氏名:	**Atsushi Mochizuki**	
所属先:	Institute for Life and Medical Sciences, Kyoto University	
Email:	mochi@infront.kyouto-u.ac.jp	
最終学位:	Ph. D. in Science	
略歴:	2018-Present Professor, Institute for Life and Medical Sciences, Kyoto University 2008-2020 Chief Scientist, Theoretical Biology Laboratory, RIKEN 2009-2015 Professor, Tokyo Institute of Technology 2002-2008 Associate Professor, National Institute for Basic Biology 1998-2002 Assistant Professor, Kyushu University 1998-1998 JSPS Fellow, Kyushu University	
研究分野:	Theoretical Biology, Mathematical Biology	

Complete control of a gene regulatory network of ascidian embryo by a few factors identified by a mathematical theory

Atsushi Mochizuki[1], Kenji Kobayashi[2], Kazuki Maeda[3], Miki Tokuoka[2], Yutaka Satou[2]

[1] Institute for Life and Medical Sciences, Kyoto University
[2] Department of Zoology, Graduate School of Science, Kyoto University
[2] Faculty of Informatics, The University of Fukuchiyama

By the success of modern biology, we have many examples of large networks consisting of many species of bio-molecules and interactions between them. It is believed that the dynamics of molecular activities based on such networks are the origin of biological functions. To understand the dynamics of complex systems, we have developed *Linkage Logic* theory, by which key molecules (FVS) to control the dynamics of a whole system can be determined from the topology of the regulatory linkages alone. We have applied the theory to a gene regulatory network (GRN) for fate specification of seven tissues (epidermis, brain, nerve cord, endoderm, notochord, mesenchyme, muscle) in ascidian embryos. From the analysis we found that dynamics of the network including more than 90 genes is controllable by manipulation of only 5 genes. We verified our prediction by combinatorial experiments of knockdown and overexpression, and obtained the results that six out of seven tissues except for muscle could be induced by experimental manipulations of these 5 genes. These successful results, at the same time, suggested that the experimentally identified GRN might be incomplete and lack the information responsible for muscle. Then, we analyzed the GRN and updated the network by combining linkage logic and experiments. We listed candidates of missing edges in the GRN under a criterion that adding one of the edges changes the FVS. We found that one of the candidates does exist actually. From an updated version of the GRN, we identified 6 (not 5) key factors. Then, we confirmed that by manipulating the activity of the 6 factors, all of seven cell types were successfully induced. The model-free approaches based on the linkage logic will promote understanding dynamics of biological systems in life sciences.