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DEVELOPMENT OF INTEGRATED MOLECULAR MARKER RESOURCES FOR RESISTANCE GENE MAPPING AND EXPLORATION OF RESISTANCE GENE DIVERSITY IN THE GENUS *SOLANUM*

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The potato is host to a plethora of pathogens which, individually and as complexes, can cause severe reductions in the yield and quality of the crop. Worldwide, potato improvement efforts focus on genetic host resistance as a viable, environment-friendly and economical alternative to chemical pest control. To date, several resistance (R) genes have been cloned from potato or related species using traditional, phenotype-driven map-based cloning approaches. Most of these R genes exist in complex families of related sequences that map to multiple genome locations. This genome redundancy of R genes at the sequence level complicates development of molecular markers. Toward long term genetic improvement of cultivated potato, our current research aims to develop an integrated system of R gene physical and genetic maps for the genus *Solanum.* Using the disease resistant diploid species *S. bulbocastanum* as a model, we have adopted a BAC-based method for the generation of single copy markers, each associated with a known genome location and a characterized R gene physical map. These markers will be useful for mapping phenotypic disease resistance and exploration of diversity near R genes.

R1, RB, and a homolog of *Mi-1* confer resistance to the late blight pathogen, *Phytophthora infestans.* We designed PCR primers from *R1, RB,* and *Mi-1.* The resulting PCR fragments were used as probes to identify corresponding BAC clones from a *S. bulbocastanum* library representing 5X genome equivalents. For each gene, 15 to ~50 homologous clones were identified, consistent with the possibility that homologs of each gene map to multiple genome locations. Each BAC clone has been end sequenced. Using an F1 mapping population, we are identifying PCR markers, developed from BAC ends, that segregate as single copy markers. As they are developed, single copy markers are being utilized to array BAC clones into contigs via a BAC end hybridization approach combined with cosegregation analysis. In a parallel study in our laboratory, a medium density AFLP linkage map is being constructed for *S. bulbocastanum.* This map will serve as a scaffold, enabling integration of the genetic map with R gene physical maps (BAC contigs) and associated single copy markers. Once completed, the integrated resource will allow assignment of segregating phenotypic disease resistance to marker "bins". We are currently exploring the potential utility of our markers for mapping in potato, tomato, and eggplant.

Finally, using our burgeoning marker resource, we are exploring genomic diversity near the *R1* and *RB* loci in a collection of 42 *S. bulbocastanum* genotypes representing the entire geographic distribution of the species, three morphologically-defined subspecies, and incorporating multiple genotypes per population. For each gene, sequence diversity of nearby single copy markers is being explored using a variety of molecular approaches. We expect our results to offer insights in the partitioning of marker diversity near R genes.