

Global Summit on

ONCOLOGY & CANCER

May 25-27, 2017 Osaka, Japan



Jiangwen Zhang

University of Hong Kong, Hong Kong

miRNA Cancer MAP: A web server prioritizing tumor associated miRNA

Recent studies have revealed the critical role of miRNAs in oncogenesis and great potential of miRNAs serving as diagnostic and prognostic biomarkers. NGS technologies have led to an exponential growth of miRNAs-related data. The mounting body of miRNA NGS data generated requires highly sophisticated tools for data analysis and integration. Currently, there are many tools available for miRNA target identification and miRNA function prediction. An integrated platform incorporating multiple data sources, methods and reported evidences would improve the accuracy and efficiency of the data analysis. Here we present our current work in this direction, miRNACancerMap, a web server inferring miRNA regulatory network in cancers. We collected miRNA-target information from multiple sources such as validated databases and sequenced-based prediction algorithms. Using text mining method, we discovered thousands of miRNA regulations in cancers from PUBMED. We have found 4,879 papers which reported hundreds of microRNAs related to cancer initiation and progression. We have also conducted data mining of miRNA NGS data from many cancer studies, e.g. genome-wide expression profiling of miRNAs and its mRNA targets. Integration of sequence-based miRNA-target interactions and expression-based miRNA-target correlations enable us to distinguish the activated regulations in cancers. And the annotation of cancer-specific evidences and functional analysis facilitate a better interpretation of the miRNA effects on cancer of the miRNA regulatory. Finally, we build up a user-friendly web server, miRNACancerMap, accessible for users to analyze the mRNAs/miRNAs of their interest and their own expression profile. And the results are presented in a comprehensive knowledge map via interactive visualization.

Biography

Jiangwen Zhang has completed his graduation from Johns Hopkins University with PhD. He has worked at Harvard University Genome Center as Senior System Biologist for years before joining University of Hong Kong in 2013. His lab has broad interest in genetic and epigenetic regulation in development and diseases. Currently, his lab is focusing on epigenetic regulation of tumorigenesis. His lab employs high throughput 'omics' assays and large scale computation to dissect the gene regulatory network and signaling pathways involved in oncogenesis.

jzhang1@hku.hk