



CDB SEMINAR

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Thursday, March 31, 2016

11:00~12:00 Auditorium C1F

Dynamics of bilaterian genome architecture evolution: insights from the octopus and hemichordate genomes

Summary

One of the major genomic factors driving bilaterian evolution is novelty in gene order (synteny) and the associated noncoding regions. The focus of this talk will be on the variation in micro- and macro-synteny across bilaterian genomes, its origins and dynamics, and its contribution to evolutionary innovation. I will describe insights from the broad genomic sampling of bilaterians over the past years, and in particular the recently sequenced genomes of a cephalopod *Octopus bimaculoides* and a hemichordate *Saccoglossus kowalevskii*. Cephalopods (octopus, squid, cuttlefish, nautilus) belong to one of the most species-rich, yet genomically under-sampled, ancient bilaterian phylum, the lophotrochozoans. Their convergently-evolved camera eyes, epibolic gastrulation, as well as complex behavior have fascinated evolutionary biologists. Through comparison to other lophotrochozoan genomes, we find that Octopus lineage has undergone a significant syntenic reshuffling, for example losing well-known linkages, such as Wnts, Forkhead, or Hox. The loss of synteny correlates with distinct (in the time domain) expansions of transposable elements (TEs). We differentiate between different classes of TEs contributing to either genome reshuffling or evolution of novel regulation and tissue-specific expression. Hemichordates, located at the base of the deuterostomes, show much better bilaterian synteny retention and representation of the ancient bilaterian genome. On top of this conservation, however, we find several prominent examples of novel synteny, and discuss their impact on our understanding of the deuterostome ancestor.

Host:

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