Proceedings of the XLIX Italian Society of Agricultural Genetics Annual Congress
Potenza, Italy – 12/15 September, 2005
ISBN **88-900622-6-6**

Poster Abstract - D.17

REAL TIME-PCR AS A TOOL TO ANALYSE GENE EXPRESSION RESPONSE TO TEMPERATURE STRESS IN DURUM WHEAT

M. CORRADI*, M. GULLÌ*, A. MARZONI*, P. RAMPINO**, C. PERROTTA**, N. MARMIROLI*

*) Department of Environmental Science, University of Parma, Italy
**) Department of Biological and Environmental Sciences and Technologies, University of Lecce, Italy

gene expression, real-time PCR, durum wheat, hsp101

Plant have both an inherent ability to survive exposure to temperature above the optimal for growth (basal thermotolerance) and an ability to acquire tolerance to normally lethal temperatures after an initial exposure to mild heat stress (acquired thermotolerance). Relatively little in known about the genetic factors involved in both type of thermotolerance in plants. One of the most studied response is the synthesis of specific proteins named “heat shock proteins” (HSP). Quantitative and/or qualitative variation in HSPs production was suggested to be correlated to the varying capacities of thermotolerant and thermosusceptible strains to acquire thermotolerance. At present in *Arabidopsis* only the HSP101 has been proven to be related to acquisition of thermotolerance. There are other signalling pathways that could be involved in thermotolerance (basal and acquired) and they depend on signalling molecules such as ABA, ethylene, active oxygen species (AOS), salycic acid (SA). Evidences are accumulating to support the hypothesis that thermotolerance is a complex multigenic process, with different gene sets involved in its development. With the purpose to analyse the expression levels of different sets of gene potentially related with thermotolerance in durum wheat, real-time reverse transcription PCR (RT-PCR) was employed on wild and domesticated durum wheat accessions, classified as sensitive or tolerant to heat stress. To asses the role of HSP101 with regards to thermotolerance, a molecular analysis was performed to elucidate the composition of *HSP101* gene family in durum wheat. Different cDNA fragments cloned from two durum wheat cultivars, Creso and Ofanto, classified as sensitive and tolerant to heat stress, confirmed the presence of two distinct genes encoding HSP101. To understand the role of each gene product in the thermotolerance trait, a multiplex Real-Time PCR reaction was performed, targeting the polymorphic regions of each gene. The expression of these genes in the two cultivars, exposed to different thermal regimes, was subsequently compared. By this approach significant differences in the expression profile of *HSP101* genes between the cultivars, in response to the same stress conditions, are evidenced. The expression of several ESTs related with thermotolerance, isolated from a wild durum wheat accession, was evaluated by real-time RT-PCR and the results obtained confirmed the multigenic determination of the thermotolerance trait.