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Gene Expression Profiling of Poplar Suspension Cells

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Objectives

This study was performed to understand the complexity of gene expression of poplar suspension cells.

Materials and Methods

A cDNA library was constructed using mRNA from poplar (*Populus alba* x *P. glandulosa*) suspension cells which were grown in the MS medium containing 1.0 mg/L of 2,4-D at 23°C in the light. The 5'-single pass sequences from randomly selected clones were determined using automatic sequencer. Sequence processing and functional classification were conducted using GeneMaster program (Ensoltek).

Results and Discussion

We present a large-scale production of expressed sequence tags (ESTs) from the poplar cells. Single pass sequences were obtained from 3,972 clones, representing 2,132 (53.7%) non-redundant groups. Putative functions were assigned to 1,864 clones, by a Blast algorithm, which could be divided into fourteen categories based on their function. The most abundant transcripts were an extensin-like protein (140) and an unknown protein (69).

Table 1. Functional classification of poplar ESTs.

Putative Function	%
Cellular transport	6.2
Interaction with cellular environment	1.4
Transcription	4.6
Energy	4.2
Cell rescue and defense	4.3
Cell cycle and DNA processing	5.7
Metabolism	11.1
Unclassified protein	4.7
Subcellular localization	0.9
Protein synthesis	12.1
Classification not yet	0.8
Protein fate	9.2
Cellular communication	1.7
Cellular organization	33.1

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