Researchers help unlock the secrets of gene regulatory networks

February 3 2009

A quartet of studies by researchers at the California Institute of Technology (Caltech) highlight a special feature on gene regulatory networks recently published in the *Proceedings of the National Academy of Sciences* (*PNAS*).

The collection of papers, "Gene Networks in Development and Evolution Special Feature, Sackler Colloquium," was coedited by Caltech's Eric H. Davidson, the Norman Chandler Professor of Cell Biology. His coeditor was Michael Levine, professor of genetics, genomics and development at the University of California, Berkeley.

"The control system that determines how development of an animal occurs in each species is encoded in the genome, and the physical location of the sequences where this code is resident is being revealed in a new area of systems biology--the study of gene regulatory networks," says Davidson. Gene regulatory networks are the complex networks of gene interactions that direct the development of any given species.

The papers in the collection focus on the gene regulatory networks of a variety of organisms, including fruit flies, soil-dwelling nematodes, sea urchins, lampreys, and mice.

"These networks lie at the heart of the regulatory apparatus, and they consist of genes that encode proteins that regulate other genes, and the DNA sequences which control when and where they are expressed," says Davidson, who authored a paper in the special feature about a gene regulatory network found in sea urchin embryos. He and Levine also coauthored a perspective in the same issue of the journal on the properties of gene regulatory networks.

In one paper, Ellen V. Rothenberg, one of the two Albert Billings Ruddock Professors of Biology at Caltech, examines, in mice, the intricate developmental pathway that causes blood stem cells to differentiate into T cells, a varied class of immune system cells that help the body fight off infection.

The paper, Rothenberg says, represents a "codification of everything we know about T cell development. We've found that getting the right balances of the various regulatory signals is absolutely crucial for the T cells to come out right. It gives one a sense of how subtle and sophisticated the regulation can be."

Another study in the special feature by Marianne Bronner-Fraser, the second Albert Billings Ruddock Professor of Biology, focuses on the gene regulatory network underlying neural crest formation in the lamprey, the most primitive living vertebrate. The neural crest is a group of embryonic cells that are pinched off during the formation of the neural tube--the precursor to the spinal cord--and then migrate throughout the developing body to form other nervous system structures.

The study "reveals order and linkages within the network at early stages," Bronner-Fraser says. "Because the neural crest cell type represents a vertebrate innovation, our work in lampreys shows that this network is ancient and tightly conserved to the base of vertebrates," she says.

The fourth of the Caltech papers, by Paul W. Sternberg, the Thomas Hunt Morgan Professor of Biology at Caltech and an investigator with the Howard Hughes Medical Institute (HHMI), and his colleagues, looks at a postembryonic gene regulatory network in Caenorhabditis elegans, a soil-dwelling worm commonly studied by developmental biologists. The gene regulatory network studied by Sternberg and his colleagues controls the formation of the worm's vulva, which connects the uterus with the outside and allows the passage of sperm and eggs.

References:

Davidson's paper, "Gene regulatory network subcircuit controlling a dynamic spatial pattern of signaling in the sea urchin embryo," coauthored with Caltech postdoctoral scholar Joel Smith, was funded by the National Institutes of Health's (NIH) Institute of Child Health and Development and General Medical Sciences Institute and a California Institute of Regenerative Medicine (CIRM) fellowship to Smith.

Rothenberg's paper, "A gene regulatory network armature for T lymphocyte specification," represents a collaboration between Rothenberg and Hamid Bolouri, a visiting associate at Caltech, with support from the NIH, the Albert Billings Ruddock Professorship, the Louis A. Garfinkle Memorial Laboratory Fund, the Al Sherman Foundation, and the DNA Sequencer Royalty Fund. The paper was coauthored by Caltech senior postdoctoral research scholar Constantin Georgescu, and William Longabaugh of the Institute for Systems Biology in Seattle.

Source: California Institute of Technology