Poster Abstract - D.19

EXPRESSION PROFILING IN RESPONSE TO HIGH TEMPERATURE DURING TOMATO FLOWER DEVELOPMENT

F. GIORNO*, I. MASSARELLI*, 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 **) 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

gene expression, cDNA microarrays, heat stress, tomato flower development, fruit set

In tomato, high temperature severely impairs fruit set when it occurs during flower-to-fruit transitions, often decreasing yield in this crop species by 70%.

In this study, the effect of heat stress (HS) on tomato was flower development was investigated in two genotypes with high (cv Saladette) and poor (cv Pullrex) fruit set ability under HS using expression profiling and the TOM1 cDNA microarray.

Plants of the genotypes Pull and Saladette were grown under controlled temperature conditions, in greenhouse at $26^{\circ}C/20^{\circ}C$ day/night (optimal condition) and high temperature ($36^{\circ}C/25^{\circ}C$ day/night). Heat stress was imposed on flowers at different developmental stages, including gametogenesis, fertilization and anthesis, all of which are known to be very HS sensitive. cDNA targets used to probe the TOM1 array were obtained from RNAs from control and HS floral buds of three developmental stages.

Statistical analysis of the obtained profiles of three biological replicas for each stage, allowed us to identify several sequences differentially and significantly regulated by HS (~400 clones, t-test p-value < 0.05) during flower development in the two different tomato genotypes.

To the regulated ESTs belong sequences corresponding to genes coding for transcription factors, signal transduction factors, protein related to flower and gamete development, enzymes involved in primary or secondary metabolism and in cell wall structural changes, ribosomal proteins, heat shock proteins and other stress-responsive gene products.

Preliminary results indicate the anthesis as the developmental flower stage where major transcriptional changes occur under heat stress.

This work was supported by MIUR projects FIRB PlantSTRESS and FISR GENEFUN.