DEVELOPMENT OF A DArT MICROARRAY FOR COMPARATIVE STRUCTURAL GENOMICS AND MAPPING OF AGRICULTURALLY SIGNIFICANT GENES IN WILD POTATO SPECIES

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Efficient access to genetic variability is important for breeding programs. For potato improvement, the approximately 180 wild species represent a valuable source for agriculturally significant genes, including genes for disease resistance and cold tolerance. We specialize in a group of 20 wild potato species that collectively comprise the tertiary genepool for cultivated potato. These species are sexually incompatible with cultivated potato, but genes from these species can be accessed using bridge crosses, somatic hybridization, and gene cloning and transformation. To improve access to agriculturally significant genes from tertiary genepool species, we have initiated an effort of comparative structural genomics using the Diversity Array Technology (DArT) marker platform. The first phase of this project was development of the DArT microarray. We used five diverse tertiary genepool species for array construction: *Solanum commersonii*, *S. bulbocastanum*, *S. polyadenium*, *S. chacoense*, and *S. pinnatisectum*. Six accessions for each species were included. Now, DArT array validation via phylogenetic comparison is ongoing. In this phase of our study, deduced relationships between the five species used in array construction plus *S. circaeifolium* and *S. cardiophyllum* will be compared with those reported previously based on morphological and molecular markers. Congruence between the DArT phylogeny and previously reported phylogenies (an expected result) will be interpreted as validation of the DArT array. For *S. commersonii*, *S. bulbocastanum*, *S. chacoense*, and *S. pinnatisectum*, parental genotypes have been designated based on crossability studies and preliminary phenotypic evaluations conducted by our laboratories. F1 mapping populations have been generated for each species. Linkage maps will be constructed for each species based on a common set of DArT markers, allowing comparison of genome structures. Significantly, the maps generated will allow efficient mapping of genes conditioning agriculturally significant phenotypes. In support of this effort, large-scale phenotypic analyses are ongoing. Currently phenotypic tests include evaluation of all available accessions of *S. commersonii* (133 accessions) and *S. chacoense* (61 accessions) for foliar resistance to *Phytophthora infestans*. 