

A highly conserved tandem kinase *Wtk1* allele confers diverse resistance responses of *Yr15*, *YrG303* and *YrH52*

Valentyna Klymiuk^{1,2,3}, Andrii Fatiukha^{1,2}, Dina Raats^{1,2}, Valeria Bocharova^{1,2}, Lin Huang^{1,2}, Lihua Feng^{1,2},
Samidha Jaiwar¹, Curtis Pozniak³, Gitta Coaker⁴, Jorge Dubcovsky^{5,6}, Tzion Fahima^{1,2}

¹Institute of Evolution, University of Haifa, Israel; ²Department of Evolutionary and Environmental Biology, University of Haifa, Israel; ³Crop Development Centre and Department of Plant Sciences, University of Saskatchewan, Canada; ⁴Department of Plant Pathology, University of California, Davis, USA; ⁵Department of Plant Sciences, University of California, Davis, USA; ⁶Howard Hughes Medical Institute, USA

The wild emmer wheat (*Triticum turgidum* ssp. *dicoccoides*; WEW) yellow (stripe) rust resistance genes Yr15, YrG303 and YrH52 were discovered in natural populations from different geographic locations. They all localize to chromosome 1B but were thought to be non-allelic based on differences in resistance response. We recently cloned Yr15 as a *Wheat Tandem Kinase 1* (*WTK1*) and showed that these three resistance loci co-segregate in fine-mapping populations and share identical full-length genomic sequence of functional *Wtk1* (Fig 1).

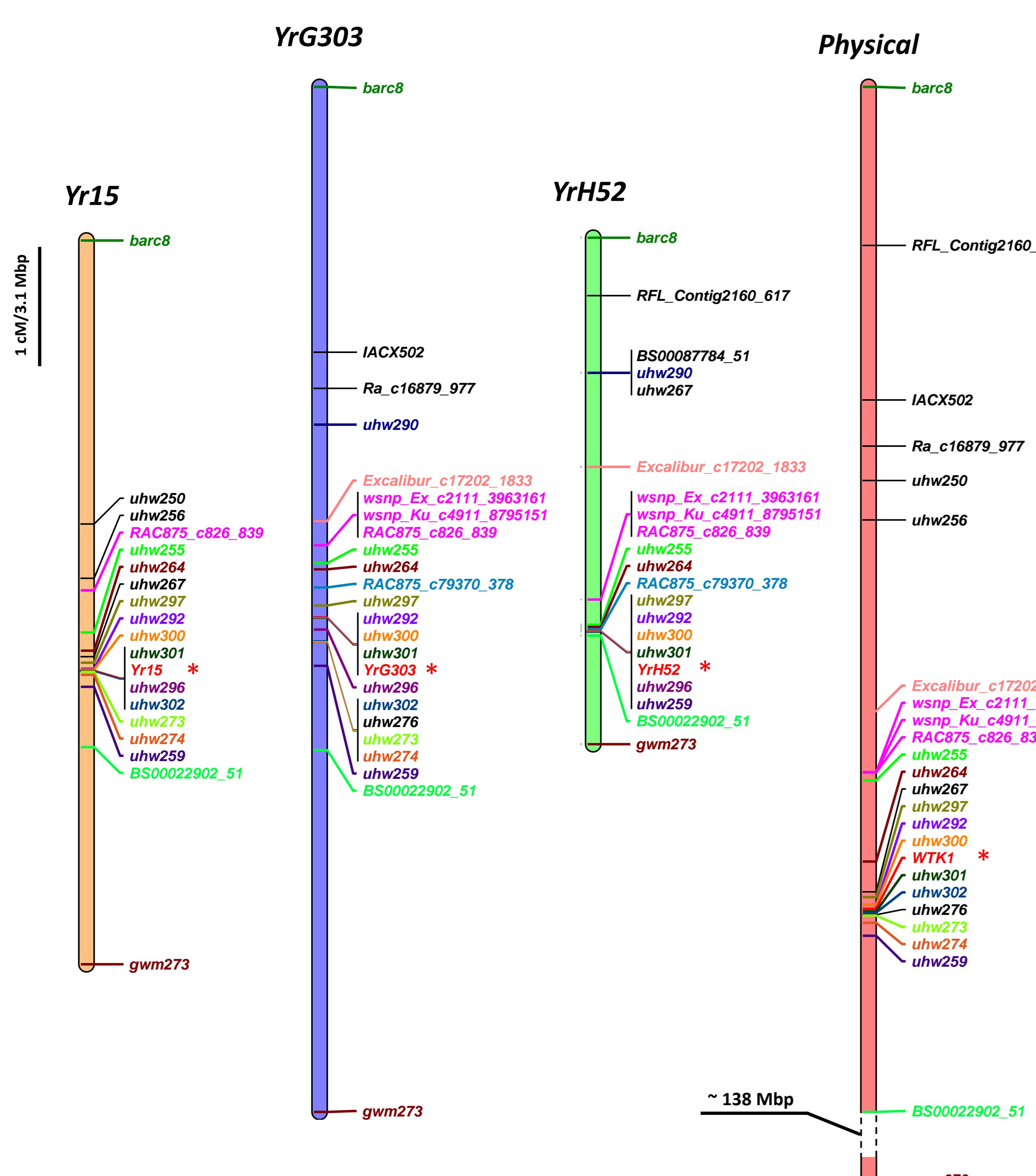


Fig. 1 Genetic and physical maps of Yr15, YrG303, and YrH52 showing the same position for all three genes that correspond to WTK1. The consensus physical map represents three reference genomes, based on 1BS pseudomolecules of WEW Zavitan, *T. durum* Svevo, and *T. aestivum* Chinese Spring.

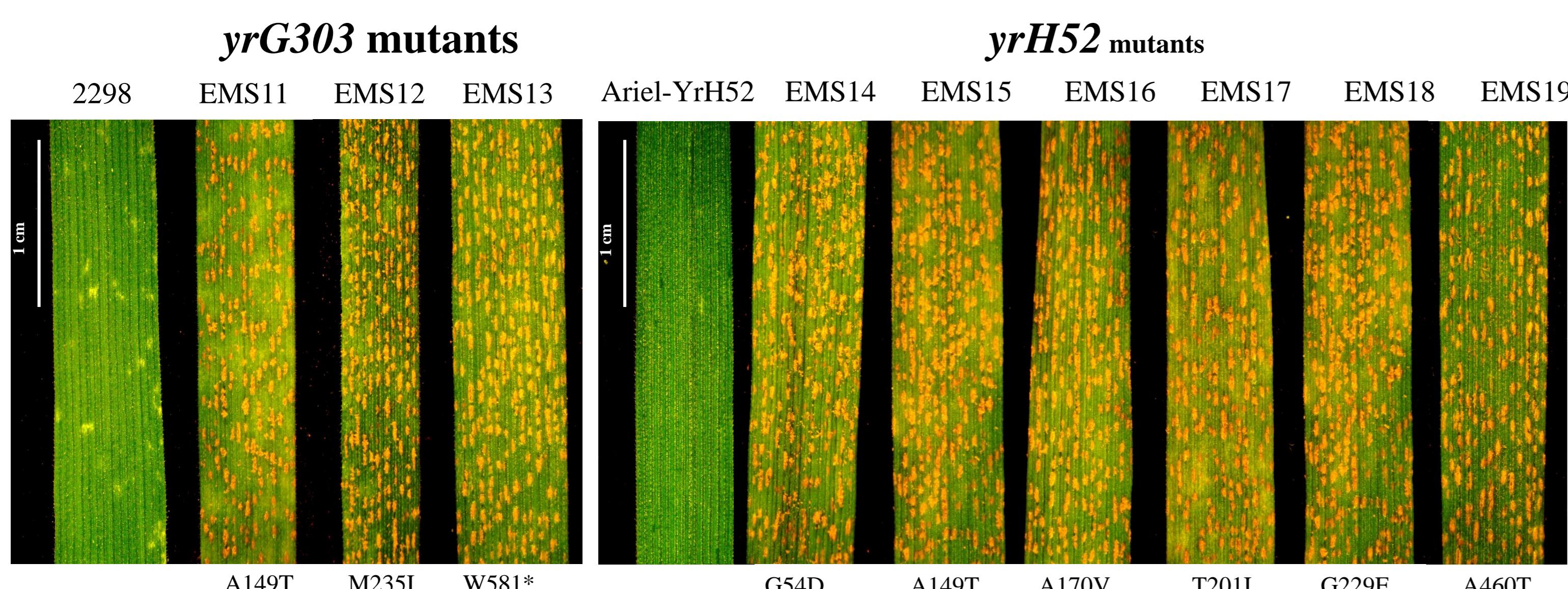


Fig. 2 Susceptible reaction of *yrG303* and *yrH52* mutants to *Pst* inoculation at 14 dpi with *Pst* isolate #5006. 2298 and Ariel-YrH52 are wild-type *YrG303* and *YrH52* hexaploid introgression lines, respectively, used to develop mutants

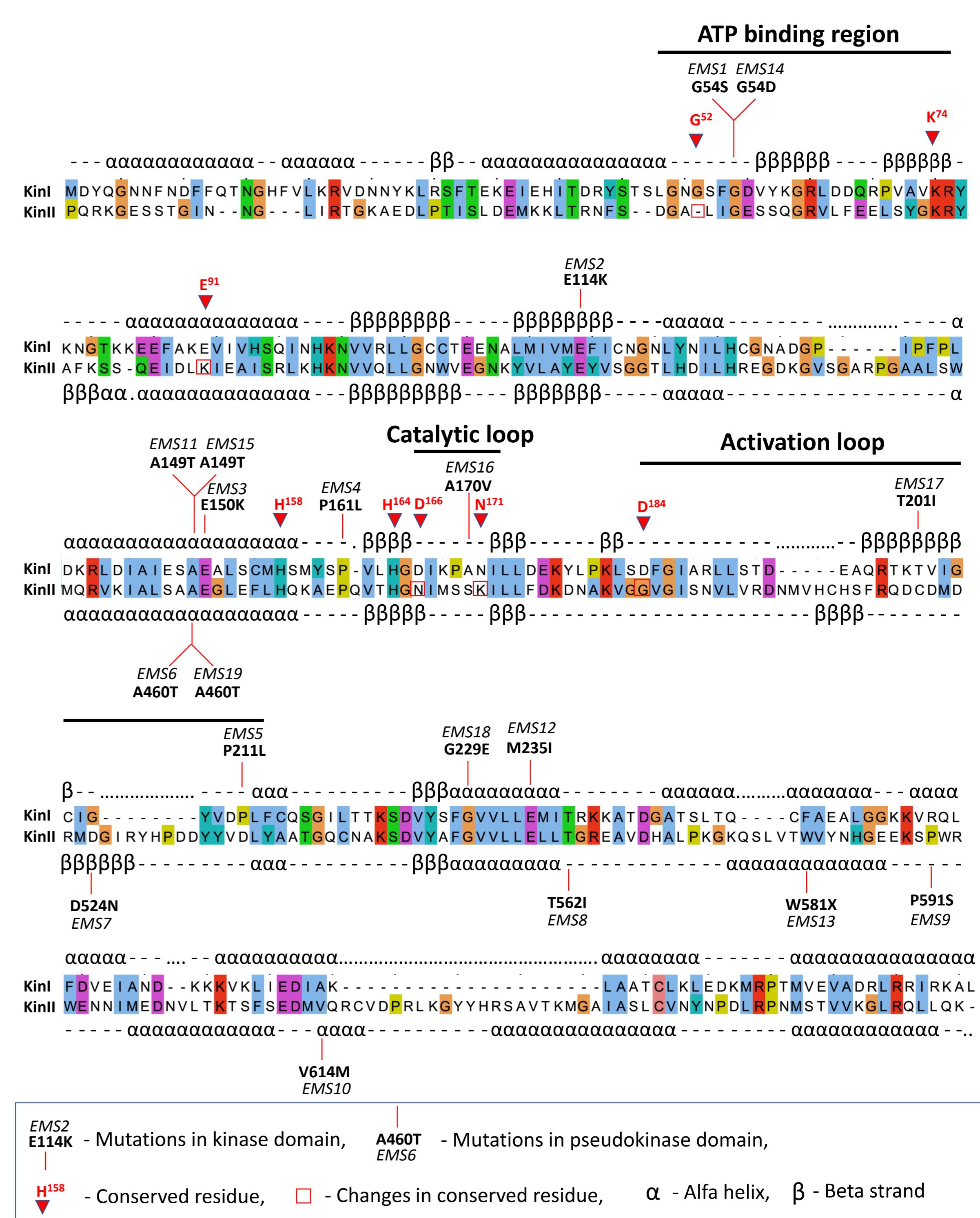


Fig. 3 Primary and secondary structures of WTK1 kinase and pseudokinase domains alongside positions of knockout EMS mutations in *yr15*, *yrG303*, and *yrH52* susceptible mutants. Vertical lines indicate EMS mutations that block resistance. KinI, kinase domain; KinII, pseudokinase domain.

Independent EMS mutagenized susceptible *yrG303* and *yrH52* lines carried single nucleotide mutations in *Wtk1* that disrupted function (**Fig. 2**). A comparison of the mutations for *yr15*, *yrG303* and *yrH52* mutants showed that while key conserved residues were intact, other conserved regions in critical kinase subdomains were frequently affected demonstrating their importance for functionality (**Fig. 3**). Introgression of *Wtk1* into multiple genetic backgrounds resulted in variable phenotypic responses, suggesting that *Wtk1*-mediated resistance is part of a complex immune response network. This information will be useful for future work on the possible molecular mechanism of *Wtk1* and its role in plant innate immunity. The *Wtk1*-mediated resistance network is diverse in WEW natural populations subjected to natural selection and adaptation, confirming that WEW natural populations have potential to serve as a good source for evolutionary studies of different traits and multifaceted gene networks.

More detailed information can be found in a published article:
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to yellow rust are encoded by a single locus *Wtk1*. *Journal of*
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