COMPARISON OF GENE REGULATORY NETWORKS BETWEEN FRUIT FLY AND SEA URCHIN

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One well supported theory of molecular genetics is that genes are grouped into networks. Studies of embryonic development show that systems of gene networks are coordinated to guide growth and differentiation of cells. From this observation and others, a theory has been proposed that there are different kinds of gene regulatory networks that are interconnected. These networks can be seen as a hierarchy of four different types of subcircuits; kernels, plug-ins, switches and gene batteries. Kernels are foundational networks that rarely undergo change. Plug-ins take on a more general role and operate in diverse networks. Switches act as on-off controls to other subcircuits. Gene batteries encode structural or functional proteins to carry out a specific task, and are not involved in regulation.

A better understanding of these hierarchies can be achieved by comparing the genomes and genomic interactions of the fruit fly (*Drosophila melanogaster*) and the sea urchin (*Strongylocentrotus purpuratus*) in early embryonic development. This comparison should allow a better understanding of how these networks are conserved, how they change and what affect those changes have in evolution.