

## CHLOROPLAST DNA SEQUENCE VARIABILITY IN CULTIVATED AND WILD POTATO SPECIES

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Based on cpDNA restriction polymorphism, the chloroplast genomes of cultivated and wild potatoes have been classified in five main types geographically differentiated: A, C, S, T, and W, being the T-type by far the most frequent in the European cultivated potato (*S. tuberosum* subsp. *tuberosum*). We have recently sequenced the plastidial genome of *S. tuberosum* (DQ386163). Further, the complete cpDNA sequence of the wild potato *S. bulbocastanum* is available in GenBank (DQ347958). Herein, we report a detailed comparative analysis between the sequences of the two species, and the variability highlighted in 18 tuber-bearing *Solanum* species by sequencing specific intergenic regions.

Comparative analysis with the sequence of the wild potato *S. bulbocastanum* has revealed a number of mutations throughout the genome of the common potato, including 28 deletions, 40 insertions and 345 base substitutions. Out of 114 genes, 67 are conserved between the wild and cultivated potato, whereas 47 have shown some differences. In particular, 22 genes are different both in the nucleotide and in the derived amino acid sequence, and 25 only in the nucleotide sequence. The *psaJ* and *ndhF* genes showed a different length between the two species. Thirty two repeats (16 direct and 16 palindromic) have been identified in *S. tuberosum* and *S. bulbocastanum*. The two sets of repeats have been compared and differences have been observed both in the length and in the presence / absence of the repeats in the genome of the two species.

Since the large majority of indels and substitutions were observed in the intronic and intergenic regions, four of them (*trnK-rps16*, *rps16-trnQ*, *trnS-trnG*, *petN-psbM*), showing high variability between *S. tuberosum* and *S. bulbocastanum*, have been sequenced in other sixteen potato species. Such analysis identified several molecular markers that differentiated all species investigated. In comparison to *S. tuberosum*, *S. polyadenium*, *S. cardiophyllum*, and *S. bulbocastanum* have shown the highest polymorphism.

Results of the present study will improve the understanding of genetic variability at the cytoplasmic level in *Solanum* spp., allowing new phylogenetic and taxonomic studies and a better characterization of genotypes used in conventional and non-conventional breeding approaches.