



A gene co-expression network predicts functional genes controlling the re-establishment of desiccation tolerance in germinated *Arabidopsis thaliana* seeds.

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MAIN CONCLUSION: During re-establishment of desiccation tolerance (DT), early events promote initial protection and growth arrest, while late events promote stress adaptation and contribute to survival in the dry state. Mature seeds of *Arabidopsis thaliana* are desiccation tolerant, but they lose desiccation tolerance (DT) while progressing to germination. Yet, there is a small developmental window during which DT can be rescued by treatment with abscisic acid (ABA). To gain temporal resolution and identify relevant genes in this process, data from a time series of microarrays were used to build a gene co-expression network. The network has two regions, namely early response (ER) and late response (LR). Genes in the ER region are related to biological processes, such as dormancy, acquisition of DT and drought, amplification of signals, growth arrest and induction of protection mechanisms (such as LEA proteins). Genes in the LR region lead to inhibition of photosynthesis and primary metabolism, promote adaptation to stress conditions and contribute to seed longevity. Phenotyping of 12 hubs in relation to re-establishment of DT with T-DNA insertion lines indicated a significant increase in the ability to re-establish DT compared with the wild-type in the lines cbsx4, at3g53040 and at4g25580, suggesting the operation of redundant and compensatory mechanisms. Moreover, we show that re-establishment of DT by polyethylene glycol and ABA occurs through partially overlapping mechanisms. Our data confirm that co-expression network analysis is a valid approach to examine data from time series of transcriptome analysis, as it provides promising insights into biologically relevant relations that help to generate new information about the roles of certain genes for DT.

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