

of *Citrus* are believed to be of interspecific origin. By studying SNP and InDel polymorphisms of 27 nuclear genes on 45 genotypes of *Citrus* and related taxa, the average molecular differentiation between species was estimated, and the phylogenetic relationship between “true citrus fruit trees” was clarified. A total of 16238 bp of DNA was sequenced for each genotype, and 1097 SNPs and 50 InDels were identified. Nuclear phylogenetic analysis revealed that *Citrus reticulata* and *Fortunella* form a clade clearly differentiated from the other two basic taxa of cultivated citrus (*Citrus maxima*, *Citrus medica*). A few genes displayed positive selection patterns within or between species, but most of them displayed neutral patterns. The phylogenetic inheritance patterns of the analysed genes were inferred for commercial *Citrus* species. The SNPs and InDels identified are potentially very useful for the analysis of interspecific genetic structures. The nuclear phylogeny of *Citrus* and its sexually compatible relatives was consistent with their geographic origin. The positive selection observed for a few genes will orient further work to analyze the molecular basis of the variability of the associated traits. This study presents new insights into the origin of *Citrus sinensis*.

S01P09

New insights on limes and lemons origin from targeted nuclear gene sequencing and cytoplasmic markers genotyping

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It is believed that *Citrus medica*, *Citrus maxima*, *Citrus reticulata* and *Citrus micrantha* have generated all cultivated *Citrus* species. Depending on the classification, lemons and limes are classified either into two species, *Citrus limon* and *Citrus aurantifolia* (Swingle and Reece) or into more than 30 (Tanaka). In order to study the molecular phylogeny of this *Citrus* group, we analyzed 20 targeted sequenced nuclear genes and used 3 mitochondrial and 3 chloroplastic markers for 21 lemons and limes compared with representatives of the 4 basic taxa. We observed 3 main groups, each one derived from direct interspecific hybridizations: (1) the Mexican lime group (*C. aurantifolia*), including *Citrus macrophylla*, arising from hybridization between papada (*C. micrantha*) and citron (*C. medica*); (2) the yellow lemon group (*C. limon*) that are hybrids between sour orange (*Citrus aurantium*, which is believed to be a hybrid between *C. maxima* and *C. reticulata*) and citron; and (3) a rootstock lemon/lime group (Rough lemon and Rangpur lime) that are hybrids between the acid small mandarin group and citron. We also identified different probable backcrosses and genotypes with more complex origins. None of the analyzed limes and lemons shared the *C. medica* cytoplasm, while this taxon is the common nuclear contributor of all limes and lemons. Limes and lemons appear to be a very complex citrus varietal group with the contribution of the 4 basic taxa. Neither the Swingle and Reece nor the Tanaka classifications fit with the genetic evidence.

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Diversity of citron (*Citrus medica*) and phylogenetic analysis of related citron hybrids using molecular markers and essential oil compositions

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It is commonly accepted that citron (*Citrus medica*) was the first citrus fruit to reach the Mediterranean area about 3 centuries B.C. The fragrance due to the essential oils is probably the main characteristic that has contributed to the reputation of this fruit in all Mediterranean countries for multiple uses including cosmetics, food, medicinal, ornamental and also as religious symbol. The Citron group is supposed genetically low diversified compared to mandarins and pummelos. To assess the diversity of the citron group we analyzed the molecular polymorphism of nuclear and cytoplasmic genetic markers and the variation in composition of essential oils from leaves and peels of 24 varieties of citron or apparent hybrids of citron.