G121

**Gene Expression Profiling at Early Stage of Head Regeneration in the Earthworm (*Perionyx excavatus*) Using Expressed Sequence Tags**

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To better understand early stage of head regeneration, we have generated 5'-end sequence of 1,410 expressed sequence tags (ESTs) from cDNA library of regenerating tissue. Individual ESTs sequences were clustered by the SeqMan II progam and annotated using Blastx and Blastn similarity analyses. Of the 1,410 clones, 632 clones (44.9%) matched to known genes and 695 clones (49.2%) had no match to any known sequences in GenBank. The remaining 83 clones (5.9%) were eliminated because of ribosomal and mitochondrial sequence. Of the 632 unique genes, 219 genes (34.6%) appeared to be singletons while 413 genes (65.4%) represented by two or more ESTs. A total 632 known genes were functional categories into 13 groups according to their biological functions. The largest group of known genes was protein synthesis co-factor, tRNA synthetases and ribosomal protein (22.4%). Further analysis of these genes may provide new insight into the epimorphic regeneration and mechanism of normal development as well as differentiation.

G122

**Transcriptome Analysis in the Midgut of the Earthworm (*Eisenia andrei*) using Expressed Sequence Tags**

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In order to investigate the transcriptome of earthworm midgut, Expressed sequence tag (EST) analysis was conducted using a complementary DNA (cDNA) library made from the midgut mRNA of the earthworm, *Eisenia andrei*. Of the 1248 clones, 538 clones (43.1%) were identified as known genes by BLAST searches and 563 clones (45.1%) as unknown genes. The remaining 147 clones (11.8%) were eliminated because of short sequence, ribosomal and mitochondrial sequences. Of the 538 unique genes, 156 genes (29%) appeared to be singletons while 382 genes (34.1%) represented by two or more clones. These known genes were categories into 6 groups according to their biological functions. The largest group of known genes was genes involved in protein expression (35.3%) followed by genes related with metabolism (30.5%), cell/organism defense and homeostasis (23.0%), cell structure and mobility (5.4%), cell signaling and cell communication (3.5%), and cell division (0.4%). The most abundantly expressed gene, the fibrinolytic enzyme, accounted for almost 3% of overall expression, indicating it has important function in the midgut. The high percent of clones showing no homology to any known genes in the GenBank databases indicate that a great number of novel genes exist in the midgut of the earthworm.

G201

**Hot Pepper Microarray Analysis from Low Temperature-induced cDNA Library Reveals that Cold Response Is Related to Regulation of Protein Function and Versatile Signals**

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Plants response to changes due to low temperature of 4℃ by regulating expression of a set of genes which is related to environmental stresses. In this study, with cDNA microarray demonstrates that major response of low temperature is regulation of protein stability and membrane fluidity in hot pepper (*Capsicum annuum* L.). We isolated differentially expressed cold-elevated or cold-repressed genes among 2,500 genes in hot pepper. As the result, 1,652 cDNAs for cold-inducible genes were isolated, and among them 250 were independent cold-inducible. Fifty five genes were also identified as unknown function, but related low-temperature stress. The data could be divided into 8 classes such as cold-repressed, cell cycle regulation, protein degradation, metabolism, transcriptionfactor, transport, signal transduction, and unknown genes. The results were clustered using K means method. The representative data were confirmed by northern blot analyses on stress conditions. Among them, 39% is related to protein synthesis and stability, and 27% to membrane fluidity. These results are similar to cold response patterns in cyanobacteria. Therefore, we came to a conclusion that plant and cyanobacteria had similar defense mechanism to the low temperature stress.

G202

**Control of Self-incompatibility by $CO_2$ gas in Brassica Campestris: $CO_2$ Gas Effect in Elimination of Self-incompatibility**

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In Brassica campestris, self-incompatibility (SI), a genetic barrier that prevents self-fertilization, can be overcome by $CO_2$ gas treatment. In this study, we investigated two genetically dissimilar (but display strong SI at self-pollination) Brassica campestris lines, 733 and 734. The 733 line did not respond to the gas treatment still rejecting self-pollen, suggesting that the plant is insusceptible for $CO_2$ gas treatment, while the 734 line was susceptible as previously reported. Confocal laser microscopy showed that the insusceptibility of 733 line was because the plant did not allow self-pollination. Transmission electron microscopy was also taken to observe structural alteration of papillar cells caused by $CO_2$ gas in the 734 line. RT-PCR analysis using specific primers for SLG gene transcript revealed that $CO_2$ gas treatment in the susceptible line resulted in decrease of the transcript amount, suggesting that $CO_2$ gas may regulate SLG gene expression during the bypass of SI.