

Systems analysis of chilling stress induced transcriptomes in *Arabidopsis thaliana*

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Cold or chilling stresses are severe environmental factors affecting plant growth and development, limiting crop productivity and influencing geographical distribution of plant species and varieties. The evolution of plants from temperate regions has resulted in the emergence of several mechanisms contributing to their cold resistance. Among them cold acclimation, when plant adaptation to chilling temperature makes them tolerant to freezing. Molecular and physiological processes underlying cold response and tolerance are widely studied. However, current knowledge is incomplete and contradictory. The aim of this study is to overview the data on chilling-stress induced gene expression with the help of systems biology methods. For this, we perform meta-analysis of all available chilling-stress-induced transcriptomes in *Arabidopsis thaliana* from different studies and compare them with the data on 370 TF binding regions. Totally, from 30 microarray and 10 RNA-seq experiments we found half of Arabidopsis genome to be differentially expressed in response to cold at least in one experiment. Among them, the most robust genes were selected to reconstruct the gene network. TFs which binding regions were overrepresented in the differentially expressed genes provide a new dimension to the network. Functional annotation of chilling-stress induced genes and their comparison with the phytohormones metabolism and signalling pathways provided us a clue for the molecular mechanism of cold acclimation.

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