Identification of new resistance genes against leaf rust in wheat Swiss wheat landraces

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Background

Leaf rust (Lr) is one of the important foliar diseases in wheat causing significant yield losses. The combination of both quantitative and qualitative resistances has been proposed the best strategy to achieve stable, broad-spectrum and long-lasting resistance to Lr.
Genome-wide association study (GWAS) was used for assessment of the genetic diversity of modern and landraces wheat varieties on Lr resistance gene or quantitative trait loci (QTL) and for identification of associated molecular markers.

Material and Methods

- ~540 wheat varieties (improved cv., landraces, spelt)
- 3 sites with different soil and climate conditions
- Statistical analysis

Phenotyping

- Each variety was individually observed and Lr disease severity was evaluated over time.

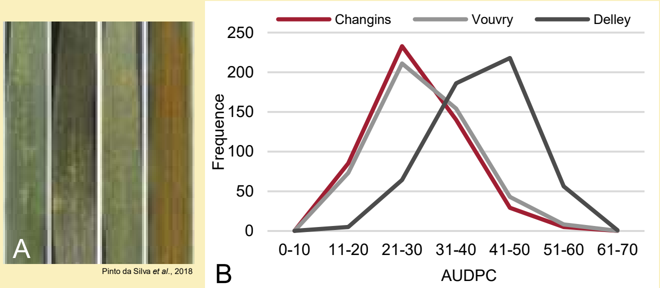

Fig.1: (A) Pictures of LR infection with gradient of severity, (B) Distribution of values of Area Under Disease Progression Curve (AUDPC) at Changins, Vouvry and Delley.

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Genotyping

- All wheat varieties sown were fully sequenced with 25K single nucleotide polymorphisms (SNP) assay
- After filtering, a total of 23'000 high-quality SNPs were retained for further analyses.

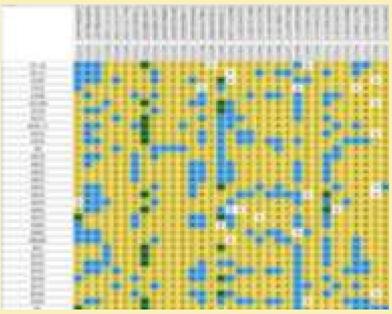

Fig.2: Sample of table indicating for each variety (lines) SNPs for a given markers (columns).

Genome-Wide Association Study (GWAS)

- An important number of markers related to Lr resistance has been identified in the study population.
- High significance (p>0.00001) were observed for markers on chromosomes 1D, 6B, 7A and 7D
- Interestingly, several markers highlighted potential candidate gene/QTL on chromosome 2D. This is the first report of Lr resistance genes on chromosome 2D in winter wheat genome.

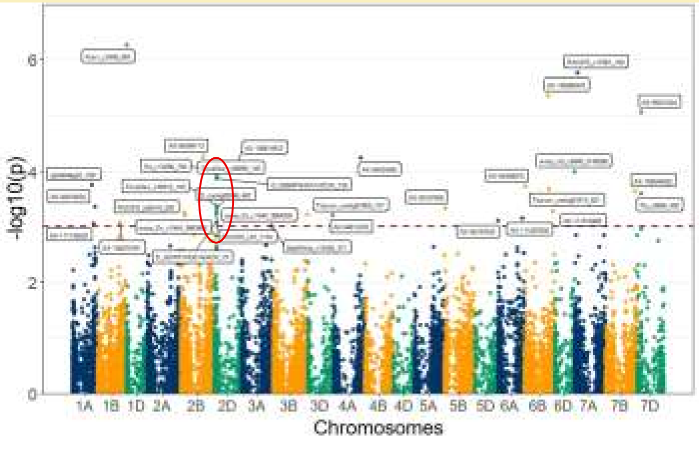

Fig.3: Manhattan plot showing markers significantly (p>0.001) linked to leaf rust resistance genes/QTLs on each chromosome.

Summary

This project aims to screen an extensive series of modern varieties and landraces from Wallis (CH) in search of new qualitative and quantitative resistances against leaf rust effective under field conditions. By combining high-quality disease phenotyping tools and GWAS, we will tap resistance sources, develop markers in order to getting insight into LR resistance mechanisms, and identify resistance genes. This work will provide direct applications for practical breeding.

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