Project FY22-BA-012: Fusarium Head Blight Resistance for Montana Barley

---

1. **What are the major goals and objectives of the research project?**
   Our objectives fall within the research priorities as follows:
   1) Continue crossing resistant material from other programs and identified in this program into lines adapted to Montana; field screen resulting progeny in different environments (VDHR objective #1).
   2) Continue to pyramid resistant lines and screen for resistance in the field for future genotype mapping (VDHR objective #3).
   3) Phenotype resistance in four 2-row NAM families in the field (VDHR objective #3).
   4) Collect and identify Fusarium species in the Montana FHB disease complex (PBG objective #12).

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

   What were the major activities?

Objective 1: In Fall 2023, Dr. Sherman made 7 crosses related to scab resistance. These crosses will be evaluated in the field as F4 rows in 2025 and will be evaluated for both agronomic characteristics and FHB resistance. In summer of 2023, 7 families consisting of 100-200 were grown as head rows and visually selected for agronomics. A total of 22 families of 10-20 lines each were evaluated agronomically as F5s. The most agronomically adapted of the 56 families were evaluated for FHB resistance in 2024. We have harvested these plots, evaluated for DON, and are currently analyzing agronomic data.

Additionally, we planted lines in 2024 that have shown promise at the EARC screening nursery in previous years at three locations: Sidney, Langdon, and Fargo in order to evaluated them for disease severity, incidence, index, FKD, and DON. We have planted these lines for evaluation at other locations in 2025.

Objective 2 and 3: We screened over 400 lines in 2024 produced from pyramiding different sources of resistance in small hill plots in our nursery and included a subset of the 2-row nested association mapping (NAM) panel. We sent in seed for DON analysis for many of these lines. Dr. Sherman's graduate student has evaluated the data from 2022 and 2023 to determine if we can use this to map potential FHB resistance. In 2024, we collected plant tissue from the mapping population and sent it to Fargo for genotyping. We used the results to evaluate our 2023 severity and DON results from these lines.

Objective 4: We have identified 350 isolates collected in 2019 and 2022 from two regions in Montana. We have completed chemotyping the *F. graminearum* isolates, and for the second time identified 3-ADON isolates in Northeast MT on durum. Montana Wheat and Barley Committee has funded an experiment in which we are testing these lines in the field on durum to determine if there is any difference in virulence, DON, and fungicide sensitivity in the field between the 15-ADON and 3-ADON isolates. This experiment was planted in 2024 and the work is ongoing.

What were the significant results?

Objective 1: We have identified several lines since initiation of this project that have decreased DON production in multiple years and locations. These have or will be evaluated for agronomic characteristics and integrated into Dr. Sherman's breeding program. Two specifically, 2017-43-18 and 2017-43-20,

show consistent resistance over years and locations when compared with resistant controls and have heading dates and height similar to our regional varieties Hockett and Buzz. Resulting lines from these crosses will be integrated into our hill plot screening as early as 2027. We will continue to collect additional data on them in multiple locations in 2025. A summary table for these lines is included below (Table 1). In the table the green highlight indicates lines used for breeding, yellow highlight indicates that the line was in the top 10 evaluated for low DON production that year, L indicates Langdon screening nursery, M indicates Minnesota screening nursery, and F indicates Fargo screening nursery.

Table 1: Average DON amounts in promising barley lines from Montana State University Breeding Program.

Line	2019	2020	2022	2023	2024	2021 L	2021 M	2023 L	2023 F	2024 L	2024 F
2017-40-17	1.2	1.8	6.6			49.4	12.8				
2017-41-16	1.7	0.9				32.3	2.65				
2017-41-6	1.1	0.7	5.7	6.6		43.9	3	41.1			
2017-69-13	1.9	1.4				56	4.45				
2019-27-46		1.8	5.9			64.9					
2017-40-10	1.8	1.9	7.1		11.9	50.7	7.3			44.55	7.5
2017-42-18	1.5	0.8	2.5	4.6		62.7	1.4	22.2		22.2	2.7
2017-42-2	1.7	1.1				27.7	0.08				
2017-43-18	1.7	1.5	2.9	3.7		37.7	3.2	38.05	15.65	43.85	2.1
2017-43-19	1.3	0.6				31.1	2.3				
2017-43-20	1.3	0.6	2.1	4.9		23.4	3.1	22.15	12.9	30.8	2.1
2017-43-22	0.9	1.2	3.4	4.3	7.9	54.3	0.865	26.8	21.7		5.8
2017-44-18	0.8					21.6	0.65				
2017-44-23	1.1					27.5	3.85				
2017-46-10	1.8		3.3	6.5	14.3					41.2	9
2017-46-19	1.4	2.1	3	3.5		52.2	3.54	63.95	26.95		7.65
2017-47-6	1.5	1.2	4.2	4.8		38.2	2.15	25.1	9.75		
2019-23-22			2	4.3							
2021-45-7			3.1	4.1				28.75			
2021-45-11			2.5	6.1							
MT18F00607			1.9	2.6				33.35	38.9		
MT19_H11_03			2.1	3.3					23.5		
MT22_Y076_16										77	4.9
MT22_Y079_10										57.15	6.33
MT22_Y080_15										62.75	6.8
Stander		6.1	16.8	22.8	30.6	62	13.05			70.45	23.1
Bearpaw		2.3	3	6.1	14.1	31.3		20	35.25		
Pinnacle		1.5	8.7	8		36.2	1.9			34.3	10.35
Hockett		3.2	2.3	8.1	18.9	42.2				44.75	17.5
Conlon					11.9		4.7			34.1	5.9
Chevron		1.1				53.2					

Green highlight indicates lines used for breeding.
Yellow highlight indicates that the line was in the top 10 evaluated for low DON production that year.
L indicates Langdon, ND screening nursery
M indicates Minnesota screening nursery
F indicates Fargo screening nursery.

Objective 2 and 3: Results from this analysis show that there are four QTLs on chromosomes 4, 5, 6, and 7 that coincide with DON levels (Fig. 1) and three QTLs associated with heading date (Fig. 2). We will repeat this analysis in 2025. We have planted three replications of the mapping population and controls and determine if we can replicate these results. Additionally, we will take a more traditional severity and incidence data to provide a disease index as well as height and heading date for further evaluation.

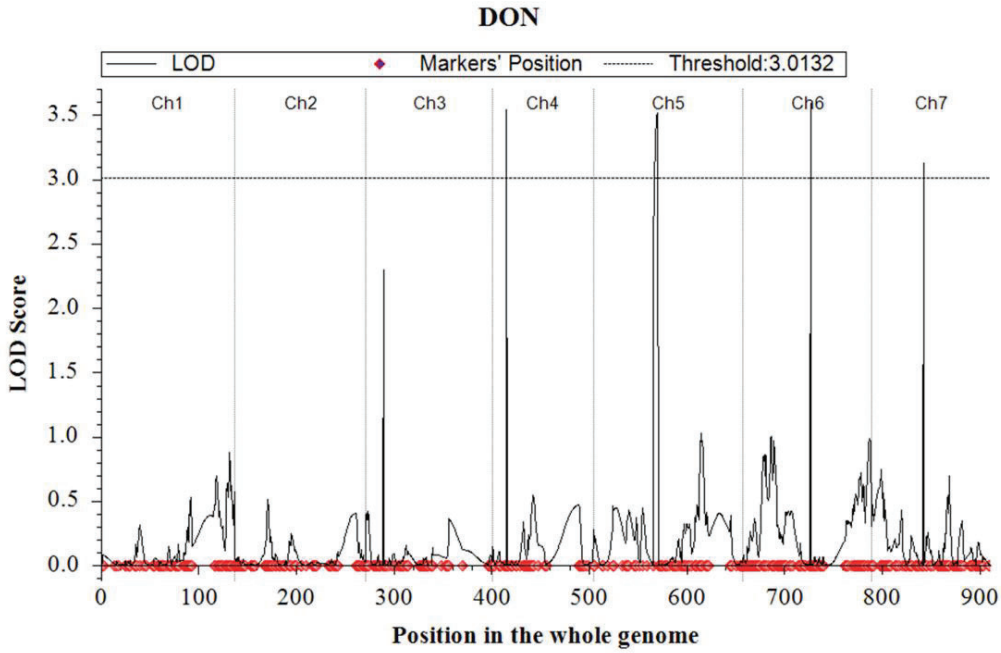

Figure 1: DON levels from 2-row NAM panel mapped to QTLs.

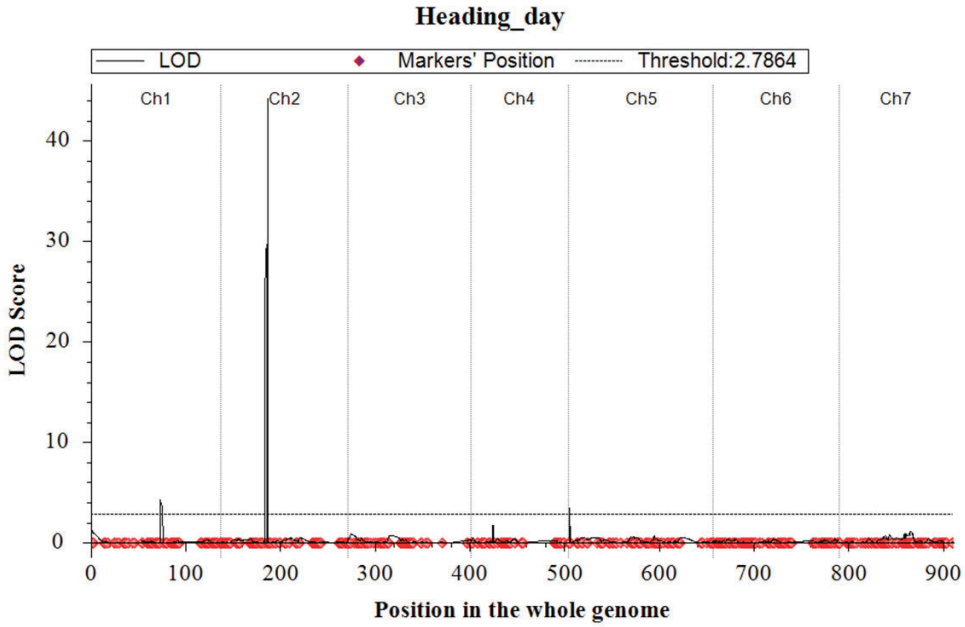

Figure 2: Heading date from 2-row NAM panel mapped to QTLs.

List key outcomes or other achievements.

We have identified two lines that have consistently had DON production that was statistically similar to our resistant controls over multiple years and locations. These lines are not suitable for direct release but can be used for crosses in the development of regionally adapted varieties.

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

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

Funding from this project paid for a graduate student to conduct genotyping and attend the 2024 FHB Forum to present our research results.

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

Results from our work have been presented at field days including at the location of our screening nursery in summer 2024. Research results were also presented at the FHB Forum in 2024.

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

We have planted this year's screening nursery, and we have had good germination and vigor. Corn spawn has been placed, and the misting has been installed. We will begin conidia applications at the end of June to barley plants at heading and we will measure disease about two weeks later. Seed will be harvested, evaluated, ground, and sent in for DON analysis. Early in 2026, the barley breeder will utilize our potentially resistant material for crosses.