

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).

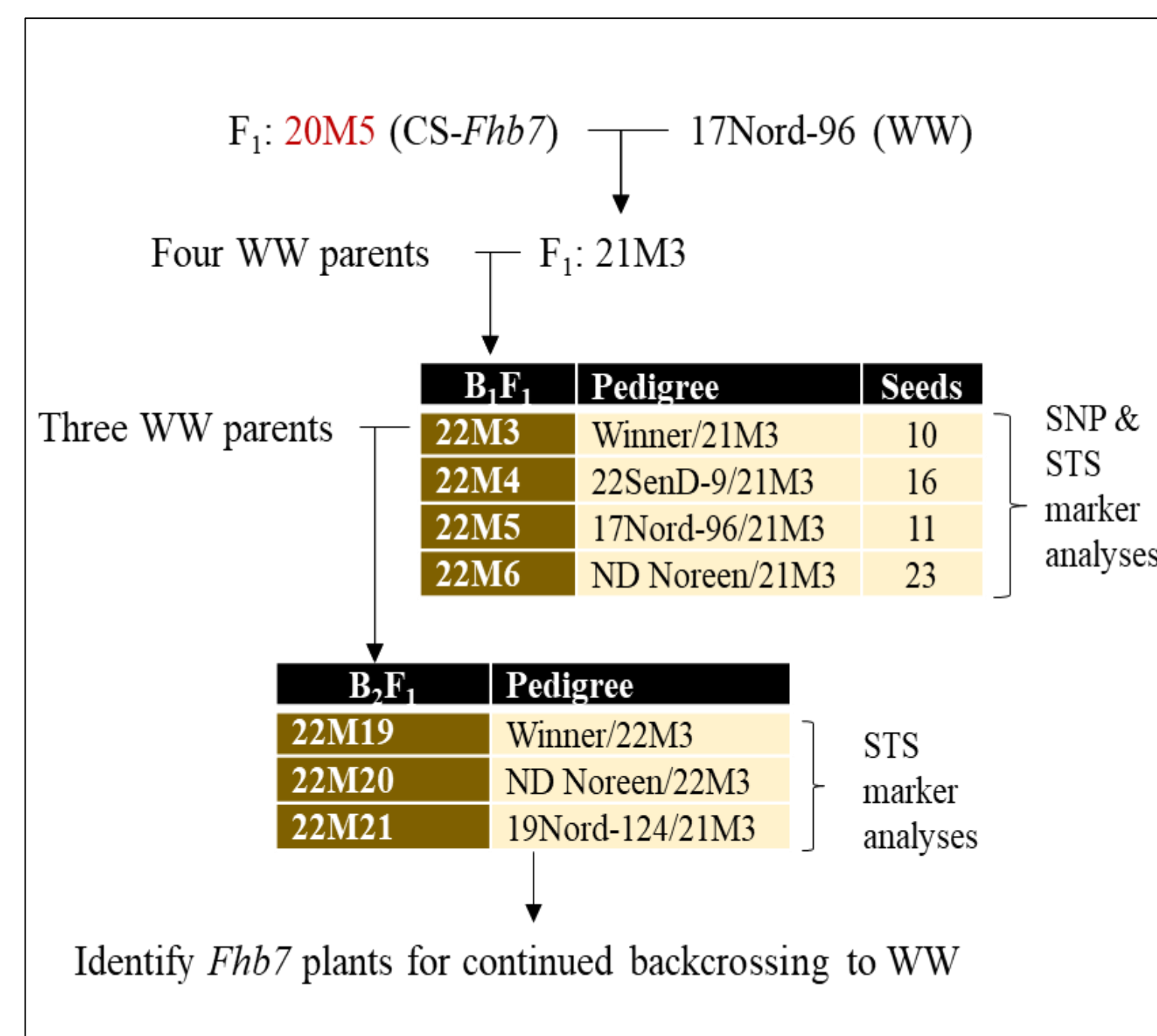


Figure 1: Modified backcrosses to transfer *Fhb7*.

- 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.

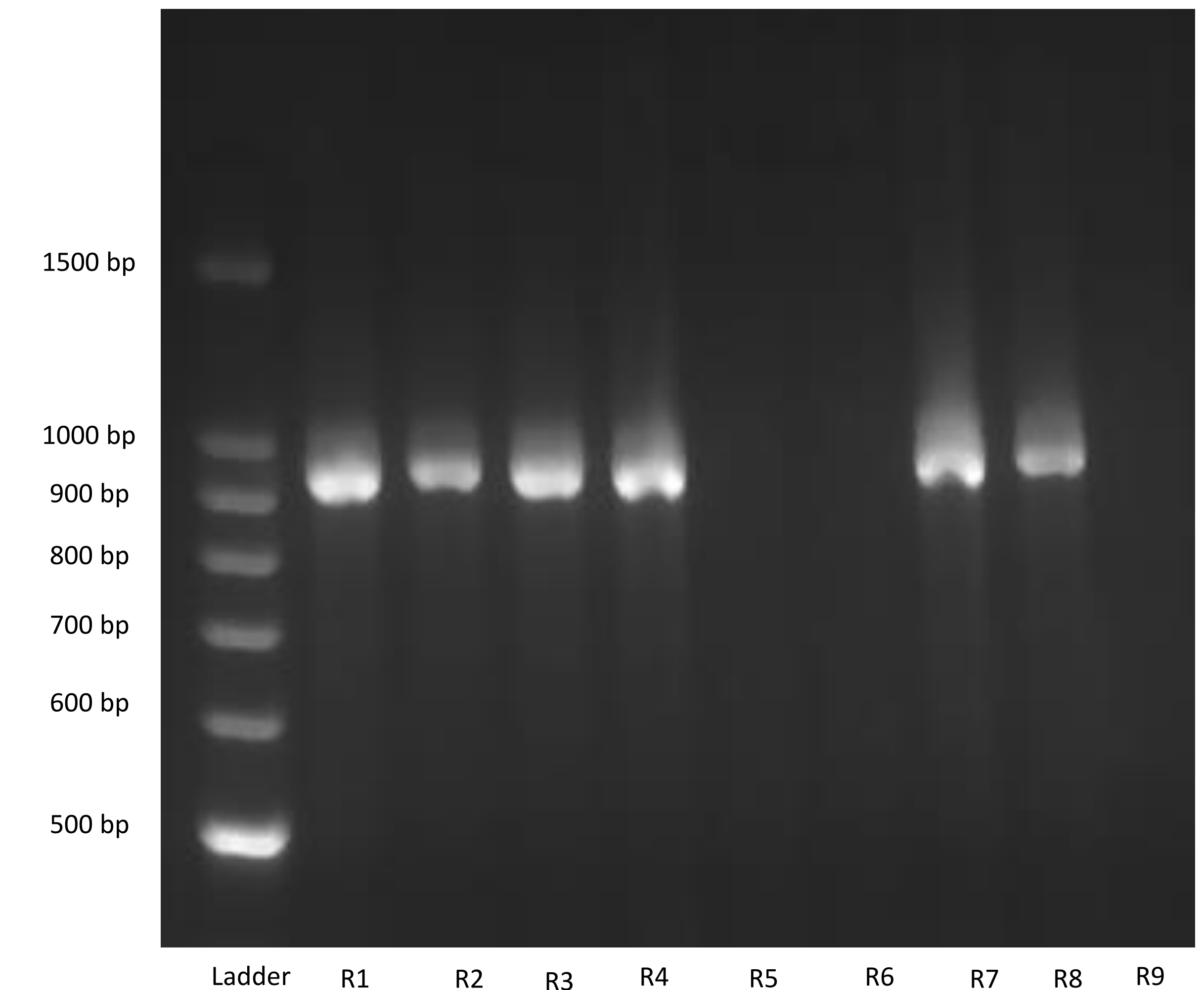


Figure 3: Use of STS marker *Xwgc2315* (dominant) to detect *Fhb7* using gel electrophoresis

	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

This is a cooperative project with the U.S. Wheat & Barley Scab Initiative funded by the U.S. Department of Agriculture under agreement numbers FAR0031913 and FAR0035988. Additional funding was provided by the NDSU College of Agriculture, Food Systems, and Natural Resources (Fund number FARG008155). Bipin Neupane and Bradley Bisek helped to execute the project. We thank Dr. Xiwen Cai for providing the *Fhb7* translocation and marker information and Mary Osenga USDA, Fargo for doing the SNP genotyping.



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