



Echinoderm genome evolution represented in Echinobase, a whole phylum model organism database

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Abstract

The ancient marine phylum, Echinodermata, has existed for half a billion years and encompasses extraordinarily diversity including the brittle stars, sea stars, sea urchins, sea cucumbers and crinoids. They play key ecological roles in ecosystems ranging from the intertidal zone to the depths of the abyssal plains. These animals are widely used in developmental biology to study gamete fertilization and early morphogenic processes such as gastrulation. They were also the phylum in which system biology was born and used to build the first gene regulatory networks. Echinobase is a model organism knowledgebase supporting echinoderm research by linking genomic data from this diverse set of organisms to other gene centric data types such as gene expression, gene function, gene interactions and publications. Inter-relating data over this evolutionary distance is challenging. Data in different fields is bridged using a set of ontologies- controlled vocabularies with relationships between terms. One of the central ontologies is the Echinoderm Anatomical Ontology or ECAO, which captures the anatomy of developing echinoderm embryos and embryonic stages for the entire phylum. We also bridge Echinoderm data to biomedical models through the use of DIOPT, an orthology prediction suite. In this instance the standard echinoderm model, the purple sea urchin, is vertically mapped to the human genome to identify potential orthologs. The same system also horizontally maps the purple urchin genome to other echinoderm genomes. The matrix of conserved relationships then permits genes in any of the represented species to be linked to the vast data on genetic diseases, protein-protein interactions and gene function available from human and other vertebrate datasets. While early phases have focused on conservation across the phylum, we have also been identifying paralogs within each species. As gene duplication plays a key role in diversification and evolution we hope to move from tools to study conserved features and processes to the evolution of this phylum.