

# Differential expression of genes involved in the lignan synthesis in flax varieties with different content of secoisolariciresinol diglucoside

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Lignans prevent the onset and development of diabetes, cardiovascular and oncological diseases. Linseed is the richest source of lignans, with secoisolariciresinol diglucoside (SDG) being the main flax lignin; however, flax varieties significantly differ in the SDG content. On the Illumina platform, we performed transcriptome sequencing of capsules of five flax genotypes that vary in SDG content. As a result, we obtained about 10 thousand reads for each sample. For evaluation of gene expression, reads were trimmed with Trimmomatic, mapped to the *Linum usitatissimum* reference genome (GenBank assembly: GCA\_000224295.2) using STAR, quantified using BEDTools, and analyzed using edgeR. Expression levels for a particular gene were quantified as read counts per million (CPM). It is known that *PLR* family genes encoding pinoresinol-lariciresinol reductases, *DIR* genes encoding dirigent proteins, and *UGT* genes, the products of which are UGT-glycosyltransferases, are involved in SDG synthesis, therefore we compared the expression levels of these genes in capsules of flax varieties with diverse content of SDG. Genotype-specific differences in expression were identified. Besides, for the identification of polymorphisms in the studied genes, variant calling was performed using FreeBayes for genome regions corresponding to the genes of *PLR*, *DIR*, and *UGT* families, and single-nucleotide polymorphisms (SNPs) were revealed. The obtained results contribute to the understanding of the role of *PLR*, *DIR*, and *UGT* genes in the determination of lignan content in flaxseed. This work was financially supported by the Russian Science Foundation, grant 21-16-00111.