

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

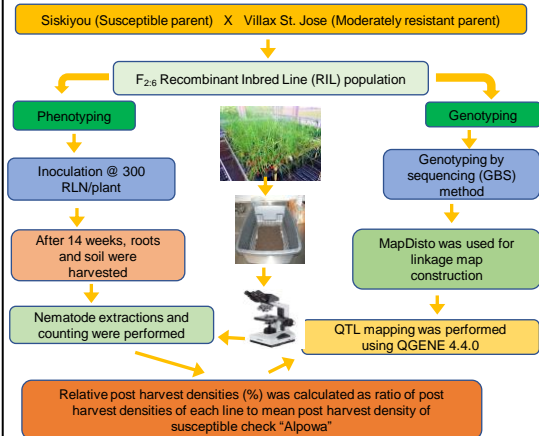
Introduction

- Root-lesion nematode (RLN), *Pratylenchus neglectus*, is an important pathogen of wheat
- Utilizing host resistance is the most economical and environment-friendly way to control RLN
- To date, no RLN-resistant commercial wheat cultivar has been reported, and sources of resistance in wheat are scarce
- Previous studies have reported high levels of resistance in rye and triticale.

Objective

- To identify quantitative trait loci (QTL) associated with *P. neglectus* in triticale.

Material and Methods



Results

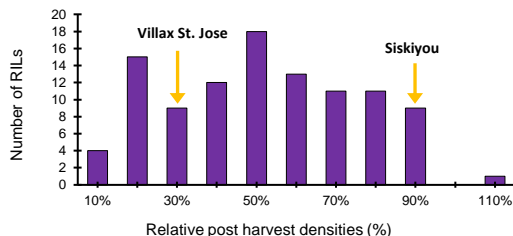


Figure 1. Histogram of average relative postharvest *P. neglectus* densities of $F_{2.6}$ Siskiyou x Villax St. Jose recombinant inbred line (RIL) population evaluated for reaction to *P. neglectus*.

Genetic map of LTC918

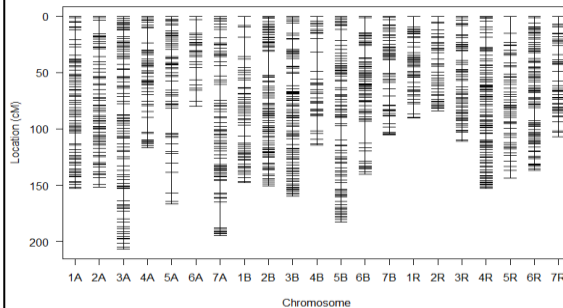


Figure 2. Genetic map of triticale was constructed using 141 $F_{2.6}$ recombinant inbred line (RIL) population derived from a cross between Siskiyou and Villax St. Jose. A total of 3,589 GBS-SNPs and seven chromosome 5R-specific SSR markers were used to construct a linkage map covering 21 linkage groups covering all wheat and rye chromosome and spanned 2,890.33 cM in total genetic distance (Wen et al. 2018)

Results

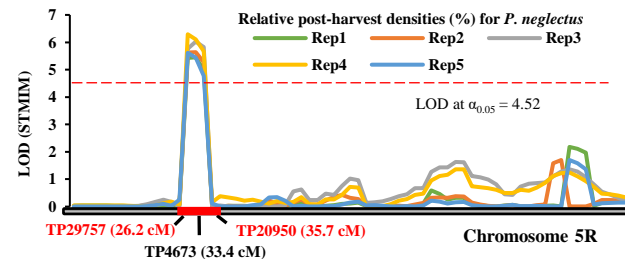


Figure 3. Single-trait multiple interval mapping (STMIM) function analysis to identify QTL showing resistance to *Pratylenchus neglectus* on rye chromosome 5R in the Siskiyou x Villax St. Jose $F_{2.6}$ recombinant inbred line population. The marker loci are shown on the X-axis and Y-axis represents 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 of 4.52 at 95% level of confidence.

Conclusions and Future Work

- 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* resistance into wheat germplasm.
- A single resistance QTL was identified on chromosome 5R for *P. neglectus* and explained 24.6% of the total phenotypic variation (Figure 3).
- GBS-SNP marker TP4673 underlies the peak of the QTL (9.5 cM interval) and flanked by TP29757 and TP20950 (Figure 3).
- The identified QTL needs to be validated in different genetic backgrounds to confirm its stability.
- The PCR-based molecular markers associated with this QTL will be helpful in fine-mapping and to better understand the genetics of RLN resistance