

【Grant-in-Aid for Young Scientists(S)】

Integrated Science and Innovative Science (New multidisciplinary fields)



Title of Project : A systems-level understanding of gene networks for the development and evolution of the chordate body plan

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Research Area : Basic genome science

Keyword : Genomic regulation

【Purpose and Background of the Research】

Recent analyses have shown many instances of developmental mechanisms conserved during evolution, while these studies have also revealed a much larger number of instances of divergence. However, to precisely determine the degree of conservation and divergence, we need a systems-level understanding of development. Because animal development is organized by the genome and the minimal functional unit of development is a cell, comprehensiveness and single-cell resolution are necessary.

Gene expressions during the animal developmental process are directed by gene regulatory networks. Precise positioning of blastomeres in the embryo is an important factor in order for the gene regulatory networks to work properly, while the architecture of the embryo is directly or indirectly regulated by the gene regulatory networks. Therefore, the relationship between the gene networks and the architecture of the embryo should be understood.

【Research Methods】

We use the ascidian, *Ciona intestinalis*, as a model system. Ascidiaceans belong to the subphylum Urochordata or Tunicata, which is the sister group of the vertebrates. The simple architecture of the ascidian larva represents the basic chordate body plan. The simplicity and compactness of the genome facilitates genome-wide studies.

The ascidian tadpole-type larva comprises approximately 2600 cells that form a small number of tissues including the central and peripheral nervous systems, epidermis, endoderm, notochord, mesenchyme and muscle. The most prominent feature of the ascidian development is that there are quite few cells in the developing embryo.

The *Ciona* genome is approximately 160 Mb in size and encodes approximately 16000 genes. The *Ciona* genome contains less paralogs than vertebrates. This relative simplicity and limited redundancy facilitates the analysis of the molecular mechanisms involved in the formation of the chordate body plan.

In our previous studies, we have been

analyzing gene regulatory networks responsible for the embryonic development of *Ciona intestinalis* on a genome-wide scale and at single-cell resolution. In this project, we continue the effort to reconstitute the regulatory networks in the *Ciona* embryos. We also are describing gene expression profiles of every cell up to the early gastrula stage by microarray analyses.

【Expected Research Achievements and Scientific Significance】

The development of ascidian embryos at early stages has been modeled in computer simulations (Tassy, et al. *Curr Biol* 16. 2006. 345-358). Taking advantages of this '3D virtual embryo', the resultant networks and expression profiles will be mapped to individual cells, and the gene networks will be modeled very precisely in three dimensions.

Because the body plan is the product of the gene network, we must start with understanding of the network for studying the evolutionary change in body plans. A systems-biological understanding of the *Ciona* embryogenesis will give important insights into the origin of the chordate body plan.

【Publications Relevant to the Project】

Imai, K. S., Stolfi, A., Levine, M. and Satou, Y. Gene regulatory networks underlying the compartmentalization of the *Ciona* central nervous system. *Development* 136, 285-293. (2009).

Imai, K. S., Levine, M., Satoh, N. and Satou, Y. Regulatory blueprint for a chordate embryo. *Science* 312, 1183-1187. (2006).

【Term of Project】 FY2009-2013

【Budget Allocation】 80,200 Thousand Yen

【Homepage Address and Other Contact Information】

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