Award ID:
R1106

Project Title:
Recruitment of First-Time, Tenure-Track Faculty Members

Award Mechanism:
Recruitment of First-Time, Tenure-Track Faculty Members

Principal Investigator:
Kim, Jonghwan

Entity:
The University of Texas at Austin

Lay Summary:

My scientific interests have focused on understanding transcriptional regulatory networks in which combinations of hundreds of transcription factors and their genomic targets are tightly involved. Understanding these interactions is critical for elucidating global gene expression program required in generating cellular diversity during normal development as well as abnormal development such as tumor formation.

As a graduate student at University of Texas at Austin, I worked in the laboratory of Dr. Vishywanath R. Iyer where I was exposed to a new concept of biology which can be represented by the terms 'high-throughput and genome-wide'. I was especially interested in a new technology developed by Dr. Iyer and others for global mapping of protein-DNA interactions in vivo. I used this technique to identify chromosomal downstream targets of transcription factors in yeast and cultured human cell lines. During this time, I obtained significant high-throughput biology skills, such as handling microarrays, large-scale data generation and storage, and data analysis with bioinformatics tools; all important methodologies for my current and future research program. I also became interested in applying systems biology tools that I focused on during the course of my Ph.D to the problems of stem cell research.

After completing the Ph.D training in 2005, I started postdoctoral research in Dr. Stuart H. Orkin's laboratory at Harvard Medical School and Children's Hospital Boston with the hope of studying functions of numerous transcription factors that play important roles in embryonic stem cells by combining multiple large-scale data sets generated by gene expression profiling, global mapping of protein-DNA interaction and protein-protein interactome data in systematic ways. During my postdoctoral training, I have specialized in a number of projects including the constructions of an extended core transcriptional regulatory network, and a Myc-centered network in embryonic stem cells using a method called in vivo biotinylation. Using the data generated from the network study in stem cells, I addressed one of the important questions in stem cell and cancer biology fields, which is a common signature observed in both types of cells. I found that a Myc-related signature is shared in various human cancers and predicts human patient outcome, suggesting that the shared feature of ES cell and cancer signatures reflects largely the features of a Myc regulatory network, and not an ES cell specific core network.

Taken together, these results emphasize the importance of understanding common features between the pluripotent stem cells and various human cancers, and my research

to date demonstrates a gradual progression into embryonic stem cell biology and cancer biology. For my future project, I plan to identify novel modulators controlling common signatures shared by cancer cells and stem cells and to further elucidate the regulatory mechanism of these common signatures to facilitate cancer treatment.