

Our results demonstrate that the citron group has a relatively high allelic diversity, probably due to multiple introductions of several varieties. Self-fertilization was the mode of reproduction, which most frequently led to the development of commercial varieties with specific aromas and flavors such as the cultivar ‘Corsican’, a putative ‘Common Poncire’ self-crossed hybrid. However, some varieties appeared to be interspecific hybrids related to citron but only by male parent. This varietal diversity was probably favored by spreading seeds to extend the cultivation of citron in Mediterranean countries. The chemical diversity does not always correspond to genetic diversity but nevertheless reveals specific profiles for some genotypes.

S01P11

Analysis of genetic diversity in Tunisian citrus rootstocks

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Breeding and selection of new citrus rootstocks are nowadays of the utmost importance in the Mediterranean Basin because the citrus industry faces increasing biotic and abiotic constraints. In Tunisia, citrus contributes significantly to the national economy, and its extension is favored by natural conditions and economic considerations. Sour orange, the most widespread traditional rootstock of the Mediterranean area, is also the main one in Tunisia. In addition to sour orange, other citrus rootstocks well adapted to local environmental conditions are traditionally used and should be important genetic resources for breeding. Prior to initiation of any breeding program, the exploration of Tunisian citrus rootstock diversity was a priority. Two hundred and one local accessions belonging to four facultative apomictic species (*Citrus aurantium*, sour orange; *Citrus sinensis*, sweet orange; *Citrus limon*, lemon; and *Citrus aurantifolia*, lime) were collected and genotyped using 20 nuclear SSR markers and four InDel mitochondrial markers. Sixteen distinct Multi-locus genotypes (MLGs) were identified and compared to references from French and Spanish collections. The differentiation of the four varietal groups was well-marked. Each group displayed a relatively high allelic diversity, primarily due to very high heterozygosity. The Tunisian citrus rootstock genetic diversity is predominantly due to high heterozygosity and differentiation between the four varietal groups. The phenotypic diversity within the varietal groups has resulted from multiple introductions, somatic mutations and rare sexual recombination events. This diversity study enabled the identification of a core sample of accessions for further physiological and agronomic evaluations. These core accessions will be integrated into citrus rootstock breeding programs for the Mediterranean Basin.

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Characteristics of ‘Pompia’ a natural citrus hybrid cultivated in Sardinia

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The ‘Pompia’ is a probable citrus natural hybrid sporadically growing in the “Baronia” area (East Sardinia, Italy). The origin and taxonomic classification of this *Citrus* taxon is unknown. The fruit shows a yellow-amber flavedo at maturity and large size (weight from 200 to 700 g), irregular shape, light-yellow pulp, and low juice content. The traditional use as food is limited to the thick albedo after removal of the flavedo tissue and of the acid, non-edible pulp, and candying. This research had as its objective a morphological study of nine accessions selected from four orchards of ‘Pompia’ in order to sample the observed variability of trees, shoots, leaves, and fruits. The results of morphological determinations showed a high similarity of ‘Pompia’ samples to lemon and citron species for thorns, fruit size and colour. The presence of small petiole winglets was observed only on one accession. AFLP, RAPD, and SCAR analysis allowed the comparison of ‘Pompia’ with seven *Citrus* species: citron, lemon, pummelo, grapefruit, bitter orange, and mandarin. The analysis with molecular markers demonstrated a close genetic relationship among ‘Pompia’, lemon, and citron. Moreover, the elaboration of the phenotypic and molecular analysis allowed evidencing a high level of similarity of the nine ‘Pompia’ accessions. Seven of them probably genetically correspond to the same clone.