Identification of Quantitative Trait Loci for Resistance to Pratylenchus neglectus in Triticale

DSU NORTH DAKOTA STATE UNIVERSIT Gurminder Singh^{1,2}, Zhaohui Liu², Justin D. Faris³, and Guiping Yan² Time 1Department of Plant Sciences, North Dakota State University, Fargo, ND, USA: 2Department of Plant Pathology, North Dakota State University, Fargo, ND, USA: 3USDA-ARS Cereal Croos Research Unit, Edward T. Schafer Agricultural Research Center, Fargo, ND, USA Zone Introduction Results Results Root-lesion nematode (RLN), Pratylenchus neglectus, is an 20 important pathogen of wheat 18 Rep1 Villax St. Jose 6 16 Siskiyou Number of RILs Utilizing host resistance is the most economical and environment-Rep4 Rep5 -5 14 (STMIM) friendly way to control RLN 12 4 10 To date, no RLN-resistant commercial wheat cultivar has been 3 reported, and sources of resistance in wheat are scarce <u>6</u> 2 Previous studies have reported high levels of resistance in rye and triticale. 50% 10% 30% 70% 90% 110% TP29757 (26.2 cM) TP20950 (35.7 cM) Objective Relative post harvest densities (%) TP4673 (33.4 cM) Figure 1. Histogram of average relative postharvest P. neglectus densities of To identify quantitative trait loci (QTL) associated with P. neglectus F2:6 Siskiyou x Villax St. Jose recombinant inbred line (RIL) population in triticale. evaluated for reaction to *P. neglectus*. **Material and Methods** Genetic map of LTC918 Siskiyou (Susceptible parent) X Villax St. Jose (Moderately resistant parent) of 4.52 at 95% level of confidence. 1 # 50 F2:6 Recombinant Inbred Line (RIL) population **Conclusions and Future Work** # \pm Genotyping Phenotyping ŧ 100 ₫ + Genotyping by Inoculation @ 300 sequencing (GBS) 150 RLN/plant method resistance into wheat germplasm. After 14 weeks, roots 200 MapDisto was used for explained 24.6% of the total phenotypic variation (Figure 3). and soil were linkage map harvested construction 1A 2A 3A 4A 5A 6A 7A 1B 2B 3B 4B 5B 6B 7B 1R 2R 3R 4R 5R 6R 7R Chromosome flanked by TP29757 and TP20950 (Figure 3). Nematode extractions and QTL mapping was performed Figure 2. Genetic map of triticale was constructed using 141 F2-5 recombinant counting were performed using QGENE 4.4.0 ٠ inbred line (RIL) population derived from a cross between Siskivou and Villax its stability. St. Jose. A total of 3,589 GBS-SNPs and seven chromosome 5R-specific

Relative post harvest densities (%) was calculated as ratio of post harvest densities of each line to mean post harvest density of susceptible check "Alpowa'

SSR markers were used to construct a linkage map covering 21 linkage groups covering all wheat and rye chromosome and spanned 2,890.33 cM in total genetic distance (Wen et al. 2018)



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Figure 3. Single-trait multiple interval mapping (STMIM) function analysis to identify QTL showing resistance to Pratylenchus neglectus on rye chromosome 5R in the Siskiyou x Villax St. Jose F2:6 recombinant inbred line population. The marker loci are shown on the X-axis and Y-axis represents the LOD score. The red region on X-axis represents the QTL region associated with P. neglectus resistance. The red highlighted loci on X-axis represents the flanking marker and black highlighted represent the loci underlying the QTL peak. The dotted lines indicate the LOD cutoff

- This is the first report in triticale to identify resistance QTL associated with RLN.
- This work provides a foundation for the introgression of rye-derived P. neglectus
- A single resistance QTL was identified on chromosome 5R for P. neglectus and
- GBS-SNP marker TP4673 underlies the peak of the QTL (9.5 cM interval) and
- The identified QTL needs to be validated in different genetic backgrounds to confirm
- The PCR-based molecular markers associated with this QTL will be helpful in finemapping and to better understand the genetics of RLN resistance

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