

Progress Toward Fine Mapping of *Ph5*, a New Late Blight Resistance Gene in Tomato

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Late blight (LB), caused by the oomycete *Phytophthora infestans*, can devastate tomato and potato crops within days, rendering their economically important products useless. Responsible for the Irish potato famine, LB re-emerged as an important plant disease in the 1970s, with annual control costing billions. Current LB control methods include cultural practices and the heavy use of fungicides. Although three LB resistance genes have been reported in tomato (*Ph-1*, *Ph-2*, *Ph-3*), new, aggressive isolates have overcome all three resistance genes, necessitating the search for new and durable sources of LB resistance. Through extensive germplasm screening with 7 *P. infestans* isolates in the field, high tunnel, greenhouse and growth chamber, we have identified several highly resistant accessions of the wild tomato species *Solanum pimpinellifolium*. One accession, PSLP153, was selected for further study. An F₂ mapping population was developed from a cross between NCEBR-2 (*S. lycopersicum*, susceptible parent) and PSLP153. Using a selective genotyping approach and F₂ and F₃ populations, a new late blight resistance gene, *Ph-5*, was mapped to the long arm of chromosome 1. Near isogenic lines (NILs) are being developed to fine map *Ph-5*. To develop the NILs, a series of backcrosses is being made using NCEBR-2 as the recurrent parent. Currently, an F₄BC₂ population is being developed. Extensive foreground and background marker assisted selection (MAS) will be conducted in this and further backcross generations. It is anticipated that by a combination of phenotypic selection for LB resistance and MAS for *Ph-5*, NILs will be generated by the BC₄ generation. Once NILs and subNILs are developed, *Ph-5* will be fine-mapped using the substitution mapping approach.