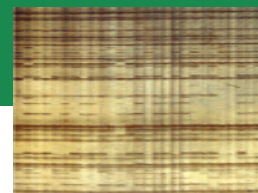


Host Resistance: Molecular Approaches



Host Resistance as Solution to the Late Blight Problem: Lessons Learned from Genetic Analysis and Future Prospects

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Since its first outbreak in Ireland in the last century, late blight has remained a threat to potato cultivation throughout the world. Breeding for host resistance using major genes was the first approach to solve the problem. The resistance obtained was not durable, however. Breeding for quantitative or field resistance does yield cultivars with good levels of resistance, which is thought to be more durable. As long as field resistant cultivars are not superior to (or at least equivalent to) established, susceptible varieties with respect to agronomic qualities other than late blight resistance, they are not commercially competitive. They are not competitive because, until today, susceptible varieties can be protected effectively against late blight by frequent fungicide treatments. However, effectiveness of chemical treatment is not durable either and begins to deteriorate. Nothing on this planet is durable. There are only different rates of change. Methods to safeguard the potato crop against late blight should evolve, therefore, at the same rate or slightly faster than the pathogen, which is co-evolving with its host. The best method should be one that is versatile and able to keep pace with adaptive changes of the pathogen.

What are the future options for protecting the cultivated potato against late blight, besides conventional breeding for resistance and agrochemistry? New and safe protective fungicides based on analysis of the genome of the pathogen *P. infestans* may be developed in the future. Such possibilities are just emerging from genome analysis of human pathogens. Biological control of *P. infestans* may be a possible

alternative. On the other hand, resistance of the host may be achieved by genetic engineering of a completely new resistance mechanism or, alternatively, by making better use of resistance mechanisms that have naturally evolved in the plants on this planet. In my view, the last option will be the safest and most versatile.

Understanding of how plants resist pathogens on the molecular level is required. As in human disease, treating the symptoms is possible. Curing the disease truly requires knowledge of the causal relationships involved. Physiological, biochemical and molecular analyses of host-pathogen interactions have provided us with a wealth of information on individual components of the resistance response. More recently, genetic analysis of qualitative and quantitative resistance to late blight using DNA markers has provided us with a first (still rather incomplete) genome-wide view on the complexity of the genetic control of the resistance phenomenon. Both lines of research together, in combination with the powerful new tools of genome analysis, may be the key for the identification and manipulation of those genes that control resistance or susceptibility to late blight in the field.

What lessons have we learned so far from genetic analysis of resistance to late blight using DNA markers? First, major genes for resistance to late blight (R genes) are closely linked to factors controlling quantitative resistance. This suggests that there is no real difference between quantitative and qualitative resistance to late blight as far as the nature of the genes involved. The differences observed on the phenotypic level may be the result of allelic variation at the same or closely related loci. Second, some R genes are organized in clusters as

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is seen in other host-pathogen systems (flax and flax rust, for example). Third, genetic factors affecting quantitative resistance to late blight have been found on all twelve potato chromosomes, underlining the multigenic nature of this resistance phenotype. Fourth, R genes as well as QTL for late blight resistance are linked to "resistance gene like sequences" (RGLs). This suggests that RGLs are candidate genes for controlling resistance to late blight. Few QTL are linked to loci encoding pathogenesis-related genes (PR genes) which are also candidate genes. Fifth, the genetic factor(s) that has the most prominent and consistent effect so far on quantitative resistance to late blight is closely linked to genes for late maturity. In fact, it may be the same gene(s) that has pleiotropic effects on late blight resistance and plant maturity. Breeding for resistance to late blight seems to have selected mainly alleles at this QTL (located on potato chromosome V) because most cultivars with good levels of field resistance are

late maturing. The challenge for breeding research will be to identify, with the help of DNA markers, superior alleles for resistance at QTL other than the ones linked to plant maturity. Sixth, QTL alleles, which increase susceptibility to late blight, are often dominant over alleles that increase resistance. Segregation ratios at QTL for late blight resistance are also often distorted, with susceptibility alleles being more frequent. DNA markers should be the tools for identifying those rather infrequent genotypes in a hybrid population with superior QTL alleles for late blight resistance.

Molecular cloning and characterization of R genes will open the door for identification, isolation, and manipulation of genes controlling field resistance to late blight. Positional information on QTL and candidate genes for late blight may be used to identify and select superior alleles for late blight resistance from cultivated and wild potato species.