

0203-SM-104 Developing marker information for genetic diversity and FHB resistance in barley.

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PROJECT ABSTRACT

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Fusarium head blight (FHB) is the most serious disease in decades to impact the malting barley crop of the upper Midwest. Our work has focused on identifying quantitative trait loci (QTL) for resistance to FHB and accumulation of deoxynivalenol (DON) in germplasm relevant to Midwest barley improvement. To enhance our understanding of the genetics of host resistance to FHB and develop new tools to manipulate FHB resistance, we propose to continue our work to study the genetics of Chevron and Frederickson derived resistance in barley. We will continue development of near-isogenic lines (NILs) for QTLs identified in the Chevron/M69 population and begin construction of fine maps of important regions. We will development NIL for QTLs identified in the Frederickson population and begin construction of a population for fine mapping QTL. We will also initiate construction of a new mapping population (Atahualpa x M81) to identify QTL that will complement those previously identified. We will enhance our SSR genotype database of FHB resistant sources and elite barley germplasm to facilitate analysis of genetic diversity and comparative analysis of FHB mapping efforts. The desired outcome of this research project is to generate genetic information and a set DNA marker tools that will facilitate germplasm enhancement of FHB resistance in barley. This project is relevant to the U.S. Wheat and Barley Scab Initiative and fits within the biotechnology area of research.