

## **TRANSCRIPTOME ANALYSIS OF TOMATO FLOWERS AT HIGH TEMPERATURE**

F. GIORNO\*, I. MASSARELLI\*, A. MARI \*\*, V. CARBONE\*\*, R. NURCATO\*,  
A. BARONE\*\*\*, S. GRANDILLO\*, R.M. ALBA\*\*\*\*, J.J. GIOVANNONI\*\*\*\*, L. MONTI\*,  
A. LEONE\*\*\*\*\*, S. GRILLO\*

\*) CNR-IGV, Institute of Plant Genetics, Via Università 133, 80055 Portici, Italy

\*\*\*) CNR-ISA, Institute of Food Science, Via Roma 52, 83100, Avellino, Italy

\*\*\*\*) Department of Soil, Plant and Environmental Sciences, University of Naples 'Federico II',  
Via Università 100, 80055 Portici, Italy

\*\*\*\*\*) Boyce Thompson Institute for Plant Research, Tower Road, Ithaca, New York 14853, USA

\*\*\*\*\*) Department of Pharmacological Sciences, University of Salerno, Via Ponte don Melillo,  
84084 Fisciano (SA), Italy

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Tomato fruit-set and productivity are severely reduced by heat stress (HS) events that often occur at the transition from flower to fruit during tomato growing season. The mechanisms underlying the failure of tomato fruit setting at high temperature are still not fully understood due to the complexity of the events which are induced in the flower in response to environmental (high temperature) as well as to developmental signals (gametogenesis, fertilization, anthesis and embryogenesis).

To analyze transcriptome changes in tomato flower under HS condition different molecular approaches as SSH (Suppression Subtractive Hybridization), TOM1 cDNA microarray and qRT-PCR analyses were used on tomato genotypes, with high (cv Saladette) and poor (cv Pull) fruit-set ability, grown under different temperature regimes. Microarray and SSH results, obtained from RNA samples of floral buds of different developmental stages, indicated that in response to HS a complex network of genes are differentially activated in the two different genotypes. The genes identified belongs to different functional classes and are involved in abiotic/biotic stress response, cell wall modification, pollen germination and development, signal transduction, sugar and amino acid metabolism, differentially.

The results obtained, confirmed by qRT-PCR, clearly indicated that gene expression responsiveness to HS conditions in tomato flower is both genotype- and stage-dependent. In addition, stage and genotype specific differences were found for some physiological and biochemical parameters as pollen vitality and germinability, soluble sugars and polyamines content estimated on developing flower buds in the two contrasting genotypes grown under HS or control temperature. The changes in gene expression and the physio-biochemical adjustments observed will be discussed altogether for a comprehensive understanding of a crucial processes for tomato productivity at high temperature.

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