

Could an 8 million-year-old gene help the citrus industry?

After 100 years of assertions about the roots of citrus, a global group of scientists – including a University of Florida professor – has traced the evolutionary history of Florida's signature crop up to 8 million years ago in the Himalayas of Southeast Asia.

Through analyses of 60 types of citrus whose genomes they sequenced, scientists identified 10 natural citrus species, according to their new study, published today in *Nature*. By sequencing genomes, scientists can find out all the genes controlling inheritable traits of an organism.

In addition to providing an evolutionary framework for citrus, the study also contains practical applications for current growers and consumers, said Fred Gmitter, a UF/IFAS professor of horticultural sciences and co-author of the paper. For the study, Gmitter worked with researchers from the US Department of Energy Joint Genome Institute and the Instituto de Investigaciones Agrarias.

With the new research, scientists can now work with more citrus genomic information, Gmitter said. This is especially relevant now that the citrus industry is reeling from the devastating citrus greening disease.

"That means that researchers who might be looking for genes to target for citrus greening resistance now can search through the many genomes of tolerant types and compare with sensitive types," said Gmitter, a faculty member at the UF/IFAS Citrus Research and Education Center.



That way, they can better select the most likely genetic targets to be effective against Huanglongbing (HLB), or citrus greening, he said. That knowledge could prove valuable down the road for breeders, growers and the public, Gmitter said.

"All of the clear understanding of relationships of the different kinds of citrus that we have revealed helps to inform plant-breeding strategies and approaches to develop cultivars tolerant of HLB or cultivars that are more delicious and nutritious," Gmitter said.

To get their results, scientists extracted DNA from varieties of citrus for which they wanted to know the genome sequence. Researchers used various DNA sequencing machines to produce very small pieces of the entire genome, Gmitter said.

"It is like creating an immense jigsaw puzzle that overlap to some degree, and then assembling these pieces into larger groups, and assembling the larger groups into even larger parts of the genome," Gmitter said.

The new research clarifies the genomic nature of the sweet orange, which might lead to more types of fruit that can be converted to USDA Grade A orange juice, he said.

This would be a good thing for growers, processors and consumers because their favorite fruit would no longer be in such short supply, prices might decrease and the refreshing beverage would be more accessible.

"By improving the condition and understanding of our genetics and breeding knowledge base, the science becomes open to exciting new possibilities in genetic improvement," Gmitter said. "And as citrus breeders, our goals have always included improvements in characteristics that benefit not only producers, but consumers as well."

For more information:

Brad Buck

University of Florida

+1 (352) 294-3303

bradbuck@ufl.edu

www.ifas.ufl.edu

Publication date: 2/8/2018

© 2018 FreshPlaza. All rights reserved.

