

Comparison of tuber proteomes of potato (*Solanum* sp.) varieties, landraces and genetically modified lines

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Background

Crop improvement by genetic modification is still controversial. One of the major issues is the potential for unintended effects. Comparative safety assessment includes targeted analysis of key nutrients and anti-nutritional factors but broader scale profiling or "omics" methods could increase the chances of detecting unintended effects. Comparative assessment should consider the extent of natural variation and not simply compare genetically modified (GM) lines and parental controls.

The aim of this work was to provide an insight into the extent of variation in potato tuber proteome by analysing a large selection of potato genotypes. In addition, several previously characterised GM potato lines were studied for possible unintended effects.

Materials

A total of 32 non-GM potato genotypes:

- 21 cultivars of tetraploid potato (*S. tuberosum*)
- eight landraces
- three diploid genotypes of *S. phureja*

10 GM potato lines, including vector-only and wild type controls

Two-dimensional electrophoresis of potato genotypes

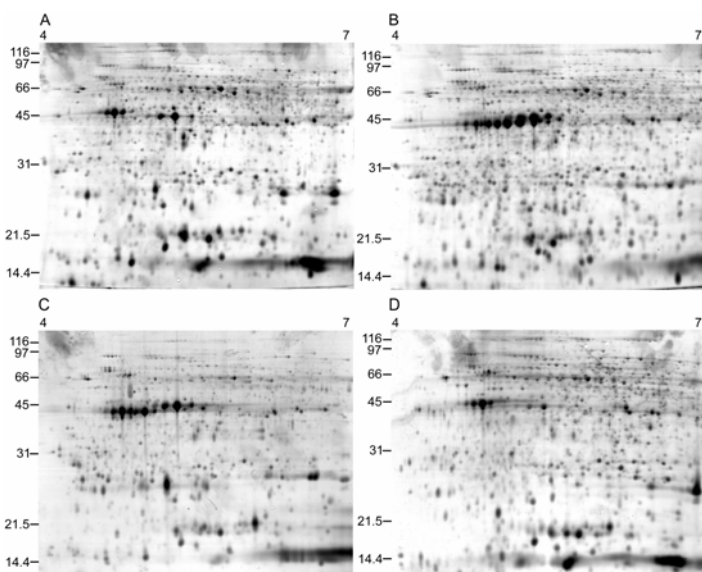


Figure 1. Two-dimensional gel electrophoresis images of tuber proteins of a range of potato genotypes. A: cv. Désirée; B: cv. Maris Piper; C: landrace accession TBR3369 (1); D: *S. phureja* accession PHU4637 (1).

Results

The expression of 1077 individual protein spots out of 1111 was significantly different among the non-GM genotypes. A total of 1932 spots were detected in all genotypes.

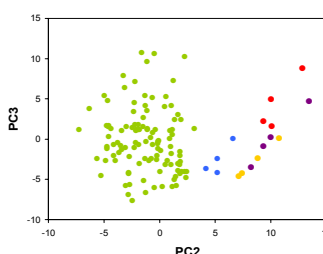


Figure 2. Principal component scores for the tetraploid *S. tuberosum* varieties and landraces (●), landrace TBR3302 (2) (●), and the diploid *S. phureja* PHU.4637 (●), cultivars Inca Sun (●) and Mayan Gold (●). Differences among the tetraploid *S. tuberosum* varieties and landraces were not as clear.

Only nine proteins out of 730 showed significant differences between GM lines or their controls. There was no clear separation between any of the lines in principal component analysis.

Furthermore, cv. Maris Piper and *S. phureja* were clearly separated from each other and from all GM and non-GM Désirée samples, while no separation was observed between wild-type Désirée and transformed lines.

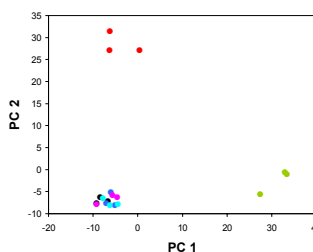


Figure 3. Principal component scores for Désirée WT (● and ●), GM lines Sam35S 3 (●) and W2GBSS VO4 (●), cv. Maris Piper (●) and *S. phureja* PHU.4637 (●).

Conclusions

- Genotypic variation was extensive; most of the proteins detected showed differences between varieties and landraces
- The effects of transformation on the proteome were much less clear
- Proteomic screening can provide much more information on crop composition than targeted analysis alone

References

Lehesranta S.J, Davies H.V, Shepherd L.V.T, Nunan N, McNicol J.W, Auriola S, Koistinen K.M, Suomalainen S, Kokko H.I, Kärenlampi S.O (2005): Comparison of tuber proteomes of potato (*Solanum* sp.) varieties, landraces and genetically modified lines. Plant Physiology, in press.