

## **GENOME SEQUENCE AND ANALYSIS OF THE TUBER CROP POTATO**

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*Solanum tuberosum*, genome sequencing, genome annotation, haplotype diversity, tuber biology

Potato (*Solanum tuberosum* L.) is the world's most important non-grain food crop and is central to global food security. It is clonally propagated, highly heterozygous, autotetraploid, and suffers acute inbreeding depression. Here we use a homozygous doubled-monoploid potato clone to sequence and assemble 86% of the 844-megabase genome. We predict 39,031 protein-coding genes and present evidence for at least two genome duplication events indicative of a paleopolyploid origin. As the first genome sequence of an asterid, the potato genome reveals 2,642 genes specific to this large angiosperm clade. We also sequenced a heterozygous diploid clone and show that gene presence/absence variants and other potentially deleterious mutations occur frequently and are a likely cause of inbreeding depression.

Gene family expansion, tissue-specific expression and recruitment of genes to new pathways contributed to the evolution of tuber development. The potato genome sequence provides a platform for genetic improvement of this vital crop.