

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

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Among all animal species, a few have the remarkable capacity to regenerate a missing part of their body after amputation. The early process of epimorphic regeneration in which dedifferentiation and cell proliferation are involved, provides a useful model to investigate the mechanism of normal development as well as differentiation. To better understand early stage of head regeneration, we have generated 5'-end sequence of 1,592 expressed sequence tags (ESTs) from cDNA library of regenerating tissue. Individual ESTs sequences were clustered by the SeqMan II program and annotated using Blastx and BlastN similarity analyses. Of the 1,592 clones, 723 clones (45.4%) matched to known genes and 624 clones (39.2%) had no match to any known sequences in GenBank. The remaining 245 clones (15.4%) were eliminated because of short sequence, ribosomal and mitochondrial sequence. Of the 323 unique genes, 216 genes (66.8%) appeared to be singletons while 107 genes (33.2%) represented by two or more ESTs. A total 323 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 (12.1%) followed by intermediary synthesis and catabolism enzymes (11.6%), transportation and binding proteins for ions and other small molecules (6.1%), cytoskeleton and membrane proteins (5.1%), intercellular signal transduction pathway molecules including kinase and signal intermediates (4.8%), stress response, detoxification, and cell defense protein (4.3%), protein degradation and processing, proteases (2.2%), extracellular matrix proteins and cell adhesion (1.8%), transcription factors and other gene regulatory proteins (1.6%), transportation and binding protein for proteins and other macromolecules (1.3%), RNA processing, polymerizing, splicing, and binding protein, and enzymes (1.1%), signaling receptor, including cytokine and hormone receptors, and signal intermediates (0.7%) and cell replication, histones, cyclins and kinase, DNA polymerase, DNA modification (0.6%). Further analysis of these genes may provide new insight into the epimorphic regeneration and mechanism of normal development as well as differentiation.