

# Genome-wide identification, functional annotation and expression profiling of cyclophilin protein family responsive to leaf rust resistance in bread wheat (*Triticum aestivum* L.)

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**Introduction:** Out of three rusts affecting wheat crop, leaf rust caused by *Puccinia triticina* L. is the most common and prevalent in almost all wheat growing regions in the world. Cyclophilins (CYPs) are a group of highly conserved proteins and have been found to be crucial in pathogenesis (Singh et al. 2017). In plants, the differential gene expression of CYPs has been observed in response to both biotic and abiotic stresses (Marivet et al. 1992; Romano et al. 2004). the role played by CYP gene in imparting leaf rust resistance in wheat has not been studied. Therefore, we conducted a comprehensive genome wide identification of wheat CYP genes (*TaCYPs*) followed by their interaction, and change in expression profile during leaf rust infection. Efforts have been also made to develop miRNA-SSRs from CYP genes for their future use in wheat molecular breeding aimed at enhancing leaf rust resistance .

**Material :** Two wheat genotypes; one leaf rust susceptible wheat genotype "Chinese Spring (CS)" and one CS derived resistant genotype "Transfer (TR)", were used for comparative expression profiling. The wheat genotype TR carries a dominant seedling leaf rust resistance gene "Lr9". Single spore derived inoculum of one of the most prevalent and virulent pathotype 220 77-5 (syn. 121R63-1) of *P. triticina* Eriks., was used for inoculating the seedlings of the two wheat genetic stocks.

## Methodology



## Results

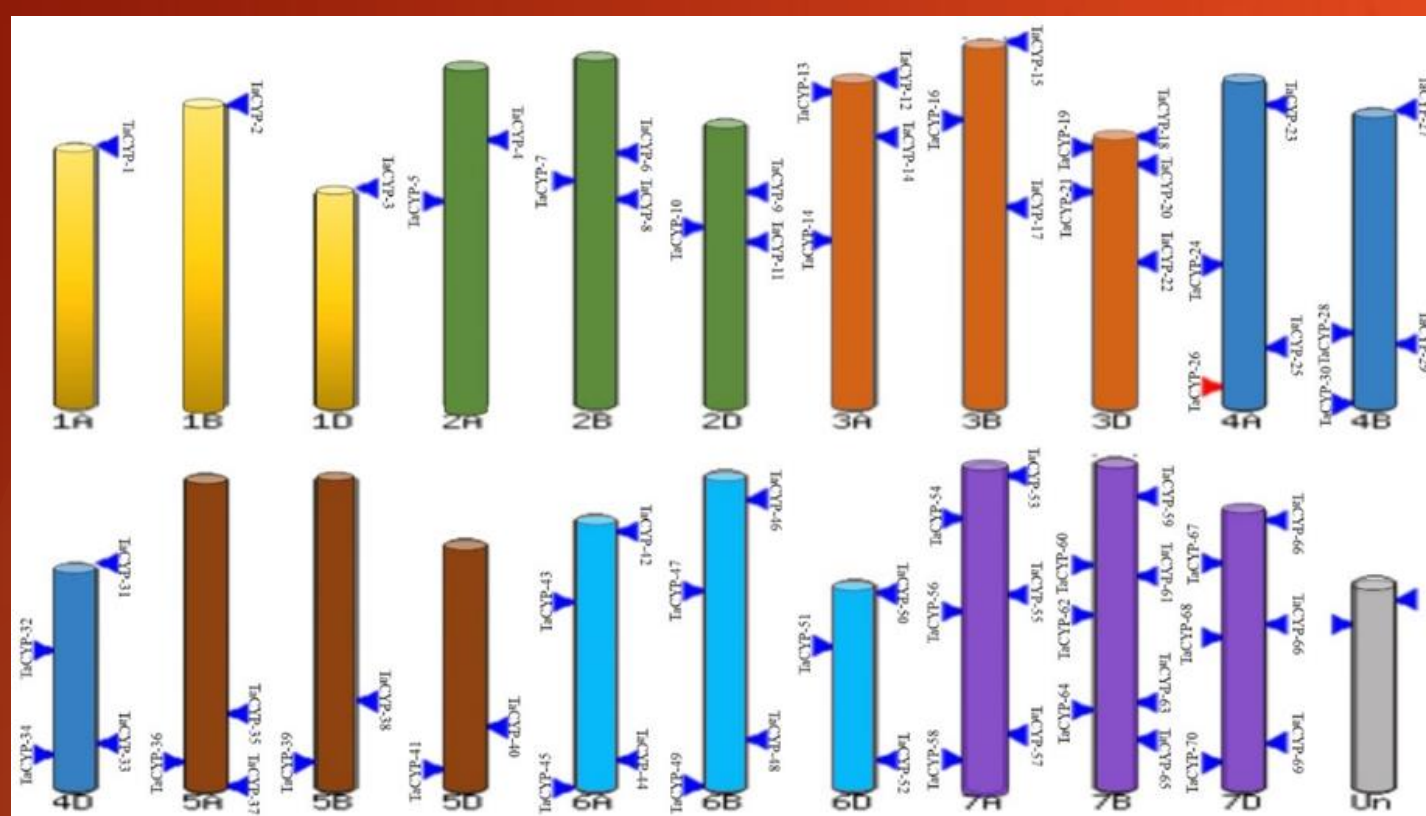


Fig 1. The physical positions of the all 81 *TaCYP* genes to corresponding chromosomes

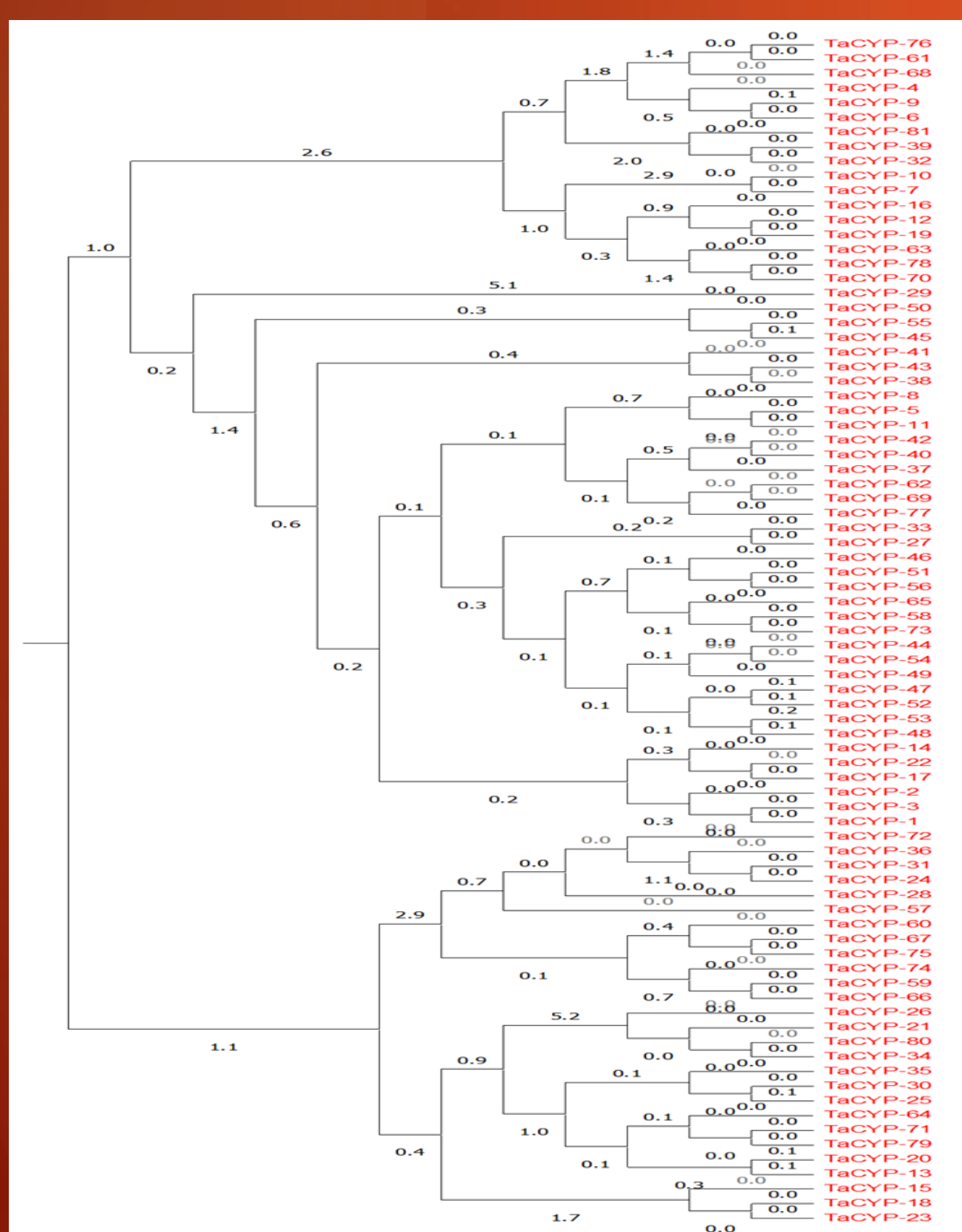


Fig. 2 Phylogenetic grouping of all the identified 81 *TaCYP* proteins

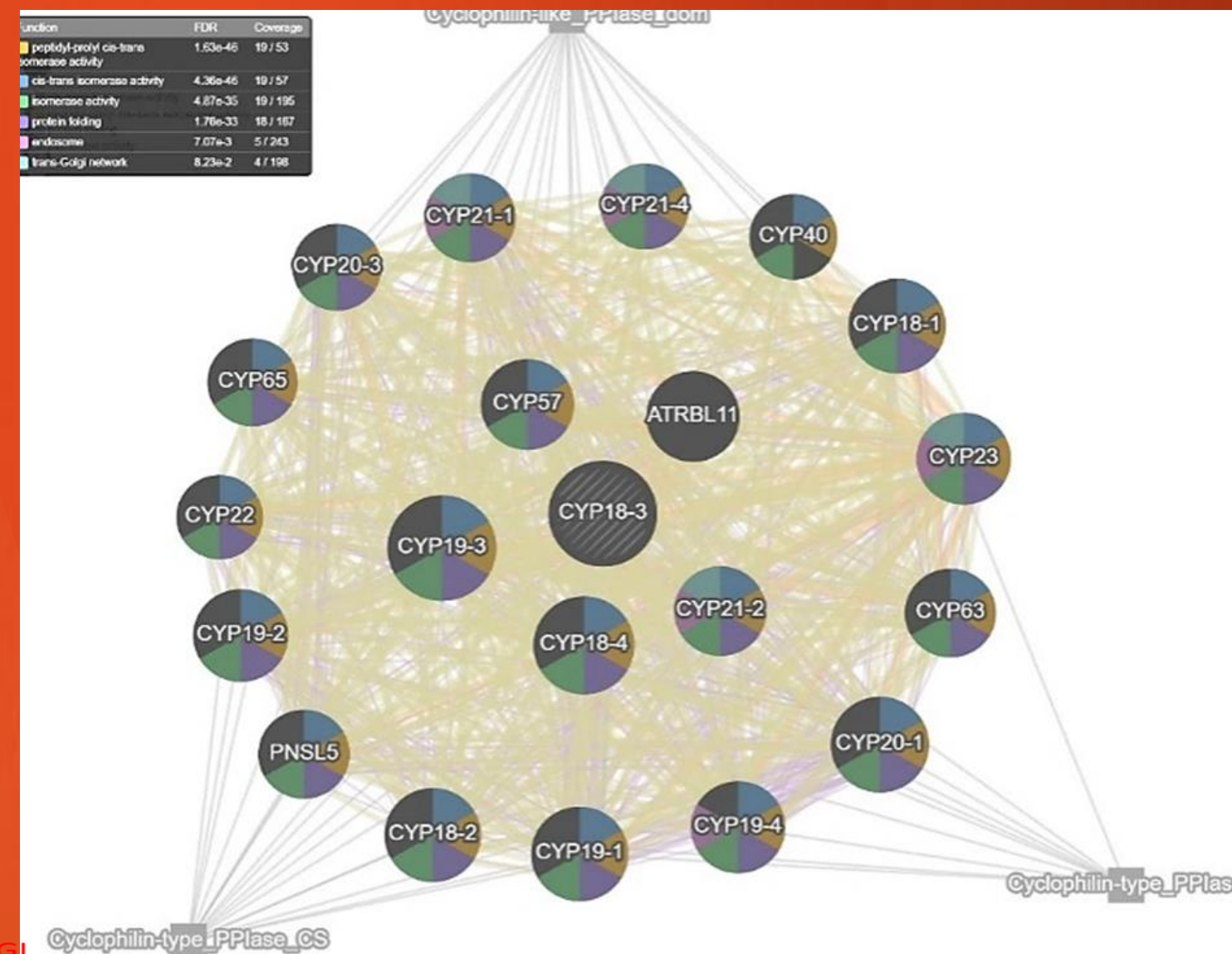


Fig. 3 Predicted protein-protein interaction networks information of all the identified wheat *TaCYP* proteins



Fig. 4 Expression profiling of all the identified 81 *TaCYP* genes under high level stress-diseases by the software expVIP calculated using available RNA-seq data.

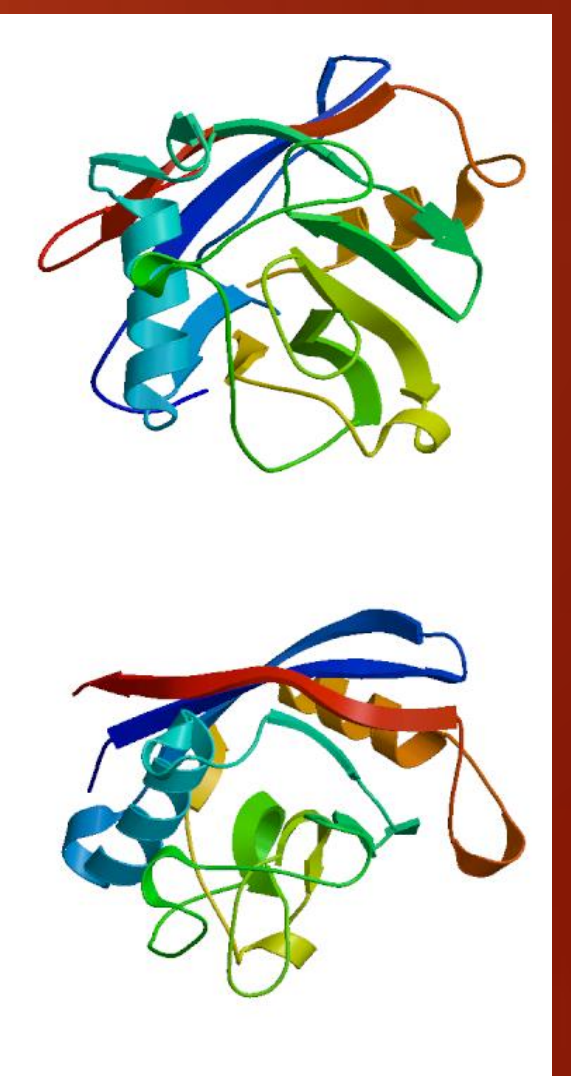


Fig. 5 3D structures of 2 representative proteins

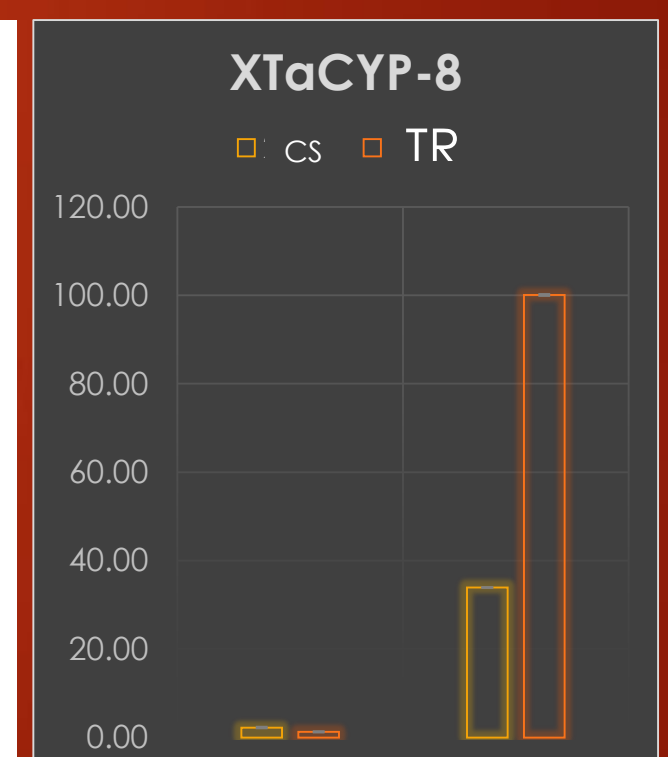


Fig 6. Differential expression of *TaCYP-8* gene against inoculation to leaf rust diseases.

**Conclusion:** Our research is its first report conducted genome-wide analysis of CYP genes in wheat for leaf rust disease. Current outcomes not only lengthen earlier conclusions associated with the role of CYP genes but also unboxed critical role of CYPs to minimize the problem of leaf rust disease in the second most important cereal crop of the world. Identified genes and developed markers will help in future wheat genetic development/improvement programs for leaf rust/pathogen stress physiology.

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