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PROJECT 1 ABSTRACT
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In studies at the University of Minnesota we have observed that higher deoxynivalenol (DON) accumulation tended to occur in point-inoculated spikelets of Fusarium head blight (FHB)-resistant barley germplasm compared to FHB-susceptible germplasm in the first 72 h after inoculation (Evans et al., 2000). Studies by other researchers, using near-isogenic lines (NILs) of wheat, have shown that resistance to DON accumulation maps in regions of the genome that are not associated with FHB severity, suggesting that resistance to disease development and DON accumulation may be independent (Zhou et al., 2002). The studies by Zhou et al. (2002) were conducted on grain of NILs at harvest, much later than the observations we have made in barley.

The barley breeding program has further investigated the genetics of the accumulation of DON within point-inoculated spikelets shortly after inoculation and, in collaboration with the small grains pathology program. This research (Mesfin et al., 2003; Smith et al., 2004) has led to the identification of a single QTL on chromosome 3 in a Fredrickson/Stander mapping population. This QTL explained 18 and 35% of the variation for DON accumulation in barley spikelets within the first 72-h after point-inoculation with macroconidia of a single isolate of *F. graminearum* in two respective experiments. Furthermore, this QTL was validated in two subsequent experiments using NILs for the QTL region. In all of these experiments, toxin accumulation was determined in whole spikelets, which included the palea, lemma and the developing barley kernel or seed. Given the importance of DON to the malting barley industry from concern over potential health risks and its role in virulence in FHB, it is essential to develop a better understanding of the biology of toxin accumulation in this host-parasite interaction.

The goal of this proposal is to better define the host-parasite interaction during pathogenesis of barley with *Fusarium graminearum*. Our specific objectives are;

1) to characterize the effect of the single QTL we have identified by investigating host-parasite interactions on toxin accumulation (in paleas and lemmas, and kernels) in NILs differing in the alleles at the identified QTL
2) use toxin-time course experiments to investigate the effect of the identified QTL on DON accumulation and link this to ergosterol accumulation in host tissues (a measure of fungal colonization)
3) determine the affect of this QTL on toxin accumulation in barley from early in infection through to harvested grain, and
4) investigate the stability of the effect of the identified QTL by using a wider range of isolates of *F. graminearum* than has previously been examined.