

Evaluation of Wild Wheat Introgression Lines in *Triticum aestivum* for Resistance to *Puccinia graminis* f. sp. *tritici*

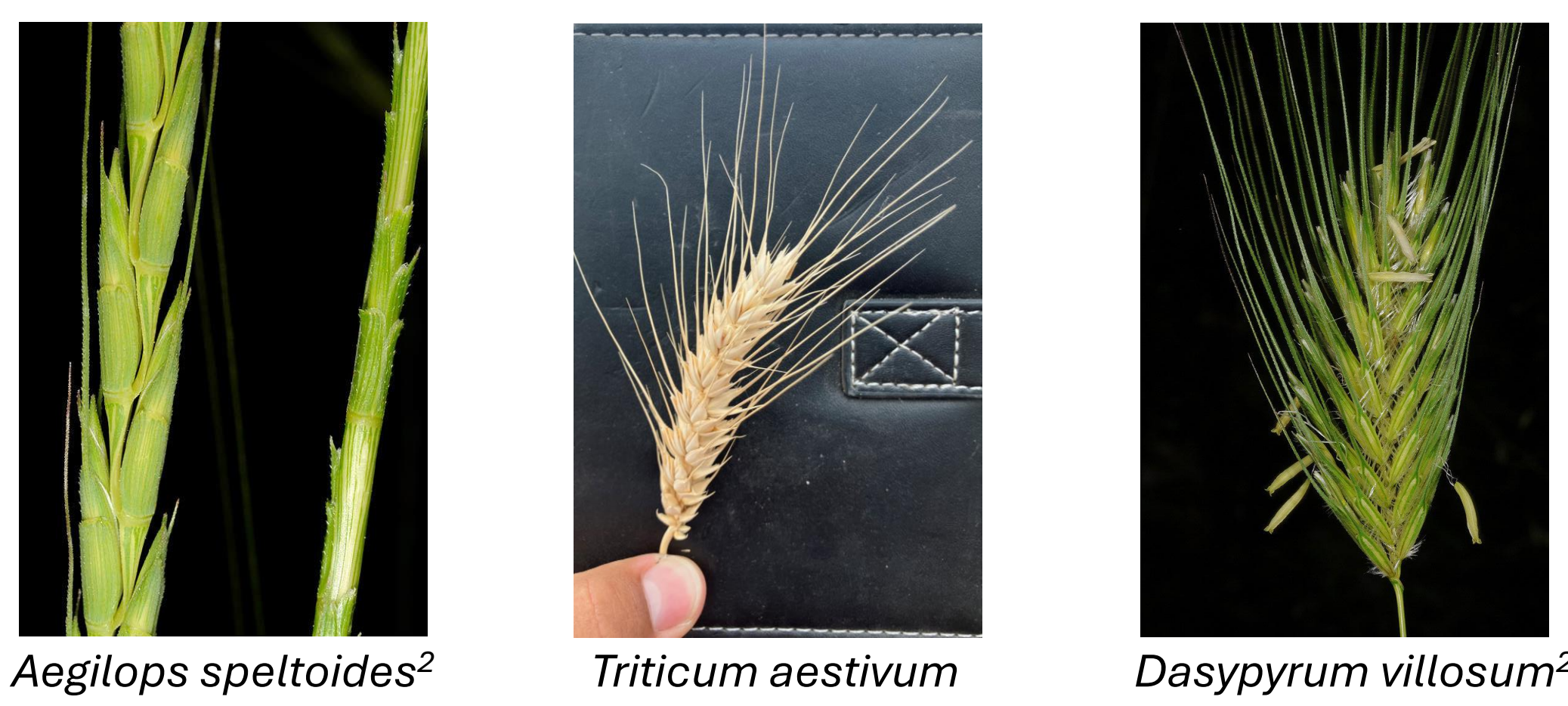


Mark Marchetti¹, Jason D. Zurn^{2,3}, Yoonha Ju^{2,3}, Jaime Knight^{2,3}, Benjamin Osae^{2,3}, Dal-Hoe Koo^{2,3}, Eduard Akhunov^{2,3}
¹ Texas A&M University, College Station, TX, U.S.A. ² Kansas State University Department of Plant Pathology, Manhattan, KS, U.S.A. ³ Kansas State University Wheat Genetics Resource Center, Manhattan, KS, U.S.A



Introduction

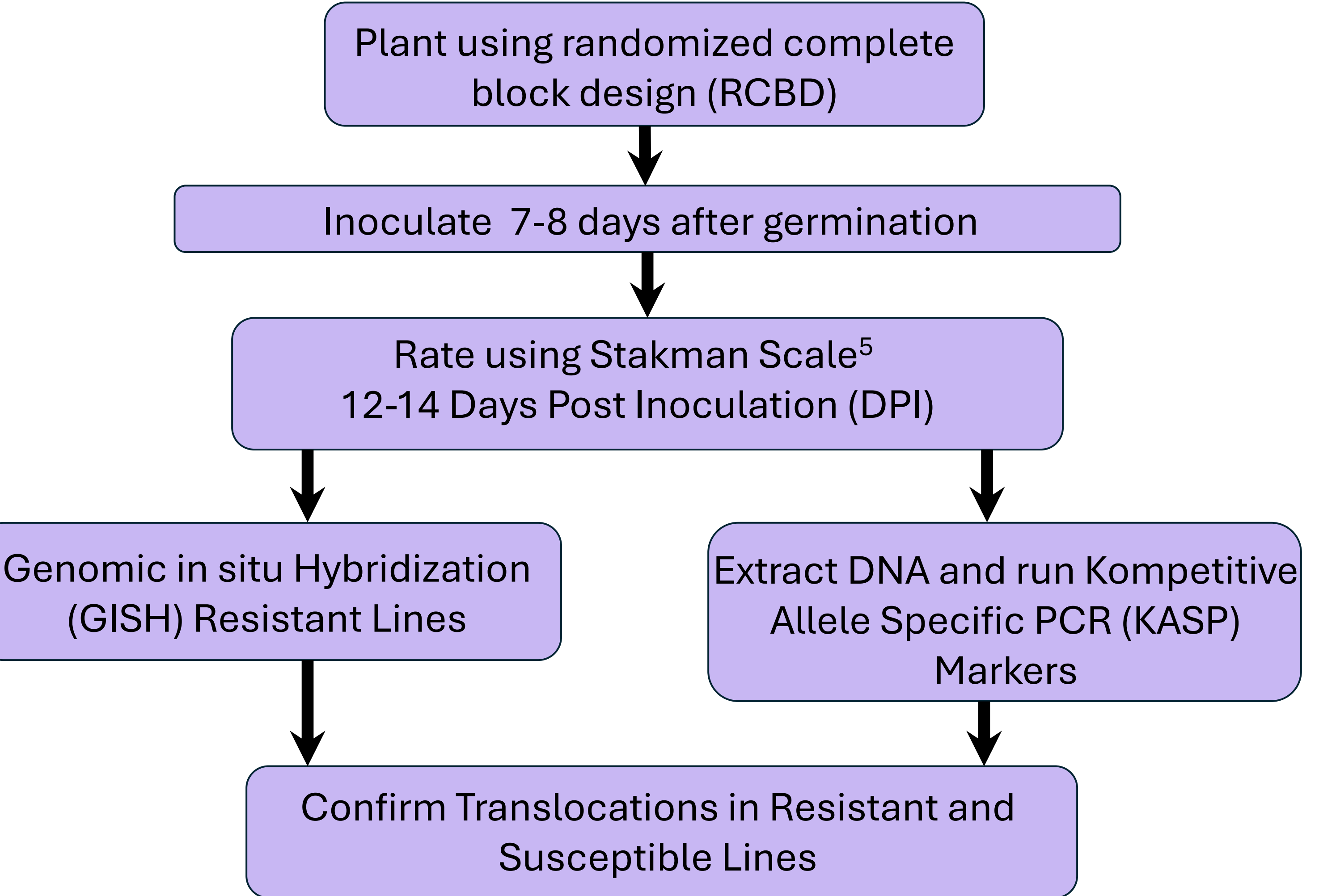
- Fungal diseases cause from 15-20% yield loss annually¹
- Substantial yearly crop losses necessitate resistant wheat variety development
- Wild wheat relatives have previously been identified as valuable sources of disease resistance (i.e., *Sr33* from *Ae. tauschii*, *Sr35* from *T. monococcum*, *Sr52* from *D. villosum*, etc.)⁴
- The Wheat Genetics Resource Center (WGRC) at K-State developed 24 wild wheat introgression lines (Robertsonian translocations, **RobT**) from *Aegilops speltoides* and *Dasypyrum villosum*.
- The WGRC is internationally-recognized for maintaining a gene bank of 2,500 wheat species accessions and housing 2,200 cytogenetic stocks, encouraging sustainable wheat research by broadening the genetic base.



❖ Objective:

- 1) Evaluate the resistance of 24 wheat-wild relative introgression lines to wheat stem rust.
- 2) Identify and confirm alien chromosome segments conferring stem rust resistance through cytological analysis and genetic markers.

Materials and Methods



Results

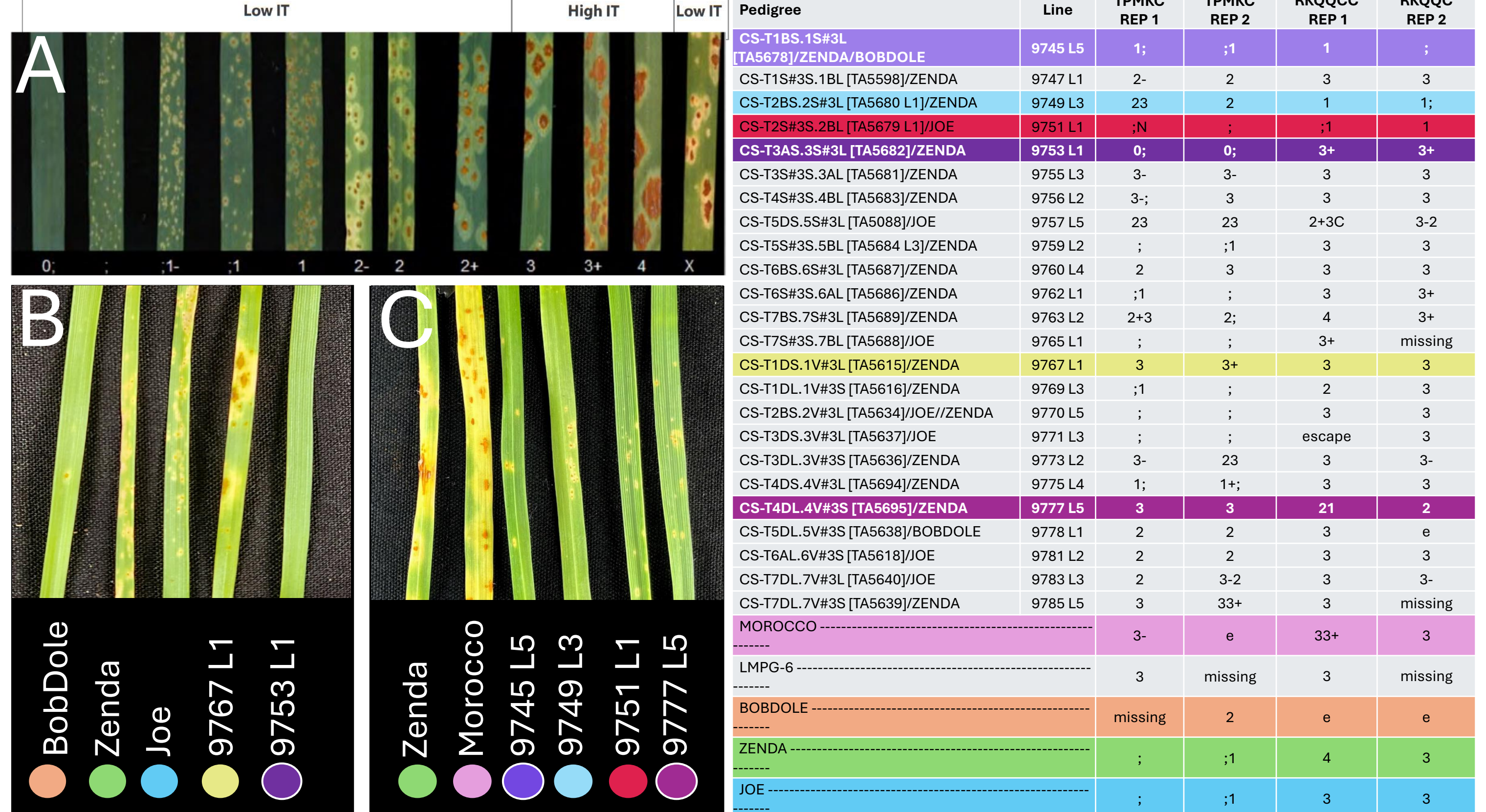
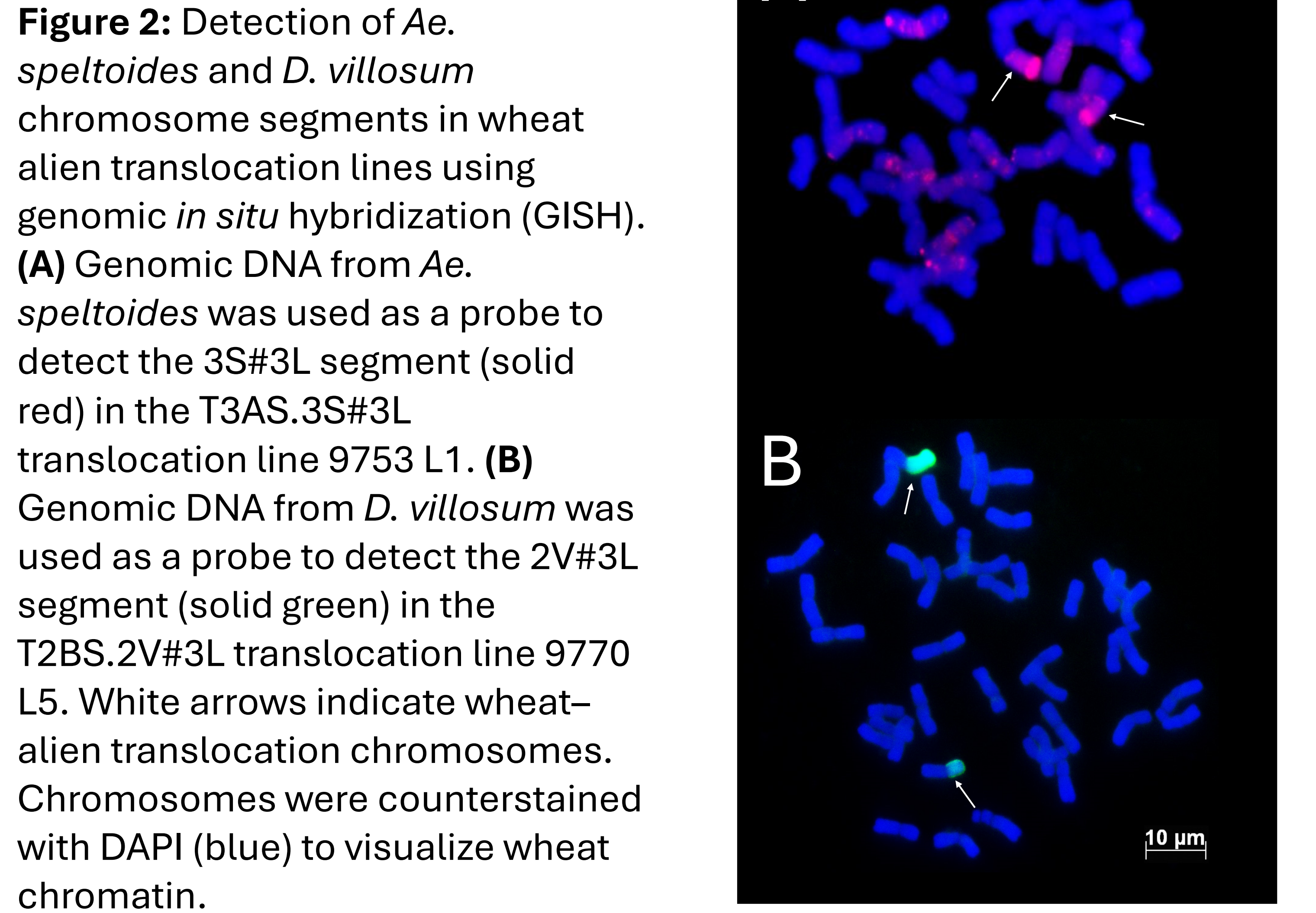


Figure 1: (A) The 24 introgression lines were scored using the Stakman Rust Scale³ at 12 DPI and displayed variable responses to wheat stem rust. (B) 9753 L1, containing an *Ae. speltoides* introgression, is more resistant than its wheat parent 'Zenda' to race TPMKC. (C) After race RKQCC screening, the introgressions from *Ae. speltoides* provided resistance in 9745 L5, 9749 L3, and 9751 L1 and *D. villosum* provided resistance in 9777 L5.

Pedigree	Line	TPMKC REP 1	TPMKC REP 2	RKQCC REP 1	RKQCC REP 2
CS-T1BS.1S#3L [TA5078]/ZENDA/BOBDOLE	9745 L5	1;	1;	1	;
CS-T1S4S3S.1BL [TA5598]/ZENDA	9747 L1	2;	2	3	3
CS-T2BS.2V#3L [TA5680 L1]/ZENDA	9749 L3	23	2	1	1;
CS-T2S4S3S.2BL [TA5679 L1]/JOE	9751 L1	;	;	1	1
CS-T3AS.3S#3L [TA5682]/ZENDA	9753 L1	0;	0;	3+	3+
CS-T3S4S3S.3AL [TA5681]/ZENDA	9755 L3	3-	3-	3	3
CS-T4S4S3S.4BL [TA5689]/ZENDA	9756 L2	3-	3	3	3
CS-T5DS.5S#3L [TA5088]/JOE	9757 L5	23	23	2+3C	3-2
CS-T5S4S3S.5BL [TA5684 L3]/ZENDA	9759 L2	;	;	3	3
CS-T6BS.6S#3L [TA5687]/ZENDA	9760 L4	2	3	3	3
CS-T6S4S3S.6AL [TA5686]/ZENDA	9762 L1	1	1	3	3+
CS-T7BS.7S#3L [TA5689]/ZENDA	9763 L2	2+3	2;	4	3+
CS-T7S4S3S.7BL [TA5688]/JOE	9765 L1	;	;	3+	missing
CS-T1DS.1V#3L [TA5615]/ZENDA	9767 L1	3	3+	3	3
CS-T1DL.1V#3S [TA5616]/ZENDA	9769 L3	1;	;	2	3
CS-T2BS.2V#3L [TA5634]/JOE/ZENDA	9770 L5	;	;	3	3
CS-T3DS.3V#3L [TA5637]/JOE	9771 L3	;	;	escape	3-
CS-T3DL.3V#3S [TA5636]/ZENDA	9773 L2	3-	23	3	3-
CS-T4DS.4V#3L [TA5694]/ZENDA	9775 L4	1;	1+;	3	3
CS-T4DL.4V#3S [TA5695]/ZENDA	9777 L5	3	3	21	2
CS-T5DL.5V#3S [TA5638]/BOBDOLE	9778 L1	2	2	3	e
CS-T6AL.6V#3S [TA5611]/JOE	9781 L2	2	2	3	3
CS-T7DL.7V#3L [TA5640]/JOE	9783 L3	2	3-2	3	3-
CS-T7DL.7V#3S [TA5639]/ZENDA	9785 L5	3	33+	3	missing
MOROCCO		3-	e	33+	3
LMPG-6		3	missing	3	missing
BOBDOLE		missing	2	e	e
ZENDA		;	1	4	3
JOE		;	1	3	3

Table 1: Introgression lines displayed variable infection types with some whole-arm introgressions providing resistance and others disrupting resistance pathways resulting in loss of resistance. Lines with infections types 0, fleck (;), 1, and 2 are considered resistant. Parental wheat lines were resistant to race TPMKC but not RKQCC. Resistance was identified in lines containing introgressions from *Ae. speltoides* and *D. villosum*.



Results

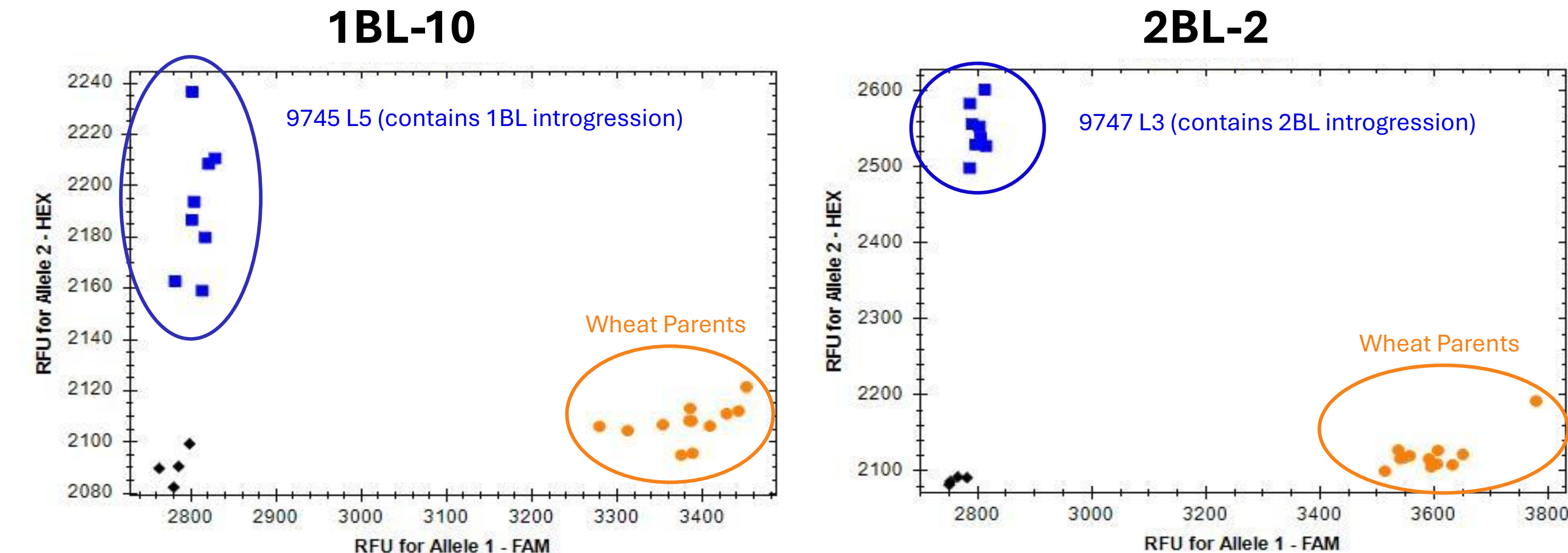


Figure 3: KASP Markers were run to validate chromosomal translocations. The X-axis represents the fluorescent intensity corresponding to Allele 1 (wheat) and the Y-axis represents that corresponding to Allele 2 (translocation). Examples above show *Ae. speltoides* introgressions on chromosomes 1BL and 2BL. These markers will prove practical for tracking the introgressions in breeding material.

Conclusions

- Whole-arm introgressions resulted in both resistance through the incorporation of R-genes and susceptibility by disrupting immune response pathways.
- 3AL introgression from *Ae. speltoides* in 9753 L1 resulted in immunity to race TPMKC but not race RKQCC.
- 1BL introgression from *Ae. speltoides* in 9745 L5 and 4DS introgression from *D. villosum* in 9777 L5 are likely new R-genes and warrant further investigation.
- The resistance found in 9749 L3 and 9751 L1 from *Ae. speltoides* may be due to the presence of *Sr47* and *Sr39/Sr32*, respectively.
- Introgressions were validated with full confidence through GISH and KASP markers.
- The results expand the R-gene repertoire in wheat.
- Future work will focus on characterizing the host-defense mechanisms associated with the newly discovered genes.

References

1. Figueroa, M., Hammond-Kosack, K. E., & Solomon, P. S. (2018). A review of wheat diseases-a field perspective. *Molecular plant pathology*, 19(6), 1523-1536. <https://doi.org/10.1111/mpp.12618>
2. POWO (2025). "Plants of the World Online. Facilitated by the Royal Botanic Gardens, Kew. Published on the Internet; <https://powo.science.kew.org/>.
3. Prof. Z.A. Pretorius, University of Free State, South Africa.
4. Rahmatov, M., Rouse, M. N., Steffenson, B. J., Andersson, S. C., Wanyera, R., Pretorius, Z. A., ... & Johansson, E. (2016). Sources of stem rust resistance in wheat-alien introgression lines. *Plant Disease*, 100(6), 1101-1109.
5. Stakman EC, Stewart DM, Loegring WQ. 1962. Identification of physiological races of *Puccinia graminis* var. *tritici*. Washington, USA: US Department of Agriculture, Agricultural Research Service, E617 (revised).

Acknowledgements

• National Science Foundation Industry-University Cooperative Research Center (NSF IUCRC) grant #1822162
• This work is supported by the NIFA Research and Extension Experiences for Undergraduates (REEU) Program grant no. 2024-68018-42431/project accession no. 1032359 from the U.S. Department of Agriculture, National Institute of Food and Agriculture.

