

## Potato Germplasm Panel

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A SNP marker platform will be used to genotype the entire germplasm panel set. Adopting standardized genotyping platforms and developing user-friendly tools for analysis will help translate genome sequence information and increase access to the breeding community. At the same time such approaches will help elucidate the genes and gene systems under selection during domestication and breeding. Standard germplasm panels (approximately 480 lines per crop) will be developed that represent a balance between relevant breeding lines and populations for association mapping of relevant traits or marker-assisted-selection.

In potato, the germplasm panel will be grouped according to specific market classes (russet fresh, russet frozen processing, round white fresh, round white chip-processing, red, yellow-flesh, novelty) and will include a broad genetic-base to survey the allelic diversity for important traits. With a well-designed panel, we should be able to examine changes due to breeding for a processing market versus a fresh market and assess linkage disequilibrium. In potato pedigree information has been well-established for North American cultivars since the mid-1800s.

A subset of the panel will be lines chosen with cold sweetening resistance. Another set will be important varieties and advanced lines of value to the breeding community (See letters of support from 11 breeding programs in US.). Selection will be based upon parental value in breeding and mapping, historical significance, whether they contain introgressions from other *Solanum* species, genetic diversity, processing ability, starch content, appearance, and resistance to major diseases. To provide a taxonomic perspective, a set of *Solanum* species and accessions that have been introgressed into 4x germplasm will be included in the panel. Lastly, a tetraploid mapping population from a russet x russet cross, segregating for vitamin C and reducing sugar concentration, will be chosen for genotyping, while a 2x mapping population (De Jong) will be used for mapping the SNPs.

Breeders will be able to access data from this panel to design future crosses for mapping or breeding purposes. These crosses would allow the breeders to develop mapping populations that have marker diversity and also segregate for the economic traits of interest beyond the initial scope of SolCAP traits. Genotyping of these populations could then be done by the central genotyping facilities via funds allocated through the small grants program, while the phenotyping is conducted by the breeder in the target region.

The majority of the material selected for the germplasm panel (mapping population and clones (varieties, parents and genetic stocks) will be field tested for two years over two environments to collect samples for phenotypic metabolite analysis and other important agronomic traits. De Jong (Cornell University) and Novy (USDA/ARS ID) will provide clean seed of the clonal material and mapping population, respectively, for the replicated field tests. Thill (Univ. of Minnesota) and Yencho (North Carolina

State University) will provide the sites for mapping population evaluations, while Jansky (USDA/ARS, WI) and Vales (Oregon State University) will evaluate the clonal material. Tubers will be collected for sugar and Vitamin C analysis and will be shipped to Cornell University for analysis. K. Haynes (USDA/ARS, MD) will manage the distribution of seed; provide experimental design, data management and analysis of the phenotypic data for potato.