

Marker-assisted selection of QTL PiX_{spg} in potato diploid backcross populations

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As most of the R-genes identified in Solanum wild species have been overcome by Phytophthora infestans, the UMR APBV team aims at identifying and studying quantitative traits loci (QTL) involved in late blight resistance.

A segregating population (96D32) obtained by crossing a susceptible dihaploid S. tuberosum clone (Rosa H1) with a resistant clone belonging to the wild potato relative S. spegazzinii has been studied for late blight resistance using a stem assay. A major QTL originating from the wild species has been identified. Using genetic map developed by Caromel (2004), this QTL has been mapped to chromosome X and is named PiXspg. It explains between 30 to 40% of the phenotypic variation according to the stem resistance component. A fine mapping of PiXspg has been carried out, leading to the development of two SSR markers (SSR223 and SSR74) and three CAPS markers (P10c8, TG403F1 and P8h11) that are closely linked to the QTL (Quélennec et al., 2009). The usefulness of these markers is evaluated in a marker-assisted selection program.

Materials and Methods



In population 06D24, the presence of the markers is associated with lower REC values whereas no QTL for REC was detected in the 96D32 population.

Conclusions and Perspectives

In 3 out of the 4 studied populations, the molecular markers linked to PiX_{spg} appear to be useful to predict the late blight stem resistance of the clones. The usefulness of these markers will be also evaluated for marker-assisted selection at the tetraploid level.

However, as the presence of PiXspa is not always correlated with stem resistance, it is likely that other genomic regions and/or epistatic interactions are involved in the expression of this trait.

References Caromel (2004) Thesis Quélennec *et al.* (2009) Bioexploit Meeting (Poster)



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