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PROJECT 1 ABSTRACT
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Breeding for FHB resistance is daunting because of the lack of a single assay to assess disease infestations. An ELISA system was developed which we used to evaluate mapping populations and the North American Barley Scab Evaluation Nursery. In both instances there was no genotype x environment interaction that is normally ubiquitous in field experimentation investigating Fusarium Head Blight. Clearly, the ELISA assessment of *Fusarium* had less variability than FHB scores or DON analysis suggesting ELISA may be a better method for phenotyping genetic mapping and breeding populations, as well as evaluating nurseries. The hypotheses we want to test are whether ELISA quantification of 1) mapping populations will provide accurate phenotype of disease resistance and, thus, new quantitative genetic information, 2) breeding populations will identify superior parents low in FHB/DON, and 3) wheat FHB nurseries will have lower variability in assessing *Fusarium* infection than disease severity, visual scabby kernel, or DON evaluations. A total of 1,500 samples from existing mapping, breeding and nurseries from barley genetic (Kevin Smith, Univ. Minnesota) and breeding programs (Kevin Smith; Rich Horsley, NDSU; Blake Cooper, Busch Ag) as well as a wheat nursery (Jim Anderson, Univ. Minnesota) will be grown in the field, inoculated with *Fusarium*, evaluated for FHB at mid-dough development, and grain harvested. Harvested grain will be analyzed for DON and *Fusarium* with ELISA. Data will be analyzed by analysis of variance, CV's compared, and rank correlations calculated for all possible two-way comparisons. ELISA data will be used by breeders and geneticists to find molecular markers unique to ELISA, select parents for breeding, and screen advanced breeding nurseries for FHB resistance. Resource allocation will be calculated to estimate efficiency of screening for each method used.