

# Levels of intra-specific AFLP diversity in tuber bearing potato species with different breeding systems and ploidy levels

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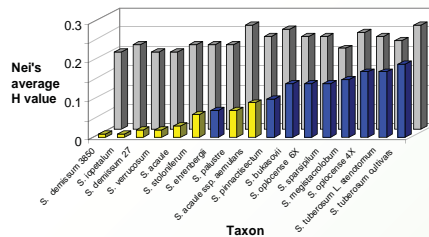
We have examined levels of intra-specific AFLP polymorphism in wild and cultivated potato taxa differing in geographic origin, ploidy and breeding system. Six AFLP primer (4 *PstI/MseI*, 2 *EcoRI/MseI*) combinations have yielded 449

polymorphic markers on 619 plants, representing 17 genebank accessions (18-24 plants sampled) of 15 potato taxa as well as a 'pseudo-population' comprising a single individual from each available accession of each taxon.

## Levels of average heterozygosity within accessions and taxa

Diversity measurements were calculated using different methods and gave very similar results. The histogram below shows the average accession diversity statistics (Nei's H value) for the 17 *Solanum* accessions (yellow for inbreeder, blue for outbreeder). The taxon average diversities are shown behind in grey.

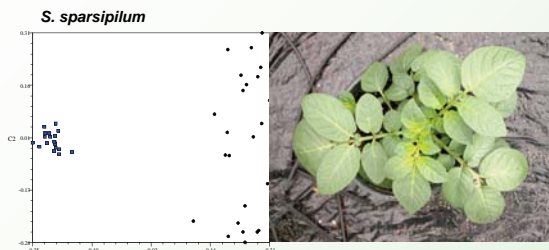
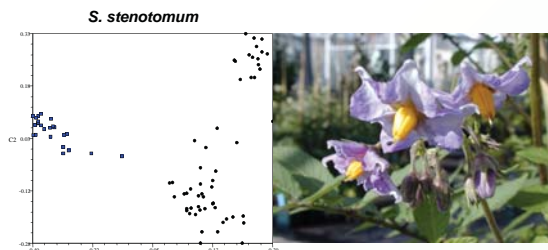
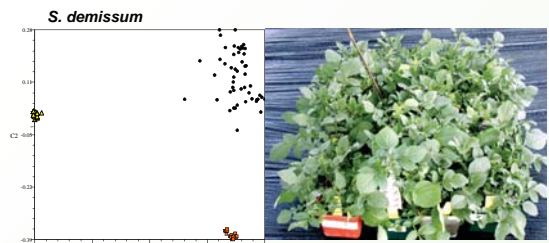
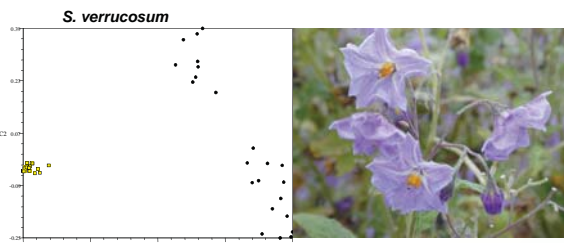
Histogram showing Nei's H values for inbreeding & outbreeding *Solanum* accessions



The histogram largely confirms that inbred accessions show lower amounts of genetic diversity than outbred ones. The least diverse accessions are allohexaploid species *S. demissum* and *S. iopetalum*. The most diverse accessions are cultivated species *S. tuberosum* ssp. *tuberosum* and *S. stenotomum*. Interestingly the outbreeder *S. ehrenbergii* shows an uncharacteristically low level of population diversity, and the allotetraploid inbreeders allotetraploids *S. stoloniferum* and *S. acaule* ssp. *aemulans* show relatively high levels of diversity.

## Relationships between individuals in a single accession to individuals from different accessions of the same species

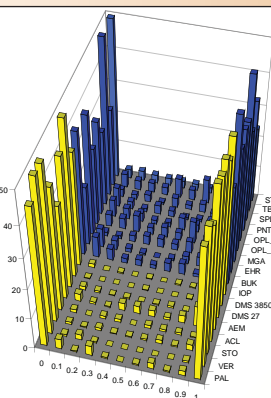
The AFLP marker data for each taxon were used to generate a similarity matrix (Jaccard), which were used to analyze the relationship between plants in each selected accession (coloured points) to those representing the same taxon using PCO analysis.



The PCO plots for the four selected taxa clearly show the very high degree of genetic relationship among individuals from each accession, as well as the relatively large genetic separation between any such individual with an individual from any different accession of the same taxon. This suggests any single plant is highly representative of the population from which it is drawn. The clustering for the two inbreeders shown (two accessions of *S. demissum*, *S. verrucosum*) is considerably greater than for the two outbreeders shown (*S. stenotomum*, *S. sparsipilum*).

## Allele frequencies of AFLP markers in accessions

Histogram showing AFLP allele frequencies for inbreeding & outbreeding *Solanum* accessions



The histogram shows the AFLP allele distributions for inbred accessions (yellow) and outbred accessions (blue) sampled. It is clear that outbred accessions contain a greater proportion of alleles with intermediate allele frequencies. The mean allele frequencies are ~91% for inbreeders (range 87-97%) and 77% for outbreeders (range 69-85%). By contrast the proportion of 'taxon marker fragments' that were present in the sampled accessions were 57% (range 47-69%) for inbreeders and 67% for outbreeders (range 49-81%). These data suggest that outbred accessions should be maintained as larger populations to reduce chances of allele loss during genebank maintenance.

### Acknowledgements

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