Utilising Molecular Diversity in the Commonwealth Potato Collection

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As it becomes possible to explore the natural variation in plants at the gene and sequence level, new ways of making precise and effective use of the natural wealth in genebanks become possible. SCRI maintains a genebank of international status, the Commonwealth Potato Collection (CPC). Comprising over 1300 accessions of 77 species, the collection houses germplasm accumulated by collecting missions to S and C America from 1938 onwards. Anticipating this shift in the exploitation of genebanks, we have converted the Commonwealth Potato Collection to DNA form and are preparing for molecular-based exploitation by characterising accessions at the DNA level.

CPC material has been extensively utilised for potato breeding using traditional approaches. An example with great impact on UK agriculture is the exploitation of the H1 gene for Potato Cyst Nematode (PCN) resistance from CPC1673, an accession of *Solanum tuberosum* ssp. *andigena*. Other examples include the use of accessions of *S. demissum* to introgress late blight resistance into cultivated potatoes, and *S. vernei* to introgress a second form of resistance to PCN. These have led to the breeding of disease resistant cultivars such as Maris Piper, Pentland Dell, and Stirling.

Figure 1 Four species in the CPC: *Solanum oplocense, S. cardiophyllum, S. ochranthum* and *S. bukasovii* (clockwise from top left).

Making efficient use of the CPC for potato breeding and other scientific endeavours relies heavily on understanding the relationships of species and the genomes within them. Taxonomies of *Solanum* published to date are generally based on morphological information and where molecular data exist they are frequently from methods with low information content such as RFLPs. In late 2001 we initiated a molecular genetic analysis of the CPC, together with material obtained from other collections in the United States and Peru, using a combination of techniques targeting both the nuclear and chloroplast genomes. Currently we are completing an analysis based on the highly-multiplex Amplified Fragment Length Polymorphism (AFLP) assay, which has involved the deployment of six AFLP primer combinations on approximately 2000 DNA samples, each of which generates in the order of 80-100 AFLP fragments. This study will allow a comprehensive, structured phylogenetic analysis of potato germplasm, leading to the identification of a core collection of material for more detailed genetic, biochemical, and metabolic studies. The data is now helping to generate better phylogenies, throwing light on the origins of species including polyploid hybrid species groups. One particular surprise has been the apparently artificial nature of series Tuberosa.

We have converted the genebank to a curated collection of DNA from both individual seedlings and bulks representing the entire variation in the accession. These resources are now being applied in the search for novel alleles, including those for higher carotenoids and vitamin C, targets which may be amenable to molecular genetic studies of genes for pathway enzymes and controlling loci. Application of direct methods of understanding the basis of genetic variation in these traits will ensure that potato varieties in the future can combine desirable traits in much more efficient ways, and hence supply the products required for future targeted and sustainable food production.