

Diversification of FHB Resistance QTL in Winter Wheat Germplasm

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Introduction

- Genetic resistance of wheat to Fusarium Head Blight (FHB) is determined by interactions of multiple quantitative trait loci (QTL) and influenced by genotype X environment interaction.
- “Larger effect”, “validated” single resistance QTL, such as *Fhb1*, *Qfhs.ifa-5A*, *Qfhb.rwg-5A.2*, *Fhb6*, etc. have been described (literature) and are being widely used in breeding programs.
- “Genetic background” or “native” resistance (presumably from unknown, “smaller effect”, and “unvalidated” QTL) is more difficult to use but can significantly complement the validated, “larger effect” resistance QTL.
- Diversifying the available “larger effect” and “background” resistance QTL in NDSU winter wheat (WW) germplasm will greatly benefit FHB resistance breeding.

Objectives

- Transfer the newly-available FHB resistance QTL, *Fhb7*, through modified backcrosses to our WW breeding material.
- Employ a testcross analysis to evaluate 14 well-adapted WW genotypes for their FHB Type II general (GCA) and specific (SCA) combining abilities.

Materials and Methods

Introgression of *Fhb7*:

- Spring wheat accession XWC14-255-3-1 was provided by Cai (2021) and carries a small translocation (7BS-7BL-7EL) from *Thinopyrum elongatum* that harbors *Fhb7*. Crosses and backcrosses to winter wheat (Fig. 1) were initiated with F₁: 20M5 that was heterozygous for *Fhb7* (in Chinese Spring background).

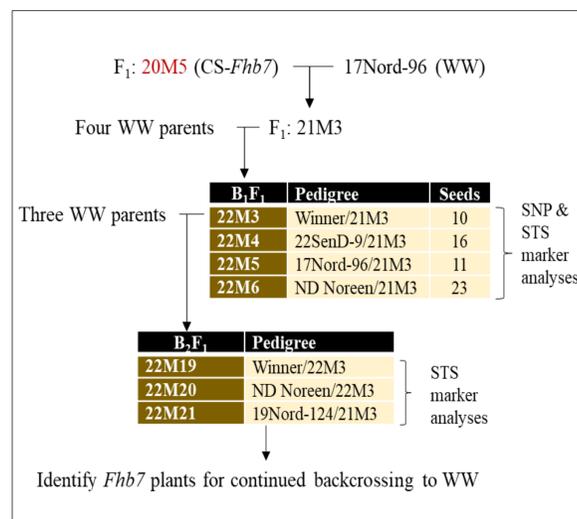


Figure 1: Modified backcrosses to transfer *Fhb7*.

- F₁: 20M5 was crossed with 17Nord-96 and their F₁ was backcrossed to four different winter wheat backgrounds (crosses 22M3-6; Fig. 1). A total of 81 genotypes including the progenies and parental control were analyzed using (i) the *Xwgc-2315* STS marker (Zhang, 2022) as well as (ii), the Illumina 90K SNP array (USDA-ARS, Fargo).
- Among the B₁F₁ progeny, a single plant with reduced height, high fertility and promising phenotype was chosen for making a second backcross to three well-adapted winter wheat genotypes (crosses 22M19-21; Fig. 1). The material is being vernalized for continuation of marker analyses and backcrosses.



Figure 2: B₁F₁ plant 22M3-9 tested positive for the presence of *Fhb7*, had the most acceptable phenotype and was used for further backcrosses

Testcross analyses to detect background resistance QTL:

- Fifty-six F₁ crosses of a 14 X 4 testcross analysis were completed and the F₁ planted in a completely randomized greenhouse trial (four replicates) that includes the 18 parents. Following vernalization, the trial will be moved to a greenhouse for testing FHB Type II resistance.
- Statistical analyses to quantify GCA and SCA combining ability will be done according to the line X tester method (Kempthorne, 1957).

Results and Discussion

Introgression of *Fhb7*:

- F₁ hybrids with 17Nord-96 were tall with poor phenotype.
 - Sixty B₁F₁ were obtained following crosses with four winter wheats (Fig. 1). Comparison of chromosome 7B-associated SNP markers among parental controls and the 60 B₁F₁ revealed three SNP loci: Excalibur_c24639_562 (534.63 cM); tpb0026f23_1134 (547.82 cM) and Excalibur_c16245_840 (458.56 cM); (Fig. 4) that produced a consistent haplotype which appeared to be associated with the *Fhb7* translocation. This haplotype occurred in the primary *Th elongatum*/CS amphiploid (2n=56); the *Th elongatum*-CS disomic addition 7E (2n=44); the translocation line XWC14-255-3-1 and 30 B₁F₁. The haplotype was absent from all the wheat parents and the remaining 30 B₁F₁.
 - The amplification of the dominant STS marker coincided perfectly with the presence of the *Fhb7* haplotype across all genotypes, confirming *Fhb7*'s presence among the segregates and its location at the distal end of 7BL.
 - A B₁F₁ plant (22M3-9; Fig. 2) with *Fhb7*, desirable semi-dwarf phenotype, early maturity and large fertile spikes was used for further backcrosses employing three winter wheat parents.
- Testcross analyses:**
- The parents and F₁ hybrids of a 14 X 4 testcross analysis will be evaluated for FHB resistance in December 2022.

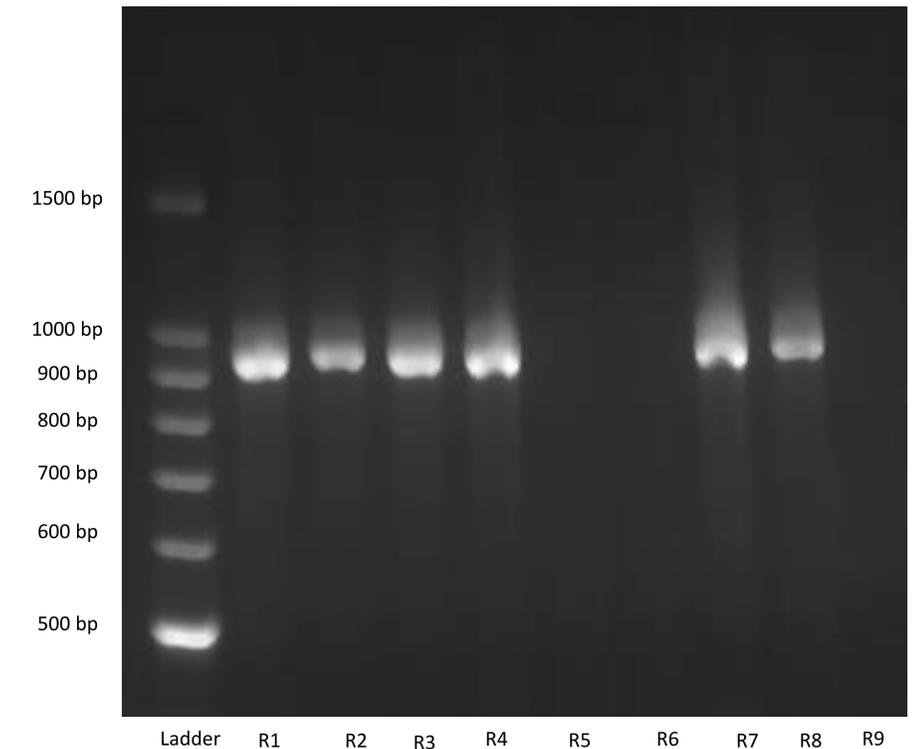


Figure 3: Use of STS marker *Xwgc2315* (dominant) to detect *Fhb7* using gel electrophoresis

	R1	R2	R3	R4	R5	R6	R7	R8	R9
Excalibur_c16245_840	AB	AB	AB	AB	AA	AA	AB	AB	AA
Excalibur_c24639_562	AB	AB	AB	AB	AA	AA	AB	AB	AA
tpb0026f23_1134	AB	AB	AB	AB	AA	AA	AB	AB	AA

Figure 4: Three SNPs co-segregated with the *Xwgc2315* STS marker located at the distal end of chromosome 7B.

References

- Zhang, W., Danilova, T., Zhang, M., Ren, S., Zhu, X., Zhang, Q., ... & Cai, X. (2022). Cytogenetic and genomic characterization of a novel tall wheatgrass-derived *Fhb7* allele integrated into wheat B genome. *Theoretical and Applied Genetics*, 1-11.
- Kempthorne, O. 1957. An Introduction to Genetic Statistics, John Wiley & Sons, New York, NY, USA

Acknowledgments

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