Metabolism of Terpene: A Comparison Between Two Different Citrus Species

Takita, M.A.; Sakamoto, T.R.T.; Machado, M.A.

Centro de Citricultura Sylvio Moreira, Instituto Agronômico de Campinas, SP, Brazil

The citriculture is a very important player in the Brazilian agribusiness. Because of that, the Centro de Citricultura Sylvio Moreira showed a deep interest and participated in the International Consortium for the Citrus Genome Sequencing, which was responsible for sequencing the genome of a haploid mandarin, Citrus clementina (7x coverage – Sanger). In a parallel work, one of the groups of the Consortium led a work in which the genome of sweet orange, C. sinensis was sequenced (30x coverage – Sanger and 454). To better understand of the Citrus biology in relation to the secondary metabolism, in particular the metabolism of terpenes, which are determinant for the aroma and flavor in Citrus, these two genomes were used for comparative analyses. In the Phytozome platform (www.phytome.org), search for the terpene keyword led to the identification of 57 different families in sweet orange and 66 in clementine. This clearly shows that clementine has more genes related to the terpene metabolism than sweet orange but they are rather redundant since it was not observed the complete absence of any gene in the genomes using the Blast tool. The few differences identified were structural and very small. There is only one that was more noticeable but the coding sequence is partial. Nevertheless the similarity for the proteins in the genomes is not high not even with transcripts from other Citrus species or related genus. This gene encodes a terpene synthase and may respond for subtle differences in the aroma and taste of clementine.

Word Keys: genome, mandarin, secondary metabolism, sweet orange

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