

FHB Screening of CDC Barley Selections, 2016-2020

Project objectives

Fusarium head blight (FHB) of barley, most commonly incited in Saskatchewan by *Fusarium graminearum* Schwabe, is currently the most important disease in this crop. Barley production has suffered millions of dollars of economic loss each year over the past decade to FHB.

Genetic tolerance to FHB is also the most environmentally desirable method to deal with this disease since it avoids the financial cost of chemical control, or agronomically undesirable practices such as stubble burning or heavy tillage. Molecular markers can improve the efficiency of incorporating genetic resistance into breeding lines, especially for diseases that are difficult and/or expensive to evaluate. For example, molecular markers we have developed for the Un8 barley smut resistance gene (through the ADF project “Developing improved markers to ensure the development of barley cultivars resistant to true loose smut.”) have greatly improved our ability to incorporate resistance into barley lines, a process that otherwise is time consuming (multiple generations are needed to phenotype the disease) and prone to inaccurate phenotyping (due to disease “escapes”). FHB evaluation of barley lines also suffers from similar difficulties as true loose smut evaluation and would therefore also benefit from the use of molecular markers.

The purpose of this research is to evaluate new CDC barley germplasm (with unknown levels of FHB resistance) and advanced CDC breeding lines (with FHB resistant parentage) for FHB resistance/low DON accumulation within the collaborative FHB nurseries already established across Canada.

The research will also aim to improve predictive NIR calibrations of barley grain DON content for use as an inexpensive screening tool in the CDC ARB Online - Research Project Application - File# 20150126 7/14 barley breeding program.

The research will also continue screening a limited number of samples within the CDC and will evaluate a set of adapted barley lines showing a range of tolerance to FHB and DON accumulation for the purpose of identifying QTL linked to FHB tolerance that could be used as an early generation screening tool in the CDC barley breeding program prior to entering lines into the collaborative FHB nurseries.