

Poster presentation

## Shared transcriptional correlations in seed formation and in plants response to drought

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### Background

Plant seed formation involves considerable water loss, while, at the same time, the dehydrated tissues exhibit desiccation tolerance preserving their vitality. Some of the genes expressed at these specific life stages are known to be involved in response to externally imposed water stress (e.g. osmotic stress and salt stress). Since functionally related genes are often co-expressed, revealing shared transcriptional correlations in response to the above dehydration processes in *Arabidopsis thaliana* plants may offer new tools for manipulating desiccation tolerance in plants.

### Materials and methods

Dehydration-related DNA microarray datasets from AtGenExpress [1,2] were normalized (MAS 5.0) and log<sub>2</sub> transformed. One thousand genes from each dataset with detectable and variable expression across conditions were selected for further analysis as follows: Pearson Correlation Coefficients (PCCs) were calculated for each pair of genes. Networks of transcriptional correlations were created from gene pairs with PCCs bigger than 0.8 or smaller than -0.8 (positive and negative transcriptional correlations, respectively). After removing transcriptional correlations related to common factors other than dehydration (i.e. circadian rhythm, temperature etc.) we intersected the networks of osmotic stress, salt

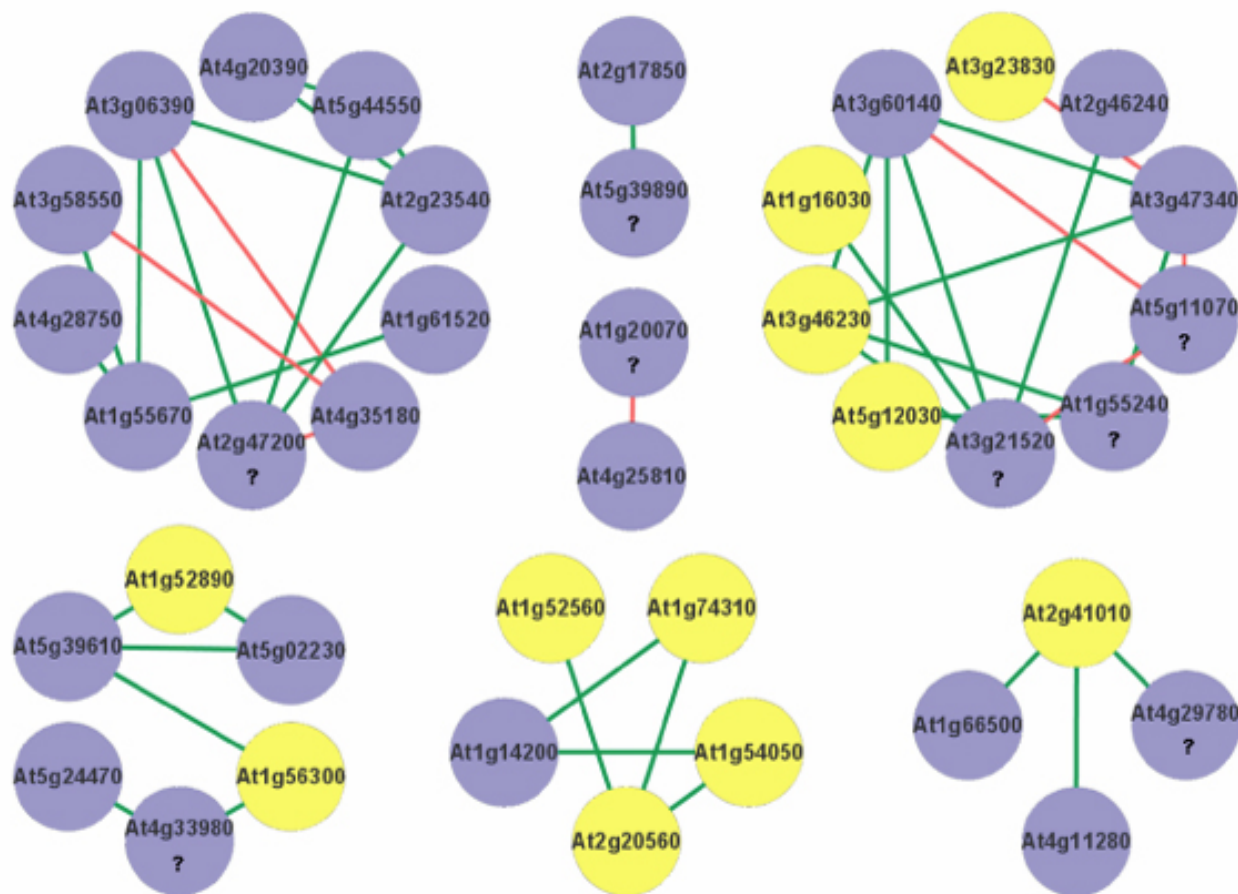
stress and stages 8–10 of seed formation using Cytoscape [3].

### Results

We identified new transcriptional correlations shared by plant responses to dehydration and by the acquisition of desiccation tolerance in the final stages of seed formation (Fig. 1). We found striking enrichment (ten times more than on the ATH1 array) with genes related to plants response to dehydration, such as genes of molecular chaperons. Transcripts of their homologues are also abundant in the resurrection plant *Selaginella lepidophylla* during dehydration [4]. About 20% of the genes are of unknown biological function. Based on our results, we propose these genes play a role in plant response to dehydration. Similar results were obtained with networks of shoots exposed to dehydration stresses.

### Conclusion

Computational approach allowed us to detect transcriptional correlations and to suggest a role in plant response to dehydration for genes with unknown function. Understanding transcriptional regulation during dehydration is an important first step in deciphering – and for future manipulation – of plant drought tolerance.



**Figure 1**

Shared transcriptional correlations in drought-stressed roots and in seed formation. Yellow: genes annotated as being involved in plant response to dehydration. Question marks – genes of unknown function. Green and red edges represent positive and negative transcriptional correlations, respectively.

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