

Transcriptomic characterization of *Fusarium* resistance QTL *Fhb1* and *Qfhs-ifa.5A* in wheat near-isogenic lines

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Abstract

Fusarium head blight (FHB) is a devastating disease on wheat leading to severe losses in yields and grain quality. Resistance to the causative fungus *Fusarium graminearum* is constituted by the effect of multiple quantitative trait loci (QTL). In an effort to identify genetic determinants underlying two validated resistance QTL to *F. graminearum* in wheat, *Qfhs.ndus-3BS* (syn. *Fhb1*) and *Qfhs.ifa.5A*, we generated NILs from a cross of the susceptible spring wheat cultivar Remus and the QTL donor line, the highly resistant CM82036, a descendant of Sumai3×Thornbird. Four NILs from a BC5F2 population were selected for the presence of either QTL resulting in NIL1 harboring both QTL, NIL2 (*Fhb1*), NIL3 (*Qfhs.ifa.5A*) and NIL4 (no QTL). We investigated differences in gene expression levels related to treatment, genotype, QTL and time point from three individual replicates using the Affymetrix 44k wheat GeneChip. Probe set contrasts were calculated for *Fusarium* challenged and constitutive expression differences caused by *Fhb1* or *Qfhs-ifa.5A*. In total, we identified 631 transcripts responding to *Fusarium* stress when calculating the average expression change between mock and *Fusarium* inoculated samples of all five investigated genotypes ($P \leq 0.05$, fold change ≥ 2). The vast majority of transcripts (625) were only detected 72 hai, less at 24 hai (48) and only few at 8 hai (18). 322 of the *Fusarium* responsive probe sets were ge-

notype independent and higher expressed in all *Fusarium* infected lines. QTL specific contrasts were calculated by subtracting the *Fusarium* responsive background from NIL4 (no QTL) from the *Fusarium* responsive transcripts observed in single QTL NILs: 72 hai 339 genes were up-regulated in lines lacking the resistance conferred by *Qfhs-ifa.5A* but only one in presence of *Qfhs-ifa.5A*. Ten genes are higher expressed in absence of *Fhb1* and one in presence of *Fhb1*. 54 transcripts exhibit constitutive expression differences for *Fhb1*. Thereof 17 genes are higher expressed in presence of *Fhb1*. Among others these encode for an extensin-like cell wall protein and a wax synthase which may contribute to resistance. 28 genes were constitutively higher and 63 less expressed when comparing only the mock-inoculated samples in genotypes differing in *Qfhs.ifa.5A*. Of 16 probe sets corresponding to defense related genes, we identified three heat shock protein 20 that are significantly more expressed. Among the defense related genes showing the highest fold changes we found a lipid-transfer protein at least 51× higher expressed in the *Qfhs-ifa.5A* lines and a MDR-like ABC transporter, which is a least 2× higher expressed.

Keywords

Affymetrix GeneChip, *Fusarium* head blight, near-isogenic lines, *Triticum aestivum*

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