



CDB SEMINAR

Date: Wednesday, October 12
Time: 16:00~18:00
Place: 7F Conference room of Building A

1. 16:00-17:00

Speaker: **Fabio Piano**

< New York University, Department of Biology,
Center for Comparative Functional Genomics >

Title: “Global molecular mechanisms and evolution of early embryogenesis in *C.elegans* and its relatives”

Summary :

Caenorhabditis elegans represents a good model to study the molecular mechanisms underlying early embryogenesis and its evolution. By combining global functional analyses (based on RNAi phenotypes, protein-protein interactions and transcriptional profiling) we have generated a network representing the functional relationships and physical interactions across the genes required for early embryonic development. The topology of this global network suggests that early embryogenesis is achieved through the coordination of a limited set of molecular machines. Using the combined data, we derived a first-draft of these machines and the connections between them. These analyses allow us to successfully predict functions of novel proteins. Furthermore, comparing these functional analyses with the natural diversity in early embryonic development across Rhabditids allows us to identify potential modules targeted by evolution to generate developmental diversity.

2. 17:00-18:00

Speaker: **Kristin C. Gunsalus**

< New York University, Department of Biology,
Center for Comparative Functional Genomics >

Title: **“Annotating the phenome:
data mining and data integration”**

Summary :

Functional genomic technologies have enabled the genome-scale characterization of different aspects of gene function, resulting in first-generation functional "maps". Such "-omic" approaches include gene expression profiling (the transcriptome), phenotypic profiling (the phenome), and protein interaction mapping (the interactome). A long-term goal of our research is to gain a comprehensive understanding of the molecular networks underlying *C. elegans* early embryogenesis. As part of this work, we have been developing approaches and tools focusing on systematic phenotypic analysis, data mining, and integration with other "-omic" datasets, which have general application in other systems.

Host: **Asako Sugimoto** <Developmental Genomics, CDB>
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