عنوان مقاله:

A Meta-Analysis of Comparative Transcriptomic Data Reveals a Set of Genes Involved in the lignin synthesis in Nicotiana tabacum

محل انتشار:

اولین همایش بین المللی و دهمین همایش ملی بیوانفورماتیک ایران (سال: 1400)

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خلاصه مقاله:

Lignin is the second component of plant biomass and provides mechanical strength to tree trunks and confersimpermeability to vascular tissues. It is mainly involved in defense mechanisms against biotic and abioticstresses. This study was designed to explore the gene expression regulatory networks of this pathway intobacco under drought stress conditions. We retrieved four datasets from different gene expression studieson tobacco in drought stress conditions from Gene Expression Omnibus. Preprocessed reads were aligned tothe reference genome with Hisat۲. HTSeq was used to count the number of reads mapped to each gene. Themeta-analysis approach evaluated differentially expressed genes by the combined data (P-value ≤ ۰.۰۵). Inaddition, based on the R Package Weighted Gene Co-Expression Network Analysis (WGCNA), we identifiedsome modules related to the lignin biosynthesis pathway. The gene network analysis also identified severalhub genes such as FAS۱and PPC۲.۵۱ which may play crucial roles in the lignin biosynthesis pathway. Theprevious study represents that FLAs are cell wall structural glycoproteins that mediate cellulose depositionand cell wall development and they are abundant in the xylem. It is also shown PP۲C signaling cascadeprovides land plants with a hormone-modulated, resulting in a tolerance strategy allowing them to supporttissues built of cells with thicker cell walls. In the present study, we identified several hub genes. The resultsshowed that these hub genes may have vital roles in regulation of lignin biosynthesis. The current findingsprovide an overall insight into lignin biosynthesis and can expand the potential for engineering genome-scalepathways and systems metabolic engineering to alter the production of lignin by plants.

کلمات کلیدی:

Phenylpropanoid pathway; RNA-seq data; Meta-analysis; co-expression; WGCNA