

W317

Genome Sequence Comparisons Reveal Interspecific Hybridizations and Admixture in Citrus**Domestication***Date: Saturday, January 11, 2014**Time: 10:01 AM**Room: Pacific Salon 3**Fred G. Gmitter , University of Florida, IFAS-CREC, Lake Alfred, FL**G. Albert Wu , DOE Joint Genome Institute, Walnut Creek, CA**Simon Prochnik , DOE Joint Genome Institute, Walnut Creek, CA**Patrick Ollitrault , CIRAD, UMR AGAP, Montpellier, France**Manuel Talon , Centro de Genomica, IVIA, Moncada, Valencia, Spain**Marcos Antonio Machado , Centro de Citricultura Sylvio Moreira, IAC, Cordeiropolis, SP, Brazil**Michele Morgante , Università Di Udine, Istituto di Genomica Applicata, Udine, Italy**Olivier Jaillon , Genoscope, Evry, France**Daniel S. Rokhsar , DOE Joint Genome Institute, Walnut Creek, CA*

Citrus is the most globally significant tree fruit, but its history of domestication is not well understood. Cultivated citrus types are believed to be direct selections from, or hybrids of, several progenitor species; however, the identities of these species and their contributions to modern cultivars remain unclear and controversial. A collection of different genomes of mandarins, pummelos, and oranges, including a high quality reference sequence from a haploid Clementine mandarin, has been assembled. By comparative analyses we show that these cultivated types were derived from two progenitor species, *C. maxima* and *C. reticulata*. Although it was determined that the sequenced cultivated pummelos represent selections from *C. maxima*, the cultivated mandarins proved to be introgressions of *C. maxima* into a distinct second population identified as the ancestral wild mandarin species, *C. reticulata*. Sweet and sour oranges were found to be hybrids between these two species. Sweet orange, the most widely cultivated citrus, arose as the offspring of previously admixed individuals. Sour (or Seville) orange was found to be an F1 hybrid of pure *C. maxima* and *C. reticulata* parents, indicating that wild mandarins were at least a part of the early breeding germplasm. Sequence analysis also revealed that at least one Chinese “wild mandarin” actually represents a citrus species distinct from *C. reticulata*, suggesting the possibility that other unrecognized wild citrus species may be identified. Understanding the phylogeny of cultivated citrus by comparative genome analysis will clarify taxonomic relationships and potentially lead to previously inconceivable opportunities for genetic improvement.

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