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Poster Abstract – C.01

TRANSCRIPTIONAL REGULATION OF HEAT SHOCK GENES IN DURUM WHEAT

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Heat stress is one of the major constraint to plant growth development and yield. This stress causes damages at the whole plant as well as at tissue, cellular and molecular level. The most prominent aspect of the response to this environmental injury is the massive synthesis of a group of proteins, the so called heat shock proteins or HSPs. These proteins are mainly chaperones or proteases that play the essential role of preventing and minimising the deleterious effect of heat at cellular and molecular level. Moreover, they have a role in helping cells to recover from the stress during the post-stress phase. The response to stress can be differently efficient depending mainly on the plant genetic background; some genotypes are able to cope better with the stress and for this they are called thermotolerant. High temperature tolerance in plants has two components: the inherent thermotolerance that is the constitutive component resulting from evolutionary thermal adaptation of species to their habitat, and acquired thermotolerance that is the ability of a plant to survive lethal temperatures, after an exposure to a mild heat stress (acclimation). Many reports indicate that HSP101 has a central role in thermotolerance, in many different eukaryote species. In plants to date many cDNAs and genomic clones relative to HSP101 have been isolated and characterised in many species (i.e. *Arabidopsis thaliana,* soybean, rice, maize, pea, beans), and different forms of HSP100 were identified indicating that this is a member of a small family of genes strongly induced by heat and with molecular weight ranging from 100.9 to 109.4 kDa. In particular, in *Triticum aestivum,* the species most similar to that of our interest i.e. *T. durum,* three different coding sequences are present in *GeneBank* The sequences reported code for different isoforms of HSP101, in addition there are evidences that in this species *HSP101* gene family could be represented by a small number of genes in each of the sub-genomes of hexaploid wheat. They also report that, in addition to heat stress, expression of HSP101 mRNAs in wheat leaves is induced by dehydration and ABA.

We report the isolation and characterisation of four cDNAs coding for different forms of HSP101 in durum wheat, evidencing that, in this species the *HSP101* genes are, at least, two per haploid genome. Expression analysis was performed using duplex real-time RT-PCR to quantify the relative abundance of the various *HSP101* isoform transcripts under different stress conditions. This approach in fact allows both precise measurement of steady state mRNA levels and discrimination among very closely related genes. Duplex real-time PCR was set up to analyse the expression of *HSP101* allelic variants in two durum wheat cultivars characterised by a different behaviour under heat stress.