

Identification of new resistance genes against yellow rust from Swiss wheat varieties

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Background

Yellow rust (Yr) is one of the most important foliar diseases in wheat causing significant yield losses. The combination of both quantitative and qualitative resistances has been proposed as the best strategy to achieve stable, broad-spectrum and long-lasting control of the disease.

A genome-wide association study (GWAS) was used for assessment of the diversity of quantitative and qualitative resistances in modern wheat varieties and wheat landraces.

Objective: Identification of molecular markers associated to putative novel sources of effective resistance against Yr in Swiss wheat varieties.

Material and Methods

- 539 wheat and spelt varieties (improved cv., landraces)
- Phenotyping at three sites with different soil and climate conditions
- 3 years (2019-2022)
- Each variety was individually phenotyped and the dynamics of disease severity evaluated over time
- All varieties were genotyped with 25K single nucleotide polymorphisms (SNP) assay



Results

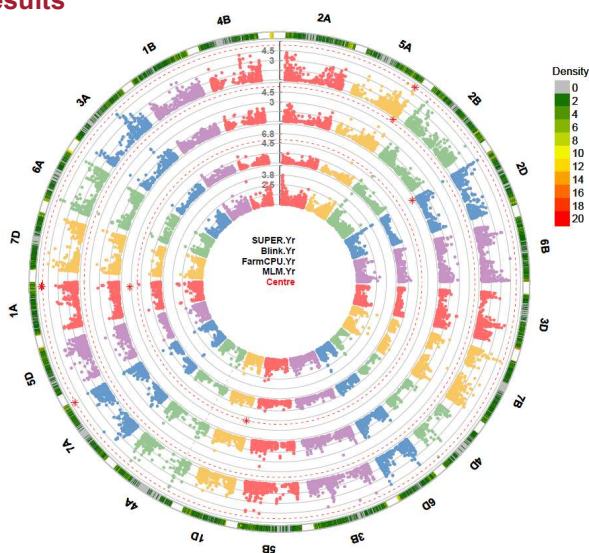


Fig.1: Circular Manhattan plot of highly associated SNPs with resistance against Yr displaying four methods of GWAS-analysis: MLM, BLINK, FarmCPU and SUPER.

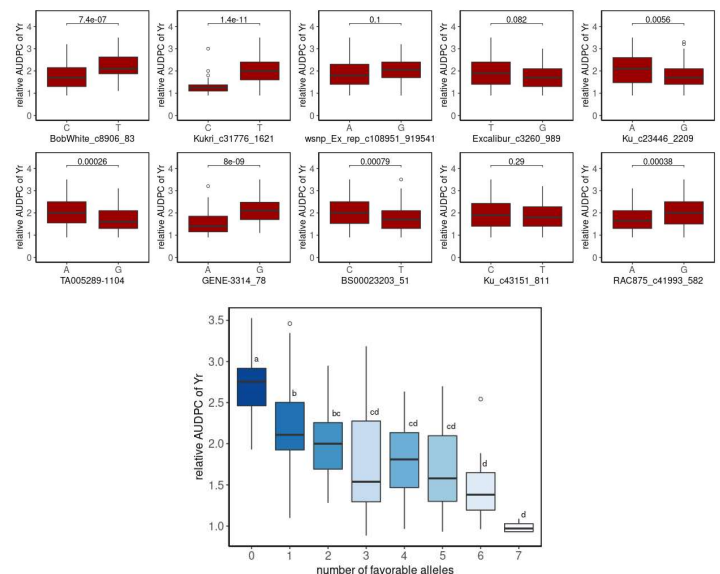


Fig.2: Boxplots for SNPs significantly associated with Yr responses at adult plant stage.

- Ten significant (FDR-adjusted p-value < 0.05) marker-trait association (MTA) for rAUDPC of Yr were detected with three different models.
- Seven out of ten rAUDPC scores for the favorable alleles were significantly lower than those for unfavourable alleles reducing rAUDPC up to 35% compared with lines without favorable SNP alleles.
- The more favourable allele (significantly decreasing the Yr infection) a genotype has, the less susceptible it will be against Yr infection.
- Three markers (wsnp_Exp_rep_c108951_91954190, Excalibur_c3260_989, Ku_c43151_811) revealed three putative candidate genes/QTLs on chr 1A, 1D and 7A.

Conclusion & Perspectives

By combining high-quality disease phenotyping tools and GWAS, the results obtained in the present study will be highly useful for identifying new QTLs for durable resistance against *Puccinia striiformis* using existing natural genetic resources. The novel markers provide important genomic information to initiate marker-assisted selection as well as fine mapping and cloning of the underlying genes and QTLs. Marker-trait association identification will be extended to leaf rust and FHB resistance for which encouraging results have already been obtained.



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