

INTEGRATED APPROACHES TO INVESTIGATE THE GENETIC BASES OF CITRUS CLEMENTINA SELF-INCOMPATIBILITY

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Seedlessness is a highly desirable trait for fresh fruit and one of the main factor contributing to its market value. In citrus the lack of seeds can be due to different mechanisms such as the occurrence of female or male sterility, or the presence of self-incompatibility (SI) reactions that prevents seed formation in the absence of cross pollination. SI mechanism is based on the discrimination between self- and non-self pollen, in fact the female determinant, an S-RNase, and the S-locus F-boxes protein (SLF), the male determinant, can either inhibit or promote the growth of pollen tubes in the style. Several S-RNase and SLF homologs were identified in citrus accessions, but, currently there is no evidence to indicate that other genes are responsible for the SI response in citrus. In the present work we analysed two clementine (*Citrus clementina* Hort. ex. Tan) varieties, 'Comune' (self-incompatible) and its natural self-compatible mutant 'Monreal'; real-time PCR were carried out on mRNAs isolated from the unpollinated and self-pollinated stigmas and styles of the two mandarins at different time-points after the anthesis. Results highlighted that the S-RNase expression is higher right before the pollen tube arrest, so these samples were chosen to perform an RNA sequencing (RNA-seq) in order to identify candidate genes differentially expressed in the pistil. Along with this, the 'Monreal' has been sequenced using Illumina next-generation technology (PE-150 reads) with an average read depth of 100x and compared with the reference genome of 'Comune'. The comparison of the two genomes using SNPeff software allowed the identification of 2,110 single-nucleotide polymorphisms (SNPs) predicted to induce nonsense and frame-shift mutations in nearly 1,000 genes. Among those SNPs, almost 100 appear to be involved

in ovary/seed formation and/or plant reproductive development. The integration of the genetic and transcriptomic results will provide novel insights to understand the mechanism controlling SI in citrus and in particular to identify candidate genes that will be used to obtain new seedless cultivar through biotechnological approaches.