CDB SEMINAR

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Friday, February 1

17:00~18:00 C1F Auditorium

Genome evolution and the origins of the innate immune repertoire: insights from the coral *Acropora* and other "lower" animals

Summary

With perhaps as few a dozen different cell types, anthozoan cnidarians, a group which includes corals and sea anemones, are amongst the simplest true animals at the morphological level. However, in terms of the total number and types of genes they are comparable with the most complex of animals - the vertebrates. The coral genome contains a large number of genes once thought of as vertebrate-specific, including clear homologs of many key components of the vertebrate innate immune repertoire; considerable effort is presently being directed into exploring the roles of these in combating coral disease. Anthozoan genomes also contain a significant number of "non-metazoan" genes - genes only previously known from members of the other kingdoms of life. These are not the products of recent lateral gene transfers, but long-term residents of cnidarian genomes that potentially increase the biochemical complexity of the organism. The unexpected complexity and heterogeneity of the coral transcriptome represents a major challenge in understanding the functional biology of corals; essentially, one cannot predict how corals will respond based on what is known about other animals.

Many of the key genes and pathways of vertebrate immunity appear to have much earlier origins than has been assumed previously and are represented in the genomes of the coral and sea-anemone. Surveys of recently released whole-genome sequences and large EST (expressed sequence tag) datasets imply that both the canonical Toll/Toll-like receptor (TLR) pathway and a prototypic complement-effector pathway, involving C3 and several membrane attack complex–perforin proteins, are present in corals and sea anemones, members of the basal phylum Cnidaria. However, both pathways are likely to have degenerated substantially in *Hydra*, leaving open the molecular mechanism by which antimicrobial activities are induced in this textbook cnidarian. Surprisingly, the cnidarian genomes also encode a protein related to deuterostome RAG1 (recombination activation gene 1). The finding that RAG1 is likely to have originated from a Transib transposase implies that it might be possible to use in silico approaches to identify its target loci in 'lower' animals.

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