A hidden layer of genetic regulation revealed by RNA structurome and interactome studies

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Abstract

The most remarkable findings in the past two decades in biology include how the mammalian genome is largely transcribed and how versatile functions RNA molecules can have. RNA structure and interactions may play a critical role in defining its function and regulation. However, due to lack of information, our knowledge on these RNA languages is very limited. In this talk, I will describe our recent effort in using new chemistry and deep sequencing techniques to probe RNA structures and interactions on a genome-wide scale. The study provides both the landscape and also the variation of structural transcriptome of species including human, mouse and virus. Analysis reveals structure features of stable and dynamic elements, long-range interactions, alternative structures, etc., in the context of biological processes including translation, RNA methylation, and RNA-protein interaction etc. Our results demonstrate that by leveraging on the power of next generation sequencing we can now approach to the structural dimension, i.e., a hidden layer of the complexity of post-transcriptional regulation.

Bibliography

Dr. Qiangfeng ZHANG, Ph.D., is an assistant professor and principle investigator in the Tsinghua-Peking Center for Life Sciences, School of Life Sciences, Tsinghua University. Dr. Zhang received his B.S. and his first Ph.D. from University of Science and Technology of China in 2000 and 2006, respectively, and his second Ph.D. from Columbia University in 2012. He worked as a postdoc at Columbia and Stanford, before he joined Tsinghua in 2015. Dr. Zhang's research interest focuses on the new area of Structural Systems Biology by combining computational and high-throughput experimental investigations. Through analysis of the conservation of local structural elements in the whole protein structural space, Dr. Zhang developed a coarse-grained structural modeling method that can accurately and effectively reconstruct protein-protein interaction networks s on a genome-wide scale (Nature 2012, PNAS 2010). Dr. Zhang also co-developed high-throughput experimental methods that use 1) enzymatic cleavage, or 2) small molecule probing, 3) crosslinking, combined with next generation sequencing techniques to profile in vitro and in vivo structures of the whole transcriptome (Nature 2014, Nature 2015, Cell 2016). The results reveal the structural-functional relationships of RNA molecules, and how RNA structures may be associated with disease. Dr. Zhang also involved in the development of a technique to identify protein-RNA interactions, a method is specifically useful for the study of non-coding RNA regulation and functions (Cell 2015). Dr. Zhang's most current interests are to apply these structural systems biology methods to study protein-RNA interactions, non-coding RNA structure, function and evolution, as well as their involvement in human disease, in particular cancer and infectious diseases caused by RNA viruses, with the ultimate goal of their precise medicine and treatment.