CICABO

Étude de la résistance génétique au virus des pieds chétifs chez l'orge et le blé tendre d'hiver

Britta RUCKWIED[1], Anne RICHTER[1], Martin SCHWEERS[1], Torsten WILL[1], Delphine TAILLIEU[2], Ellen GOUDEMAND-DEGUE[2], Elise COCCIANTELLI[3], Constance LAVERGNE[3], Rachel GODDARD[3], Gabriel BEUDIN[4], Auberi AVALLE[5], Guillaume ROULLET[5], Yann MANES[6]*, Chami BERGER[6], Alexis OGER[6]*

1 - Julius Kuhn Institute
2 - Florimond Desprez
3 - Limagrain
4 - RAGT
5 - Unisigma
6 - Syngenta France S.A.

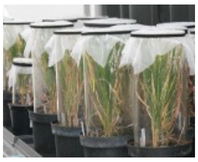
Coordinateurs du projet : **Yann Manès et **Alexis OGER alexis.oger@syngenta.com***

RÉSUMÉ

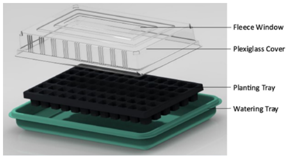
The wheat dwarf virus (WDV), is transmitted by the leafhopper *Psammotettix alienus*. Symptoms in infected plants are: dwarfism, significant reduction in tillering and leaf chlorosis. When infection occurs at the seedling stage during early autumn, yield losses can reach up to 80%, highlighting the substantial economic impact of this disease. In the centre and north-east of France, symptoms have become increasingly prevalent in recent years. The effectiveness of conventional insecticides is limited due to the high mobility of the leafhoppers. Plant breeding offers a promising approach for disease control and partial resistance has already been identified for wheat.

MATÉRIEL - MÉTHODES

The CICABO project aims to identify genetic resistance to WDV in diverse wheat germplasm and make it available for breeding by identifying QTL. Workflow.

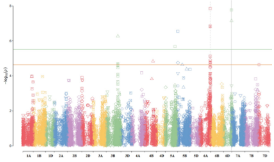


Leafhopper rearing

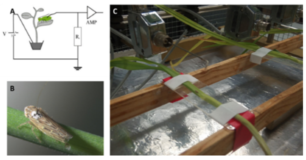


Artificial WDV infection

Phenotyping



GWAS

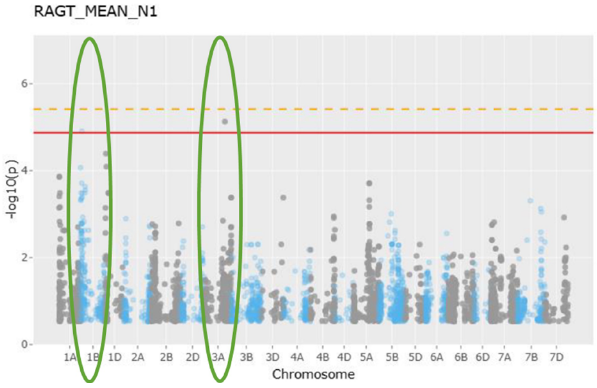


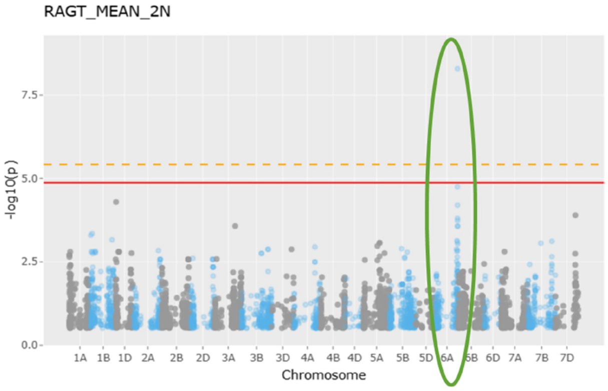
Leafhopper feeding

Phenotyping of 83-247 genotypes was conduted in the field and under artificial inoculation. Genotyping based on the Illumina 25K chip (Trait Genetics), followed by GWAS analysis. Detection of leafhopper resistance included feeding behavior observation by electrical penetration graph technique.

FIELDS TRIALS RESULTS

Phenotyping & GWAS

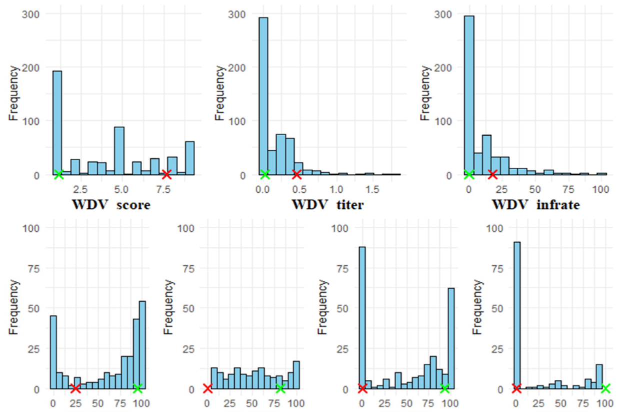


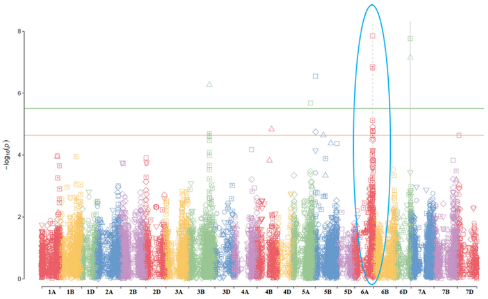


- ▶ Only one location used for the analysis out of 16
- ▶ Major QTL for WDV resistance on chromosome 6A
- ▶ Additional QTL on 1B and 3A

CONTROLLED CONDITIONS RESULTS

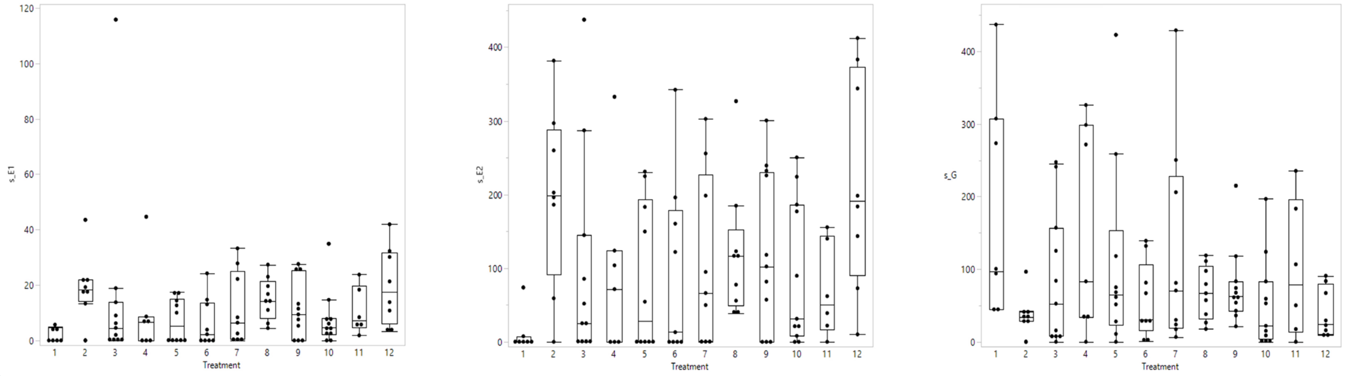
Phenotyping & GWAS





- 3 highly WDV resistant accessions (DBW020, DBW118, DBW154)
- Major QTL for WDV resistance on chromosome 6A
- Additional QTL on chromosomes 4D and 6D

Leafhoper feeding behaviour



- Accession (DBW020) with high resistance to *P. alienus*
- Resistance located inside sieve elements

CONCLUSIONS

QTL WDV / wheat	Field conditions	Controlled conditions
Common, overlapping major QTL	6A (599–602 Mbp)	6A (601–603 Mbp)
Additional QTL identified in regions with described minor QTL	1B, 3A	1B, 3B, 4B, 4D, 5A, 5B, 6A, 6D
Putative novel QTL		4D, 6D

Genetics

Genetic architecture of WDV resistance proved to be complex, involving multiple QTLs with moderate effects and suggesting the existence of complementary mechanisms of direct virus resistance and vector resistance.

Breeding

The WDV resistance associated haplotype is carried by DBW020 and DBW110, reinforcing their relevance together with the discovered vector resistance in DBW020 for breeding programmes targeting joint vector/virus resistance.

Limitations

- Heterogeneous infection pressure
- WDV/BYDV co-infection
- Phytoplasma co-infection
- Variable transmission efficiency of WDV