同济大学 TONGJI UNIVERSITY

报 告 人：郭天南 研究员

西湖高等研究院（西湖大学）

主 持 人：岳锐 教授

时　　间： 2017 年 12 月 29 日 10:00-11:00

地　　点： 医学楼 1101

Education and Employment

2006 年毕业于华中科技大学同济医学院临床医学七年制，同时获得武汉大学生物科学双学位；
2007-2008 年曾在新加坡国立肿瘤中心从事医学研究工作；
2012 年获得新加坡南洋理工大学博士学位；
2012-2017 年在瑞士苏黎世联邦理工大学 Ruedi Aebersold 教授实验室从事博士后研究；
2017 年 1 月至 7 月在澳大利亚悉尼大学儿童医学研究所 ProCan 任 Scientific Director，肿瘤蛋白质组 Group Leader，悉尼大学医学院兼聘高级讲师；
2017 年 8 月加入西湖高等研究院任研究员。

Research focus

We have developed a high-(sample)-throughput proteomics pipeline using pressure cycling technology and Data-Independent Acquisition (DIA)/SWATH mass spectrometry, and applied the PCT-SWATH pipeline to understand intra-tumor heterogeneity. Compared to alternative proteomic technologies, the PCT-SWATH pipeline offers the following benefits: 1) analysis of over 20 samples per mass spectrometry instrument per working day; 2) reproducible analysis of small amount of biopsy-level tissue samples (< 1 mg wet tissue weight); 3) generation of a comprehensive digital proteome map which can be in silico mined perpertually; 4) practical conversion of clincial specimens into digital biobank. Benefited from this methodology, we quantified the proteome-level spatial intra-tumor heterogeneity in prostate tumors. We found that protein biomarkers exhibited distinct heterogeneity pattern which has to be taken into account in clinical applications. We also quantitatively compared the genomic, transcriptomic and proteome heterogeneity in prostate cancers, and uncovered buffering effect at protein level.

Reference

Tiannan Guo, Petri Kouvonen , Ching Chiek Koh , Ludovic C Gillet , Witold E Wolski , Hannes L Röst , George Rosenberger , Ben C Collins , Lorenz C Blum , Silke Gillessen , Markus Joerger, Wolfram Jochum , Ruedi Aebersold. Rapid mass spectrometric conversion of tissue biopsy samples into permanent quantitative digital proteome maps. Nature Medicine. 2015. 21, 407–413.