

Gene expression analysis of related wheat lines with contrasting levels of head blight resistance after *Fusarium graminearum* inoculation

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Abstract

Eight spring wheat genotypes with contrasting phenotypes for *Fusarium* head blight (FHB) resistance were used in this study: the highly resistant line CM82036, the highly susceptible cultivar Remus, four BC₅F₂ near isogenic lines (NILs) for *Fhb1* and *Qfhs.ifa-5A* and two doubled haploid (DH) lines from a CM82036/Remus mapping population differing in *Fhb1* and *Qfhs.ifa-5A*. At anthesis the flowering heads of the plants were single floret inoculated by *F. graminearum* or water. The inoculated spikelets were harvested at several time points after inoculation and dissected into the generative and vegetative parts for RNA preparation. Differential gene expression was monitored with two complementary methods: 1) cDNA-AFLPs and 2) the Affymetrix wheat

GeneChip. At early time points (8-24 h) after inoculation only few genes were differentially expressed, at later time points (48-72 h) after inoculation an increasing number of differentially expressed transcripts was evident. A comparative analysis of the data on identified candidate genes gained by the two complementary approaches will be presented.

Keywords

cDNA-AFLP, gene expression, microarray, transcriptomics, *Triticum aestivum*

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