

ABSTRACT

Citrus is by far the most economically important genus of the subfamily Aurantioideae. It is believed to have originated in the south-eastern region of Asia, in an area that includes China, India and the Indochinese peninsula and nearby archipelagos. Although many different studies have been done, *Citrus* taxonomy is still controversial due to the large degree of morphological diversity found within this group, the sexual compatibility between the species and the apomixis of many genotypes. In this PhD thesis a broad diversity within the *Citrus* genus, citrus relatives and other taxa from the Aurantioideae subfamily has been studied in order to clarify their organization and phylogeny using different types of molecular markers and different genotyping platforms. The mandarin germplasm plays a major role in citrus rootstock and cultivar breeding, but its genetic organization is still largely unknown. Therefore, an analysis in depth of diversity and organization has been done.

The development of nuclear Insertion-Deletion (indel) markers, for the first time in citrus, has allowed us to demonstrate its utility for diversity and phylogenetic studies in the genus *Citrus*. In combination with SSR markers, the contribution of three basic edible taxa (*C. reticulata*, *C. maxima* and *C. medica*) to the genomes of secondary species and modern cultivars has been quantified. Their mosaic genetic structure has also been determined from the data obtained by sequencing 27 nuclear genes involved in the biosynthesis of quality compounds of citrus and genes involved in plant stress response. Nuclear phylogenetic analysis revealed that *C. reticulata* and *Fortunella* form a clade that is clearly differentiated from the clade that includes two other basic taxa of cultivated citrus (*C. maxima* and *C. medica*), which is consistent with the geographic origin of the species studied. From this study, SNP molecular markers with a high phylogenetic value has been developed and tested for transferability into genetically related genera. They performed very well within the *Citrus* genus and should be useful for germplasm fingerprinting at a much broader diversity level.

The genetic organization within the mandarin germplasm (198 'mandarin-like' genotypes from two germplasm collections, INRA-CIRAD and IVIA), and its introgression by other taxa was studied with 50 and 24 nuclear SSRs and indel markers respectively, and four mitochondrial (mtDNA) indels. It has been shown that many genotypes, believed to be pure mandarins, have introgression from other basic taxa in their genomes. Five parental groups have been determined within the germplasm analysed. Moreover, many genotypes have been originated from the cross between these mandarins, leading to a very complex hybrid structures. Furthermore, some mandarin genotypes have a non-mandarin maternal origin as determined by mtDNA markers.

This PhD thesis has released new information about the phylogenetic relationships of taxa within the *Citrus* genus and relative species, as well as secondary commercial species. New sets of complementary markers had been developed. The genetic organization of the mandarin germplasm was revealed and a proper characterization of two citrus germplasm collections was obtained. These contributions will help in the breeding of new, high-quality citrus cultivars and will contribute to optimizing the conservation and characterization at genetic and phenotypic levels of the citrus genetic resources.