

Foliar and tuber late blight resistance in a *Solanum tuberosum* breeding population

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Abstract

The purpose of this research was to identify the genetic basis of foliar and tuber resistance to *Phytophthora infestans* in a potato breeding population developed from a cross between two tetraploid *Solanum tuberosum* lines, NY121 and NY115. The parent with high foliar resistance, NY121, was highly susceptible to tuber blight. Foliar resistance was assessed in field trials, while tuber blight was assessed both in the field and in the laboratory. A quantitative trait locus (QTL) explaining ca. 50% of the phenotypic variance for foliar resistance was located on the lower arm of linkage group V, and was loosely associated with tuber blight resistance (significantly in one of two trials). This QTL was confirmed in a separate sample from the same population. Tuber blight detected via laboratory assays was not correlated with tuber blight incidence in the field. Most markers associated with tuber blight resistance were not associated with foliar resistance and most markers associated with foliar resistance were not associated with tuber blight resistance.

Key words: late blight — quantitative trait loci analysis — tuber blight — resistance — *Phytophthora infestans*

Late blight, caused by the oomycete *Phytophthora infestans* (Mont.) de Bary, is one of the most devastating diseases of potato. Both foliage and tubers can be affected. Host resistance is recognized as potentially the most effective and environmentally acceptable method to control late blight. Unfortunately, most commercially cultivated potato varieties have little resistance to foliar and/or tuber blight. The introgression of single, dominant resistance genes (R-genes) from wild *Solanum* species into cultivated *Solanum tuberosum* has not proven durable for disease management. Monogenic R-gene resistance in potato has been easily overcome by the appearance of new races of *P. infestans* (Niederhauser and Mills 1953, Stewart et al. 2003). This type of resistance has been termed 'qualitative' because it is very effective against some races of the pathogen, but ineffective against others, and appears to be non-additive. R-genes which confer resistance to *P. infestans* in the foliage, do not always impart resistance to the tubers (Roer and Toxopeus 1961, Park et al. 2005). Because of the lack of success in controlling late blight with R-genes, a more intensive effort has been initiated to produce resistant potato cultivars without R-genes. This 'non-R-gene' resistance is assumed to be polygenic and to be effective against all races of *P. infestans*.

Analyses of numerous breeding populations of *S. tuberosum* crossed with wild *Solanum* species have detected both qualitative and quantitative resistance in foliar tissue. However, there have been both positive and negative correlations between foliar and tuber blight resistance (Stewart et al. 1992, 1994, Platt and Tai 1998, Oberhagemann et al. 1999, Park et al. 2005). For example, in crosses between *S. tuberosum* and four wild *Solanum* species (*S. vernei*, *S. kurtzianum*, *S. stenotomum*, and *S. chacoense*) Oberhagemann et al. (1999) detected a quantitative trait locus (QTL) on chromosome V, which was associated with foliar resistance and tuber susceptibility. In another study foliar and tuber resistance were found to segregate in combination and independently in four mapping populations analysed by Park et al. (2005). Therefore, the relationship between foliar resistance and tuber resistance remains complex. The goal of the present study was to identify QTL for foliar and tuber blight resistance for use in marker assisted selection.

Materials and Methods

Plant material: The population evaluated (Y36) was derived from a cross between NY121 (female parent) and NY115 (male parent). A total of 1872 seedlings of Y36 were grown in pots in 1999. After applying mild selection for tuber type and appearance, four tubers were saved from each of 1622 progeny. Further selection for tuber appearance and yield at harvest reduced the Y36 population to a total of 313 clones. A subpopulation of 94 clones for initial marker analysis was selected from the 313, where 41 clones were chosen because they had exhibited resistance to race Ro2 of the golden cyst nematode (*Globodera rostochiensis*); 35 were chosen because they had tested susceptible to Ro2; an additional 18 were chosen because they exhibited some degree of resistance to late blight in greenhouse trials. After the 2004 trial, in which five polymorphic markers were linked to blight resistance (see Results), an additional 126 progeny were selected randomly from the remaining 219 clones to further test the linkage of these five markers.

Marker development and mapping: Genomic DNA was isolated from leaves of NY121, NY115 and Y36 clones with a DNeasy kit (Qiagen, Valencia, CA, USA), following the manufacturer's instructions. Extracted DNA was prepared for amplified fragment length polymorphism (AFLP) analysis by digestion with *Pst*I and *Mse*I, ligation of adaptors, and preamplification with non-selective Pst and Mse primers, as described by Vos et al. (1995). A total of 57 Pst+2/Mse+3 selective primer pairs was used for final amplification. Selective Pst primers were labeled with 33P prior to amplification. Products were separated on a denaturing polyacrylamide gel, which was then dried and exposed to film. Amplification products that

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