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**Project ID:** FY18-BA-006

**ARS Agreement #:** *New*

**Research Category:** BAR-CP

**Duration of Award:** 1 Year

**Project Title:** Interstate Spring 2-rowed Malting Barley Breeding for FHB Resistance and Reduced DON.

### PROJECT 1 ABSTRACT

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The overall goal of this project is to develop spring 2-row malting barley varieties with FHB resistance and adaptation to the northeastern U.S.

The project objectives are to:

- 1) Evaluate FHB resistance in spring malting barley varieties in a Uniform Eastern Spring Malting Barley nursery coordinated by Richard Horsley at North Dakota State University,
- 2) Evaluate FHB resistance in malting barley varieties in the New York State Regional Spring and Winter Malting Barley testing program,
- 3) Evaluate FHB resistance and agronomic traits in our NY spring 2-row elite line training population, and
- 4) Use genomic selection to develop spring 2-row malting barley varieties with FHB resistance and adaptation to the northeastern U.S.

Expected outcomes include published results of our state regional trials for both spring and winter malting barley including FHB and malting quality data. This project will identify both spring and winter FHB resistant germplasm, characterize potentially novel sources of resistance, and develop elite spring 2-rowed malting barley varieties that are adapted to NY and have resistance to FHB and low DON accumulation for growers, processors and consumers. Results of our trials will be disseminated by hard copy, email and online.

Approach: For objectives 1 to 4 we will grow all entries in our FHB misted field evaluation nursery in three replicates. We use a backpack CO<sub>2</sub> sprayer to apply a spore suspension three to four times bracketing the flowering times of the entries. Each plot is scored for incidence and severity approximately 21 days post flowering. Each plot is harvested and sampled for DON and percent damaged kernels. Results will be reported to the uniform nursery coordinators and in our annual small grains testing reports. We have 1400 lines from seven elite biparental crosses that will be evaluated in two locations in an augmented design. A subset of 350 lines will be evaluated in our misted inoculated FHB nursery. Genomic selection models will be trained using agronomic data from the 1400 lines and using FHB data from the 350 lines. Selected lines will be increased in a winter nursery for regional evaluation in 2018 and 2019.

Stakeholders and end users will benefit from the increased availability of FHB resistant varieties and more consistent malting quality.