

A novel approach to crop genetics



A traditional maize field in Mexico, with tomatillos growing beneath the maize plants.

Photo by Jeffery Ross-Ibarra/UC Davis

Plant domestication is also a focus for Assistant Professor Jeffrey Ross-Ibarra, an anthropology-student-turned-plant-biologist who is fascinated with what plant domestication and crop evolution can tell us about our world. He recently received a three-year \$448,000 grant from the USDA/CSREES for a project that that could revolutionize crop genetics.



Ross-Ibarra

genomic regions that might affect that trait.

Ross-Ibarra's project, "Scanning for Yield: High-Throughput Discovery of Candidate Agronomic Loci for Marker-Assisted Selection in Maize" takes a different approach, by first identifying genes with the signature of adaptation using population genetics and then

using a broad array of genetic tools to identify the phenotypes to which these genes contribute.

"Marker-assisted selection has become one of the most important tools of modern plant breeding, but its success relies on the availability of markers that associate with agronomic traits," Ross-Ibarra says. "While traditional approaches such as QTL and association mapping have been successful at identifying these markers, they suffer from several important disadvantages, such as the context-dependence of the markers identified."

Ross-Ibarra is looking at it from the bottom up.

"Bottom up approaches begin by assaying genetic diversity in hundreds of loci, preferably from a sample of about 100 individuals representing both the domesticate and its wild ancestor," he says. "The genome shows signs of selection, and that's what you're looking for, statistical signs of selection. If one gene had a particularly big effect on yield, for example, you would expect

"Domestication fundamentally changed the course of human history, yet there is still so much about it we don't understand," Ross-Ibarra says. "Who were the domesticators? What were their cultivation methods? What happened to crops, genetically, during the adaptation process?"

What we do know is domestication produced dramatic shifts in phenotypes, or observable characteristics or traits. Researchers have long been trying to identify the genes and genetic mechanisms that contributed to those phenotypic changes – and not just to better understand crop evolution.

"Discovering the genes and genetic mechanisms that contribute the phenotypic changes associated with domestication could also facilitate trait manipulation through modified breeding strategies," Ross-Ibarra explains.

Most research along this line has followed what some call the "top-down approach," which starts by identifying a phenotype of interest then seeks

Repositories

Preserving and protecting precious germplasm



We live in a world of accelerating change affecting climate and crop pests and pathogens, while demands for safe, healthy, plentiful food continue to rise. Adapting crops to shifting conditions requires many things, including genetically diverse germplasm.

Germplasm is living tissue from which new plants can be grown – a seed, a leaf, a stem, pollen or even just a few cells. Germplasm contains the information for a species' genetic makeup. Researchers travel far and wide to collect wild forms of our cultivated species, which provide a wealth of genetic diversity, but that valuable resource could be lost without repositories where germplasm can be properly stored, multiplied and distributed.

The Department of Plant Sciences houses several such seed and gene collections for a wide variety of crops – wheat, lettuce, strawberries, beans, cereal, stone fruits, grapes, nuts, the list goes on. To understand the importance of these collections, let's take a closer look at one such repository: the C.M. Rick Tomato Genetics Resource Center.

The tomato, like other cultivated crops, lost much of its genetic diversity during domestication and migration. As a result, tomato breeding progressed slowly in the early part of the 20th century. But all that began to change in the 1940s when (not coincidentally) plant geneticist and botanist Charles Rick joined the faculty at UC Davis in what was then the Division of Truck Crops (now part of Plant Sciences). For the next half century, Rick criss-crossed the Andes, the Galapagos and elsewhere, gathering more than 1,000 wild tomato specimens, many of which are now extinct in their native habitat. With his growing collection, Rick made landmark contributions in plant genetics, evolution and genome mapping. As a byprod-

(from Page 9) that it would increase in frequency and decrease in diversity, and those areas will show up in your statistical analyses. We may find that the candidate gene most associated with yield controls root density or nitrogen uptake or some agronomic trait we hadn't even considered."

Ross-Ibarra and his team will genotype 60,000 single nucleotide polymorphisms in a stratified chronological sample of more than 500 maize lines, including wild teosintes, landraces, early inbreds, and modern inbreds. They will use statistical methods to identify candidate

agronomic loci (CAL) that have increased in frequency due to selection during maize improvement. Because of the central role yield has played in maize improvement, they predict many of these CAL will be associated with yield. They will directly test this prediction in yield trials comparing the efficiency of selection using their list of CAL to selection using random markers or phenotype alone.

"Bottom-up approaches are relatively new, and many of the methodologies are still being developed, but we believe they have the potential to revolutionize crop genetics," Ross-Ibarra says.