Molecular diversity in a potato germplasm collection

Karen McLean[1], Gavin Ramsay[1], Robbie Waugh[1], David Spooner[2], Glenn Bryan[1]
[1]Scottish Crop Research Institute, Invergowrie, Dundee DD2 5DA, Scotland
[2]University of Wisconsin, Madison, Wisconsin, USA

Scottish Crop Research Institute

Introduction

We have recently completed the first stage of a comprehensive molecular genetic analysis of the Commonwealth Potato Collection (CPC), held at SCRI in botanical seed form. The CPC consists of approximately 80 species represented by around 1200 individual accessions. In addition, 380 samples were included in the analysis from the USDA collection which is held at Sturgeon Bay, USA.

As an initial step in the use of the data we have performed a phenetic analysis on the entire data set to establish putatively misidentified accessions. Data analysis was carried out in Bionumerics software (Applied Maths) using a Dice algorithm and the dendogram produced using UPGMA clustering.

Germplasm Studied

380 accessions were included in the study to look at intra-accession variability within different groups. These were made up of 20 - 24 individuals from the same accession which were chosen to represent several different categories defined by ploidy level and breeding system.

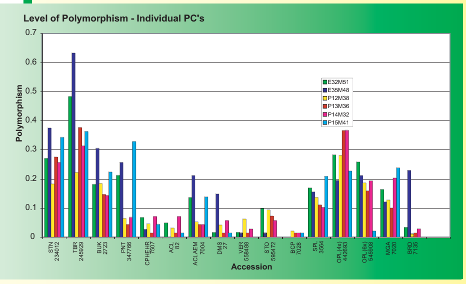
Category	No. of Accessions
2x Cultivated	150
4x Cultivated	447
Other cultivated	2
2x Wild	519
4x Wild	226
6x Wild	111
Unknown	57
Total	**1512**

Intra-accession Material Studied

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

Ongoing studies include measuring the levels of between and within accession diversity. Different species appear to have different levels of polymorphism across different primer combinations.

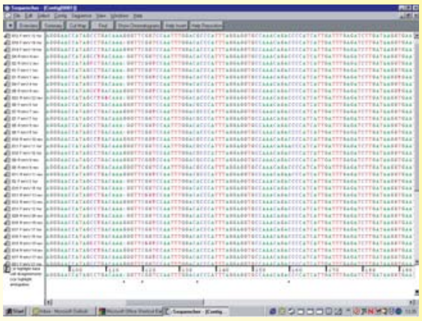
DNA was extracted from single plant samples grown from seed. AFLP analysis was carried out using *Eco* R1/*Mse*1 and *Pst*1/*Mse*1 primer combinations. Bands were selected for scoring depending on their reliability on each of the gels for a particular primer combination. In this way errors due to scoring difficulties were reduced. A total of 877,000 bands have been scored on the 162 AFLP gels in this study.



Bands Scored per Primer Combination

Primer	No.of Bands Scored
EAACMCCA	62
EACAMCAC	78
PACMACT	96
PAGMACC	75
PATMAAC	73
PCAMAGG	67
Total	**451**

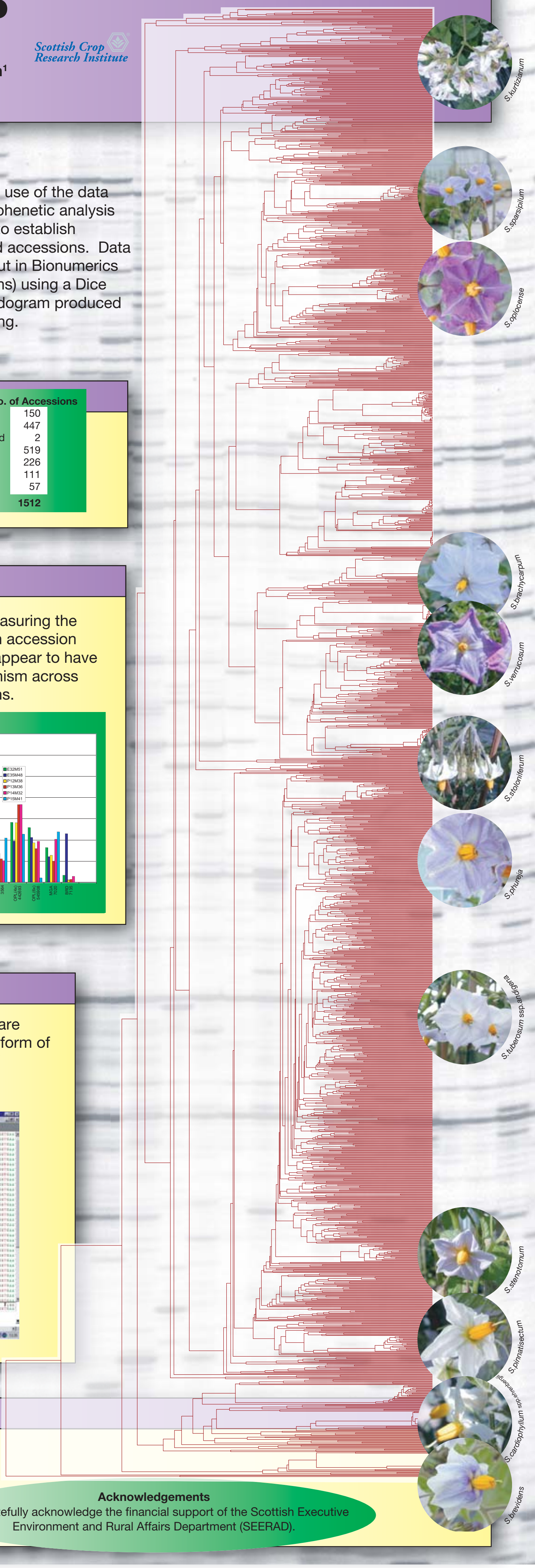
Gel scoring was carried out using AFLP Quantar software supplied by Keygene. Scored data are exported in the form of Excel files which can then be imported into a variety of phylogenic analysis packages



An analysis of the same material using organelle-derived markers and gene sequences is underway. Initial work on the analysis of chloroplast data from 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.

Ongoing Work

- Complete the analysis of the current data set.
- Complete cpDNA analysis.
- Perform taxonomic genetic analysis of a core set of the CPC - around 200 individuals - using gene sequence data.



Acknowledgements
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