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Yuan Guo, Caisheng Qiu, Songhua Long, Ping Chen, Dongmei Hao, Marta Preisner, Hui Wang, Yufu Wang

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Digital gene expression profiling of Flax (*Linum usitatissimum* L.) stem peel identifies genes enriched in fiber-bearing phloem tissue

Yuan Guo [a], Caisheng Qiu [a], Songhua Long [a], Ping Chen [a], Dongmei Hao [a], Marta Preisner [b], Hui Wang [a], Yufu Wang [a,*]

[a] Institute of Bast Fiber Crops and Center of Southern Economic Crops, Chinese Academy of Agricultural Sciences, Changsha 410205, China

[b] Faculty of Biotechnology, University of Wrocław, Wrocław 51-148, Poland

Abstract

To better understand the molecular mechanisms and gene expression characteristics associated with development of bast fiber cell within flax stem phloem, the gene expression profiling of flax stem peels and leaves were screened, using Illumina's Digital Gene Expression (DGE) analysis. Four DGE libraries (2 for stem peel and 2 for leaf), ranging from 6.7 to 9.2 million clean reads were obtained, which produced 7.0 million and 6.8 million mapped reads for flax stem peel and leave, respectively. By differential gene expression analysis, a total of 975 genes, of which 708 (73%) genes have protein-coding annotation, were identified as phloem enriched genes putatively involved in the processes of polysaccharide and cell wall metabolism. Differential expression genes (DEGs) was validated using quantitative RT-PCR, the expression pattern of all nine genes determined by qRT–PCR fitted in well with that obtained by sequencing analysis. Cluster and Gene Ontology (GO) analysis revealed that a large number of genes related to metabolic process, catalytic activity and binding category were expressed predominantly in the stem peels. The Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis of the phloem enriched genes suggested approximately 111 biological pathways. The large number of genes and pathways produced from DGE sequencing will expand our understanding of the complex molecular and cellular events in flax bast fiber development and provide a