Association Mapping of Fusarium Head Blight in a French winter wheat population

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A devasting disease

First observed in 1884 in England, *Fusarium* Head Blight (FHB) is now a worldwide pathogen that causes significant quality and yield losses in wheat.

FHB is also responsible for accumulation of mycotoxins in the grain, which can make it unfit for consumption; the European recommendations limit at 0.125mg/kg the level of mycotoxins produced by *Fusarium* in grain.

The deployment of resistant cultivars appears to be the most effective strategy to control the disease, but we observed that the most resistant varieties are mainly exotic with poor agronomic interest in Europe (Buerstmayr *et al.*, 2002) (1). The understanding of the mechanisms of resistance in exotic material would help to develop adapted varieties in Europe, but unfortunately these mechanisms still remain unknown.

The objectives of this study are the confirmation of QTL previously found in the western-European winter wheat germplasm and the identification of the most important FHB resistance loci that can be used in breeding programs.

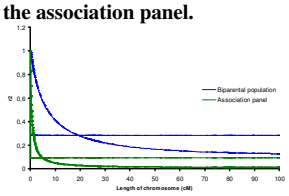
Linkage Disequilibrium Analysis

For the genetic analysis, 1,500 DArT markers were genotyped by Triticarte Pty. Ltd. (http://www.diversityarrays.com), and we also used 500 SSR markers. This number of markers allowed a good distribution over the genome.

A genetic map was thus developed and we compared the Linkage Disequilibrium between a biparental population and the association panel.

We observed a decline in LD around 5 cM for the association panel and a decline around 20 cM for our biparental population, which potentially permit us to obtain markers more closely linked to the QTL regions with the association panel.

Decline of LD between marker over genetic distance.



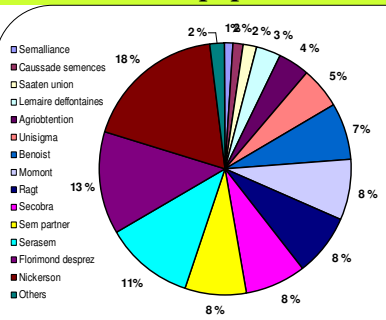
Association studies

Association studies were performed with the program TASSEL (http://www.maizegenetics.net) and R scripts using the population structure coefficients derived from the SSR marker data to correct for population stratification. To control for multiple testing, Bonferroni tests were used.

Association for *Fusarium* infestation showed that the Rht-D1 gene is the most associated locus with the resistance. We also found 13 markers previously reported to be associated with the resistance to FHB (*) and 6 new ones.

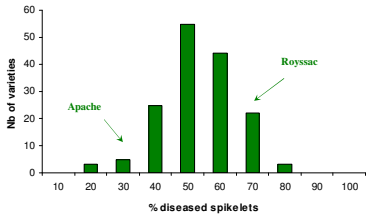
Chromosome	P-value	Chromosome	P-value
1B*	3.08X10-4	4A*	6.13x10-4
1D*	0.0013	4D (Rht-D)	7.14x10-6
2A*	0.0011	4Ds	4.28x10-5
2Bs*	0.0025	5A*	2.94X10-4
2Bl	7.56x10-5	5Bs*	0.002
3A*	0.0097	5D	0.0018
3Bs*	0.0048	6A	0.0015
3Bl*	0.002	7As*	4.70X10-4
3Ds	0.0072	7Al*	2.91X10-5
3Dl*	0.0034	7D	6.13X10-5

Association population and phenotypic data



In order to identify potential new FHB resistance genes in the French elite winter wheat lines, we selected a set of 195 wheat cultivars developed by various breeding companies.

The first year of field trial evaluation showed good diversity for infestation. Apache and Royssac, respectively a resistant and sensitive varieties, were used as controls.

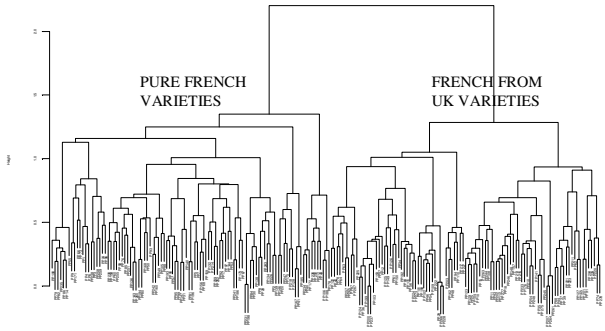


Histogram of % diseased spikelets 450 degree days after flowering time

Structure of the panel

The substructuring of the panel was assessed using the program STRUCTURE (Pritchard *et al.* 2000) (2) and with the calculation of Cavalli-Sforza Chord distance to produce a dendrogram derived from UPGMA cluster analysis.

We clearly observed 2 substructures in this panel explained by the origin of the varieties (Pure French varieties and French from UK varieties).



Conclusions - Perspectives

The first year of evaluation in this French elite germplasm allowed to confirm previously identified loci and to detect new ones potentially involved in FHB resistance. A second year of field trials was conducted in 2009 and an association analysis on this new set of data will be performed. The confirmed associated loci will then be densified by SNP markers.

Next to this French panel, we try to confirm the result on a new set of varieties to cross validate the results.

The knowledge of presence or absence of positive alleles linked to the different QTL for FHB resistance in segregation in breeding material is of great interest to efficiently pyramid resistance genes in new wheat cultivars.

Ref : (1) Buerstmayr H., Lemmens M., Hartl L., Doldi L., Steiner B., Stierschneider M., Ruckenbauer P., (2002) *Theor Appl Genet 104:84-91*
(2) Pritchard JK., Stephens M., Donnelly P., (2000) *Genetics 155:945-959*