

**PI: Franckowiak, Jerome D.****Project ID: 0304-FR-109****Research Area: VDUN****Project Title: Enhanced resistance to Fusarium in two-rowed barley.****PI's E-mail: [jfrancko@badlands.nodak.edu](mailto:jfrancko@badlands.nodak.edu)****ARS Agreement #: 59-0790-9-034****Duration of Award: 1 Year**

## PROJECT 1 ABSTRACT

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Development of two-rowed barley (*Hordeum vulgare*) cultivars for the Upper Midwest having better resistance to Fusarium head blight (FHB), *Fusarium graminearum*, is the primary research goal. Secondary goals include 1) identification of two-rowed barley lines that exhibit more resistance to FHB, 2) accumulation of genes for FHB resistance in two-rowed barley lines adapted to North Dakota (ND), and 3) examination of genetic factors in chromosomes 2H and 4H that restrict incorporation of FHB resistance into Midwest barley cultivars. A modified pedigree scheme is being used to generate breeding lines having more FHB resistance and adaptation to ND. Utilization of East Asian cultivars as a source of FHB resistance (*Rfg*) genes is being expanded and more emphasis is being placed on single crosses than three-way crosses. The FHB reactions of lines and populations will continue to be evaluated in FHB screening nurseries in China and ND. Advanced lines are being tested in ND for other diseases, agronomic traits, and malt quality using field plots, disease nurseries, and laboratory facilities. Promising lines will be considered for release to growers.

A group of linked genes in chromosome 2HL near the six-rowed spike 1 (*vrs1*) locus has limited progress in combining essential agronomic traits with *Rfg* genes. Agronomic effects of maturity (*Eam6*) and plant height (*hcm1*) genes in 2H and their interactions with the intermedium spike-c (*Int-c*) and early maturity 9 (*eam9*) loci in 4H are being investigated. Data collected on the Harrington/Morex (HM) doubled-haploid population will be used to study the relationship between the *Eam6* locus and *Rfg* genes. FHB response and maturity data from single-seed descent populations involving *eam9*, which is present in early maturing East Asian cultivars, will be collected. Combining FHB and maturity data with molecular marker information may better define the interactions between maturity genes and FHB reactions in two-rowed barley. Alternatives to the *Eam6* gene for early maturity are being studied, but the most promising ones, *Eam5*, *eam9*, and *eam10*, are short-day responsive genes that have few phenotypic effects in ND. Preliminary results indicate that only two-rowed lines with the *Eam6* gene are well adapted to ND.