

Creation of Near-Isogenic Wheat Lines for Use in Validating the Effect of a Novel Source of Fusarium Head Blight Resistance

Matt Nelson, Brian Seda, Ed Quirin and Dr. James Anderson
Department of Agronomy and Plant Genetics

Introduction



Fusarium Head Blight, also known as scab, is the most serious disease affecting wheat production in the upper Midwest. Scab is caused by the fungus *Fusarium graminearum*. Scab is the major reason for the dramatic loss of wheat production in the 1990's and is still a major problem today. Therefore, identifying a novel source of genetic resistance in wheat is very important. Dr. James Anderson's lab identified a quantitative trait locus (QTL) region on the long arm of chromosome 3B that appears to be conferring resistance to scab. The purpose of this research is to create near-isogenic wheat lines (NILs) to validate and quantify the effect of the QTL on Fusarium Head Blight infection.

Figure 1: Comparison between a healthy and infected wheat head. The head on the left is healthy while the head on the right is infected by *Fusarium graminearum*, which causes premature bleaching and seed destruction.

Provided by usda.gov

Materials and Methods

- Mapping project by Ed Quirin identified QTL of interest
- Microsatellite marker GWM108 was identified as the most significant marker for this QTL
- QTL validation by NIL's was demonstrated to be effective in Pumphrey *et al.* 2007
- Eleven validation populations were created
 - Recombinant Inbred Lines from the mapping population were selected as resistant parents based upon field resistance scores
 - Moderately susceptible University of Minnesota breeding lines were chosen as the susceptible parents
- Populations were self pollinated to the F₅ generation, and 2772 resulting individuals were grown in Fall 2009 greenhouse
- DNA was extracted at USDA Small Grains Genotyping Lab in Fargo, ND
- DNA fragment sizes were analyzed using polyacrylamide gel electrophoresis

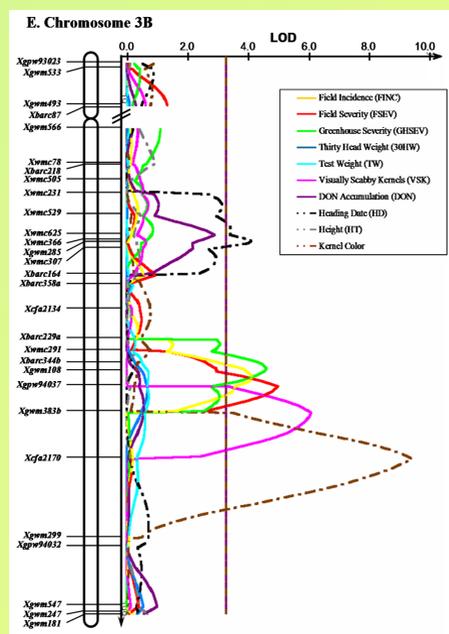


Figure 2: Mapping results showing GWM108 linked to scab resistance QTL on chromosome 3BL.

Provided By Ed Quirin

References

Pumphrey, M., Bernardo, R., & Anderson, J. (2007). Validating the Fhb1 QTL for Fusarium Head Blight Resistance in Near-Isogenic Wheat Lines Developed from Breeding Populations. *Crop Science*, 47(1), 200-206.

Results and Discussion

- Thirty-six families per population and seven individuals per family were grown
- DNA from the individuals was pooled together based on family groups
- Families that were segregating for the marker allele were identified
 - Resistant allele at 192 bp
 - Susceptible allele at 205 bp
- One population (204) was discarded due to monomorphism at the marker locus
- DNA from individuals within segregating families were screened with GWM108
- Heterozygous individuals were selected
- Selected individuals, as shown in table 1, were advanced to the next generation based upon seed quantity and planted in the Spring 2010 greenhouse
- Reduced seed quantity resulted from induced stress due to height constraints

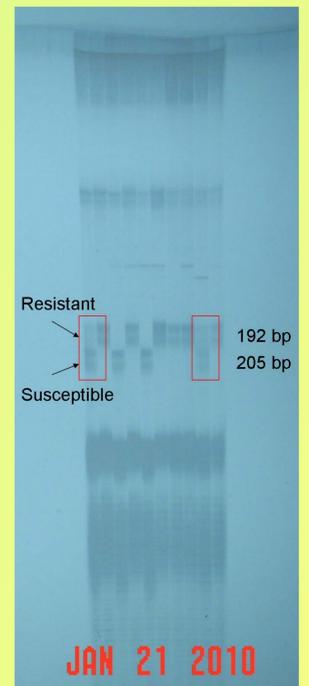


Figure 3: Polyacrylamide gel identifying heterozygotes with both the resistant and susceptible bands.

127	205	206	207	208	209	210	211	253	254
3-4	6-1	11-2	19-5	7-5	12-7	4-5	4-7	1-4	8-6
20-4	18-4	15-2	27-2	7-6	18-5	8-4	18-6	6-2	27-1
30-7	18-5	16-1	30-2	23-5	26-2	8-6	27-2	20-3	27-7
	21-9		30-5	23-6	26-5	19-7	27-3	20-6	
	28-7			28-5	27-7	25-2			
	8-6				28-6	25-7			
	27-1				28-7				
	27-7				34-3				

Table 1: These are selected heterozygous individuals. Bold numbers indicate population. The cells below the population indicate family with first number and individual within family with second number

Future Work

- Screen progeny from heterozygous individuals
- Identify resistant and susceptible homozygous individuals resulting in NIL's
- Conduct field trials to quantify magnitude of resistance imparted by resistant allele

Acknowledgements

I would like to thank: Jennifer Flor, Brian Seda, Ed Quirin, Dr. Anderson, Margaret Krause and Samantha Miller from the Wheat Lab

I would like to thank: Shiaoman Chao from the USDA Lab Undergraduate Research Opportunity Program Grant