

Blast from the past: understanding the impact of maize wild relatives in modern maize and leveraging lost traits to improve fertilizer use efficiency

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Maize (*Zea mays* spp. *mays*) was domesticated around 9,000 years ago from teosinte *parviglumis* (*Zea mays* spp. *parviglumis*) in the lowlands of current southwest Mexico. From there maize was brought to the highlands of Mexico where it received significant introgression of highland teosinte *mexicana* (*Zea mays* spp. *mexicana*). Recent genomic studies have shown that modern maize contains significant introgression from teosinte *mexicana*, highlighting the important role of wild relatives in modern maize.

Our research represents two complementary perspectives on the role of ancestral diversity in maize nitrogen efficiency. First, we highlight evidence of ancient *mexicana* introgressions that persist in modern maize, including alleles associated with nitrogen metabolism. Second, we describe how the development of new maize × teosinte mapping populations and genomic resources for maize's wild relatives are enabling the discovery of extant teosinte alleles — lost during domestication — that can be reintroduced to improve modern maize. Many of these alleles are associated with microbiome-mediated nitrogen processes, including traits that suppress microbial nitrification and denitrification.