

Genomic Analysis on the Specific ESTs Expressed in the Dark Grown Soybean Hypocotyls

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In order to unravel the molecular mechanism during the hypocotyl elongation in the dark grown soybean seedlings (*Glycine max*), 118 expressed sequence tags(ESTs) were generated from randomly selected clones of cDNA library prepared from hypocotyls from dark grown soybean seedlings. Database comparisons of the ESTs revealed 84 non-redundant clones showed a high similarity with previously identified genes. Among these, 79 clones showed a homology with previously identified plant genes. The deduced amino acid sequences of 5 clones had a homology to proteins that have been reported from non-plant sources.

These ESTs were classified into 11 categories according to their function. Many transcriptional factors and putative ion channels have been identified. Base on these findings, it can be suggested that many new genes are induced during the hypocotyl elongation in the dark grown soybean seedlings.