W355: Evaluation of Variability in the Sweet Orange Germplasm through Next Generation Clonal Fingerprinting

Saturday, January 14, 2017
08:19 AM - 08:38 AM
Pacific Salon 3

The great phenotypic variability characterizing the sweet orange [*Citrus sinensis*(L.) Osbeck] germplasm arises from spontaneous bud mutations, causing a diversification into major groups (common, Navel and blood oranges). A huge divergence also occurred within each varietal group. The genetic basis of such variability, also including nutritional and qualitative traits (ripening time, colour, fruit shape, acidity, sugars), is currently uncharacterized, and therefore not exploitable. With the aim of describing the somatic mutation events in the sweet orange group a deep-sequencing of 20 Italian and foreign accessions was performed by Illumina platform, allowing the identification of single nucleotide polymorphisms (SNPs), structural variants (SVs) and large deletions, specific to each varietal group or clone-specific. A subset of SNPs used for the design of two 384 SNP - GoldenGate Assays allowed to genotype 225 CREA sweet orange accessions. The developed markers represent the first reliable molecular tools able to unambiguously fingerprint each somatic mutant. Moreover, they might be used to associate mutations with phenotypic traits, and are a powerful tool for traceability. By using the GoldenGate assay, we have been able to fingerprint several blood orange clones starting from DNAs isolated from leaves or juice. These tools will potentially provide the consumer with a guarantee on the quality and origin of juices, avoiding eventual frauds.

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