The evolution of maize during early, post-domestication expansion across the Americas

Matthew Hufford, Ph.D.
Iowa State University

Maize, like many crop species, colonized a much larger area following its domestication in a narrow center of origin. Many population genomic questions regarding the demography of maize during this expansion remain unanswered. Based on high-depth re-sequencing data from 31 maize landrace genomes spanning the Americas, we conduct genome-wide demographic analyses. We reveal a continuous genetic bottleneck in maize landraces starting from approximately 10,000 BP and lasting to 1,000 BP, with a substantially stronger bottleneck in Andean maize. These results suggest a history of serial founder effects making maize, in this respect, similar to humans and other recently expanding species. The Andean landraces, located at the expansion wave front of maize, demonstrate the lowest genetic diversity, the highest level of derived homozygous genotypes and runs of homozygosity, and the highest genetic load. Previously detected introgression from teosinte (Zea mays ssp. mexicana) into Mexican highland landraces was also confirmed and unreported introgression was found extending into the Guatemalan highlands and the southwestern US. Our work has practical implications for maize breeding. For example, efforts to improve Andean material may be particularly challenged by its high level of genetic load, a symptom of its evolutionary history.