

Computational reconstruction of transcriptional cascades induced by plant hormones

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Reconstruction of hierarchical transcriptional cascades (TCs) orchestrated by plant hormones is the key for understanding the molecular mechanisms underlying different plant traits. Despite recent progress in methods for automatic inference of gene regulatory networks (GRNs), there is still a shortage of computational approaches for the large-scale reconstruction of TCs, which define GRN architecture. Here, we introduce an original three-step procedure to reconstruct hormone-induced TCs based on the integrated analysis of differentially expressed gene lists and a representative collection of transcription factor binding profiles. We applied this procedure to reconstruct TCs induced by auxin and ethylene in *Arabidopsis thaliana*. We identified transcriptional subnetworks, which operated before hormone treatment and were switched off upon hormone application, and the ones, which were switched on by the hormone. Moreover, we illustrated the functioning of the auxin-induced TC in regulation of chlorophyll biosynthesis. Our results demonstrate a promising outlook of using a new approach for computational reconstruction of TCs. This work was supported by the RSF grant no. 20-14-00140.

Take-home message:

A new three-step procedure based on the integrated analysis of differentially expressed gene lists and a representative collection of transcription factor binding profiles enables automatic reconstruction of transcriptional cascades.