

# Evaluation of Fusarium Head Blight Resistance QTL on Agronomic and Quality Traits of Soft Red Winter Wheat Populations

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## 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  $F_2$  populations as indicators of expression levels of quantitative trait loci (QTL) prior to extensive backcrossing is explored in this study.

## MATERIALS AND METHODS

Four high yielding FHB susceptible KY breeding lines were crossed with VA01W-476 (two FHB resistance QTL plus native resistance) to generate backcross and forward cross progeny.  $F_2$  individuals were genotyped and analyzed according to resistance alleles of each QTL.

Effectiveness of QTL in reducing FHB in  $F_{2,3}$  lines was assessed in a misted, inoculated scab nursery. Traits measured included Rating (1-9), Severity, Incidence, FHB Index (Severity \* Incidence) and FDK (Fusarium damaged kernels). FDK and DON (deoxynivalenol) were predicted with Near Infrared Reflectance (NIR, Perten Instruments, DA7200). FDKNIR and DONNIR measurements were compared with actual values.

$BC_1F_3$  progeny from four genetic backgrounds were grown in a 2 rep RCB yield test in Lexington, KY, 2011 and 2012. The Solvent Retention Capacity (SRC) and Sedimentation (SDS) tests utilized the ability of whole wheat meal to retain different solvents to evaluate wheat quality including gluten strength. Population 2 lines were screened with 961 Diversity Array Technology (DART) and the results were used to estimate the percentage of recurrent parent in each backcross derived line.

Associations with resistance and agronomic traits were analyzed using SAS 9.3. Backcross and  $F_2$  derived progeny were compared for suitability as breeding populations.

## 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 1).
- Populations 1 to 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.
- $R^2$  for disease traits in the scab nursery ranged from 55 to 77 %.

Table 1. Yield and test weight of  $BC_1F_3$  lines, over 3 environments (2011 and 2012).

Population	Pedigree	Statistics	YIELD	TEST WEIGHT		HEIGHT	Number of lines different yield from checks	%lines NS
				(lb/bu.)	(in)			
1	(KY99C-1051-03-1 / VA01W-476 // KY99C-1051-03-1)	$R^2$ (%)	64.0	99.6	96.5	32	18.8%	
		CV	1.3	5.3				
		Mean	10.6	57.9				
2	(KY97C-0321-05-2 // KY97C-0321-05-2 // VA01W476)	$R^2$ (%)	99.6	97.6	96.8	90	23.3%	
		CV	8.7	2.3	5.0			
		Mean	64.8	57.4	33.4			
3	(KY97C-0519-04-05 // KY97C-0519-04-05 // VA01W476)	$R^2$ (%)	96.4	78.1	93.0	32	21.9%	
		CV	15.1	19.5	6.4			
		Mean	51.6	54.5	31.7			
4	(KY97C-0540-01-03 // KY97C-0540-01-03 // VA01W476)	$R^2$ (%)	93.8	95.3	95.8	90	13.3%	
		CV	10.6	2.3	5.0			
		Mean	58.5	59.1	33.3			
5	(KY98C-1446-02-1 / VA01W-476 // KY98C-1446-02-1)	$R^2$ (%)	91.9	95.5	91.8	36	41.7%	
		CV	13.0	2.6	4.8			
		Mean	56.0	55.7	33.5			
6	(KY97C-0508-01-01 // KY97C-0508-01-01 // VA01W476)	$R^2$ (%)	92.5	74.8	97.4	72	12.5%	
		CV	13.9	9.9	5.1			
		Mean	62.8	58.3	34.0			
7	(KY98C-1474-02 / VA01W-476 // KY98C-1474-02)	$R^2$ (%)	92.5	76.3	94.7	64	57.8%	
		CV	14.0	8.8	6.2			
		Mean	57.4	55.6	34.2			

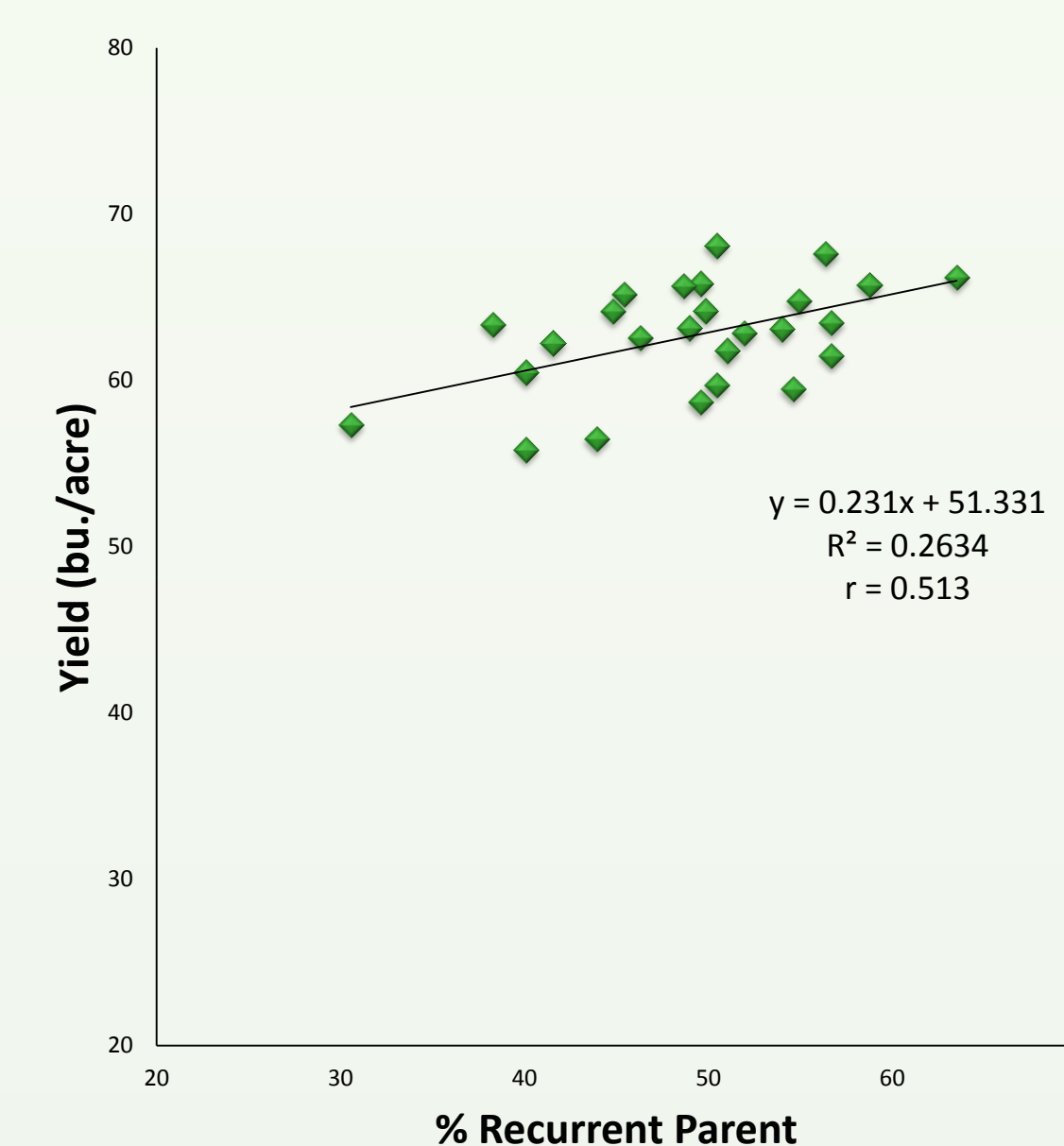


Figure 1. Relationship between yield and percentage of recurrent parent measured with DART in population 2,  $BC_1F_3$  lines, over 3 environments (2011 and 2012).

Table 2. Means for FHB traits evaluated in  $F_{2,3}$  lines according to the presence of resistance (R) or susceptible (S) alleles at QTL (*Fhb1* and *2DL*), Lexington, KY, 2012.

		N	RATING	SEVERITY	INCIDENCE	FHBINDEX	FDK	FDKNIR	DONNIR
			(1-9)	(%)	(%)	(%)	(%)	(ppm)	
<b>POP2 (KY97C-0321-05-2//VA01W476)</b>									
<i>Fhb1</i>	S	112	1.9 *	15.6 NS	31.1 NS	5.5 NS	10.2 *	9.5 NS	14.7 *
	R	78	1.4	16.8	30.1	6.2	9.1	8.8	13.9
<i>2DL</i>	S	92	1.8 *	16.0 NS	31.1 NS	6.0 NS	10.6 *	9.6 NS	14.8 NS
	R	98	1.7	16.1	30.3	5.6	8.9	8.9	14.2
<i>Fhb1+2DL</i>	S	50	1.9 *	15.5 NS	31.0 NS	5.7 NS	10.1 *	10.0 NS	15.4 *
	R	36	1.3	16.9	28.6	6.2	8.1	8.5	13.7
<b>POP3 (KY97C-0519-04-05//VA01W476)</b>									
<i>Fhb1</i>	S	87	2.1 NS	13.5 NS	36.3 NS	5.4 NS	8.3 NS	6.4 NS	10.5 NS
	R	78	2.2	29.0	32.4	7.3	8.6	6.1	10.0
<i>2DL</i>	S	89	2.5 **	27.7 NS	38.7 **	7.8 NS	9.2 **	7.1 **	11.2 **
	R	76	1.8	12.7	29.5	4.4	7.5	5.2	9.2
<i>Fhb1+2DL</i>	S	51	2.5 *	13.8 NS	41.3 *	6.6 NS	8.8 *	7.0 **	11.1 **
	R	40	2.0	14.9	29.8	5.1	7.4	4.8	8.8
<b>POP4 (KY97C-0540-01-03//VA01W476)</b>									
<i>Fhb1</i>	S	160	2.4 **	13.2 NS	36.7 **	5.5 **	7.4 **	6.8 *	11.1 NS
	R	112	1.8	12.2	31.1	4.2	6.3	6.2	10.6
<i>2DL</i>	S	152	2.2 NS	13.2 NS	35.3 NS	5.1 NS	7.6 **	7.0 **	11.7 **
	R	120	2.1	12.4	33.2	4.8	6.1	6.0	9.9
<i>Fhb1+2DL</i>	S	90	2.5 *	13.0 NS	37.1 **	25.0 NS	8.2 **	7.2 **	11.9 **
	R	50	1.8	12.9	29.0	21.7	5.7	5.6	9.5
<b>POP6 (KY97C-0508-01-01//VA01W476)</b>									
<i>Fhb1</i>	S	112	1.9 **	15.6 NS	31.2 NS	5.5 NS	10.2 *	9.5 NS	14.9 **
	R	78	1.4	16.8	30.1	6.3	9.1	8.8	13.9
<i>2DL</i>	S	92	1.8 NS	16.0 NS	31.1 NS	6.0 NS	10.6 **	9.6 NS	14.8 NS
	R	98	1.7	16.1	30.3	5.6	8.9	8.9	14.2
<i>Fhb1+2DL</i>	S	50	1.9 **	15.5 NS	28.6 NS	6.2 NS	11.1 **	28.9 *	30.1 **
	R	36	1.3	17.0	31.0	5.7	8.1	25.1	23.3

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

- Correlation between Wheat meal Flour Protein and Flour Softness Equivalent predicted by NIR was  $-0.33$ . As expected, whole grain NaCO SRC was negatively correlated with Flour Yield ( $r = -0.72$ ). SDS was associated with Lactic Acid SRC (which predicts gluten strength (Guttieri et al 2001), with correlations around  $r = 0.4$  among all 7 populations.
- Fhb1* individually reduced FDK in 3 / 4 populations. *2DL* individually reduced FDK in all populations (Table 2).
- FDK was significantly reduced by the presence of *Fhb1 + 2DL* by 20, 16, 31 and 27 % in populations 2, 3, 4 and 6, respectively. Rating was significantly reduced by the presence of resistance alleles.
- Correlations between FDKNIR and actual FDK were 0.77, 0.67, 0.71 and 0.53 for populations 2, 3, 4 and 6, respectively. Correlations between DONNIR and FDK were 0.74, 0.68, 0.62 and 0.55 for populations 2, 3, 4 and 6, respectively.
- Significant QTL effects on FDK were also detected using NIR in populations 3, 4 and 6.

## CONCLUSIONS

$F_2$  populations should be used for genotyping, ensuring QTL are effective before extensive backcrossing. *Fhb1* and *2DL* often reduced disease and will remain important in our marker-assisted selection. Our preliminary results indicated that  $BC_1$  populations may be a useful source of breeding lines.

## REFERENCES

Guttieri, M.J., Bowen, D., Gannon, D., O'Brien, K., and Souza, E. 2001. Solvent retention capacities of irrigated soft white spring wheat flours. *Crop Sci.* 41:1054-1061.

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