P21

Genome-wide analysis of the repertoire of TRIM genes in sea urchins

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The eukaryotic TRIM (TRIpartite Motif) super-family represents one of the largest classes of putative E3 ubiquitin ligases involved in several processes, including epigenetic control of development and disease. In the post-genomic era, new approaches allow genome-wide studies of gene family. In particular, we performed a comprehensive analysis of the TRIM repertoire in selected sea urchin species. By combining iterations of *ab initio* predictions and pairwise comparative methods, we first retrieved the full complement of TRIM genes in *Strongylocentrotus purpuratus*, whose full genome sequence was available. Interestingly, such a DNA sequence set includes not previously classified, echinoderm-specific, TRIM genes as well as multiple copies of known ones. We also retrieved a landscape of cDNA sequences from staged EST libraries, indicating that most of these genes are actively transcribed during development. Phylogenetic analysis of the deduced proteins, using set of TRIMs from various species, revealed a degree of genetic variation between species. Worth of mention, we predicted the occurrence of transposition events involving some of these genes, according with the documented rapid evolution of this family. Next, we adopted heuristic algorithms and post-processing steps to investigate the evolutionarily distant *Paracentrotus lividus*, *Allocentrotus fragilis* and *Lytechinus variegatus* genomes, whose sequencing projects are actually in progress. We assembled partial pools of TRIM genes and specifically associated them to EST-derived cDNA sequences. Such a collection of data should provide a framework for unravel gene regulatory networks involving TRIM genes from an evolutionary perspective. Indeed, in the *Pl* species, we have previously isolated and functionally characterized the cDNA sequence encoding the first echinoderm TRIM factor, Strim1. Here, we identified five *strim1* genes, all sharing a intronless organization, and roughly located their *cis*-regulatory apparatus.