Project FY24-BA-002: Evaluation and development of FHB resistant germplasm for enhancing barley production

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

Major goals: Screen the ARS Aberdeen barley materials under multiple environments and develop new germplasm with low DON accumulation.

Objectives 1) Characterize FHB resistance and DON accumulation in elite barley germplasm; 2) incorporate a genomic selection approach for FHB resistance and low DON accumulation; 3) develop elite barley lines with FHB resistance, low DON accumulation and good agronomic performance.

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

What were the major activities?

1) DON data for 100 elite breeding lines was collected via collaboration with North Dakota State University and University of Minnesota for FHB screening in their nurseries. The data will be used in selecting FHB resistant lines for future cultivar release and parental uses in the crosses.

2) The genomic selection training population was updated by replacing 23 randomly selected lines of the original training population with F_3 lines from the first round of cycle 1 crosses. This new training population was characterized for FHB severity and DON accumulation at Kimberly, ID in 2024. Further characterization is planned for next season. 710 lines have been developed by single-seed descent from 21 crosses of parents chosen by genomic selection from the founder population (cycle 1 round 1), 24 crosses made between progeny of those crosses (cycle 1 round 2), and 23 crosses made in turn from progeny of those (cycle 1 round 3). F_3 seed of these were planted in the greenhouse with the intention of genotyping them using the 3K platform for the next cycle of genomic selection. Supply chain and purchasing issues resulted in a shortage of genotyping supplies at the critical time, so a generation advance was performed instead, and these lines will be genotyped for genomic selection in the F_4 generation.

3) DON content analysis was done on grain samples of four bi-parental populations planted at the Kimberly, Idaho and Fargo, North Dakota nurseries in summer. Three-year data (2021 – 2023) summarized and utilized to identify QTLs contributing to low DON content and FHB severity in barley malting lines and varieties.

What were the significant results?

1) The elite line 19ARS176-1 showed promising low DON of 7.8 ppm at Fargo location and 16 ppm at Minesota location, while the resistant control Conlon showed 34.4 ppm and 30 ppm at the two locations, respectively. The elite malting line 16ARS072-5 in current AMBA pilot scale quality testing also showed DON contents of 26.4 ppm at Fargo location and 27.0ppm at Minesota location, lower than Conlon for 34.4 ppm and 30 ppm at both locations respectively. The DON information is very useful for the breeding and stakeholders.

2) Disease severity of the genomic selection training population at Kimberly, ID was lower than previously observed (mean DON was 4.4 in 2025 and 14.7 in 2020), but sufficient to contribute information to the next round of genomic selection when added to the data from other location years already accumulated. The genomic selection Cycle 1 population is in the F_4 generation and ready for the next cycle of genomic selection using genotype and phenotype information from an updated training population.

3) Analysis of three-year data suggested the presence of QTL influencing DON level on chromosomes 1H, 2H, 3H, 4H, 5H and 7H. QTLs on 1H, 2H, 3H and 4H were detected only in one location-year while QTLs on 5H and 7H were detected in multiple location-years. Four QTLs influencing FHB score were also identified on chromosomes 1H, 3H, 5H and 7H each with single location-year.

List key outcomes or other achievements.

Linkage analysis identified QTL contributing to lower DON levels in multiple location-years on chromosomes 5H and 7H in the Aberdeen elite malting barley lines.

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

This project provided the training opportunity for two postdocs at ARS, and one undergraduate student at Idaho State University and one student from the local high school.

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

FHB inoculation methodology study that would support evaluate reaction of barley lines to FHB infection in a controlled environment was presented in poster format at the 2024 FHB Forum held in Austin, TX.

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

1) This project is not funded for the next reporting period. Hence, we will carry out some of the activities at a reduced scale using in-house resources. We will submit a revised proposal in the next funding cycle that includes continuation of some objectives from the current project while also adding new objectives.
2) May continue the elite breeding lines evaluation for FHB resistance depended on the availability of workforce.

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1. **What are the major goals and objectives of the research project?**
   To identify and characterize FHB-resistant germplasm from the following germplasm
   - Montana State University Breeding Program
   - Dr. Gongshe Hu's breeding material
   - USDA ARS Aberdeen Training Population.

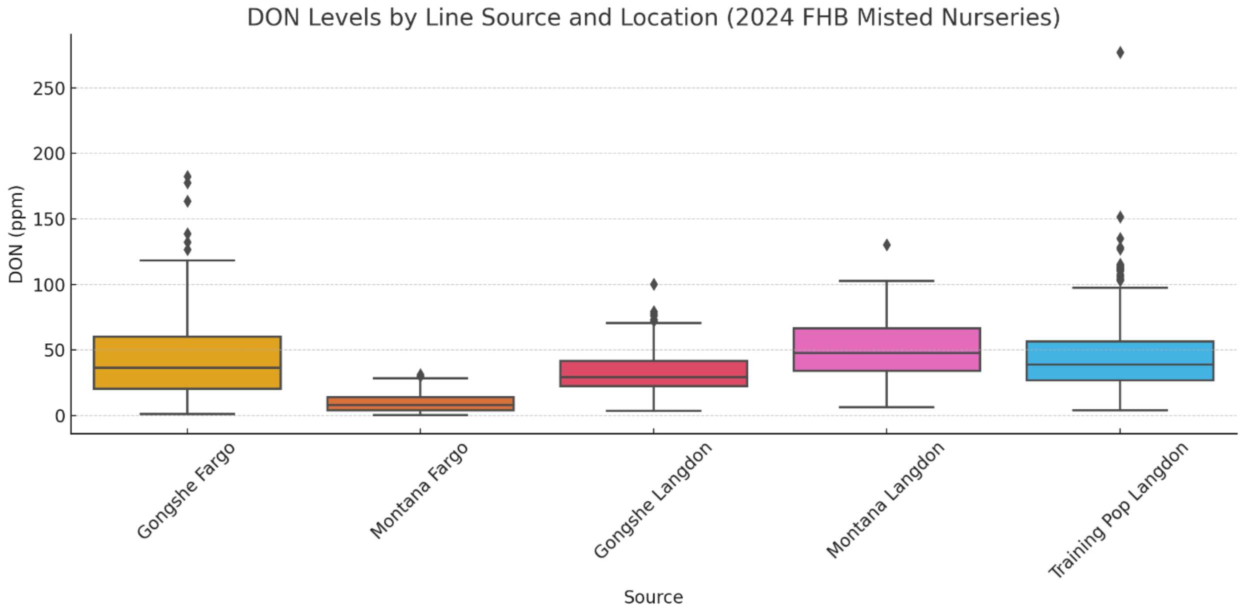
2. **What was accomplished under these goals or objectives?** *(For each major goal/objective, address these three items below.)*

What were the major activities?

In the 2024 FHB misted nurseries at Fargo and Langdon, major activities included screening diverse barley germplasm, including *Dr. Gongshe Hu's lines, Montana breeding lines, and the Aberdeen Idaho training population*, for resistance to Fusarium head blight (FHB) by quantifying deoxynivalenol (DON) accumulation. Over 980 entries were evaluated.

What were the significant results?

Montana lines at Fargo had the lowest average DON levels (mean = 10.02 ppm), indicating strong resistance under those conditions. In contrast, the same Montana lines at Langdon had a much higher mean DON (51.79 ppm), showing a strong genotype × environment interaction. Dr. Gongshe Hu's lines performed better at Langdon (mean = 32.66 ppm) than at Fargo (mean = 44.60 ppm), suggesting environmental variation influenced DON accumulation. The training population at Langdon showed a wide range of DON levels (4.1–277 ppm), making it suitable for QTL mapping and genomic prediction studies. Top resistant lines (low DON) were identified in both locations, with several entries showing <10 ppm in high-pressure nurseries. Maximum DON values varied greatly: 277 ppm (Training Pop Langdon), 182.6 ppm (Gongshe Fargo), and 130.4 ppm (Montana Langdon), confirming the effectiveness of the misted nursery in creating strong disease pressure for differentiation.



List key outcomes or other achievements.

The data we generated helped identify lines suitable for resistance breeding pipelines. This years screenings reinforced use of Conlon and Chevron as benchmark resistant checks.

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

Field interns and research specialists engaged in hands-on screening and DON sample preparation.

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

Reports have been submitted to Dr. Frank Crutcher at Montana State University, Dr. Gongshe Hu at USDA-ARS in Aberdeen, ID, and Dr. Belayneh Yimer at the USDA-ARS in Aberdeen, ID.

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

We have planted material for Dr. Crutcher and Dr. Hu again in Fargo and Langdon for the 2025 field season. The training population was not planted.