

## Identification of genes expressed in abalone tissues (*Haliotis discus hannai*) using expressed sequence tags

Yoon Kwon Nam<sup>a,\*</sup>, Sang Jun Lee<sup>b</sup>, Koung Kil Kim<sup>b</sup>, Ji Eun Park<sup>a</sup>,  
Dong Soo Kim<sup>a</sup>

<sup>a</sup>Department of Aquaculture, Pukyong National University, Busan 608-737

<sup>b</sup>National Fisheries Research and Development Institute, Busan 619-902

Gene expression in five tissues of the abalone (*Haliotis discus hannai*) was investigated using an expressed sequence tag (EST) analysis. Randomly selected clones were obtained from cDNA libraries constructed with gill (GI), digestive diverticula (DD), hepatopancreas (HP), foot/mucus (FM) and rectangular muscle (RM). Of 1,235 clones analyzed (288 clones for GI, DD, HP each, 166 for FM, and 205 for RM), 741 (60.0%) clones in total turned out to share significant similarity with the sequences from NCBI GenBank (less than  $10^{-3}$  of e-values), 423 sequences showed poor similarity ( $> 10^{-3}$ ), and 71 sequences didn't match with any sequences in GenBank. The percent unique sequence (singleton) was ranged from 56.1% (RM) to 74.7% (FM) among libraries. On the other hand, overall percent singleton was 55.3% when all the ESTs from five libraries were assembled into contigs. Analysis of the organisms represented by the best hit for each EST (e-values  $< 10^{-3}$ ) showed that 23.8% matched with mammalian entries, 24.0% with mollusks, 14.4% with insects, 11.6% with fish and 26.2% with others. The expressed patterns differed among the tissues when judged by the categorization of the sequences from each library into 10 broad functional classes. In all the libraries, the class I (no hit or poor similarity) was the largest category with an average of 40.1%. This largest class was followed by class V (general metabolisms) in DD (21.9%), GI (14.6%) and HP (16.7%), while the 'cell structure and motility' (class VI) was the second largest class in remaining two libraries (31.2% for RM and 9.6% for FM). The class IX (cell division and proliferation) was the smallest class in all the libraries (less than 3%). This report provides the first tissue-specific lists of expressed abalone genes, which could be a fundamental basis for genomics program of abalone species.