

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

Myung Sik Lee, Sung Jin Cho, Jong Ae Lee, Joo Sik Moon, Hyun Ju Cho, Bum Joon Park, Seong-Ki Kim, Jong Kil Choo, Soon Cheol Park

Department of Life Science, Chung-Ang University, Seoul 156-756, Republic of Korea

In order to understand the expression profile of earthworm midgut, we analyzed 1255 expressed sequence tags (ESTs) derived from earthworm midgut cDNA library. Among 1255 ESTs analyzed, 537 (42.8%) ESTs represented 231 unique genes of which 168 ESTs were singletons and 63 ESTs represented by two or more ESTs. A total of 571 unknown ESTs showed no significant homology. The remaining 147 (11.7%) ESTs whose lengths were less than 150 bp were removed. Among 231 identified unique genes, 168 genes (72.7%) were sequenced only once. Forty-seven genes (19.5%) appeared 2 to 6 times and 16 genes (7.8%) were sequenced over 10 times. Whereas over 70% of genes were sequenced only once, the top 10 most highly expressed genes accounted for 15.3% of transcripts analyzed in this study, indicating that the gene expression in the earthworm midgut was highly polarized. The expression of globin-related proteins including ferritin and fibrinolytic enzymes appeared to account for 6.5% and 4.1% of total ESTs analyzed in this study, respectively, suggesting that the prime functions of midgut in the earthworm would be associated with protein hydrolysis as well as extracellular globin formation. Among the known genes, the gene category involved in gene/protein expression appeared the largest one accounting 36.1% of expression in the midgut, followed by gene categories associated with metabolism (31.7%), cell/organism defense and homeostasis (20.9%), cell signaling/cell communication (3.7%), and cell structure/motility (4.8%). In view of functional groups, the most abundantly expressed genes were associated with extracellular respiratory pigment (6.3%), cellular respiration (5.2%), and fibrin hydrolase (4.0%). In addition, we were able to identify ESTs related with innate immune system of the earthworm including destabilase, a possible antagonist of transglutaminase.