

## **Analysis of Transcript Abundance in Two-row Malting Barley on Interaction with *Fusarium graminearum* Chemotypes and its Potential Application in Barley Breeding**

### Project overview

A proposal entitled “Analysis of Transcript Abundance in Two-row Malting Barley on Interaction with *Fusarium graminearum* Chemotypes” was earlier submitted to conduct an RNA-Seq (RNA Sequencing) study to make contrast of: two-row malting barley cultivars ‘CDC Kendall’ vs. ‘Norman’.

‘Norman’ was derived from ‘CDC Kendall’ using in vitro selection using mycotoxin laden growth media applied in conjunction with doubled haploid technology, and shows 25% less DON content. The study also proposes a contrast of response to *Fusarium graminearum* chemotypes: 3ADON, 15ADON and NIV.

In recent years 3ADON has progressively invaded western Canada and displaced the 15ADON chemotype that has previously dominated. The 3ADON chemotype is of concern to barley producers as it has potential to produce higher toxin levels. We also propose to evaluate NIV chemotypes which are not present in Canada, but have become common in southern-USA regions.

While NIV chemotypes generally produce less overall toxin, NIV is of concern as it has a higher mammalian toxicity than DON. The study targets time points 72 & 96 hours post infection based on prior knowledge from previous experiments. Funding was requested for a single year to cover only the cost related to sequencing.