

### POPULATION GENOMICS

## Unearthing potato evolution

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The genomes of wild tuber-bearing *Solanum* relatives hold the key to understanding the evolution and adaptive diversification of potato. To assess the genetic variations in the potato gene pool and how selection shaped the genome, Michael A. Hardigan, from Michigan State University, and colleagues resequenced 67 samples, including wild diploid species, South American landraces, North American tetraploid cultivars and outgroups. Their analysis revealed the genomic mechanism of potato domestication and diversification.

The estimation of population diversity based on single-nucleotide polymorphisms in conserved genomic regions showed that cultivars and landraces bear strikingly high levels of diversity, comparable with wild species and exceeding any previously resequenced crop.

Extensive allele sharing with wild species demonstrates that the introgression of wild alleles contributed to the diversification of cultivated potatoes. A high level of wild

introgression was detected in the tetraploid cultivated genomes, which might be explained by the high rates of unreduced gametes in wild diploids that facilitate interploidy gene flow. The introgressed regions are enriched with genes that are responsible for stress tolerance and disease resistance, indicating that the transmitted alleles from wild species have facilitated regional adaptation. Haplotype analysis of the maturity gene, *St CDF1*, suggests that introgressed wild alleles contribute to long-day adaption of potatoes in Europe and North America.

In total, 2,662 genes were found to be under selection in cultivated potatoes, but only a minor proportion were shared between the cultivars and landraces. This supports the idea that lowland cultivars and highland landraces were differentially selected. The most highly selected genes exert a series of biological functions, including circadian rhythms, carbohydrate metabolism and glycoalkaloid biosynthesis, among others. Of these, the selection of genes that modulate pollen development is likely attributable to the shift in asexual reproduction in landraces and cultivars.

This study provides a genomic perspective on the domestication and diversification of potato and highlights the high diversity of cultivated populations underpinned by wild allele introgression.

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