

CHARACTERIZATION OF SOC1-LIKE GENES IN TOMATO BY INTEGRATING GENOMICS, GENETIC DIVERSITY, GENOME EDITING AND GENE CO-EXPRESSION NETWORK PLATFORMS

DEL BUFALO A.*****, GENTILE D.*****, FABRIANI M.*, D'ORSO F.**,
IANNELLI M. A.*, ALBERTINI E.*****, FRUGIS G.*

*) CNR, Institute of Agricultural Biology and Biotechnology (IBBA), Unit of Rome, Italy

**) CREA, Centre for Genomics and Bioinformatics, Unit of Rome, Italy

***) Department of Biology and Biotechnologies “Charles Darwin” (BB CD), Sapienza University, Rome, Italy

****) Department of Agricultural, Food And Environmental Sciences - Università degli Studi di Perugia, Perugia, Italy

Solanum lycopersicum, flowering time, transcription factors, genetic diversity, Gene Coexpression Networks

The time at which flowering occurs, besides having adaptive value in natural populations, plays a major role in agricultural production as it affects the quality and quantity of leaf, flower, seed and fruit products, ease of harvest and marketing. Flowering is under the control of a complex genetic network that integrates environmental and endogenous signals, such as photoperiod, temperature and hormonal status. Transition to reproductive growth occurs in the shoot apical meristem (SAM). The signaling pathways that are activated by various endogenous and environmental cues ultimately converge to a few floral integrator genes at the SAM to activate floral meristem identity.

To develop innovative molecular technologies and strategies for precision breeding, the SMART-BREED project focuses on target transcription factors (TF) with a proven role in plant architecture traits that are important for the production and adaptation of horticultural species. In this framework, genes homologous to the *MADS-box SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1* (*SOC1/AGL20*), a main floral integrator which is highly conserved in plant species, are being identified and characterized in tomato.

Based on orthology prediction and construction of a custom phylogenetic tree using the *Arabidopsis thaliana* *SOC1* gene as seed, five *SOC1*-like genes were identified in the genome of *Solanum lycopersicum* (SL4.0) and in the wild tomato species *Solanum pennellii*. Two of them, *TOMATO MADS-box 3* (*TM3*) and *SISTER OF TM3* (*STM3*) have been characterized as important regulators of tomato inflorescence, the others are not yet characterized. Gene expression was analyzed both *in silico* and by qRT-PCR in a developmental series of the tomato model system Micro-Tom. Two uncharacterized *SOC1*-like genes displayed interesting transcriptional profiles during transition to flowering. Regulatory genomic regions were analyzed and conserved MADS-domain protein binding motifs (CArG box) identified. Alignment of genomic sequences identified an insertion of 1135 bp in the promoter of a *SOC1*-like gene that characterizes the domesticated tomato, and may underly differences in *SOC1*-like transcriptional regulation with the wild *S. pennellii* species. Screening of the genomes of 1135 *Arabidopsis* natural accessions identified putative adaptive *SOC1* allelic variants that are being also searched in tomato in a translational approach. The role of *SOC1* orthologues candidates in flowering transition, and the importance of the identified genomic variations in their regulatory regions, will be validated by genome editing. Gene coexpression network (GCN) will integrate the previous analyses to dissect the genetic regulatory networks ruled by the tomato *SOC1*-like genes. All the information will be integrated to develop advanced molecular markers for prioritization of tomato cultivars in the framework of the National Research Centre for Agricultural Technologies (Agritech).