Late blight resistance of potato mapping populations in front of naturally evolving pathogen populations

FÉDÉRATION NATIONALE DES PRODUCTEURS DE PLANTS DE POMME DE TERRE

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Context

Non specific resistance to *Phytophthora infestans* has become an objective for our breeders. To be able to deal with such a complex polygenic trait in breeding programs, one can use molecular markers linked to quantitative resistance loci (QRL).

Here we present phenotypical results obtained on two segregating families. Experiments have been done during years of important evolution in the pathogen populations (2005 to 2009). However, despite we could observe the erosion of R gene(s) efficiency, partial resistance factors present in the source of resistance were still efficient.

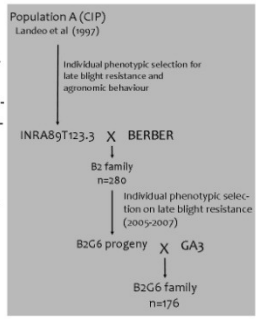
Which type of material did we study ?

Genealogy of the material is detailed on the figure.

- INRA89T123.3 is the source of resistance coming from CIP A population.
- Berber is a susceptible variety.
- GA3 is a susceptible genotype of another mapping family.
- B2G6 progeny exhibited specific resistance associated with partial resistance.

Standards were included in the experiment. Results obtained on Robijn (partial resistance) and Désirée are presented.

Blacks differentials were also included each year in the experiments.



What did we measure ? How ?

B2 family was experimented each year between 2005 and 2007. B2G6 was experimented in 2009.

The experimentations took place in Ploudaniel, France (oceanic conditions) under natural conditions of contamination.

Bintje was used as a spreader.

Disease progress curves were constructed using a mean of 10 notations each year. Each genotype was visually scored using a scale of foliage destruction (Dowley et al, 1999).

rAUDPC, deltaa and deltat (Andrivon et al, 2006) parameters were computed.

Each genotypes was observed in 3 replicates (except in 2009, 2 replicates for B2G6 family)

Statistical tests were made using SAS software.

View of the experiment, july 20th 2009

Perspectives

- Continue the evaluation of the new generation of material and the behavior of resistance factors in front of the new pathogen populations,
- Evaluate the proportion of QRL detected in the first generation which is also efficient in the second one,
- Compare QRL detected across the progenies.

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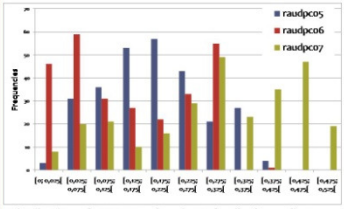
5 GROCEP, Station de Lavergne, 87370 Laurière, France
6 FN3PT , Roudouhir, 29460 Hanvec, France

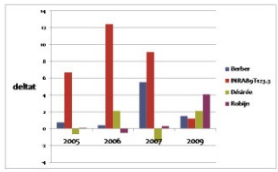
Euroblight, Arras, 3-6 mai 2010

Erosion of the R gene(s) efficiency

In the first generation of material (B2 family), segregation of the resistance factors is observed and is subjected to a strong year effect. Important Year effect is also observed on parental clones and standards



Distribution of rAUDPC values in B2 family depending on the year

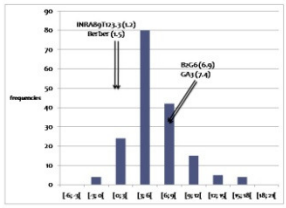


Evolution of the deltat values between 2005 and 2009 for parents of the family and two controls. Berber and INRA 89T123.3 were not planted in 2008. Standard déviations were equalt to 2,5 in 2005, 3 in 2006, 4,7 in 2007 and 2,7 in 2009.

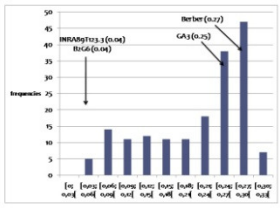
A rather rapid erosion of the R gene(s) efficiency has been observed through the decreasing value of the period without symptom on the material as compared with susceptible control (deltat)

Factors of partial resistance are not masked by R gene(s) in 2009

Additional intra progeny crosses have been made leading to a new generation that has started to be observed in 2009, concomitantly to the observed loss of efficiency of R gene(s). It was then easier to observe the efficiency of partial resistance factors that were previously masked by R gene(s) and only visible in the R gene free proportion of the family.



Distribution of deltat values in B2G6 , values of the parents and grandparents are indicated



Distribution of rAUDPC values in B2G6 , values of the parents and grandparents are indicated

Interests and limits to experiment in natural conditions of contamination

- Our site of experiment can be considered as a "hot spot" for experimentation on late blight resistance. Late blight occurs every year without the need to use artificial inoculum. The pathogen pressure is high due to optimal climatic conditions;
- Isolates sampled each year and characterized since a long time by phytopathologists (Andrivon's team), are characterized by a complex pattern of virulences (Corbière, pers. comm.) and were able to overcome most of the S. *demissum* R genes except R5 in 2006 and R9 which was never infected during the period of the experiments (differentials results).
- Between 2005 and 2009, changes have occurred in the pathogen population in France (Andrivon, communication during this congress) including the increase of A2 mating type and the pattern of virulences. Our site was concerned despite it was slightly different from the others in France probably due to the presence of the Inra breeding material where a lot of resistance genes are experimented (Corbière, pers. comm.).

Limits of experimenting in such conditions are:

- Composition of the inoculum is not controlled
- Population of isolates is always evolving

However, experimenting an overall selection in such conditions is interesting because

- Resistance factors are submitted to a high and diverse pressure of pathogen
- We can see what happen in "real life" to the resistance factors we are dealing with
- Partial resistance phenotype is now supposed to be accessible even if R gene(s) are segregating in the material

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