Identification of Quantitative Trait Loci for Fusarium Head Blight Resistance in a Winter Wheat Population

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U.S. Wheat & Barley Scab Initiative

Introduction

Host plant resistance for Fusarium head blight (FHB) is a primary method to control the devastating losses in wheat. Combining alleles from multiple resistance sources and of multiple resistance types will likely produce cultivars that possess improved resistance. Asian sources of FHB resistance that have the 3BS locus, *Fhb1*, are arguably the most widely used sources in wheat breeding programs worldwide. Resistance sources from Europe have also been identified, such as Arina and Dream. Additionally, in the Eastern U.S. cultivars such as Goldfield, Ernie, Truman, Freedom, and Roan have been identified as having native resistance to FHB (i.e. independent of Asian sources)(5). The objective in our study was to identify quantitative trait loci (QTL) for resistance to FHB in IL97-1828. The Illinois soft red winter wheat line IL97-1828 does not have a known source of FHB resistance in the parentage. Identifying QTL for multiple FHB parameters in IL97-1828 will allow wheat breeders to combine multiple types of resistance to improve host resistance.

Materials and Methods

- Plant material: 242 $F_{5:6}$ recombinant inbred lines (RILs) developed from a cross between the resistant line, IL97-1828 and the susceptible line, Clark.
- Experimental design: randomized complete block design with two replications at a single location (Urbana, IL) in 2009 and at two locations (Urbana, IL and Wooster, OH) in 2010.
- At the Crop Science Research and Education Center in Urbana, IL plots were evaluated for FHB in an inoculated grain spawn and irrigated nursery.
- At the Snyder Farm of the Ohio Agricultural Research and Devlopment Center (OARDC) near Wooster, OH plots were inoculated according to methods described by Sneller et al. (5).
- Plots were evaluated for FHB symptoms approximately one month after heading date as follows:
  - Incidence – estimate of the percentage of infected heads.
  - Severity – mean of the number of infected spikelets per head based on seven heads.
- Fusarium damaged kernels (FDK) percentage was assessed post-harvest as a visual estimate of FDK percentage by comparison to known standards.
- Deoxynivalenol (DON) concentration was quantified by Gas Chromatography – Mass Spectrometry at the University of Minnesota (Dr. Yanhong Dong). DON concentration was not obtained for plots in Wooster, OH.
- FHB index was calculated as follows: (incidence × severity)/100
- ISK index was calculated as follows:
- [(0.3 × incidence) + (0.3 × severity) + (0.4 × FDK)]
- Genotyping:
  - DNA was extracted from lyophilized seedling tissue using a modified CTAB extraction protocol.
  - Quantified and diluted DNA was sent to Triticarte Pty. Ltd. (Cranberra, Australia) for genotyping using DArT markers.
  - A small set of SSR markers were analyzed on the population using polymerase chain reaction (PCR) to amplify marker regions.
- Linkage Map Construction and QTL identification:
  - Joinmap 3.0 (7) with a logarithm of odds (LOD) score of 5.0 was used to construct a linkage map from 214 DArT and 16 SSR markers.
  - Composite interval mapping was done using PLABQTL (6) with a significant LOD threshold of 10% set at 2.7 and 5% at a LOD of 3.0.
- Statistical analysis:
  - Data were analyzed using PROC MIXED of SAS v9.2 (4).
  - PROC UNIVARIATE NORMAL PLOT was used to check residuals for normality and to assess homogeneity of error variance across years and locations

Literature Cited

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7. Van Ooijen, J.W. and R.E. Voorrips. 2001. JoinMap® version 3.0: Software for the calculation of genetic linkage maps. Plant Research International, Wageningen, the Netherlands.

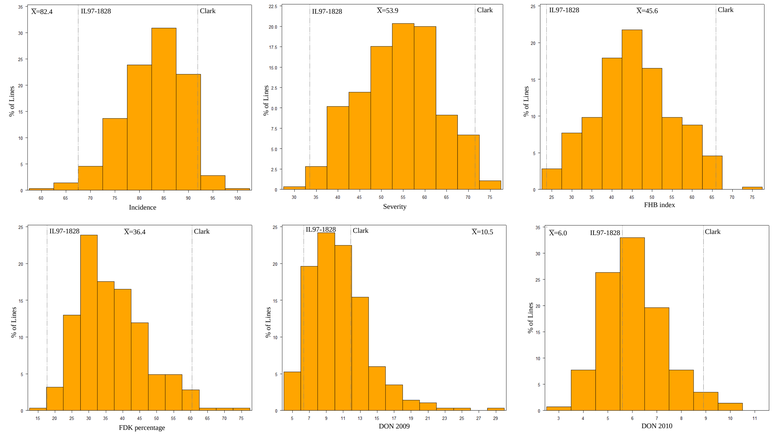

Figure 1. Frequency distributions of 242 wheat recombinant inbred lines developed from a cross between IL97-1828 and Clark for Fusarium head blight incidence, severity, FHB index, and FDK percentage averaged over three environments as well as DON concentration for Urbana, IL in 2009 and 2010.

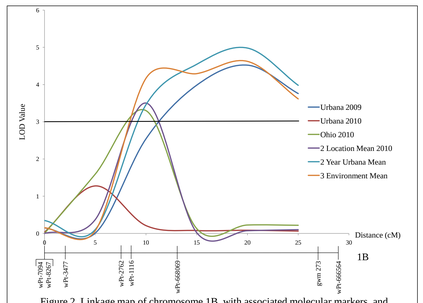

Figure 2. Linkage map of chromosome 1B, with associated molecular markers, and QTL graphs for Type I resistance to FHB.

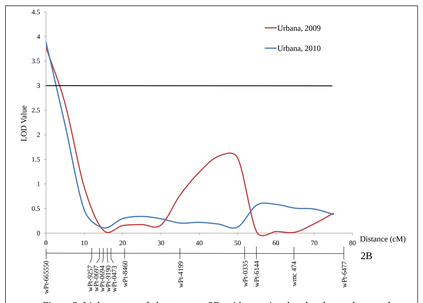

Figure 3. Linkage map of chromosome 2B, with associated molecular markers, and QTL graphs for resistance to DON accumulation.

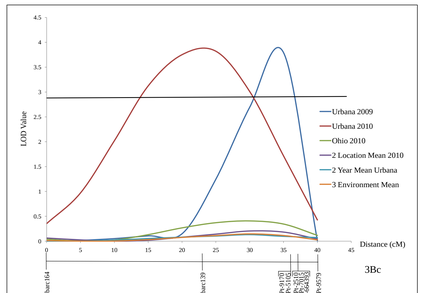

Figure 4. Linkage map of chromosome 3BSc, with associated molecular markers, and QTL graphs for resistance to FDK percentage.

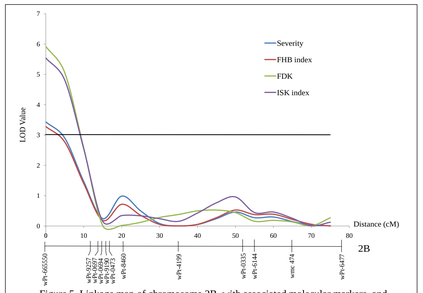

Figure 5. Linkage map of chromosome 2B, with associated molecular markers, and QTL graphs for FHB severity, FHB index, FDK percentage, and ISK index averaged over three environments.

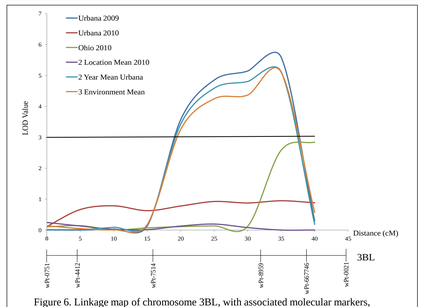

Figure 6. Linkage map of chromosome 3BL, with associated molecular markers, and QTL graphs for resistance to FDK percentage.

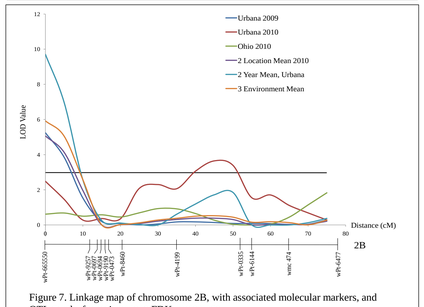

Figure 7. Linkage map of chromosome 2B, with associated molecular markers, and QTL graphs for resistance to FDK percentage.

Disclaimer

Any opinions, findings, conclusions, or recommendations expressed in this publication are those of the authors and do not necessarily reflect the view of the U.S. Department of Agriculture.

Results

- All FHB resistance measurements had broad and continuous phenotypic distribution (Figure 1, ISK index not shown).
- DON concentration was analyzed on an individual year basis because of the heterogeneity of variance across years.
- QTL were identified on six chromosomes: 1A, 1B, 1D, 2B, 3BSc, 3BL, 4A. (Table 1).
- All QTL came from the resistant parent IL97-1828, and were minor explaining between 2.9% and 8.7% of the phenotypic variance.
- No QTL were identified consistently across all environments, and three QTL (1A, 1D, and 4A) were only detected in a single environment for a single parameter.
- Eight additional QTL were significant when dropping the LOD critical value from 3.0 (α=0.05) to 2.7 (α=0.1); however, all of these additional QTL were detected in other environments or for other parameters.
- Two QTL were detected from data collected in Ohio. A single QTL at critical value 3.0 on chromosome 1B was detected for incidence. An additional QTL at critical LOD value of 2.7 was detected on the long arm of chromosome 3B for reduction in FDK percentage.
- Only a single QTL was detected for Type I resistance across all three environments. This QTL, located on chromosome 1B (Fig. 2), explained up to 6.2% of the phenotypic variance.
- A QTL for reduction in DON concentration on 2B was detected for both years in Urbana. This QTL explained 4.5% and 6.5% of the phenotypic variance for 2009 and 2010, respectively. (Fig. 3)
- A region on 2B explained up to 8.67% of the phenotypic variance for FDK percentage (Fig. 7) and the same region explained up to 8.7% of the phenotypic variance for ISK index.
- Two QTL were detected on separate linkage groups that mapped to chromosome 3B. These regions do not appear to be near the 3BS loci of *Fhb 1*. One region appears to be near the centromeric region on 3BS, and the other on the long arm of chromosome of 3B. Both of these regions were significant for reduction in FDK percentage (Figs. 5 and 7).

Conclusions

- All QTL were in similar regions to QTL previously reported (3), indicating these regions are important for FHB resistance in different genetic backgrounds.
- Many QTL identified in this study were coincident with a few FHB resistance parameters. It is unclear whether it is pleiotropy or multiple genes linked at the same loci, but breeders would be able to indirectly select for reductions in other FHB measurements.
- The region on 2B was significant for reduction in FDK and DON concentration. As a result, this region appears important for the prevention of symptoms in IL97-1828. This QTL is potentially coincident with regions previously identified for FDK reduction in Ernie (1), and IL94-1653 (2).
- Further work is needed to confirm these QTL in different genetic backgrounds, and to identify markers closely linked to QTL for use in marker assisted selection.

Table 1. Summary of significant quantitative trait loci (QTL) for Fusarium head blight (FHB) resistance traits in a wheat recombinant inbred line (RIL) population derived from a cross between IL97-1828 and Clark for disease incidence, severity, FHB index, FDK percentage, ISK index, and DON concentration.

			2009 Urbana, IL			2010											
						Urbana, IL			Wooster, OH			2 Loc. Mean			2 Year Urbana, IL Mean		
Trait	Chr†	cM‡	LOD	A§	R²(%)#	LOD	A	R²(%)	LOD	A	R²(%)	LOD	A	R²(%)	LOD	A	R²(%)
Incidence	1B	8.5 - 13.1	4.52*	4.79	4.60	… ¶	…	…	3.30	4.12	3.40	3.50	1.16	4.60	4.98	2.84	5.50
Severity	1B	1.7 - 13.1	…	…	…	3.43	2.84	3.99	…	…	…	3.86	2.46	4.20	2.93††	2.40	3.92
	2B	0.0 - 34.6	4.07	3.40	4.98	4.94	3.41	8.48	…	…	…	…	…	…	2.82	2.06	7.25
	3BL	31.6	2.88	2.98	5.54	…	…	…	…	…	…	…	…	…	3.09	2.23	3.35
	4A	9.8	3.18	2.93	3.84	…	…	…	…	…	…	…	…	…	…	…	…
FHB index	1B	1.7 - 13.1	3.61	3.53	4.80	3.10	2.79	4.31	…	…	…	4.28	2.82	4.80	3.72	2.88	5.85
	2B	0 - 34.6	…	…	…	4.73	3.46	8.01	…	…	…	…	…	…	…	…	…
	3BL	31.6	…	…	…	…	…	…	…	…	…	…	…	…	3.07	2.37	3.05
FDK	1A	2.9	…	…	…	3.62	2.50	4.41	…	…	…	…	…	…	…	…	…
	2B	0 - 34.6	5.24	3.62	6.39	3.65	3.21	5.90	…	…	…	5.06	2.73	4.00	9.71	3.51	8.67
	3BSc	23	3.79	3.16	4.48	3.82	2.52	5.56	…	…	…	…	…	…	…	…	…
	3BL	31.6 - 38.7	5.59	4.05	7.29	…	…	…	2.85	3.50	2.70	2.74	2.14	5.38	5.11	2.67	5.37
ISK index	1B	0.0 - 13.1	…	…	…	2.85	1.44	1.94	…	…	…	2.86	1.53	4.51	3.04	1.86	3.43
	1D	0.0	…	…	…	3.02	3.33	3.53	…	…	…	…	…	…	…	…	…
	2B	0.0 - 34.6	3.62	2.64	6.61	4.64	2.23	7.70	…	…	…	3.75	1.69	5.20	3.86	2.07	7.10
	3BL	31.6	4.82	3.30	7.72	…	…	…	…	…	…	…	…	…	4.85	2.13	5.96
DON	2B	0.0	3.78	0.93	4.50	3.89	0.34	6.50	-‡‡	-	-	-	-	-	-	-	-

			3 Envrionment Mean		
Trait	Chr†	cM‡	LOD	A	R²(%)
Incidence	1B	8.5 - 13.1	4.62	2.14	6.20
Severity	1B	1.7 - 13.1	3.88	2.42	6.76
	2B	0.0 - 34.6	3.43	2.11	6.61
	3BL	31.6	…	…	…
	4A	9.8	…	…	…
FHB index	1B	1.7 - 13.1	4.41	2.82	7.90
	2B	0 - 34.6	3.28	2.25	6.24
	3BL	31.6	…	…	…
FDK	1A	2.9	…	…	…
	2B	0 - 34.6	5.92	2.92	7.43
	3BSc	23	…	…	…
	3BL	31.6 - 38.7	5.10	2.84	7.06
ISK index	1B	0.0 - 13.1	2.77	1.82	4.31
	1D	0.0	…	…	…
	2B	0.0 - 34.6	5.54	2.16	8.70
	3BL	31.6	3.67	1.86	6.66
DON	2B	0.0	-	-	-

† Chromosomal location of linked marker.

‡ Location of the linked markers along the linkage group in centimorgans (cM).

§ The additive effects from the marker at the peak LOD.

Percent phenotypic variance explained by significant QTL.

* Values significant at LOD value 3.0, α=0.05.

¶ At a critical LOD value of 2.7 values were insignificant.

†† Boxed values are significant at LOD value 2.7, α=0.1.

‡‡Values could not be calculated.

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