



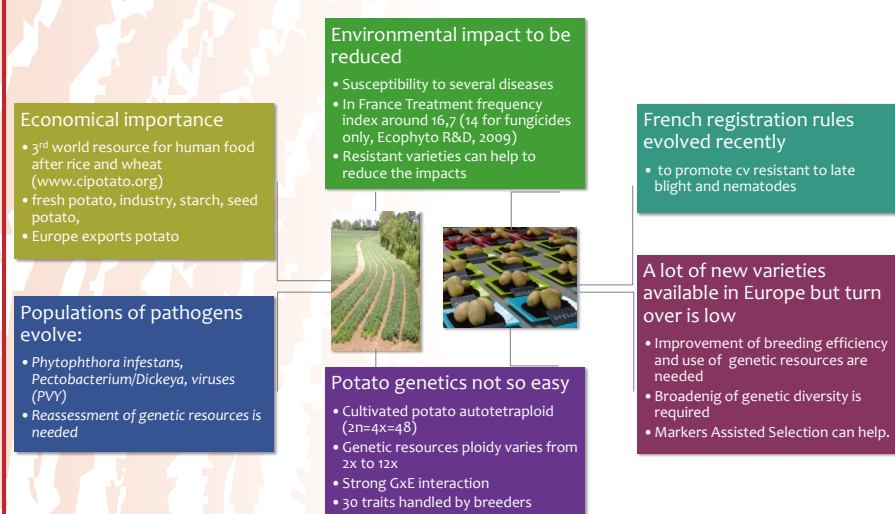
FÉDÉRATION NATIONALE
DES PRODUCTEURS
DE PLANTS DE POMME DE TERRE



Use of joint molecular tools by public and private partners for an efficient use of potato prebreeding material

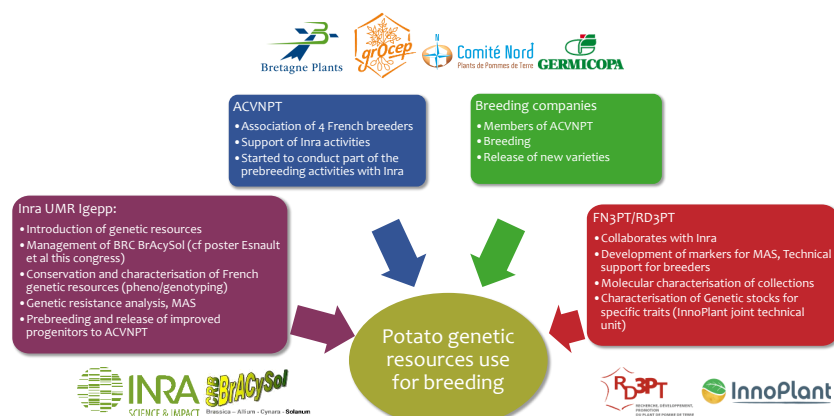
Marhadour, S.^{1,6}, Méar, A.^{1,6}, Esnault, F.⁵, Abiven, J.M.², Aurousseau, F.³, Dubreuil, H.⁴, Chauvin, J.E.⁵, Le Hingrat, Y.⁶, Kerlan, M.C.⁵

Potato: a major crop with environmental constraints and not so easy genetics



French organization around the potato genetic resources: a close partnership

Several structures are involved in the potato genetic resources evaluation, conservation and use. Roles of each partner are described on the figure.



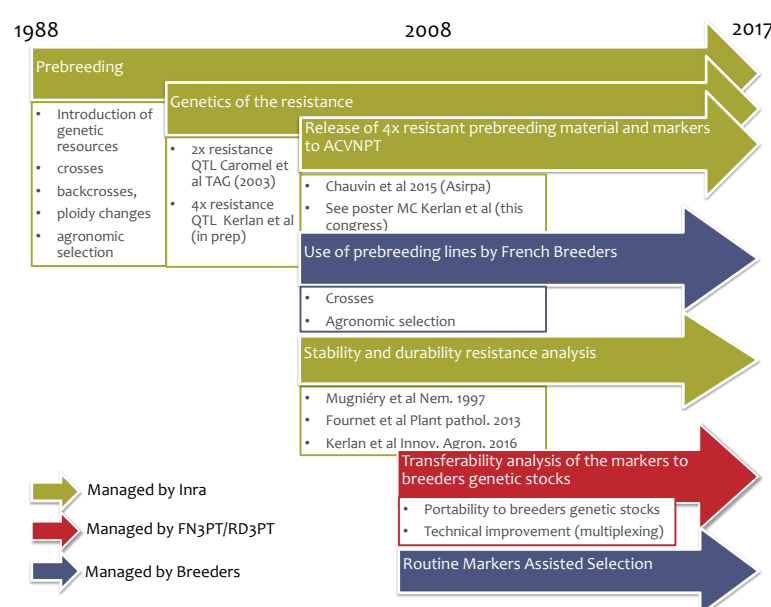
Furthermore, the French genetic resource included in the Multilateral system of Access and Benefit sharing (ITPGRFA) was set up by the French Solanum network coordinated by Inra and gathering the 4 French breeding companies plus the seed potato organisation FN3PT.

Markers Assisted Selection for resistance to *G. pallida*: from public research to routine selection in breeders' labs

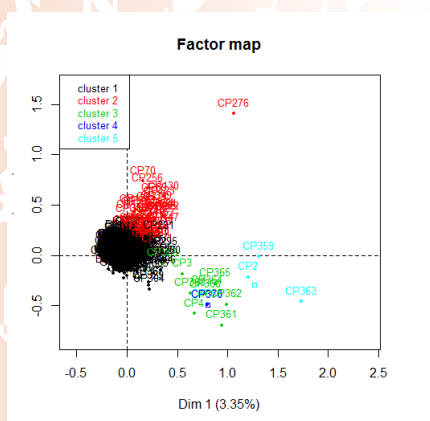
Prebreeding followed by breeding for resistance is a long lasting process. Here is described an example leading to the use of routine Markers Assisted Selection in 3 breeding companies and the improvement of the genetic resources use efficiency.

These results were obtained with several supports from French Ministry of Agriculture, EU and ACVNPT (details: see poster of Kerlan et al, this congress).

FN3PT/RD3PT tested the portability of the markers to the genetic stocks of Bretagne Plants Innovation, Comité Nord/Sipre and Grocep breeders and improved the routine use efficiency of the markers. Breeders labs perform the MAS and the selection of resistant varieties harbouring characteristics corresponding to the markets standards.



Exploring the molecular diversity of public and private collections using the same molecular tools



Two sets of potato genotypes were molecularly characterized using a joint kit of 15 SSR markers. The FN3PT/OP set is composed of 291 *S. tuberosum* genotypes and is representative of the genetic pools used by 3 breeding companies (Bretagne Plants Innovation, Comité Nord/Sipre and Grocep). The Inra set is composed of 22 related species clones and 350 *S. tuberosum* genotypes. Twenty genotypes are common to both sets.

Analysis of the molecular diversity was done using Multiple Correspondence Analysis (MCA) followed by Hierarchical Clustering Analysis (HCA).

Representation of HCA results obtained on the global set of genotypes. Genotypes are plotted relatively to axis 1 and 2. Five clusters can be distinguished. The main cluster (1) is composed of 578 genotypes of both sets. Clusters 3, 4, and 5 are outside and correspond to related species (*Solanum tuberosum andigenum* group, *S. sparsipilum* and *S. stenotomum*). CP276 corresponds to Vitelotte Noire.

We are currently analysing the molecular diversity of both sets excluding related species in order to focus on *S. tuberosum* variability. This project was part of the InnoPlant Joint technical unit programme (www.umn-innoplant.fr)

Prospects

Phenotyping genetic resources is now the issue. New diseases or evolving populations of pathogens require reassessment of these resources.

Genetic resources are a common good, however it is difficult to find public research funding and maintain forces for the preservation of PGR. We also face to a strong risk of loss of skill due to non replacement of retiring public staff.



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