

Quantitative trait analysis of FHB resistance derived from *Triticum dicoccoides*

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The devastating effect of Fusarium head blight (FHB) caused by *Fusarium graminearum* has led to significant financial losses across the Upper Midwest of the United States. These losses have spurred the need for research in biological, chemical, and genetic control methods for this disease. To date, majority of the research on FHB resistance has concentrated on hexaploid wheat (*Triticum aestivum* L.) lines originating from China. Other sources of resistance to FHB would be desirable. One other source of resistance for both hexaploid wheat and tetraploid durum wheat (*T. turgidum* L var. durum) is the wild tetraploid, *T. turgidum* L. var. *dicoccoides* (*T. dicoccoides*). Previous analysis of the 'Langdon' -*T. dicoccoides* chromosome substitution lines [LDN(Dic)] indicated that the chromosome 3A substitution line expresses moderate levels of resistance to FHB. LDN(Dic-3A) Recombinant Inbred Chromosome Lines (RICL) were used to generate a linkage map of chromosome 3A with 19 molecular markers spanning a distance of 155.2 cM. The individual RICL and controls were screened for their FHB phenotype in two greenhouse seasons. Analysis of 83 RICL identified a single major quantitative trait locus, *Qfhs.ndsu-3AS*, that explains 37% of the phenotypic or 55% of the genetic variation for FHB resistance. A microsatellite locus, *Xgwm2*, is tightly linked to the highest point of the QTL peak. The results of the genotyping show that there is a region from the *T. dicoccoides* parental line spanning *Xmwig14* locus to *Xbcd828* locus present in all of the resistant RICL. This region covers a distance of 29.3 cM spanning both the short and long arms of chromosome 3A and contains *Qfhs.ndsu-3AS*. The top five most resistant lines in the RICL population all contain this region.

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