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INFLUENCE OF GROWTH STAGE ON MOLECULAR RESPONSE OF DURUM WHEAT TO WATER STRESS

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Physical stresses, particularly drought, place major limit on cereal productivity in Mediterranean environments which are undergoing a continuous decrease of mean rainfall.

The exposure of plant to abiotic stresses determines a physiological and molecular response depending, in initial phases, on a complex cascade of stress signal transduction in which few regulatory genes control many downstream genes that contribute to stress tolerance.

Many studies describe the expression profile of stress-related genes in early developmental stages, nevertheless the plant can react to stress in different ways if different phenological stages are considered, depending on the developmental processes in course.

In this work a set of 15 stress-related genes has been analysed for expression, in terms of transcript amount, in response to water stress in different tissues and phenological stages from the third leave to the physiological maturity (dough stage) in the Ofanto variety of durum wheat.

The tested genes were selected by means of two strategies based on an *in silico* and an experimental approach. In the first case, genes coding for transcription factors involved in abiotic stress response have been selected among wheat ESTs available in public databases. Different members of DREB/CBF family and a WRKY transcription factor have been assessed with specific primer couples.

In the second case, genes with a putative role in regulation of abiotic stress response on the basis of sequence homolgy and early expression following exposure to stress, 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. The selected genes could be involved in the response to different stresses, included dehydration, in which the oxidative damage plays a key role.

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 at in post-transcriptional (RNA-binding proteins) or post-translational (ubiquitination and sumoylation pathways) control.

All tested genes appeared to be induced by stress in booting and flowering stages, while only some of them showed a clear response to the applied stress also in early stages and/or at physiological maturity, these results indicaticating a strong influence of developmental stage on gene responsiveness to water stress.