

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

MARHADOUR¹, S., PELLE², R., ABIVEN³, J.M., AUROUSSEAU⁴,
F., DUBREUIL⁵, H., LE HINGRAT⁶, Y. AND CHAUVIN², J.E.

¹ FN3PT INRA UMR APBV Keraiber 29260 Ploudaniel France

² INRA UMR APBV Keraiber 29260 Ploudaniel France

³ Bretagne Plants, Station de Création Variétale, Kerloï, 29260 Ploudaniel France

⁴ Station de recherche du Comité Nord, 76110 Bretteville du Grand Caux, France

⁵ CROCEP, Station de Lavergne, 87370 Laurière, France

⁶ SFN3PT, Roudouhir, 29460 Hanvec, France

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

Marhadour¹, S., Pellé², R., Abiven³, J.M., Auroousseau⁴, F., Dubreuil⁵, H., Le Hingrat⁶, Y. and Chauvin⁷ J.E.

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.

INRA87c133 is the source of resistance coming from CIP A population. Bamber is a susceptible variety. CA3 is a susceptible genotype of another mapping family. BxC6 progeny exhibited specific resistance associated with partial resistance.

Standards were included in the experiment. Results obtained on Rubis (partial resistance) and Délaire are presented. Black differentials were also included each year in the experiments.



What did we measure ? How ?

Bx family was experimented each year between 2005 and 2007. BxC6 was experimented in 2009.

The experiments took place in Floudanle, France (oceanic conditions) under natural conditions of contamination.

Bintje was used as a spreader.

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

HAUOPC, deltaT and deltaT (Andrion et al, 2006) parameters were computed.

Each genotype was observed in 3 replicates (except in 2009, 2 replicates for BxC6 family)

Statistical tests were made using SAS software.



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.

¹ FN3PT, INRA UR204 ARAP, Avignon, France, Prévost-Delafont, Françoise

² INRA UR204 ARAP, Avignon, France, Prévost-Delafont, Françoise

³ INRA UR204 ARAP, Avignon, France, Prévost-Delafont, Françoise

⁴ INRA UR204 ARAP, Avignon, France, Prévost-Delafont, Françoise

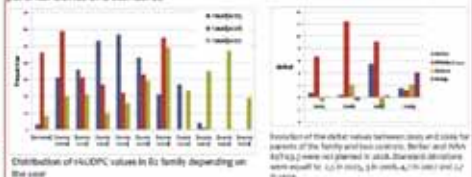
⁵ INRA UR204 ARAP, Avignon, France, Prévost-Delafont, Françoise

⁶ INRA UR204 ARAP, Avignon, France, Prévost-Delafont, Françoise

⁷ INRA UR204 ARAP, Avignon, France, Prévost-Delafont, Françoise

Erosion of the R gene(s) efficiency

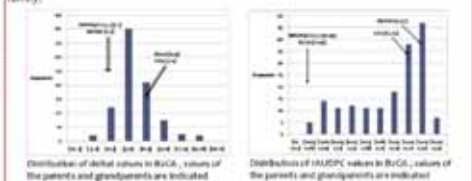
In the first generation of material (Bx family), segregation of the resistance factors is observed and is subjected to a strong year effect. Important Year effect is also observed on parental clones and standards



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.



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 (Andrion's team), are characterized by a complex pattern of virulence (Corbière, pers. comm.) and were able to overcome most of the 5 dominant R genes except R₃ in 2006 and R₅ which was never detected during the period of the experiments (differentials results).
- Between 2005 and 2009, changes have occurred in the pathogen population in France (Andrion, communication during the congress) including the increase of A₁ mating type and the pattern of virulence. Our site was concerned despite it was slightly different from the others in France probably due to the presence of the real breeding material where a lot of resistance genes are implemented (Corbière, pers. comm.).

Limits of experimenting in such conditions are:

- Comparison of the isolates 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 happens 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



This study is partially financed by the European Union through the FP6-015848 project.

