

Project FY22-GD-009: Winter Barley Mutant Resource to Increase FHB Resistance and to Reduce DON Content

1. What are the major goals and objectives of the research project?

- 1) Phenotypic Evaluation of M4 plants in head row design under misted scab nursery
- 2) Evaluation of selected mutant families in the greenhouse under point inoculation
- 3) Confirmation of the mutants and sharing the germplasm

2. What was accomplished under these goals or objectives? (For each major goal/objective, address these three items below.)

What were the major activities?

We screened Nomini mutant population of 800 me derived M3 plants under misted and GH (point inoculation). In total in GH condition 3200 plants from Nomini mutant population were screened and data was recorded and contrasting mutant phenotypes were identified.

What were the significant results?

Since our screening at the misted nursery did not yield optimum results and the disease was not visible due to very low temperature, we screened the Nomini mutant population in the GH under point inoculation with *F. graminearum* culture. Our screening of 800 M2 derived M3 families (4 plants per family and 4 heads per plant) identified 9 contrasting mutant phenotypes as compared to the wild type Nomini (Fig. 1). These 9 mutants showed significantly improved response that Nomini wild type parental lines under three different replicated tests. The results of the analysis are presented in Fig. 2 and Fig. 3.

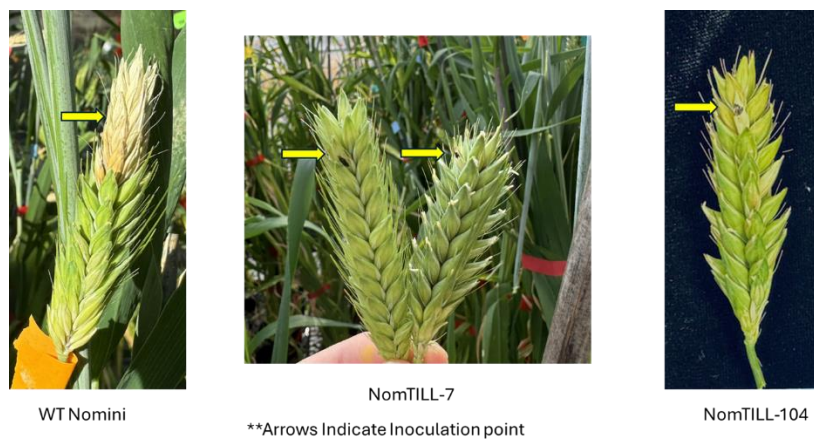


Fig. 1. Comparison of disease spread between wild type Nomini and two independent mutants (NomTILL-7 and NomTILL-104) with enhanced FHB resistance.

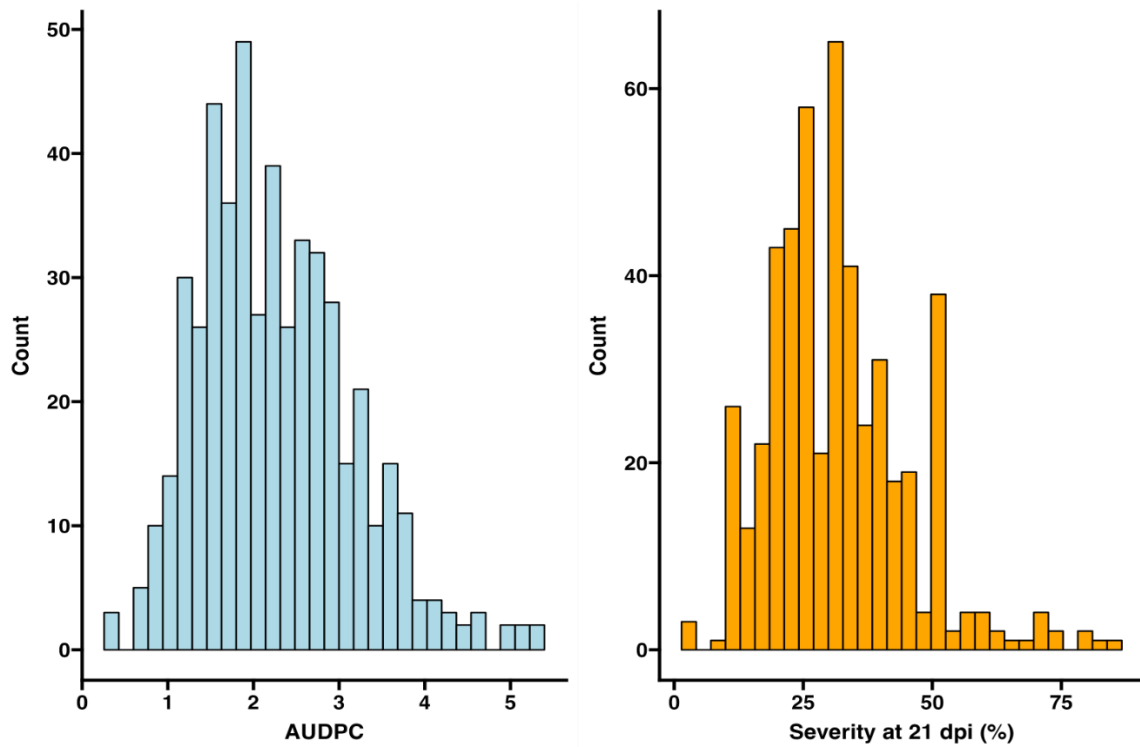


Fig. 2. Area under disease progression curve and severity index of barley mutant population under FHB inoculation.

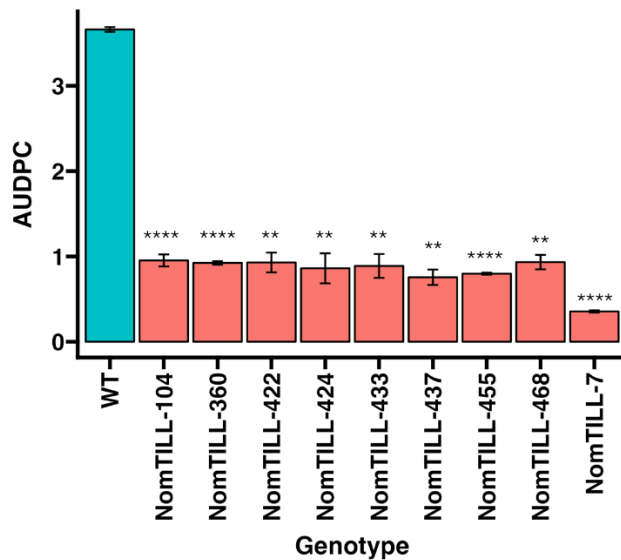


Fig. 3. Comparison of AUDPC of FHB progression in Nomini wild type and 9 independent mutants identified under at least two rounds of testing.

List key outcomes or other achievements.

Screening of Nomini EMS population for FHB resistance identified 9 independent mutants. A total of 3200 plants (from 800 M2 derived M3 families) were screened and a total of 1.1% of the population showed mutant phenotypes.

3. What opportunities for training and professional development has the project provided?

Three PhD students, one MS student, one postdoc, and three undergraduate students were trained under this project. All the trainees worked with the PI to conduct the nursery and collect and analyze data. These students also participated in conferences and commodity board meetings with their work.

4. How have the results been disseminated to communities of interest?

An undergraduate student, Ms. Victoria Chang led the GH phenotyping part of the project, and she has presented the results at the MAS-ASPB meeting in her poster presentation. She also presented her work at a meeting at Cornell University. The PI presented the results in oral presentations and disseminated updates on FHB in wheat and barley through emails. PI presented the research updates in the FHB forum as well as online project update meetings. The graduate students in the team presented the results as posters and handouts to the stakeholders in commodity board meetings. The results were published as wheat trial Factsheets and was disseminated via emails and the UMD extension system to the broader grower community.

5. What do you plan to do during the next reporting period to accomplish the goals and objectives?

The project has expired but we are working on further validation of the mutants in multiple tests. We are also working on developing MutMap populations of two most promising mutants to identify the causal SNPs related with the resistant phenotype. We will be generating some concrete data and would then request funding support from USWBSI to identify the causal susceptibility gene(s).