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Dissecting the genetics of potato tuber composition

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Potato breeders screen tens of thousands of candidate clones each year, looking for the rare individual that may become an outstanding new variety. Here, researchers work in potato-breeding plots in New York, USA. Photo by Walter De Jong.

Potatoes are an important source of nutrients in the human diet. They represent both a staple crop essential for food security and a snack food with major economic value. Potato breeders who want to improve nutritional quality are faced with a daunting challenge because at the genetic level, potato is highly heterozygous; thus, countless traits segregate each time a cross is made. Breeders need tools to help select offspring with desired nutritional profiles out of large populations.

Researchers, publishing in *Crop Science*, measured 981 compounds in cooked potatoes, including primary and specialized metabolites, and examined the inheritance of each. The levels of about half (432) were controlled by just one or a few genes. One group of compounds measured, glycoalkaloids, help protect against insects and other pests, but are also toxic to people, so need to be kept at low levels. This study found regions of three chromosomes associated with glycoalkaloids that, surprisingly, do not harbor any known glycoalkaloid genes.

Identifying genetic regions associated with desirable and undesirable metabolites will make it possible to develop simple and readily scalable genetic markers to help scientists and breeders more efficiently guide improvements in potato nutritional quality.

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Levina, A.V., Hoekenga, O., Gordin, M., Broeckling, C., & De Jong, W.S. (2021). Genetic analysis of potato tuber metabolite composition: Genome-wide association studies applied to a nontargeted metabolome. *Crop Science*, *61*, 591–603. **https://doi.org/10.1002/csc2.20398**

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