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PROJECT 1 ABSTRACT
(1 Page Limit)

Marker-assisted selection based on using a handful of DNA markers linked to the major resistance QTL for Fusarium head blight (FHB) has been making a slow progress on improving the level of resistance in wheat and barley due to its complex trait inheritance. Availability of high-density SNP arrays and rapid evolution of next-generation sequencing technologies have enabled genome-wide marker data to be obtained from a large number of samples at a more affordable cost. Marker-based plant breeding, thus, is at the transitioning stage from targeting a few major QTL linked to the traits to assessing the effects of genome-wide markers on complex trait performance. Genomic selection (GS) is such a breeding strategy that allows breeders to select for complex traits based on genome-wide marker data alone. Empirical studies conducted in both wheat and barley based on DNA marker data have demonstrated the high prediction accuracy for both FHB and DON grain content using GS. The objectives of this research are to (1) generate genome-wide SNP marker data using the cost-effective genotyping-by-sequencing (GBS) methods to facilitate the evaluation of the effectiveness of GS on improving FHB resistance and DON content for spring wheat and durum wheat breeding programs, and to (2) continue providing genotyping support for the spring barley breeding programs for their ongoing GS efforts using the targeted amplicon sequencing approach. The outcome of this research is expected to provide wheat and barley breeders with critical information to assess the benefits of GS, and enable breeders to plan and implement the GS strategies in the subsequent breeding process for developing cultivars with better FHB resistance.