

Weighted Gene Correlation Network Analysis (WGCNA) of Arabidopsis Somatic Embryogenesis (SE) and Identification of Key Gene Modules to Uncover SE Associated Hub Genes

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Abstract

Somatic embryogenesis (SE), which occurs naturally in many plant species, serves as a model to elucidate cellular and molecular mechanisms of embryo patterning in plants. Decoding the regulatory landscape of SE is essential for its further application. Hence, the present study was aimed at employing Weighted Gene Correlation Network Analysis (WGCNA) to construct a gene coexpression network (GCN) for Arabidopsis SE and then identifying highly correlated gene modules to uncover the hub genes associated with SE that may serve as potential molecular targets. A total of 17,059 genes were filtered from a microarray dataset comprising four stages of SE, i.e., stage I (zygotic embryos), stage II (proliferating tissues at 7 days of induction), stage III (proliferating tissues at 14 days of induction), and stage IV (mature somatic embryos). This included 1,711 transcription factors and 445 EMBRYO DEFECTIVE genes. GCN analysis identified a total of 26 gene modules with the module size ranging from 35 to 3,418 genes using a dynamic cut tree algorithm. The module-trait analysis revealed that four, four, seven, and four modules were associated with stages I, II, III, and IV, respectively. Further, we identified a total of 260 hub genes based on the degree of intramodular connectivity. Validation of the hub genes using publicly available expression datasets demonstrated that at least 78 hub genes are potentially associated with embryogenesis; of these, many genes remain functionally uncharacterized thus far. In silico promoter analysis of these genes revealed the presence of cis-acting regulatory elements, "soybean embryo factor 4 (SEF4) binding site," and "E-box" of the napA storage-protein gene of Brassica napus; this suggests that these genes may play important roles in plant embryo development. The present study successfully applied WGCNA to construct a GCN for SE in Arabidopsis and identified hub genes involved in the development of somatic embryos. These hub genes could be used as molecular targets to further elucidate the molecular mechanisms underlying SE in plants.

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Biography

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