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A Reference Linkage Map Of *C. clementina* Based On SNPs, SSRs And Indels

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A haploid *C. clementina* was chosen by the International Citrus Genomic Consortium (ICGC) to establish the reference whole genome sequence for Citrus. Development of a dense clementine linkage map was part of the objectives of this global

collaborative project. Two inter-specific populations between *C. clementina* and *C. maxima* were used for this purpose. 156 hybrids of Nules clementine x Pink pummelo and 200 hybrids of Chandler pummelo x Nules clementine were genotyped with 1003 markers. 306 were SSRs markers (66 from genomic libraries, 207 from ESTs and 33 from clementine BAC end sequences –BES-), 34 were Indels markers mined from BES and 663 SNPs mined from Clementine BES or identified by candidate gene sequencing. 901 markers were successfully mapped in the 9 clementine linkage groups. Segregation distortion was observed for many loci of clementine when it was used as male parent while it followed Mendelian segregation for most markers when used as female parent. However marker order was mostly conserved between the male and female maps; thus, data of the two populations were joined to establish the reference clementine genetic map. The total clementine linkage map cover 1250 cM with linkage groups from 105 cM until 210 cM. This map is strongly anchored on a large diploid clementine BAC library resource. It is a powerful tool for Citrus genetics and supports the alignment of the haploid clementine whole genome sequence in the framework of the ICGC collaborative project.