

Full Length Transcriptome Sequencing and Differential Expression Gene Analysis of Hybrid Larch under PEG Stress

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Abstract : Larch is the main afforestation and timber tree species in Northeast China, and drought is one of the main factors limiting the growth of Larch and other organisms in Northeast China. In order to further explore the mechanism of Larch drought resistance, PEG was used to simulate drought stress. The full-length sequencing of Larch embryogenic callus under PEG simulated drought stress was carried out by combining Illumina-Hiseq and SMRT-seq. A total of 20.3Gb clean reads and 786492 CCS reads were obtained from the second and third generation sequencing. The de-redundant transcript sequences were predicted by lncRNA, 2083 lncRNAs were obtained, and the target genes were predicted, and a total of 2712 target genes were obtained. The de-redundant transcripts were further screened, and 1654 differentially expressed genes (DEGs) were obtained. Among them, different DEGs respond to drought stress in different ways, such as oxidation-reduction process, starch and sucrose metabolism, plant hormone pathway, carbon metabolism, lignin catabolic/biosynthetic process and so on. This study provides basic full-length sequencing data for the study of Larch drought resistance, and excavates a large number of DEGs in response to drought stress, which helps us to further understand the function of Larch drought resistance genes and provides a reference for in-depth analysis of the molecular mechanism of Larch drought resistance.

Keywords : larch, drought stress, full-length transcriptome sequencing, differentially expressed genes

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