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INTERSPECIFIC AND INTERGENERIC SOMATIC HYBRIDS WITH *C. DELICIOSA* TEN. ENLIGHTENS NON ADDITIVE INHERITANCE IN ALLOTETRAPLOID CITRUS

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Neoregulation of parental genome expression in allopolyploid plants contributes to the expression of new phenotypes. Somatic hybrids allow combining genomes without sexual recombination and are interesting models to study the immediate effect of allopolyploidisation on the regulation of gene expression and subsequent phenotype elaboration. While most of the citrus germplasm is diploid, somatic hybridization has become an integral part of citrus variety improvement programs aiming to create new allotetraploid rootstocks or to synthesize triploid hybrids by further sexual hybridization. By protoplast fusion CIRAD obtained allotetraploid hybrids between *C. deliciosa* and 6 others citrus species: 4 belong to *Citrus* genus (*C. limon*, lemon; *C. aurantifolia*, lime; *C. sinensis*, sweet orange; *C. paradisi*, grapefruit), 2 belong to *Poncirus trifoliata* (trifoliolate orange) and *Fortunella margarita* (kumquat). Molecular analysis using 100 SSR markers did not reveal any inconsistency with total addition of parental genomes. Morphological description was done for leaves and fruits as well as the sugar and acid fruit contents. According to the traits and parental combination, codominance or dominance of one parent was observed and lead to conclude for an important contribution of interaction variance in phenotypic diversity elaboration. Analyze by GC-MS of the leaf volatile compounds of the same allotetraploid hybrids revealed a systematic global dominance of the mandarin profile. It was particularly marked regarding the absence of monoterpene aldehydes and monoterpene alcohols and the very low level of sesquiterpene hydrocarbons, sesquiterpene alcohols, and sesquiterpene aldehydes in all hybrids while these compounds were found at high concentrations for the non mandarin parents. 2-D electrophoresis analysis of the leaf proteome of two allotetraploid somatic hybrids combining *C. deliciosa* with *C. aurantifolia* and *Fortunella margarita* displayed a closer relation between the two allotetraploid hybrids and their mandarin parent than with the other parent. Similar results have been observed at transcriptome level in a genome-wide gene expression analysis on fruit pulp of allotetraploid between *C. deliciosa* and *C. limon*, using a *Citrus* 20 K cDNA microarray. The gene expression of the allotetraploid suggested a global dominance of the mandarin fruit pulp transcriptome. Particularly, genes down regulated in mandarin compared to lemon were also repressed in the allotetraploid hybrid. The study is now extended to an interspecific diallelic somatic hybridization scheme to have a wider understanding of genome interaction in allotetraploid citrus.

Keywords: Citrus, somatic hybrids, proteome, transcriptome, inheritance