EST Analysis for Aplysia Genome and Its Application for the Study of Learning and Memory

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Aplysia, a marine snail, has been used as a model system for studying the molecular mechanism of learning and memory because of its simple nervous system. However, the genetics of *Aplysia* has barely been investigated. To study the mechanism of learning and memory in cellular and molecular level in *Aplysia*, we constructed cDNA libraies of *Aplysia kurodai* central nervous system (full-length, 5'end enriched and random primed) and collected 11,493 ESTs (expressed sequence tags). We estimated that these sequences represent 4,859 sigletons in 5,953 contigs. These ESTs are sorted in respect to the roles in biological process, cellular component and biological function using the Gene ontology classification system.

Using this EST database, we have searched molecular components underlying synaptic plasticity in *Aplysia*. One of them was CPEB (cytoplasmic polyadenylation element binding protein), an mRNA binding protein that regulates polyadenylation-induced translation of mRNA containing the CPE site(UUUUAU) in 3'UTR. We found that the inhibition of CPEB expression using dsRNA blocks long term facilitation of sensory-to-motor synapse. To find the candidate of CPEB substrate, we screened putative CPE sites in assembled ESTs by bioinformatics analysis. In addition, we are performing biochemical analysis such as PAT assay to confirm the bioinformatics. Taken together, these data suggest that *Aplysia* EST provide very useful tool to characterize learning and memory related genes.