Minnesota Wheat Research and Promotion Council
CROP YEAR 2013 RESEARCH REPORTING FORM
Form Due November 15, 2013

1. PROJECT TITLE **Coordinated Effort to Isolate a Fusarium Head Blight Resistance Gene**

2. PRINCIPAL INVESTITAGATOR (S)

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4. REPORT DATE

11/15/13

5. REPORTING PERIOD

1/1/13 – 11/15/13

6. TERMINAL REPORT ___XX_____ **PROGRESS REPORT** _____

7. AMOUNT OF GRANT
$67,000

8. PUBLICATIONS

One publication related to Fusarium head blight:

Schweiger, W., B. Steiner, C. Ametz, G. Siegwart, G. Wiesenberger, F. Berthiller, M. Lemmens, H. Jia, G. Adam, G. Muehlbauer, D. Kreil and H. Buerstmayr. 2013. Transcriptomic characterization of two major Fusarium resistance QTL, *Fhb1* and *Qfhs.ifa-5A*, identify novel candidate genes. Mol. Plant Path. 14:772-785.

9: EXECUTIVE SUMMARY

Research Question:

Fusarium head blight (FHB) is a major disease problem for Minnesota wheat growers. A major resistance gene located on chromosome 3BS referred to as *Fhb1*, exhibits partial resistance to FHB. *Fhb1* has been incorporated into breeding programs and resulted in new varieties with improved resistance. However, the new varieties are still susceptible during a severe FHB epidemic. Unfortunately, the *Fhb1* gene that underlies resistance has not been isolated. We examined expression patterns resulting from wheat lines either carrying either the resistant or susceptible allele for *Fhb1*. Our goals were to either identify the *Fhb1* gene and/or gene expression patterns that are specific to *Fhb1*.

Results:

For all experiments we used two genotypes that were highly similar except they differed in whether they carried the resistant *Fhb1* gene or the susceptible *Fhb1* gene. We sequenced RNA from both genotypes from the following tissues: *F. graminearum*-inoculated spikelet samples at 96 hai; *F. graminearum*-inoculated rachis samples at 96 hai; and DON and water spikelet samples at 12 hai. We generated between 95 – 616 million sequences from the RNA from each tissue/genotype/treatment combination. We reasoned that genes exhibiting differential expression between the genotypes may be either the *Fhb1* gene or genes that are specific to the *Fhb1* response. We identified genes that were differentially expressed between the two genotypes when the genes exhibited a q-value of 0.05 and a 2-fold change in expression. We have used these data to identify gene expression patterns that are specific to the rachis and DON treatment and to identify those genes that are highly expressed in the resistant genotype in all treatments. Our results have also revealed sets of genes that are specific to the *Fhb1* resistance response. Taken together, these genes represent a rich resource for further examination of the *Fhb1* resistance response and could lead to novel strategies for FHB resistance.

Application/Use:

Having the *Fhb1* gene will result in the perfect marker for marker-assisted selection for FHB resistance in breeding programs and will be an ideal candidate for genetic engineering. This will ultimately benefit the growers through improved FHB resistant varieties.

Materials and Methods:

We used genetic stocks developed by Dr. Jim Anderson (University of Minnesota) that contain either the *Fhb1* resistant or susceptible gene. We established three experiments: (1) *F. graminearum* inoculated spikelets and the spikelets were sampled at 96 hours after inoculation; (2) *F. graminearum* inoculated spikelets and the rachis was sampled 96 hours after inoculation; and (3) deoxynivalenol treated spikelets and the treated spikelets were sampled 12 hours after inoculation. RNA from the experiments was sequenced using next generation sequencing technologies. In collaboration with Drs. Eduard Akhunov (Kansas St. University) and Klaus Mayer (MIPS, Germany), we conducted an analysis of the genes that are differentially expressed between the resistant and susceptible genotype in the three experiments.

Economic Benefit to a Typical 500 Acre Wheat Enterprise:

Fusarium head blight is a major disease problem in the wheat growing regions of Minnesota. Yield and quality losses due to this disease can be devastating. Prophylactic fungicide treatments can cost $15/ acre. In addition, in severe FHB disease years the crop is not worth harvesting. Therefore, the economic benefits to this research are large.

10: RELATED RESEARCH

My laboratory is conducting two other projects focused on Fusarium Head Blight. In the first project, we sequenced RNA from three major QTL for FHB resistance in barley and are in the initial stages of examining the data. We are seeking to identify either the gene(s) underlying the QTL and/or the genes that are specific to each QTL. These genes will be a resource for further study of the resistance response in barley. In the second project, we are evaluating transgenic wheat and barley carrying a barley UDP-glucosyltransferase (UGT). Our results show that the transgenic wheat carrying the barley UGT exhibit high levels of resistance in the greenhouse and field to FHB. These transgenic wheat exhibit resistance that is equivalent or better than the best lines used in breeding programs. We have crossed these transgenics with a wheat variety and are currently assessing resistance to FHB.

11: RECOMMENDED FUTURE RESEARCH

Future research related to FHB:

Continued research to identify the *Fhb1* gene is an important goal for two reasons including: it will provide the perfect marker for marker-assisted breeding, and it will provide a better understanding of resistance and possibly lead to novel resistance strategies.

Future research for accelerating wheat improvement:

Developing a doubled haploid (DH) facility that caters to the wheat breeders in Minnesota, North Dakota and South Dakota would accelerate progress in developing novel wheat varieties. A DH production facility would provide the opportunity to rapidly create inbred lines and accelerate the breeding cycle.

12: APPENDIX

Ten abstracts related to the project:

Kovalsky Paris, M.P., W. Schweiger, S. Shin, G. Muehlbauer, C. Hametner, R. Krska, F. Berthiller and G. Adam. 2012. A barley UDP-glucosyltranferase forming a novel zearalenone-glucoside. National Scab Forum Abstracts.
Hofstad, A., H. Jia, B.P. Millett, E. Akhunov and G.J. Muehlbauer. 2012. Identifying FHB resistance genes in wheat using a next generation sequencing approach. National Scab Forum Abstracts.
Huang, Y., S. Shin, B.P. Millett, X. Li, G. Adam, S. McCormick, K.P. Smith, B.J. Steffenson and G.J. Muehlbauer. 2012. Identification and characterization of barley genes that provide resistance to trichothecenes. National Scab Forum Abstracts.
Koeritz, E.J., A.M. A.M. Elakkad, L.S. Dahleen, R. Skadsen, T. Abebe, J. Shah, V.J. Nalam, G. Klossner, N. Tumer, R. Di, G.J. Muehlbauer, X. Li, S. Shin and R. Dill-Macky. 2012. Testing transgenic spring wheat and barley lines for reaction to Fusarium head blight: 2012 field nursery report. National Scab Forum Abstracts.
Li, X., S. Shin, R. Dill-Macky, F. Berthiller, T. Clemente, S. McCormick and G.J. Muehlbauer. 2012. Transgenic wheat carrying a barley UDP-glucosyltranferase exhibits high levels of Fusarium head blight resistance. National Scab Forum Abstracts.
Muehlbauer, G.J., S. Shin, X. Li, J. Boddu, S. Heinen, J.A. Torres-Acosta, M.P.K. Paris, W. Schweiger, T. Clemente, R. Dill-Macky, S. McCormick, M. Lemmens, F. Berthiller and G. Adam. 2012. Developing Fusarium head blight resistant wheat. National Scab Forum Abstracts.
Schweiger, W., M.P. Kovalsky Paris, G. Wiesenberger, F. Berthiller, M. Lemmens, S. Shin, J.A. Torres-Acosta, G.J. Muehlbauer and G. Adam. 2012. Functional genomics of UDP-glucosyltransferases: heterologous expression in yeast to test for deoxynivalenol detoxification capability of candidate genes. National Scab Forum Abstracts.
Schweiger, W., B. Steiner, C. Ametz, G. Siegwart, G. Wiesenberger, F. berthiller, M. Lemmens, H. Jia, G. Adam, G.J. Muehlbauer, D.P. Kreil and H. Buerstmayr. 2012. Transcriptomic characterization of the Fusarium resistance QTL *FHB1* and *QFHS-IFA.5A*. National Scab Forum Abstracts.
Hofstad, A.N., H. Jia, B.P. Millett, E. Akhunov, and G. Muehlbauer. 2013. Identifying FHB resistance genes in wheat using a next generation sequencing approach. Plant and Animal Genome XXI Abstracts.
Kovalsky Paris, M.P., W. Schweiger, G. Wiesenberger, JA. Torres Acosta, H. Michlmayr, S. Newmister, M. Lemmens, A. Malachova, S. Shin, G. Muehlbauer, T. Weigl-Pollack, P. Fruhmann, H. Mikula, C. Hametner, B. Kluger, R. Schuhmacher, R. Krska, J. Fröhlich, I. Rayment, F. Berthiller, and G. Adam. 2013. *In planta* inactivation of Fusarium mycotoxins. European Fusarium Symposium Abstracts.

One presentation related to the project:
"Developing Fusarium head blight resistant wheat", at the National Scab Initiative, Orlando, FL