**INTRODUCTION**

Despite shared traits, most morphological differentiation Citrus, Fortunella, Poncirus, Peromys and Macroptera are clearly distinguished and they are considered as separate genera. The wild relatives of these genera are usually seen as Citrus. The origin of cultivated citrus from four basic taxa (C. maxima, C. medica, C. reticulata and wild clades) is now well established. In contrast, the origin of the remaining related genera is still unclear. In the present work we analyse their nuclear and maternal phylogeny by using respectively SNPs on gene sequences and mitochondrial insertion-Deletions (indels).

**MATERIAL AND METHODS**

The varietal sample set was composed of 45 genotypes: 7 clementines-), recent hybrids from the 20th century breeding programs (1 C. aurantium), 4 wild citrus “papeda” (C. minciana, C. tylistis, C. inodora, C. medicus, C. medica, 3 Passiflora, 2 Punica, 1 Mespilus, 1 C. arboricola, 1 C. aurantifolia, 1 C. auratifolia, 1 C. tetraploidy, 1 C. aurantium). Recent hybrids were sequenced and included in the next analysis. The sequences were blasted on the reference citrus genome sequence. They display a good dispersion on chromosomes. Excepted PIP1 and NCED, which two locations were found for each gene. Therefore they will provide a good representation of the whole genome diversity and an important source of data for population genetics and phylogenetics. SNPs were mimed using BioEdit and SeqMan softwares and phylogenetic analysis done in Phylop (v. 3.68). Phyyl Best AIC Tree (v. 1.03). For maternal phylogeny, 4 mitochondrial Indels markers have been used.

**WITHIN AND BETWEEN SPECIES NUCLEAR DIVERSITY**

<table>
<thead>
<tr>
<th>Species</th>
<th>SNP/Kb</th>
<th>Freq</th>
<th>InDel/Kb</th>
<th>Freq</th>
</tr>
</thead>
<tbody>
<tr>
<td>C. reticulata</td>
<td>8.15</td>
<td>0.0032</td>
<td>0.0050</td>
<td>0.0061</td>
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<tr>
<td>C. maxima</td>
<td>3.73</td>
<td>0.0035</td>
<td>0.0050</td>
<td>0.0061</td>
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<tr>
<td>C. medica</td>
<td>3.22</td>
<td>0.0029</td>
<td>0.0047</td>
<td>0.0068</td>
</tr>
<tr>
<td>Fortunella</td>
<td>8.54</td>
<td>0.0056</td>
<td>0.0086</td>
<td>0.0085</td>
</tr>
<tr>
<td>Wild citrus</td>
<td>8.66</td>
<td>0.0056</td>
<td>0.0086</td>
<td>0.0085</td>
</tr>
</tbody>
</table>

**NUCLEAR PHYLOGENY BETWEEN RELATED GENERA AND CITRUS BASIC TAXA**

The phylogeny analysis was made joining together the 27 sequences for each genotype. The best model that fit our data was TVM+I+G+F with SH-like branch support. In the resulting tree, we account the nucleotide substitution model TVM (5 substitution classes), the proportion of invariable sites, the nucleotide frequency (F) and the Gamma distribution (G). The first species that was separated from the others was Poncirus trifoliata. After that two clearly groups were formed, one which included C. reticulata and Fortunella and the other one which formed by wild citrus, C. maxima, C. medica, Microcitrus. For the last two last genera of Australian origin are strongly associated. The only ancestor group that did not formed a well defined clade was the wild citrus.

**CONCLUSIONS**

Almost 70% of the diversity is explained by the first two axes. The basic citrus taxa are well distinguished. Only C. maxima/sinensis is clearly differentiated from the other wild citrus taxa (nos 3 not shown) and should be of inter-specific origin. Secondary species are positioned in between their supposed parents: C. sinensis between C. maxima and C. reticulata; C. paradoxi between C. sinensis and C. maxima; C. limon between C. aurantifolia and C. medica; and C. trifoliata between C. medica and C. minciana. The complete similarity of this figure with the genetic organization displayed by previous SSRs studies suggest a well defined behavior of the current SNPs markers.

REFERENCES:


