Project FY22-BA-006: Developing Fusarium Head Blight-resistant North American Winter Barleys

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1. **What are the major goals and objectives of the research project?**
   The overall goals of this project are to enhance and increase the number of winter barley varieties developed by U.S. public breeding programs that possess resistance to head blight disease caused by Fusarium graminarum. The specific objectives of this project are to: 1) coordinate a North American Barley Scab Evaluation Nursery (NABSEN) for winter barley, in which North American winter barley breeders submit their best lines for testing, 2) identify lines in the Ohio breeding program exhibiting Fusarium Head Blight (FHB) resistance in the forms of low Deoxynivalenol (DON) accumulation and low disease incidence, and 3) utilize modern breeding technologies to efficiently and rapidly introgress those resistances into elite lines for varietal release to farmers.

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

   What were the major activities?
   The FY24 Performance Reporting Period spans aspects of two field seasons, 2023–24 and 2024–25, so activities associated with both will be reported on.

   Objective 1, the winter NABSEN
   Seven U.S. public breeders contributed lines to the winter NABSEN for the 2023–24 season. A total of 47 lines from the contributors were tested that season. For the 2024–25 season, a total of 51 lines from eight U.S. public breeding programs are being tested. Cornell is a new source 2024–25. Eight checks that were vetted by the nursery participants were included. The seeds of all entries were sent to the Stockinger lab. The seed was treated with NipsIt™ SUITE Cereals OF Seed Protectant (Valent, https://www.valent.com/) following the manufacturer’s recommendation and allowed to dry. Seed was then packaged and shipped to the nursery participants September 14, 2023, and September 9, 2024, for the 2023–24 and 2024–25 season scab nurseries, respectively. The nursery was planted at eight locations, which includes Wooster Ohio. Seven of the nurseries, including the Ohio nursery, screened lines using Fusarium inoculation combined with overhead mist irrigation. The eighth is using natural infection only.

   The 2023–24 Ohio scab nursery was planted in Wooster on October 9, 2023, in a field equipped with well-water access. Each line was planted into a 0.8 m long headrow in a field measuring 32 m × 72 m. Planting format consisted of four adjacent columns of barley, each separated by two columns of a wheat spacer. Each line was planted in three reps using an alpha lattice incomplete block design.

   On April 19, 2024, which was prior to heading and was early in canopy development, the nursery was inoculated with multiple race isolates of Ohio F. graminearum using corn cob "spawn" placed in nursery rows. An overhead irrigation system was put in place on April 29, 2024.

The 2024–25 Ohio scab nursery was planted in Wooster on October 21, 2024. The field dimensions were 61 m × 42 m (200′ × 136′). Well water access, planting format, and experimental design were the same as those of the 2022–23 nursery. A total of 34 headrow trays were planted, two per pass, which included 15 experimental passes and two border passes of wheat on the flanks.

On April 29 and 30, 2025, overhead sprinkler heads were gridded at 9 m intervals along X and Y axes with sprinkler heads sitting on a 1.5 m riser. The nursery was inoculated with corn cob spawn on April 30th, 2025. Beginning May 9, 2025, and continuing to May 22, F. graminearum spore suspension was applied every third day, for a total of five spore inoculations. Inoculations were conducted in the evenings, beginning at 4:00 PM. The field was overhead irrigated intermittently for 5 minutes every 30 minutes between 5:00 AM and 9:00 AM, and again between 5:00 PM and 9:00 PM throughout anthesis, and for seven days following the time when the latest-heading line completed anthesis.

Heading date of lines were recorded.

At maturity, the reps from the 2023–24 Ohio scab nursery were hand-harvested and then threshed in a stationary lab thresher. Following harvest and threshing, three different approaches were taken to prepare the reps for grinding and DON level assessment, which were done for the purpose of maximizing the number of technical reps assessed within our 1000 sample allotment by the University of Minnesota DON testing lab. The first approach was to process each individual rep. This was done for the NABSEN set. The second was to process rep 1 as its own sample and composite an equal portion of reps 2 and 3 together. This was done for most of the advanced Ohio breeding lines. The third approach was to create a composite consisting of an equal portion of all three reps together. This was done for the Bregitzer population and a subset of the less advanced Ohio breeding lines. Individual rep samples and the composites were then ground to a fine powder using a burr mill type coffee grinder. The target quantity of sample used for DON analysis was 100 g. Ground samples were then sent to the laboratory of Dr. Yanhong Dong, at the University of Minnesota for DON analyses.

Hand-harvesting material from the 2023–24 scab nursery was completed the week of July 7, 2025.

Objective 2, the Ohio breeding program

The Ohio selection GHRIL0201-088 exhibited the lowest DON values across the entire Ohio Nursery the 2022–23 season. In addition to being the lowest DON accumulator, GHRIL0201-088 also exhibits good malting quality and high levels of resistance to lodging and stem breakage. These favorable qualities have been observed over multiple years and multiple locations. Because of the multiple highly desirable qualities we have used GHRIL0201-088 extensively as a parent in crosses. One of the crosses, to Ohio selection FL-029/WI-013-08, is now in the pipeline for a doubled haploid population development at the U.S. Wheat and Barley Scab Initiative-supported genomics facility at Oregon State University.

We also used GHRIL0201-088 as a recurrent parent and a donor parent in a reciprocal backcrossing strategy with a subset of seven Ohio lines that consistently exhibit the best malting quality when grown across Ohio. The hypothesis being that if DON accumulation levels has a heritable genetic component, then the set of reciprocal backcross sublines having 75% of the GHRIL0201-088 genome will exhibit a DON mean level that is lower than of the set of reciprocal backcross lines having 25% of the GHRIL0201-088 genome and 75% of parent 2 genome.

Each respective F1 was crossed back to GHRIL0201-088 and to the second parent in each of the GHRIL0201-088 crosses. The target number of BC1F2 seed in which the F1 was backcrossed to each parent, was 25. Up to 20 BC1F2 seeds from the rachis of the F1 were sown, the seedlings were vernalized, and the plants were taken to maturity in the greenhouse. The BC1F3 offspring from those lines were planted into headrows autumn 2024. Spring of 2025, selections at the BC1F4 from those headrows were made, and will be further evaluate for grain quality traits.

This same set of BC1F3 lines were also planted into the winter scab nursery, each line in three reps. An additional ~75 lines were planted for seed increase, which will be added to the scab nursery autumn 2025. The BC1F3 derived BC1F4 lines were genotyped using the 3K chip developed by Dr. Jason Fiedler at the USDA Fargo ND genotyping lab. A new M.S. student, Mr. Frolence Paul Fidelis has begun analyses of the genotyping data. Results from those analyses indicates allelic variation at loci polymorphic between GHRIL0201-088 and the second parent in the reciprocal backcross lines is consistent with the direction of the reciprocal backcross. Spring 2025, Mr. Fidelis phenotyped the GHRIL0201-088 backcross populations for height, lodging, and heading date.

Objective 3, utilizing modern breeding technologies to efficiently and rapidly introgress resistances into elite lines for varietal release to farmers
Autumn 2024, we rotated in a new panel of 250–300 lines, identified as the “Wong” population for testing its use as a structured population for genetic analyses of resistance to scab. Approximately 250 lines of this set share ‘Wong’ as an ancestor, either as the direct parent or grandparent. The lines in the ‘Wong’ population were developed by multiple breeding programs across North America mid-20th Century. The other lines in the panel are those to which ‘Wong’ was crossed.

'Wong' was introduced in 1941 and quickly became the dominant winter barley grown in the eastern U.S. and continued to dominate acreage for more than 20 years (Jensen, N.F. (1964). Registration of Wong barley. Crop Sci 4, 238). It is a six-row genotype that was used extensively as a parent by breeding programs across North America because of exceptionally strong straw, winter-hardiness, and resistance to powdery mildew.

The rationale for rotating in the ‘Wong’ panel is two-fold. One rationale is that our data supports there being a genetic component to the levels of DON accumulated in barley, which appears to be in large part derived from the two-row line MO B2549, a line having ‘Wong’ in its pedigree. Data for ‘Wong’ comes only from the 2020–21 nursery. DON levels of ‘Wong’ in the 2020–21 nursery were 21 ppm, which was about the same as that of the resistant check VA15H-73 (16 ppm) and MO B2549 (22 ppm). To put these numbers in perspective, DON levels for the 2020-21 nursery ranged 16 ppm (VA15H-73) to 125 ppm (Mercer, an Ohio “landrace”). Another rationale for assessing the 'Wong' panel is that the genetic relatedness of the 'Wong' population is anticipated to enhance our ability to genetically interrogate DON accumulation over that which we were able to do using the 300-line panel of completely unrelated lines. An ideal outcome from these experiments is that we would be able to use the information gained by genetic analyses of the Wong population to predict genetic resistance to F. graminearum in the Ohio winter malting barley breeding program.

What were the significant results?

A general overview of the results is presented, which is then followed by sections that focus on results under each specific objective.

For the 2023–24 Ohio nursery, no physical symptoms of disease were apparent during heading. As such we did not score for disease index. It should also be noted that Ohio experienced severe drought and high temperatures during heading and grain fill, which was a weather pattern non-conducive to F. graminearum growth.

To circumvent the lack of disease index score we assessed DON levels from as many technical reps for our plots as permitted by our allotment, rather than from a composite in an effort to increase the ability to detect variation that occurs in DON levels for each line.

DON data for the 2023–24 field season was returned to PI Stockinger March 19, 2025. A total of 1000 samples were submitted for testing. Across all samples and the entire Ohio nursery, DON values ranged 0.5 ppm – 28 ppm. The mean was 3.4. The lowest and the highest DON values observed were for two Ohio lines, both of which were recombinants derived from crosses to the spring variety 'Golden Promise'. The low DON values for the 2023–24 nursery were consistent with the lack of visible symptoms of disease.

Amongst the eight checks used, for both the NABSEN and the entire Ohio nursery, the mean DON values for the 2023–24 season ranged 1 ppm – 7 ppm (Table 1). VA15H-73 exhibited the lowest value, while Hirondella exhibited the highest value. Overall, DON values for the checks the 2023–24 season were about 1/3 those of the 2022–23 season, which in turn were about an order of magnitude lower than they were the 2021–22 season (Table 1).

In contrast to the 2023–24 Ohio nursery, the 2024–25 nursery exhibited robust scab disease symptoms. In addition to the scab nursery, head scab disease has been observed on non-inoculated barley fields in Wooster during spring 2025. The weather conditions spring 2025 were very cool, very wet, and very rainy.

Table 1. DON levels of check lines tested in Wooster Ohio 2021–22, 2022–23, and 2023–24.

		2021–22		2022–23		2023–24	
Genotype	**Row type**	**DON ppm (mean) ***	**DON ppm (std dev)**	**DON ppm (mean) ***	**DON ppm (std dev)**	**DON ppm (mean) ***	**DON ppm (std dev)**
VA15H-73	2	34	2	3	2	1	1
Endeavor	2	111	4	10	4	3	1
Calypso	2	139	3	16	3	4	1
Wintmalt	2	151	3	14	3	4	1
Atlantic	6	116	4	21	4	4	1
Thoroughbred	6	117	3	14	3	4	1
Secretariat	6	124	3	21	3	4	1
Hirondella	6	222	4	21	4	7	4

* Means derived from 24 plots per check, from all trials (8) for the 2021–22 and 2022–23 seasons, and 36 plots per check, from all trials (9) the 2023–24 season.

Objective 1, the winter NABSEN

DON levels of the winter NABSEN lines tested in Wooster Ohio the 2023–24 season is provided in Table 2. The mean DON level for this set of lines was 3.8. The lines from most of the North American breeding programs were just above or just below this mean. The one exception was the lines from the Nebraska program – all of the Nebraska lines exhibited much high DON numbers than the mean.

Compilation of the results and data from the cooperator’s 2023–24 nurseries is still in progress. Results and data from the 2024–25 nurseries is not expected until late 2025 or early 2026.

Table 2. DON levels of the winter NABSEN lines tested in Wooster Ohio the 2023–24 season.

Entry	**Program**	**Variety**	**DON (mean)**	**DON (std dev)**
NABSEN-2023-24-001	USDA-ARS Idaho	12ARS777-1	4.4	2.4
NABSEN-2023-24-002	USDA-ARS Idaho	12ARS777-2	2.1	0.6
NABSEN-2023-24-003	USDA-ARS Idaho	1316ARS627-037	2.2	0.3
NABSEN-2023-24-004	USDA-ARS Idaho	13ARS514-6	3.0	0.7
NABSEN-2023-24-005	USDA-ARS Idaho	13ARS526-8	5.0	1.8
NABSEN-2023-24-006	USDA-ARS Idaho	13ARS537-19	2.4	0.6
NABSEN-2023-24-007	U. Minnesota	2MW18_3373-001	5.3	0.9
NABSEN-2023-24-008	U. Minnesota	2MW18_4462-011	3.1	1.1
NABSEN-2023-24-009	U. Minnesota	2MW19_3013-004	1.7	0.5
NABSEN-2023-24-010	U. Minnesota	2MW19_3346-014	6.4	0.6
NABSEN-2023-24-011	U. Minnesota	TM17.125-008	5.7	1.0
NABSEN-2023-24-012	U. Minnesota	W2M001 (2MW19_3009-004)	4.2	1.2
NABSEN-2023-24-013	U. Minnesota	W2M002 (2MW19_3023-022)	2.9	0.9
NABSEN-2023-24-014	Montana State U.	MTWF6(F2)_50-1	2.7	0.4
NABSEN-2023-24-015	Montana State U.	MTWF6(F2)_50-7	5.6	1.2
NABSEN-2023-24-016	Montana State U.	MTWF6(F3)_24	4.2	1.4
NABSEN-2023-24-017	Montana State U.	MTWF6(F4)_84-127	4.2	1.0
NABSEN-2023-24-018	Montana State U.	MTWF7_4-2	2.2	0.8
NABSEN-2023-24-019	Montana State U.	MTWF7_4-3	2.3	0.1
NABSEN-2023-24-020	Montana State U.	MTWF7_6-7	3.0	0.9
NABSEN-2023-24-021	Nebraska State U.	NB17411	4.5	1.2
NABSEN-2023-24-022	Nebraska State U.	NB17431	10.6	1.8
NABSEN-2023-24-023	Nebraska State U.	NB19406	6.8	1.5
NABSEN-2023-24-024	Nebraska State U.	NB19420	6.8	1.9
NABSEN-2023-24-025	Nebraska State U.	NB22216	6.0	1.2
NABSEN-2023-24-026	Nebraska State U.	NB22229	8.3	1.0
NABSEN-2023-24-027	Ohio State U.	2011-725-02	2.6	0.5
NABSEN-2023-24-028	Ohio State U.	DH0214-007	1.4	0.2
NABSEN-2023-24-029	Ohio State U.	DH02FL-028	4.1	1.6
NABSEN-2023-24-030	Ohio State U.	GHRIL0201-103	3.7	0.5
NABSEN-2023-24-031	Ohio State U.	RIL0201-088	3.0	0.2
NABSEN-2023-24-032	Ohio State U.	RIL0257-01-011	3.2	0.6
NABSEN-2023-24-033	Ohio State U.	RIL02FL-029	5.4	2.0
NABSEN-2023-24-034	Ohio State U.	MOB2549-NT074-012	0.6	0.1
NABSEN-2023-24-035	Oregon State U.	DH141917	2.7	0.3
NABSEN-2023-24-036	Oregon State U.	DH162310	1.5	0.2
NABSEN-2023-24-037	Oregon State U.	DH150683	3.7	1.7
NABSEN-2023-24-038	Oregon State U.	DH170472	2.7	0.6
NABSEN-2023-24-039	Oregon State U.	DH180676	2.4	1.0
NABSEN-2023-24-040	Oregon State U.	Lightning	4.2	1.6
NABSEN-2023-24-041	Oregon State U.	Thunder	2.9	0.9
NABSEN-2023-24-042	Virginia Tech U.	VA20MFHB-18DH515	3.1	0.5
NABSEN-2023-24-043	Virginia Tech U.	VA21BFHB-19DH0143	2.6	0.5
NABSEN-2023-24-044	Virginia Tech U.	VA21BFHB-19DH0184	3.7	0.8
NABSEN-2023-24-045	Virginia Tech U.	VA22M-205	3.1	0.7
NABSEN-2023-24-046	Virginia Tech U.	VA22M-20DH1299	2.6	0.5
NABSEN-2023-24-047	Virginia Tech U.	VA22M-20DH1427	3.2	0.9

Objective 2, the Ohio breeding program, and the Bregitzer population

Autumn 2024, the BC1F3 offspring from reciprocal backcrosses between GHRIL0201-088 and seven Ohio lines were planted into headrow plots. Up to 20 lines from each reciprocal backcross were planted. Selections at the BC1F4 from those lines were made spring 2025. These selection will be further evaluated for grain quality traits.

DON values for the Ohio breeding program set of lines ranged 0.5–28.0 ppm, with a mean value of 3.4 ppm. GHRIL0201-088, which stood out the 2022–23 season as having the lowest DON levels across the entire nursery, exhibited DON values of 2.7, 3.0, 3.1, 3.1 for each of the four rep plots in which it was grown. These values are not substantially different from the mean for the entire nursery.

DON values for the Bregitzer population of 83 recombinant lines derived from 95SR316A × 'Charles' ranged 0.7–9.1 ppm, with a mean value of 2.5 ppm. Mean DON values for Charles were 1.1 ppm, and those of 95SR316A were 3.1 ppm. The numbers for the 2022–23 and 2023–24 seasons were much lower than those of the 2021–22 season (Table 3).

Table 3. DON levels for the Bregitzer population lines tested in Wooster Ohio the 2021–22, 2022–23, and 2023–24 seasons.

Value (or line)	Season		
	2021–22	2022–23	2023–24
High	222	15	9.1
Low	54	2	0.7
Mean	135	7.6	2.5
Charles	154	7.6	1.1
95SR316A	105	4.2	3.1

List key outcomes or other achievements.

In the preceding years' scab nursery trials (2020–21, 2021–22, 2022–23), we inoculated our scab nursery using corn spawn and asexual spores. Corn spawn inoculation took place early in canopy development, while asexual spore inoculations took place at two-day intervals at the first sign of head emergence (Zadoks 51-53) and prior to pollen dehiscence and continuing until the latest-heading line completed anthesis. However, we did not employ spore inoculation for the 2023–24 nursery. The reason being that concern was expressed by the barley scab community at the 2023 FHB Forum, that our disease pressure might be too great because our DON numbers were much higher than those observed by other barley researchers with scab nurseries. Community members suggested we eliminate the spore inoculation and rely exclusively on infection from corn cob spawn.

In hindsight however, and following return of the DON data for the 2023–24 season, we now think eliminating the spore inoculum was a mistake. DON numbers the 2023–24 season were the lowest they had been since we have been carrying out trials in our nursery. While there is still a pattern in which the susceptible check 'Hirondella' exhibits some of the highest values, the extremely low DON numbers for all lines in the trials precludes our ability to detect stratification of DON levels across lines. Thus, for the 2024–25 season we reintroduced the use of spore inoculation, at the frequence of every 3rd day throughout anthesis.

And while DON numbers for the Ohio scab nursery tend to be much higher than those observed by other barley researchers with scab nurseries, our DON numbers for the NABSEN set of lines parallels the numbers detected by the Virginia program for each given line. And DON numbers for Virginia program are also much higher than the DON numbers detected by the other researchers utilizing the scab nurseries. The high disease pressure, high DON levels, and large range in DON values exhibited by the lines in the Ohio and Virginia nursery environments suggest these environments are excellent testing grounds to screen winter barley lines being considered for cultivation across North America.

While the infection and disease pressure in the 2022–23 Ohio scab nursery was not as intense as that of the 2021–22 Ohio scab nursery, DON levels of lines defining the extreme low and extreme high ends of DON accumulation in the 2021–22 nursery also defined the low and high extremes of the 2022–23 nursery. Lines that were intermediate in DON levels between the two extremes were less well stratified in the 2022–23 nursery than they were in the 2021–22 nursery. Some of this reduced stratification may be the result of a higher level of variation relative to the absolute DON values, i.e., absolute DON values were an order of magnitude lower in the 2022–23 nursery relative to the 2021–22 nursery, yet the variation was proportionally much greater in the 2022–23 nursery than it was in the 2021–22 nursery. Nonetheless many of the recombinants in the Bregitzer population that exhibited DON values below the presumptive resistant parent 95SR316A, or above the presumptive susceptible Charles, parsed similarly in the 2022–23 nursery as they did in the 2021–22 nursery. Taken together, these findings support the notion that incorporating genetic resistance to DON accumulation through genetics and breeding is doable when multiple environments and multiple years of testing are a component of the breeding program.

Another observation made was that many of the lines in the Ohio and Virginia program exhibited DON accumulation values at the low end of the spectrum. This result suggests that these programs may also be selecting for lines that do well under high disease pressure.

3. What opportunities for training and professional development has the project provided?
The 2023–24 season this project provided tremendous learning, training, and professional development opportunities for one Ph.D. student, Madison Dahn, one M.S. student, Frolence P. Fidelis, and two Research Scholars, Nicolas E. Rueda and Genesis Vargas. Ms. Dahn led, trained and managed all members of the Stockinger program in carrying out field design, plot maps, heading date and disease data recording.

4. How have the results been disseminated to communities of interest?
Key findings from the 2021–22 and 222–23 scab nurseries were presented at the 2024 National Fusarium Head Blight Forum, Austin TX, December 8–10, 2024. Greater detail on those findings were uploaded to the Uniform Nursery Reports webpage at https://scabusa.org/reports, and entitled “2021–22 and 2022–23 Combined Report for the Winter North American Barley Scab Evaluation Nurseries.” The findings were also provided to the breeders who submitted lines to the nursery.

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

The goal of this project is to increase resistance to head scab in the winter barley varieties grown in North America, and to use all genetic means available to get closer to achieving that goal. Some of the objectives are designed to directly achieve that goal, such as the use of GHRIL0201-088 as a recurrent parent and a donor parent in the reciprocal backcrosses with the best Ohio program's malting barley lines, an objective which is expected to "raise the bar" of head scab resistance in our breeding program's lines. Other objectives are designed to provide data and results that can be applied towards the breeding objective. Use of the Wong population falls into the latter because it is expected to provide insight into the genomic regions conferring head scab resistance, which can then be used to predict head scab resistance in breeding lines being used for variety development. The Bregitzer and GHRIL0201-088 reciprocal backcross populations are also expected to provide insight into the genomic regions conferring head scab resistance.

The plan for the next reporting period is to first test whether the set of reciprocal backcross sublines having 75% of the GHRIL0201-088 genome exhibit a mean DON level that is significantly different (lower) than of the set of reciprocal backcross lines having 25% of the GHRIL0201-088 genome. This test will be followed by tests for association between DON levels of the individual lines and height, lodging, and heading date. Tests for association between DON levels of the sets of GHRIL0201-088 reciprocal backcross lines and the height, lodging, and heading date phenotypes is expected to reveal whether resistance is due to those traits enabling the plant to escape disease pressure and whether resistance in the form of low DON levels is being conferred by an independent genetic mechanism.

The plan is to also carry out the same tests for association between DON levels of the Wong population lines and height, lodging, and heading date for the next reporting period.

If the results and data from those tests with the GHRIL0201-088 and Wong populations indicate that there is a genetic mechanism affecting DON accumulation levels that is independent of height, lodging, and heading, then the next step will be to test for association between DON accumulation levels and molecular markers across the barley genome. This step would be followed by steps that address whether the regions of the genome identified in the GHRIL0201-088 population set of lines are the same as the regions of the genome identified in the Wong population set of lines. Finding the same regions in the two different populations would strongly support the identified region as having a genetic role in DON accumulation. This data would then be used to guide selection in the Ohio breeding program's lines. A subsequent next step will be to also attain a greater resolution of the regions of the genome responsible for the difference in DON accumulation levels.

Most importantly, for the next reporting period the same sets of lines in the GHRIL0201-088 and Wong populations will be planted into plots the 2025–26 season in both the scab nursery and in non-inoculated to fields so that a second year of data and results can be obtained, which will statistically strengthen any conclusions that can be made. Similarly, we will continue to plant and evaluate the Bregitzer population.

In addition to their use in the genetic analyses of DON accumulation, the reciprocal backcross lines between GHRIL0201-088 and other Ohio lines are being used for breeding winter barley for malting purposes. A total of 172 different selections at the BC1F4 from the BC1F3 offspring from the reciprocal backcrosses between GHRIL0201-088 and seven Ohio lines were made spring 2025. These selections will be further evaluated for grain and malting quality traits. Selections meeting target specs will be advanced in the breeding program 2025–26.

My lab also plans to continue coordination of the winter NABSEN for the next reporting period. At the request of stakeholders in the barley community and those operating the databases housing the results and data from coordinated nurseries we will also request that the nursery cooperators work towards collecting their data in a more standardized format, which has been provided to the coordinators by the database curators and their advisory committees.