香港浸會大學
HONG KONG BAPTIST UNIVERSITY

School of 中醫藥學院
Chinese Medicine

Computational Analysis of the Phosphoproteomic Data

Prof. XUE Yu

Department of Biomedical Engineering
College of Life Science and Technology
Huazhong University of Science and Technology, Wuhan, China

Date	:	14 Aug 2015 (Friday) 4:30 – 6:00 p.m.
Venue	:	SCM809
Language	:	English
Facilitator	:	Prof. LI Min

Abstract

Post-translational modification of proteins provides reversible means to regulate the function of a protein in space and time. Recently, mass spectrometry-based proteomic profiling of PTMs has emerged to be a hot topic, and computational analyses of the flood of data have attracted much attention. In 2008, we developed a GPS (Group-based Prediction System, http://gps.biocuckoo.org) algorithm, which can predict kinase-specific phosphorylation sites for 408 human protein kinases in hierarchy. Together with this sequence-based algorithm and protein-protein interaction information, we further developed a software package of iGPS ("*in vivo*" GPS, http://igps.biocuckoo.org) for predicting potential site-specific kinase-substrate relations (ssKSRs) and re-constructing phosphorylation networks. From the results, we observed that the eukaryotic phosphoregulation is poorly conserved at the site and substrate levels, but preferentially conserved at the pathway levels. Also, we performed a systematic prediction of POLO-like kinase (Plk)-specific phospho-binding and phosphorylation sites from phosphoproteomic data, and experimentally validated that human Mis18B is a novel interacting partner of Plk1. Based on a simple hypothesis that a kinase with higher activity phosphorylates more sites, we further developed an algorithm of kinase activity analysis (KAA) to monitor differentially active kinases among different tissues. Together with phosphoproteomic identifications, we re-constructed phosphorylation networks for mouse testes. By comparing to other tissues, we observed that a number of kinases such as POLO-like kinases (Plks), MAPKs, and CDKs with statistically more ssKSRs might have significantly higher activities, while the prediction was experimentally validated by detecting and comparing the activity-associated phosphorylation of Plk1 in testis and other tissues. Further experiments showed that the inhibition of Plk1 decreases cell proliferation by inducing G2/M cell cycle arrest. Taken together, our studies not only provided useful tool for analyzing the phosphoproteomic data, but also the prediction results are accurate for further experimental manipulation.

*** All are welcome ***