

NEXT GENERATION SEQUENCING DATA FOR SWEET ORANGE CLONAL FINGERPRINTING

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Somatic mutations are a cause of intraspecific diversity in many crops, such as citrus, grapevine and apple. In the case of sweet orange [*Citrus sinensis* (L.) Osbeck], intraspecific variability is determined only by somatic mutations. Tools for clonal fingerprinting are required by breeders and nurserymen and have important implications for traceability. With the aim of studying genomic variability and identifying mutational events responsible for varietal diversification, we deep-resequenced 22 accessions including navel, common and blood oranges using an Illumina platform. A robust and reliable set of single nucleotide polymorphisms (SNPs), structural variants (SVs) and indels, private of each accessions or common to varietal groups, was identified in natural mutants. A subset of SNPs, mobile elements insertions and indels was validated by Sanger sequencing, PCR amplifications and high resolution melting analysis, confirming the results of the bioinformatics analysis. Moreover, to identify a reliable set for traceability of specific cultivars, we collected leaf and juice samples from many Italian citrus nurseries and growing areas and used a KASP platform for their fingerprinting. These tools will be useful to prove true-to-type-ness for specific sweet orange varieties and will potentially provide the consumers with a guarantee on the origin of juices.