

Project Abstract

Project Title:	A Double Haploid Initiative to speed development of FHB resistant Soft Winter wheat	
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This proposal expands the regional Double Haploid (DH) initiative to quickly develop and release high-yielding varieties that contain effective FHB resistance pyramids. Objectives are: 1) Develop DH lines that combine multiple effective FHB resistance genes/QTL in a high-yielding background; 2) Utilize molecular markers to track FHB genes/QTL and enrich F₁ DH populations; and 3) Share new DHs with all VDHR-SWW breeders after the initial culling such that each breeder evaluates about 420 new DHs each year.

This region-wide project includes extensive phenotyping of DHs and maximizes economic return by ensuring that DHs with high cultivar potential are not discarded due to chance performance in a single environment. Each breeder will have many DHs to evaluate and better data for selection, while, each DH will have a much higher probability of being tested in the environment it performs best in. Cultivars adapted to the region with improved FHB resistance, good yield, and resistance to important diseases and insects will be developed and commercialized.

Each breeder will select crosses that combine effective FHB resistance QTL in high yielding, adapted backgrounds. Bi-parental crosses selected for DH production will have several FHB QTL, some being homozygous, to increase the frequency of DHs with multiple FHB QTL. F₁ seed of three-way crosses will be vernalized and simultaneously haplotyped by the Eastern Wheat Genotyping Lab. F₁ seedlings of three-way crosses with desired FHB QTL combinations will be submitted to the DH Lab. Some of the crosses will include the newly characterized and effective *Fhb7* gene backcrossed into an adapted, high-yielding background. Each program will develop and evaluate about 420 DHs per year and select 10 - 25% based on qualitative traits. Seed of these will be shared with all cooperators such that each breeder will receives 336 to 840 DHs annually. Previous research within the SunGrains group showed that it is common for a breeding line to be discarded by the originating breeder and to excel in a different environment and be released by a second breeder. All DHs that enter first year yield trials will undergo low coverage, genome-wide sequencing and most will be entered into the regional Genomic Selection program.