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The goal of this project is to promote collaboration between North American barley breeding programs to advance and distribute elite barley germplasm with resistance to *Fusarium* head blight. A limiting factor in the development of barley varieties with improved Type I resistance and lower DON accumulation is the number of screening nurseries available where the level of infection is sufficient to identify resistant lines from those that are susceptible. In addition, it is beneficial to screen multiple lines from different programs at common sites so head to head comparisons are valid. The coordinated screening effort will evaluate advanced breeding lines with putative FHB resistance from four barley breeding programs in the upper Midwest US and two breeding programs in Canada. The cooperative nursery is called the North American Barley Scab Evaluation Nursery (NABSEN). The NABSEN will contain the most advanced barley lines with putative FHB resistance and will be grown in eight locations across the region where FHB is affecting the crop. There will be a mix of locations for the NABSEN, with some being mist irrigated and inoculated and others grown under natural environmental conditions. Entries for the nurseries will be sent to NDSU barley pathology project in March each year. Seed will be redistributed to each collaborator where it will be sown in a replicated trial that includes checks agreed upon by all collaborators. Collaborators will collect data on FHB severity, FHB incidence and heading date. Barley samples will be collected from each entry and will be submitted to Dr. Paul Schwarz at NDSU for DON determination. FHB and DON data will be submitted to the NDSU barley pathology project in fall each year and a report will be prepared and distributed to all collaborators and the USWBSI NFO, making it freely available to all interested groups. The historic data set containing lines evaluated over the past 10 years will also be utilized in an association mapping study to determine the location of FHB resistance QTL. Markers associated with the QTL will be identified and can be utilized in MAS.