

Natural and Engineered QTL for Quantitative Resistance to Late Blight

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The improvement of potato for field resistance to late blight is conducted at CIP through molecular approaches that will eventually complement our longstanding conventional breeding work.

Humans started agriculture almost 12,000 years ago by domesticating an almost insignificant proportion of the world's plant germplasm and developed what is today agriculture. It is generally recognized that modern agriculture tends to narrow down the genetic diversity of crop plants. It has also been recently recognized that broadening the genetic base of crop plants is a valid response to new emerging constraints and threats to crop plant production, such as new pathogens or abiotic factors. An intriguing question is how to get back to this diverse germplasm to develop new crops in less than 12,000 years that will respond to these constant changes in pathogens, climates, or consumer needs.

Tremendous expectations come from the application of modern biotechnology in agriculture to broaden the genetic base of crop plants and speed up current breeding processes.

In moving valuable genes from the germplasm to crop plants, a first step is germplasm evaluation for the identification of new trait sources. The next steps involve either a genetic mapping followed by marker-assisted selection approach or a gene cloning followed by direct gene transfer approach. The research at CIP on new sources and genes conferring resistance to LB is traced from this scheme.

Valuable but unknown genes are present in the germplasm, and we need to explore this gene pool for valuable alleles contributing to LB resistance. Two well-known species host various interesting levels of resistance to LB and have already been used at CIP to develop populations with interesting levels of resistance. The selection of parental clones for these populations has so far been driven essentially by breeders' art. To base this selection on gene-based criteria, genetic diversity assessments of these germplasm collections have been done in both cases. *Solanum phureja* is a diploid cultivated potato with high levels of horizontal resistance to LB. *Solanum tuberosum* subsp. *andigena* is a tetraploid cultivated potato of the Andean region. Both collections were sampled to form a core encompassing the genetic diversity of the base collection. These core collections will be valuable resources for the identification of superior QTL alleles.

The next strategic step is the identification of chromosomal regions associated with the trait of interest. To that end, we developed a genetic mapping approach based on a cross between *S. phureja* and a dihaploid *S. tuberosum* clone. Two genetic maps were produced — one for each parent— and a QTL analysis was recently developed to identify QTL and their respective contributions to the phenotypic variation. Both parental maps revealed QTL location on chromosomes previously identified to host QTL (11 out of the 12), but some apparently at a different location. In particular, the QTL on chromosome XII seems to be at a different location from that which has been reported in the literature. Markers encompassing QTLs from both parents will be tested for LB resistance predicting power in diploid and tetraploid crosses using a resistant clone from the mapping popu-

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lation and by looking at homologous markers in our tetraploid crosses of the *S. tuberosum* subsp *andigena* material. Finally, after having confirmed the value of such potato regions for QTL for field resistance, we can get back to the germplasm core collections and test allelic variation to identify superior alleles.

The single gene approach under development at CIP uses antifungal protein genes. Here, we follow the experience of engineering resistance to another fungal pathogen of tomato by combining the chitinase and glucanase genes that have been shown to have a synergistic effect. Our approach consists of three genes: the osmotin gene from *S. phureja* and *S. commersonii*, the T₄ lysozyme gene, and the 1,3- β -glucanase gene. These genes have been reported to display antifungal activity. We plan to combine these antifungal proteins and test the hypothesis of synergistic effect on resistance to late blight.

In conclusion, the molecular approach undertaken at CIP is based on the ambitious project to prospect the germplasm biodiversity for genes associated with quantitative resistance to LB, identify QTL from identified valuable new sources, and pyramid these with effective combinations of antifungal transgenes.

Another molecular approach that we have so far been unable to undertake is looking for genes associated with disease resistance from a genome-wide stand. Having such an EST sequencing approach, we could harvest a wealth of candidate genes that would allow us to develop new gene technology systems. In addition to novelty of genes, this genome-wide strategy would allow us to get around the complications associated with patents and other IPR and leave us freedom to operate with these genes.