Phenotypic and molecular characterization of 3 breeders' collections for late blight resistance

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An association study to find reliable markers for late blight resistance

Breeding for late blight resistant varieties is a way to help growers decreasing fungicides impact. **Association mapping** is a promising way to detect markers to implement markers assisted selection in breeding schemes.

Our aim is to **construct genotypes stacking R genes and partial resistant factors** that may increase the durability of R genes. To do so, it is necessary to get reliable markers.

Here we present some preliminary results obtained on a **collection of genotypes** used in the selection processes of three breeding companies.

142 genotypes were included by Comité Nord, 96 by Bretagne Plants and 63 by Grocep. Taking into account genotypes common to at least two companies, the overall collection included 287 unique genotypes *i.e.* hybrids, varieties and progenitors bred at Inra UMR1349 Ploudaniel.

Different levels and types of late blight resistance were observed experimenting the collection in 2013 in a hot spot for late blight
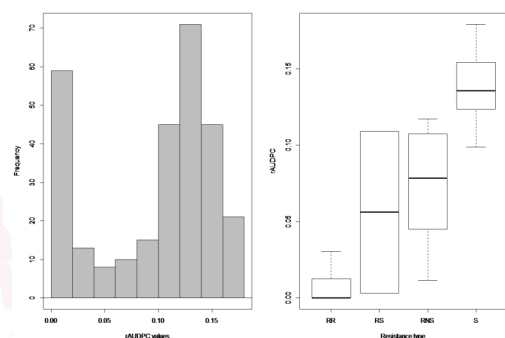

The collection exhibited a high level of phenotypic variability for resistance to late blight as illustrated on the rAUDPC histogram (left).
Different types of resistance could be deduced using an adapted combination of threshold on Δa and Δt parameters (right) according to Marhadour et al 2013. RR : strong resistance with very few symptoms, RS: R genes overcame during the epidemic, RNS: partial resistance, S: susceptible genotypes.
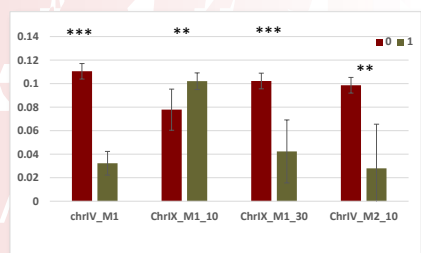
Molecular diversity showed no evident structuration

Factorial analysis: Axes 1 / 2
Axis 1 : 4.4%, Axis2: 3.1%

All together markers gave 231 bands. Results from factorial analysis on dissimilarity matrix showed no evident groups into the collection.
Axis 1 explained 4.4% and Axis 2 3.1% of the total inertia.
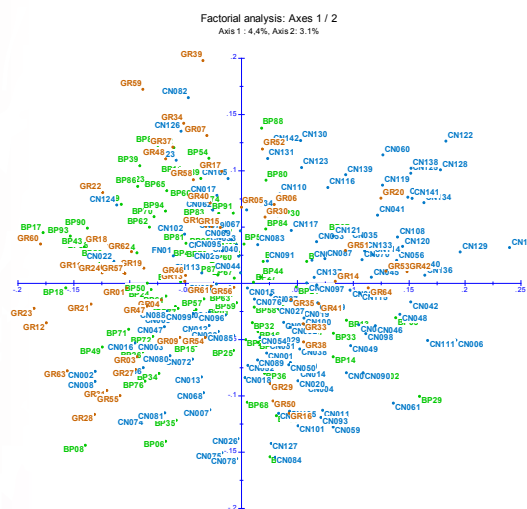
Joint phenotypic/genotypic data analysis

rAUDPC means for groups of genotypes displaying (1) or not (0) each of 4 markers revealed significantly related to variation of resistance to late blight in 2013 (p<0.0001)

Markers located on chromosomes IV and IX were significantly related to variation of late blight resistance evaluated during 2013 season, confirming the interest of the results obtained previously on segregating mapping families (Marhadour et al 2011, 2012).

Methods: Late blight experiment

- 2013: first year of experiment
- Location: Ploudaniel, France (oceanic climate)
- Augmented design trial (Petersen, 1985) , Controls in each of the 5 blocks: Robijn, Desiree, Kerpondy, Bintje and Sirtema
- 11 Blacks 'differentials included
- Natural infection conditions, 9 notations between June, 18th and July, 23rd
- Using a visual scale of foliage destruction adapted from Dowley et al. (1999). rAUDPC, Δa and Δt parameters were computed as described in Marhadour et al (2013).

Late blight experiment on July, 16th 2013

Methods: Molecular characterization

32 markers were used on the collection
- 14 markers from bibliography or from our previous own works and known to be significantly linked to variation of late blight resistance and other traits (2 CAPS, 5 PCR and 7 SSR)
- 18 SSR markers : 7 of the kit we developed for cultivar identification (Marhadour et al 2014), 11 SSR markers used by Esnault et al (2014) to characterize the potato collection conserved in CRB BrACySol

Markers were coded as dominant ones. Genetic distances (DICE) between genotypes and factorial analysis on the dissimilarity matrix were performed using Darwin software (Perrier and Jacquemoud-Collet , 2006).
Variance analysis was used to detect significant association between markers and variation of resistance using SAS software (SAS Institute Inc., Cary, NC, USA).

Prospects

Second year late blight experiment is in progress.
Additional genotyping is also in progress in order to use the full set of markers used to characterize the Inra collection. This will help us to compare the diversity of both collections.
We also intend to proceed to a high throughput genotyping of our collection using SNP markers and to use an association mapping approach.

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INRA SCIENCE & IMPACT — Bretagne Plants — grocep — Comité Nord Plants de Pommes de Terre — InnoPlant