

Next-generation SNP genotyping platforms for characterizing potato germplasm

David De Koeyer^{*1}, Katheryn Douglass¹, Martin Lague¹, Benoit Bizimungu¹,
Agnes Murphy¹, Merideth Bonierbale² and Teresa Mosquera³

¹*Agriculture and Agri-Food Canada*

²*International Potato Center, Peru*

³*Universidad Nacional de Colombia, Colombia*

**corresponding author: David.Dekoeyer@agr.gc.ca*

Abstract

High-throughput, low-cost methods for generating genotypic data within potato breeding programs are necessary to help breeders develop improved varieties faster. With the availability of the potato genome sequence and the identification of numerous polymorphisms, new genotyping strategies and marker resources for potato research are now widely available. These genome-wide markers are available for comprehensive characterization of potato genetic resources and prediction of the value of exotic potato germplasm. Several genotyping methods have been evaluated at the Agriculture and Agri-Food Canada (AAFC) Potato Research Centre to identify single nucleotide polymorphisms (SNPs), characterize potato germplasm resources, generate genetic maps, and initiate genomic selection projects. These methods include whole genome re-sequencing, targeted sequence capture, Illumina SolCAP SNP arrays, restriction site associated DNA sequencing, genotyping by sequencing, and most recently with 2b-RAD genotyping. Each of these methods has some advantages in terms of genome coverage, genotype certainty, sample throughput, and cost per sample. Diploid and tetraploid potato germplasm from the AAFC potato breeding program, the Canadian Potato Gene Resources Repository collection, the International Potato Center (Peru) breeding program, and diploid *Solanum phureja* germplasm from Colombia have been genotyped using the SolCAP SNP array and / or genotyping by sequencing. Applications of these methods for SNP discovery, detection of marker-trait associations, characterization and comparisons of diversity within gene pools and future research on prediction of breeding values will be presented. Based on our experiences, the new genotyping tools will lead to better utilization of beneficial diversity in wild potato relatives and germplasm from South America.

Keywords: potato, single nucleotide polymorphism, genetic resources