



Decoding the potato's mating language

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Left: Potato flowers showing anthers and part of the pistils. Right: In-vitro pollen germination. Styles and pollen were used to study S-RNases and SLFs. Photos courtesy of Mercedes Ames, first author on the study.

Some plant families—including the Solanaceae, where potatoes, tomatoes, and petunias belong—have a natural system that forces them to reproduce by crossing with other plants. This mechanism, called self-incompatibility, prevents self-fertilization and promotes gene exchange with other plants to remain competitive and

expand genetic diversity.

While self-incompatibility is crucial for genetic diversity in potatoes, the specific molecular mechanisms governing this process have not been fully characterized. To address this, scientists at the USDA-ARS investigated two key elements: the pistil (the part of the flower that receives pollen) and the pollen itself. The pistil makes proteins called S-RNases, and the pollen makes proteins called SLFs. If these two don't "match" correctly, the pollen is rejected. Both genes are located in a specific region of the potato DNA called the S-locus.

Using DNA and RNA data from wild and cultivated potatoes, the scientists found that SLFs are only active in pollen and are spread across a large section of chromosome 1, flanking the S-RNase gene. Both S-RNase and SLFs are very diverse, containing many different versions. This diversification predates speciation events that lead to tomatoes, petunias, and potatoes—like living fossils of plant reproduction.

This knowledge will help develop better potato breeding methods, such as diploid hybrid breeding, and improve our knowledge about gene flow in wild potato populations.

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Ames, M., Halterman, D., & Bethke, P. C. (2025). The structure and allelic diversity of the self-incompatibility locus (S-locus) in diploid potatoes inferred from genome sequences and transcriptome data from styles and pollen. *The Plant Genome*, 18, e70167. <https://doi.org/10.1002/tpg2.70167>

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