

## **TRANSCRIPTIONAL ANALYSIS IN POTATO DURING WATER STRESS**

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Plant response to abiotic stresses is a complex phenomenon involving a wide gene network. In order to preserve crop production in adverse environmental conditions is interesting to understand the molecular mechanisms that regulate the stress response and, above all, the adaptative response.

In order to study molecular events that differentiate short versus long term water stress responses, PEG (Polyetilenglycol) was used to impose either an abrupt short water stress either a gradual long term adaptation to potato cell culture.

We have previously reported that gradual acclimation of potato cells to PEG-mediated water stress induces a set of metabolic changes, including proline accumulation, de novo protein synthesis, changes in membrane lipid composition, not observed in cells exposed abruptly to water stress (Leone et al., 1994, *Plant Physiol* 106: 703-712; Leone et al., *Plant, Cell & Environ.*, 1996, 19: 1103-1109).

To have a global view of the changes in gene expression during water stress and to compare two different responses, the TIGR 10k potato array was challenged with RNA isolated from untreated, PEG-shocked and PEG-acclimated cells. The slides were hybridized, at least in six technical replicates, including dye swap, with labeled Cy3-dUTP and Cy5-dUTP retro-transcribed total RNA.

A statistical analysis of microarray data revealed that more than 300 genes were up-regulated (>2.0 fold increase) belonging to different functional categories (including transcription factors, stress-proteins, amino-acid, protein and carbohydrate metabolism, cell wall synthesis, cellular processes and others) in both PEG-shocked and acclimated potato cells. However, only 13 cDNAs were common to both treatments. Similarly, a limited number (30) of common down-regulated genes were identified in the two cell populations.

The contribution of specific gene functional classes in the acclimation or in the abrupt response to water stress was discussed on the basis of the microarray results and their differential expression by RT-PCR or Real-time RT-PCR.

The expression of some genes (hsp 80, 14-3-3, salt tolerance, adaptin, gtp-binding) was, further, analyzed in potato plant tissues (leaves and roots) in water stress conditions. An altered expression profile of hsp80, salt tolerance and gtp-binding was found in vegetative tissues in response to water deficit. Forward and Reverse genetic studies are in progress to establish the functional role of these genes in the mechanisms of plant response to stress.

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