoculated and uninoculated resistant *H. villosa* indicated that the genes involved in the salicylic acid and ethylene signal transduction pathways were upregulated by *B. graminis* inoculation in the resistant *H. villosa*. RT-PCR and transcriptome comparison in the inoculated wildtype resistant and susceptible mutant showed that the genes involved in the ethylene and jasmonic acid signal transduction pathways were upregulated by *B. graminis* inoculation in the susceptible mutant *H. villosa*, while the salicylic acid signal transduction pathway was not participated in the process. The endogenous SA concentration of wildtype and susceptible mutant *H. villosa* inoculated for different hours were measured. SA concentration in the resistant *H. villosa* increased dramatically after inoculated with *B. graminis*, while that in the susceptible mutant remained at very low level. Since genes in the ethylene signal pathway were induced in the resistant and mutant *H. villosa* and genes in the salicylic acid signal transduction pathway were induced only in the resistant *H. villosa*, the salicylic acid signal transduction pathway might be the major pathway involved in *H. villosa* resistance to the powdery mildew. Genes involved in the resistance to powdery mildew in the *H. villosa* were also identified, including pathogenesis related protein genes, defense genes, transcription factors, signal transduction components and resistance gene analogs.

**Key words** [Barley genechip](#) [Haynaldia villosa](#) [Signal transduction pathway](#) [Defense response](#) [Powdery mildew](#)

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