Proceedings of the 51st Italian Society of Agricultural Genetics Annual Congress
Riva del Garda, Italy – 23/26 September, 2007
ISBN **978-88-900622-7-8**

Poster Abstract – G.04

ON THE GLUTATHIONE S-TRANSFERASE GENE FAMILY IN *CITRUS SINENSIS*

D'AGOSTINO N.**, LICCIARDELLO C.*, REFORGIATO RECUPERO G.*,
CHIUSANO M. L.**

*) CRA-Istituto Sperimentale per l'Agrumicoltura, Corso Savoia 190, 95024 Acireale, Catania (Italy)
**) Department of Soil, Plant, Environmental and Animal Production Sciences, University of Naples "Federico II", Via Università 100, 80055 Portici (Italy)

Citrus sinensis (L) Osbeck, glutathione S-transferase, differential tissue gene expression

This study aimed to achieve a comprehensive characterization of the glutathione S-transferase (GST) gene family in *Citrus sinensis (L.) Osbeck*.

In plants, GST activity protects cells from a wide range of biotic and abiotic stresses, including pathogen attack, xenobiotic and heavy-metal, toxicity and oxidative stress. In addition, plant GSTs have been shown to be important in binding secondary metabolites like anthocyanins and cinnamic acid and hormones.

A collection of 94.127 orange Expressed Sequence Tags (ESTs) was screened in order to identify members of the gluthatione S-transferase gene family.

A total of 370 ESTs, putatively encoding GST proteins, were identified by similarity search against the UniProtKB/Swiss-Prot database. This set of sequences is submitted to a clustering/assembling procedure resulting in 62 distinct transcripts: 28 tentative consensus sequences (TCs) and 34 singletons (sESTs). Then, for each transcript the GST membership class is determined, according to the classification schema developed by *Dixon et al.* (2002). Finally, the identification of the longest Open Reading Frame (ORF), permitted to describe some transcripts as full-length mRNAs. Tissue specific expression patterns of the GST transcripts identified in this study were inferred by quering the dbEST database with respect to different tissues/developmental stages. SemiQuantitative Reverse Transcription Polymerase Chain Reaction (SemiQ RT-PCR) analyses were performed to assess the expression levels of the *in silico* assembled mRNAs in different tissues such as the albedo, flavedo, flesh, young and adult leaf and ovary tissues. Tissue samples were collected from the Moro nucellare 58-8D-1 (blood orange) and the Cadenera (common orange) cultivars.

The experimentally defined expression patterns confirmed the existence of the *in silico* predicted mRNAs, and that the GST family is composed of genes that revealed a tissue specific expression as well as of genes that are differentially expressed in the two cultivars.