



# Soft winter wheat responses to two major resistance QTL for Fusarium head blight in F<sub>2</sub> derived populations

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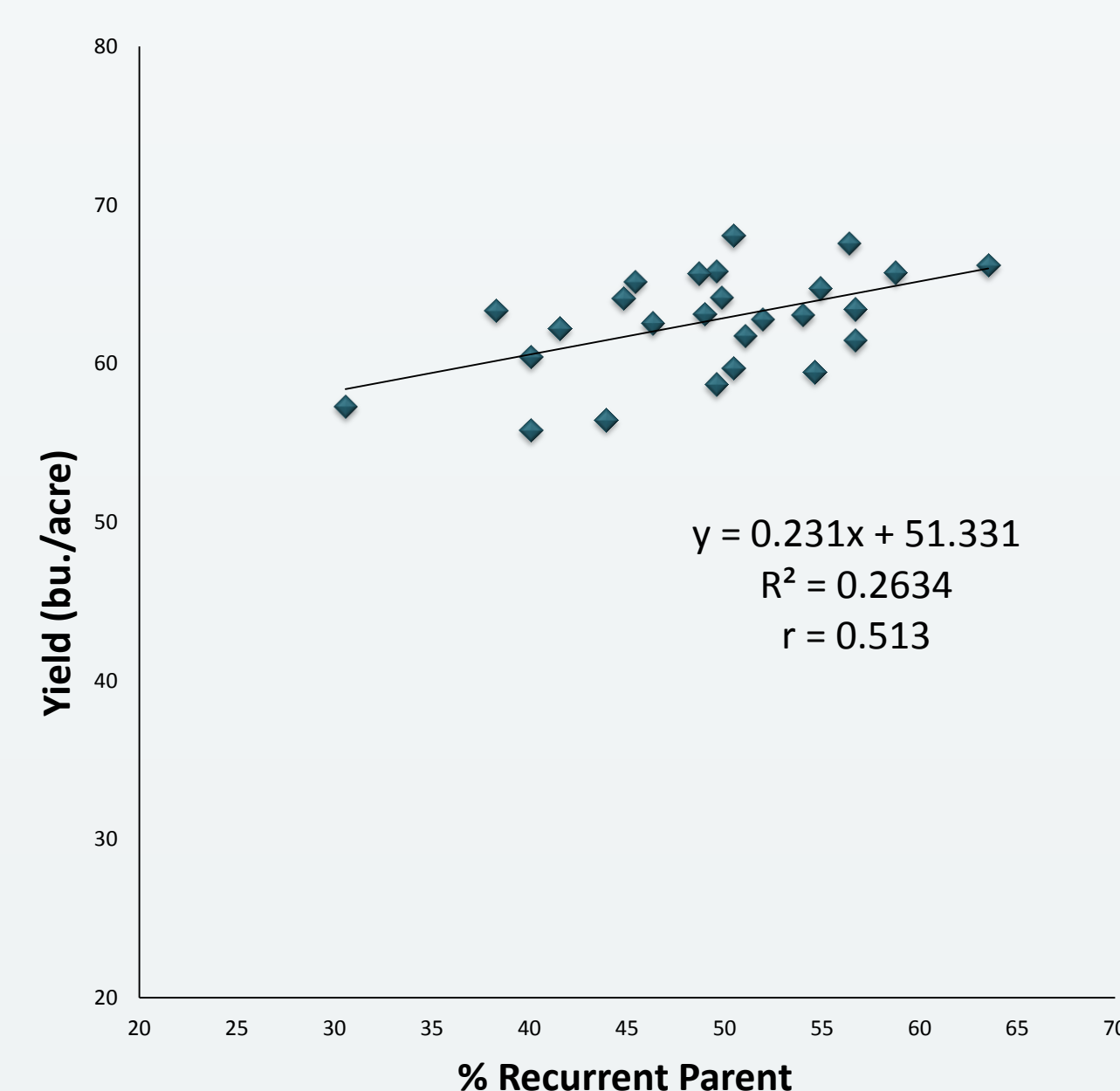
US WHEAT AND BARLEY  
SCAB INITIATIVE

## INTRODUCTION

Fusarium head blight (FHB), caused by *Fusarium graminearum* Schwabe [teleomorph: *Giberella zeae* Schein. (Petch)], is recognized as one of the most destructive diseases of wheat (*Triticum aestivum* L. and *T. durum* L.) and barley (*Hordeum vulgare* L.) worldwide. The influence of *Fhb1* (chromosome 3BS) and *QFhs.nau-2DL* (*2DL*) on FHB resistance in wheat populations was investigated. The utility of F<sub>2</sub> populations as indicators of expression levels of quantitative trait loci (QTL) prior to extensive backcrossing is explored in this study.

## MATERIALS AND METHODS

- F<sub>2</sub> derived lines from crosses between high yielding KY breeding lines to VA01W-476 (two FHB resistance QTL plus native resistance), were genotyped for the presence of resistance alleles of each QTL, *Fhb1* and *2DL*.
- BC<sub>1</sub>F<sub>3</sub> and BC<sub>1</sub>F<sub>4</sub> progeny from seven genetic backgrounds were grown in a 2 rep RCB yield test in Lexington and Princeton, KY, 2011 and 2012.
- BC<sub>2</sub> and BC<sub>3</sub> derived populations were grown in a Augmented Design yield test in Lexington, KY, 2012.
- F<sub>2:3</sub> and F<sub>3:4</sub> were grown in 2-rep RCB in misted, inoculated nursery, Lexington, KY, 2011 and 2012.
- FHB traits: Rating (1-9), Severity, Incidence, FHB Index (Severity \* Incidence), Fusarium damaged kernels (FDK) and deoxynivalenol (DON).
- FDK and DON predicted with Near Infrared Reflectance (NIR, Perten Instruments, DA7200).
- Population 2 lines were screened with 961 Diversity Array Technology (DArT) markers to estimate the percentage of recurrent parent in each backcross derived line (Figure 1).
- Associations with resistance and agronomic traits were analyzed using SAS 9.3. Backcross and F<sub>2</sub> derived progeny were compared for suitability as breeding populations.



**Figure 1.** Relationship between yield and percentage of recurrent parent measured with DArT in population 2, BC<sub>1</sub> derived lines, over 3 environments (2011 and 2012).

**Table 1.** Means for FHB traits evaluated in F<sub>2</sub> derived lines according to the presence of resistance (R) or susceptible (S) alleles at QTL (*Fhb1* and *2DL*), Lexington, KY, 2011 and 2012.

	N	RATING (1-9)	SEVERITY	INCIDENCE	FHBINDEX (%)	FDK	FDKNIR	DONNIR (ppm)	DON (ppm)
<b>POP2 (KY97C-0321-05-2/VA01W476)</b>									
<i>Fhb1</i>	S 154	3.7 NS	33.7 NS	53.6 NS	19.1 NS	16.2 NS	17.9 NS	18.4 NS	11.5 NS
	R 164	3.8	34.7	54.1	20.1	15.8	17.7	18.7	10.7
<i>2DL</i>	S 175	3.8 NS	35.4 *	54.2 NS	20.2 NS	17.0 *	17.6 NS	19.1 *	11.4 NS
	R 143	3.6	32.8	53.5	18.9	14.7	18.1	18.0	10.7
<i>Fhb1+2DL</i>	S 87	3.8 NS	35.5 NS	54.5 NS	20.3 NS	17.2 *	18.0 NS	18.9 *	12.3 NS
	R 76	3.6	34.1	54.5	20.1	14.5	18.1	18.0	10.7
<b>POP3 (KY97C-0519-04-05/VA01W476)</b>									
<i>Fhb1</i>	S 168	3.2 NS	31.8 NS	46.6 NS	17.3 NS	15.9 NS	17.0 **	19.2 **	8.7 **
	R 162	3.2	31.2	45.9	17.1	16.4	16.2	18.1	7.7
<i>2DL</i>	S 182	3.4 **	33.1 NS	49.6 **	18.9 **	18.1 **	17.6 **	20.0 **	8.8 **
	R 148	2.9	29.6	42.2	15.2	13.7	15.5	17.1	7.4
<i>Fhb1+2DL</i>	S 102	3.4 **	33.4 *	51.7 **	19.6 **	17.0 **	18.1 **	20.8 **	9.6 **
	R 82	3.0	29.3	44.7	16.2	13.2	15.2	16.9	7.4
<b>POP4 (KY97C-0540-01-03/VA01W476)</b>									
<i>Fhb1</i>	S 288	3.2 **	28.5 *	43.6 **	14.5 NS	16.2 **	16.1 NS	17.4 NS	9.9 **
	R 249	2.9	31.0	40.9	14.7	13.8	16.6	17.5	8.3
<i>2DL</i>	S 327	3.2 **	31.1 **	43.3 NS	15.3 **	16.8 *	17.3 **	18.6 **	10.1 **
	R 210	2.8	27.5	40.9	13.4	12.5	14.7	15.7	7.8
<i>Fhb1+2DL</i>	S 177	3.4 **	30.7 NS	43.9 **	15.4 NS	18.9 **	17.9 **	19.2 **	11.1 **
	R 100	2.7	29.3	37.7	13.1	12.8	15.8	16.5	7.5
<b>POP6 (KY97C-0508-01-01A/VA01476)</b>									
<i>Fhb1</i>	S 206	3.0 **	25.7 NS	37.5 NS	11.0 NS	17.2 NS	17.8 NS	20.6 NS	9.6 **
	R 170	2.5	27.0	36.7	11.5	15.9	18.0	19.9	7.9
<i>2DL</i>	S 198	2.9 **	28.0 **	38.0 NS	12.2 **	18.8 **	19.1 *	21.7 **	9.7 **
	R 178	2.6	24.4	36.1	10.1	14.3	16.5	18.8	7.8
<i>Fhb1+2DL</i>	S 98	3.2 **	28.1 NS	38.0 NS	12.2 NS	19.8 **	19.5 **	22.6 **	10.9 **
	R 70	2.1	25.6	34.5	10.4	13.1	17.0	18.7	7.0

\*, \*\*: p < 0.05 and 0.01, respectively. NS : not significant.

**Table 2.** Yield and test weight of BC<sub>1</sub> derived lines, over 3 environments (2011 and 2012). † : No seeds produced from this cross.

Population	Pedigree	Statistics	YIELD (bu./acre)			% lines NS different yield from checks		
			BC <sub>1</sub>	BC <sub>2</sub>	BC <sub>3</sub>	BC <sub>1</sub>	BC <sub>2</sub>	BC <sub>3</sub>
1	(KY99C-1051-03-1 / VA01W-476 // KY99C-1051-03-1)	Mean Range CV	61.8 53 - 78 10.6	51.5 48 - 55 6.6	†	19%	50%	†
2	(KY97C-0321-05-2 / KY97C-0321-05-2 / VA01W476)	Mean Range CV	64.8 51 - 81 8.7	73.0 40 - 87 4.4	71.3 49 - 84 9.3	23%	97%	88%
3	(KY97C-0519-04-05 / KY97C-0519-04-05 / VA01W476)	Mean Range CV	51.6 43 - 77 15.1	61.2 41 - 83 8.0	59.4 48 - 66 9.6	22%	81%	91%
4	(KY97C-0540-01-03 / KY97C0540-0103 / VA01W476)	Mean Range CV	58.5 54 - 79 10.6	53.7 43 - 69 4.4	56.1 46 - 67 8.5	13%	50%	72%
5	(KY98C-1446-02-1 / VA01W-476 // KY98C-1446-02-1)	Mean Range CV	56.0 54 - 77 13.0	61.4 52 - 68 4.1	52.6 42 - 69 9.2	42%	83%	54%
6	(KY97C-0508-01-01A / KY97C-0508-01-01A / VA01W476)	Mean Range CV	62.8 58 - 83 13.9	49.2 39 - 61 4.7	48.5 33 - 69 12.0	13%	33%	33%
7	(KY98C-1474-02 / VA01W-476 // KY98C-1474-02)	Mean Range CV	57.4 39 - 79 14.0	63.7 54 - 72 12.7	62.0 54 - 75 11.8	58%	100%	100%



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## RESULTS AND DISCUSSION

- Results suggest that although these lines have a scab resistant parent with poor agronomic performance, one backcross is enough to restore high yield potential (Table 2).
- In BC<sub>1</sub> populations 1 - 7 had 19, 23, 13, 42, 13 and 58 %, respectively, of lines with yields not significantly different (P < 0.05) from the commercial checks used in the experiment.
- BC<sub>2</sub> and BC<sub>3</sub> populations had higher percentages of populations as high yielding as the commercial checks, however, when mean yields are compared, the numbers are very similar among BC<sub>1</sub>, BC<sub>2</sub> and BC<sub>3</sub>.
- R<sup>2</sup> for disease traits in the scab nursery ranged from 46 to 96 %.
- Fhb1* individually reduced FDK in 1 / 4 populations. *2DL* individually reduced FDK in all populations (Table 1).
- Fhb1* + *2DL* significantly reduced DON by 13, 23, 32 and 36% in all populations, respectively.
- Correlations between FDKNIR and actual FDK were 0.38, 0.35, 0.44 and 0.73 for populations 2, 3, 4 and 6, respectively.
- Correlations between DONNIR and DON were 0.55, 0.77, 0.64 and 0.82 for populations 2, 3, 4 and 6, respectively.

## CONCLUSIONS

- F<sub>2</sub> populations should be used for genotyping, ensuring QTL are effective before backcrossing.
- In these 4 backgrounds, *2DL* was more effective than *Fhb1* in reducing FDK, in contrast to Balut (2012), where *Fhb1* was more effective.
- BC<sub>1</sub> populations may be a useful source of breeding lines.

## REFERENCES

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