

Molecular diversity in a large potato germplasm collection

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We have completed the first phase of a comprehensive molecular genetic analysis of the Commonwealth Potato Collection (CPC). The CPC consists of 80 species represented by around 1200 individual accessions.

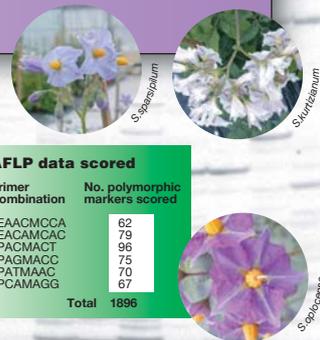
In addition, 380 samples were included in the analysis from the USDA potato collection. Six AFLP primer (4 *PstI/MseI*, 2 *EcoRI/MseI*) combinations have yielded 449 polymorphic markers, and a total of 877,000 fragments have been scored.

Germplasm Studied

Category	No. of Accessions
2x Cultivated	173
4x Cultivated	473
Other cultivated	2
2x Wild	703
3x Wild	1
4x Wild	337
5x Wild	3
6x Wild	188
Unknown	16
Total	1896

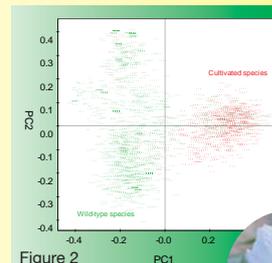
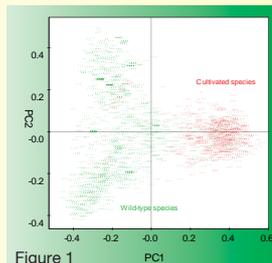
AFLP data scored

Primer Combination	No. polymorphic markers scored
EAAQMCQA	62
EACAMCAC	79
PACMACT	96
PAGMAAC	75
PATMAAC	70
PCAMAGG	67
Total	1896



PCO analysis of entire dataset

A similarity matrix (Jaccard) has been analysed using Principal Coordinates Analysis (PCO). The accompanying figures show PCO plots (dimensions 1 & 2) for two AFLP primer combinations (Figures 1 & 2). The shapes of the plots are quite similar and the vast majority of cultivated accessions cluster with a subset of wild accessions corresponding to the Brevicaule species group. Some cultivated accessions cluster anomalously with other wild species and the identity of these are being checked. Similar parallel analyses are focussing on other species groups. These data are used to 'flag' accessions as having potentially erroneous data to allow more detailed phylogenetic analyses.



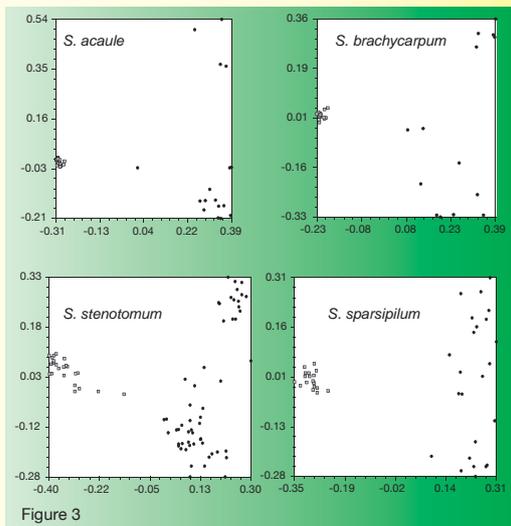
Intra-accession diversity

We have examined levels of AFLP diversity within and among 17 accessions (18-24 plants) of 15 taxa representing different ploidies and breeding systems occurring in potato.

Category	Species
2x Inbreeder	<i>S. verrucosum</i> , <i>S. brevidens</i>
4x Inbreeder	<i>S. stoloniferum</i> , <i>S. acaule</i> ssp. <i>aemulans</i> , <i>S. acaule</i>
6x Inbreeder	<i>S. demissum</i> , <i>S. brachycarpum</i>
2x Outbreeder	<i>S. stenotomum</i> , <i>S. pinnatisectum</i> , <i>S. sparsipilum</i> , <i>S. bukasovii</i> , <i>S. megistacrolobum</i> , <i>S. cardiophyllum</i> ssp. <i>ehrenbergii</i>
4x Outbreeder	<i>S. tuberosum</i> , <i>S. oplocense</i>
6x Outbreeder	<i>S. oplocense</i>

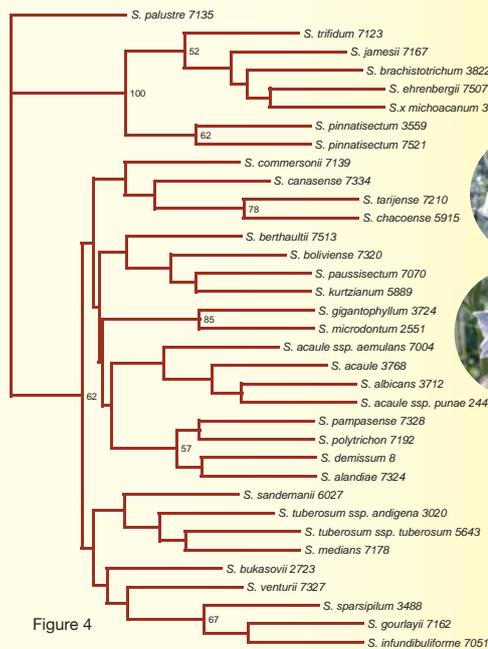
Our results show that genebank accessions of inbreeding species contain significantly less genetic diversity than outbreeders. The ratio of between/within accession diversity changes markedly from outbreeders to inbreeders. A single plant better represents an inbreeding accession than an outbreeding one. However, an outbreeding accession contains more of the genetic diversity held in the species than an inbreeding one.

Figure 3 shows PCO plots (1st and 2nd dimensions) for 4 species, showing tighter clustering of accessions of inbred taxa (*S. acaule* & *S. brachycarpum*) in comparison to outbreeding species (*S. stenotomum* & *S. sparsipilum*). Points shaded in grey represent individuals of same accession for each species.



Chloroplast DNA analysis

An analysis of the same material using organelle-derived markers and gene sequences is underway. Initial work carried out on chloroplast DNA analysis on a subset of the material surveyed by AFLP has revealed very low levels of polymorphism. Work is continuing to provide a sequence-based high taxonomic level chloroplast phylogeny of the selected material. Figure 4 shows a phylogenetic tree based on a relatively variable chloroplast sequence (NTCP9), which suffers from poor bootstrap support. It is hoped to find other such variable sequences to improve the resolution.



Summary

These data, in conjunction with phenotypic evaluations, will inform the efficient use of CPC material for potato improvement, and aid the identification of core collections. We are also using the data to analyse the genetic 'structure' of potato germplasm from a population genetics viewpoint.

Acknowledgements

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