

MOLECULAR RESPONSE TO WATER STRESS IN DURUM WHEAT IS DEPENDENT ON GENOTYPE AND WATER STRESS IMPOSITION

A.M. DE LEONARDIS*, F. NEFFAR**, L. CATTIVELLI*, A.M. MASTRANGELO*

*) C.R.A. Experimental Institute for Cereal Research section of Foggia, S.S. 16 km 675, 71100 Foggia, Italy - mastrangelo@iscfoggia.it

***) C.R.A. Experimental Institute for Cereal Research section of Fiorenzuola d'Arda, Via S. Protaso 402, 29017 Fiorenzuola d'Arda, Italy

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Plant react to stress events through the synthesis and the accumulation of a number of proteins and small molecules which contribute to the stress tolerance as a whole. This is the result of a complex cascade of perception and transduction of the stress signal, in which few regulatory mechanisms direct the expression of many downstream genes, whose protein products have a structural role in stress tolerance, or catalyse the synthesis of small molecules with osmotic properties.

The aim of this work was to individuate genes putatively involved in control of plant response to abiotic stress and to assess how intrinsic and environmental stimuli can regulate their expression.

To this effort, a set of 21 candidate genes as been analysed for transcript amount, following water stress in different tissues, phenological stages and growing condition in durum wheat.

The tested genes were selected by means of two strategies based on an *in silico* and an experimental approach. Eleven CBF genes, coding for transcription factors involved in abiotic stress response, have been selected among wheat ESTs available in public databases and have been assessed with specific primers couples.

Ten genes, originally isolated as early responsive genes (*e-cor*), have been chosen among those isolated from a subtractive library in which the oxidative stress, a common aspect to different abiotic stress types, was imposed by treating durum wheat plantlets to low temperature (3°C) in presence of light. Among the selected sequences some of them are putatively involved in the regulation of gene expression at transcriptional level, coding for zinc-finger transcriptional factors, as well as in post-transcriptional (RNA binding proteins) or post-translational (ubiquitination and sumoylation pathways) control. The selected genes were all originally described as cold-regulated, nevertheless since some component are in common between cold and drought stress were investigated in details their involvement in the latter condition.

Three durum wheat cultivars (Ofanto, Creso and Trinakria) were drought stressed at flowering stage to test the expression of the selected genes in flag leaf. Furthermore plants of the cultivar Ofanto, at the stage of third leaf, were also subjected to fast or slow dehydration process to asses the effect of the stress protocol on the identification of drought induced genes.

In the first experiment (flowering stage flag leaf), all tested genes were induced by stress in the cv Ofanto, whereas in Creso and Trinakria only some of the tested genes showed the same expression profile. When fast and slow dehydration stresses were compared (cv Ofanto third leaf stage) 7 out of 10 *e-cor* genes not show the same induction in transcript level in response to drought stress, whereas only three of the 11 CBF showed the same increase in transcript .