Genetic characterization of seedling and adult stage leaf rust resistance in a geographically diverse panel of wheat

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INTRODUCTION

Leaf rust, caused by *Puccinia triticina* (*Pt*) is among the most devastating diseases posing a significant threat to wheat production globally. Host resistance is the most effective management strategy to control rust diseases. The wheat genepool contains a large set of resistance genes, with currently having more than 150 race-specific all-stage resistance (ASR) genes identified, and many are effectively deployed in wheat cultivars. The race-specific genes provide resistance at the seedling stage. In contrast, non-race specific, adult-plant resistance (APR) is often partial resistance at the adult plant stage and more durable due to non-specificity to the pathogen races. Identification of resistance loci conferring adult plant resistance against leaf rust will help in developing durable leaf rust resistant cultivars. Therefore, exploring new sources of resistance is important for proper utilization of resistant sources.

OBJECTIVES

1. Evaluate a diversity panel against different prevalent leaf rust races in ND for seedling and adult plant resistance.
2. To identify genomic regions associated with seedling and adult plant resistance to leaf rust.

MATERIAL AND METHODS

Plant Material

A diversity panel of 365 bread wheat accessions selected from a worldwide population of landraces and cultivars was evaluated for leaf rust resistance at the seedling and adult plant stage.

Phenotyping

- Seedlings were evaluated against two leaf rust races, namely TDBJQ and TBBGS in two replications in the greenhouse facility at NDSU. The lines were scored at 2-leaf stage using a 0 to 4 scale described by Stakman et al. (1962). The IT scores from 0 to 4 were converted into a linearized scale (LS) from 0 to 9 as described by Zhang et al. (2014).
- The spring wheat lines were evaluated in field experiments conducted at two locations in North Dakota, Prosper and Langdon. Trials were inoculated with *Pt* race composite at flag leaf stage. Disease severity (DS) on the lines was scored using the modified Cobb's scale (Peterson et al.,1948) and host response to infection was determined according to Roelfs et al. (1992) .

GWAS Analysis

- The diversity panel has been previously genotyped using wheat exome capture (He et al., 2019). A filtered set of 302,524 SNPs was used for conducting the preliminary GWAS analysis.
- GWAS was performed using GAPIT3 using FARMCPU algorithm. The model used kinship matrices (K) and three components from principal component analysis (Q) to control the confounding effects of stratification.
- An arbitrary threshold $-\log_{10}(P)=5$ was used to declare an association significant for a given trait.

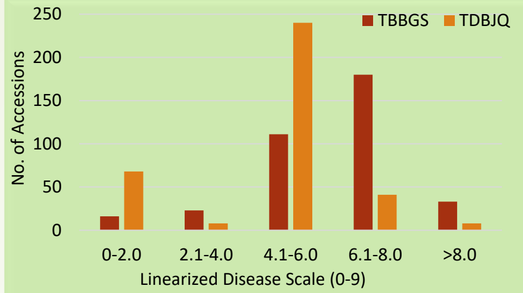

Fig 1. Distribution of seedling responses to two *Puccinia triticina* races, TDBJQ and TBBGS in wheat accessions.

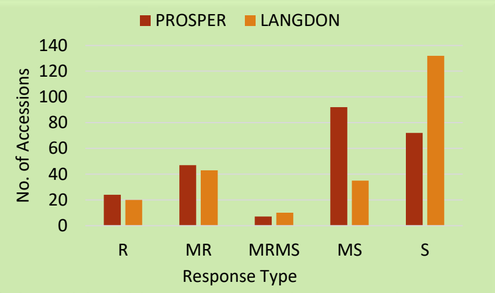

Fig 2. *Puccinia triticina* response at adult plant stage in wheat accessions evaluated at two North Dakota locations (Prosper and Langdon).

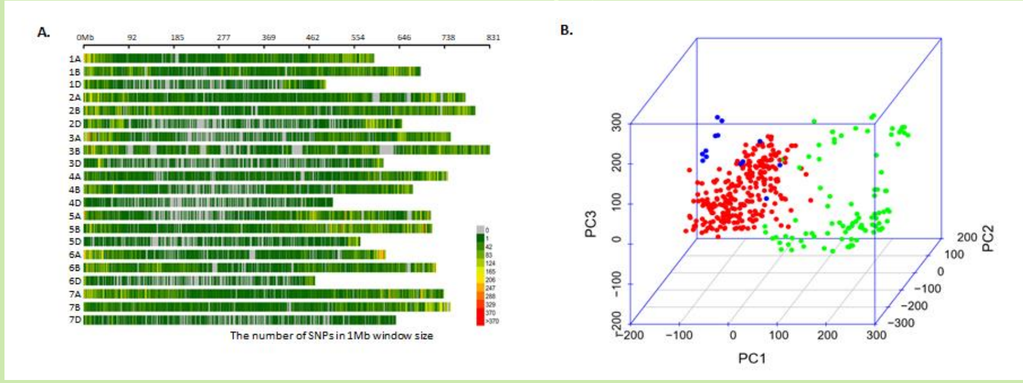

Fig 3. (A) Single nucleotide polymorphisms (SNP) density on twenty-one wheat chromosomes, and **(B)** A 3D scatter plot of principal component analysis for 365 accessions using 302,524 high quality SNPs.

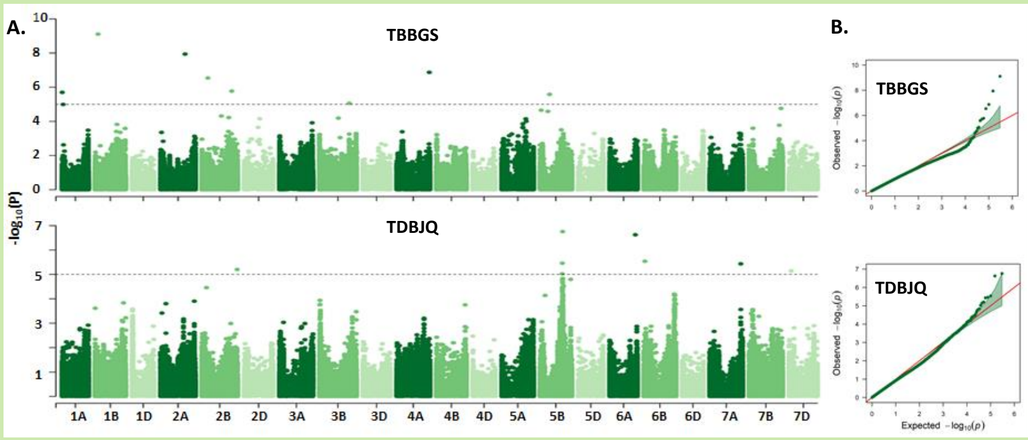

Fig 4. GWAS analysis of diversity panel for leaf rust resistance at seedling stage . (A) Manhattan Plots (B) Q-Q plots.

RESULTS

Race	SNP	Chr	Position	P. value	log10P
TBBGS	scaffold121111_1066794	1A	3,378,732	1.99E-06	5.70
	scaffold145719_3415472	1B	69,906,201	7.8E-10	9.11
	scaffold57658-1_2072082	2A	547,134,065	1.14E-08	7.94
	scaffold2319_1204793	2B	134,569,664	2.87E-07	6.54
	scaffold31412_1689540	2B	669,198,300	1.69E-06	5.77
	scaffold9253_5372146	3B	667,640,165	8.68E-06	5.06
	scaffold5465-1_658100	4A	729,862,046	1.35E-07	6.87
	scaffold131220_545501	5B	216,849,285	2.61E-06	5.58
TDBJQ	scaffold13891_739100	2B	788,841,581	6.27E-06	5.20
	scaffold92707_5188121	5B	506,312,238	1.75E-07	6.76
	scaffold126294-1_9241767	6A	572,696,744	2.38E-07	6.62
	scaffold45401_818513	6B	27,942,666	2.89E-06	5.54
	scaffold94969_1173910	7A	692,911,298	3.68E-06	5.43
	scaffold3479_289978	7D	49,873,100	7.15E-06	5.15

Table1. Summary of the significant markers associated with leaf rust resistance

- A wide distribution of seedling responses against the two *Pt* races was observed (Fig 1).
- For race TDBJQ, 20.8% of plants were highly resistant (linearized scale <= 4) and 12.1% were susceptible (linearized scale 7-9) . For race TBBGS, 10.74% of plants were highly resistant and 40.5% were susceptible.
- Majority of the lines showed susceptible response at the adult plant stage. Accessions with *R*, MR, and MRMS infection types were considered resistant to moderately resistant (Fig 2.). At Prosper (32.2% R-MR, 67.8% S) and at Langdon (30.5% R-MR, 69.5% S).
- GWAS was conducted using 302,524 high quality SNPs (Fig 3).
- GWAS for seedling response identified eight and six genomic regions associated with response to *Pt* races TBBGS and TDBJQ, respectively. (Fig 4. and Table 1).

FUTURE DIRECTIONS

- Several QTLs identified for leaf rust resistance at seedling stage.
- Associated SNPs will be validated for marker-assisted breeding.
- GWAS will be conducted to identify genomic regions associated with APR

REFERENCES

- He, F., Pasam, R., Shi, F. *et al.*. *Nat Genet* 51, 896–904 (2019).
- Peterson RR, Campbell AB, Hannah AE. Canadian Journal of Research., 26c(5): 496–500; (1948).
- Roelfs, A. P., Singh, R. P., Saari, E. E. *Rust diseases of wheat: concepts and methods of disease management* (Mexico, D.F: CIMMYT); (1992).
- Stakman, E.C., Stewart, D.M., Loegering, W.Q. United States Department of Agriculture, Agricultural Research Service; (1962).
- Zhang, D., Bowden, R.L., Yu, J., Carver, B.F., Bai, G. PLOS ONE 9(7): e103747; (2014).