Proceedings of the Joint Meeting AGI-SIBV-SIGA
Assisi, Italy – 19/22 September, 2011
ISBN **978-88-904570-2-9**

Poster Communication Abstract – 6A.29

IDENTIFICATION OF TOMATO DIFFERENTIALLY EXPRESSED GENES INVOLVED IN RESPONSE TO WATER DEFICIT

SCHIAVULLI A.*, LOTTI C.*, MARCOTRIGIANO A.R.**, PAVAN S.**, GRILLO S.***, IOVIENO P.***, MIACOLA C.**, ZONNO V.**, RICCIARDI L.**

*) Department of Agro-Environmental, Chemistry and Crop Protection, University of Foggia, Via Napoli 25, 71100 Foggia (Italy)
**) Department of Biology and Chemistry Agro-Forestal and Environmental, Genetics and Plant Breeding Unit, University of Bari, Via Amendola 165/A, 70125 Bari (Italy)
***) Institute of Plant Genetics (IGV), CNR, Portici, Via Università 133, 80055 Portici (Italy)

Solanum lycopersicum L., water deficit, gene expression analysis

Environmental stress adversely affects plant performance, resulting in significant reduction of crop yield and quality worldwide. Increasing aridity of semi-arid regions together with limited water resources has led to an exigent necessity for improving crop drought resistance.

Elucidating the molecular mechanisms of drought tolerance is critical for increasing crop production and quality. Plants do not passively accept environmental stresses, but respond actively through perception of stress signals. Responses to water deficit may occur within a few seconds or within minutes and hours when a plant withstands the imposed stress, and may arise from either tolerance or mechanisms that permits avoidance of the situation. In trying to understand responses to stresses, many genes induced by periods of water deficit have been identified and characterized. Interest has centred on differentially expressed genes, because it has been postulated that induction of genes will permit adaptation to stresses.

We present results of a study on tomato (*Solanum lycopersicum* L.) differentially expressed genes induced by water deficit. Two genotypes, selected based on drought tolerance and susceptibility, were grown in "semi-controlled" conditions (i.e. outdoor and protected from rainfall by transparent plastering covering), with three water stress treatments, and in greenhouse with two water stress treatments. We investigated the expression of 15 genes candidate to be involved in response to water deficit One gene, ERD15, showed a differential expression profile between[0] the two genotypes grown under the "semi-controlled" conditions, while 5 genes, including the same ERD15, were differentially expressed in greenhouse.

We are currently carrying out a proteomic approach to further analyze genotypic drought responsiveness.