



“Clostridium difficile: Functional Genomics Studies”

Date: 12 January 2015 (Monday)
Time: 2:30pm – 3:30pm
Venue: G5-217, Green Zone, 5/F (Lift no. 2), Academic 1,
City University of Hong Kong, Kowloon Tong

Speaker:

Prof. Yung-Fu Chang
Professor, Department of Population Medicine and Diagnostic Sciences,
College of Veterinary medicine, Cornell University

Abstract

C. difficile is the most common cause of nosocomial diarrhea in North America and Europe. Genomes of individual strains of *C. difficile* are highly divergent. We have applied both proteomic and transcriptome approach to determine how divergent strains respond to environmental changes. Tandem Mass Tag (TMT) labeling and nanoLC-MS/MS driven proteomics was used to investigate the responses of four *C. difficile* strains to nutrient shift and osmotic shock. We detected 126 and 67 differentially expressed proteins in at least one strain under nutrition shift and osmotic shock respectively. During nutrient shift, several components of the phosphotransferase system (PTS) were found to be differentially expressed which indicated that the carbon catabolite repression (CCR) was relieved to allow the expression of enzymes and transporters responsible for the utilization of alternate carbon sources. Some classical osmotic shock associated proteins such as GroEL, RecA, CspG, CspF and other stress proteins such as PurG and SerA were detected during osmotic shock. Furthermore, the recently emerged strains were found to contain a more robust gene network in response to both stress conditions. The transcriptomes of two historic and two recently isolated hypervirulent strains were analyzed following nutrient shift and osmotic shock. Illumina based RNA-seq was used to sequence these transcriptomes. Our results reveal that although *C. difficile* strains contain a large number of shared and strain specific genes, the majority of the differentially expressed genes were core genes. We also detected a number of transcriptionally active regions that were not part of the primary genome annotation. Some of these are likely to be small regulatory RNAs. Finally, a comparative genomic study of *C. difficile* and *C. sordellii* is also presented.

About the Speaker

Dr. Yung-Fu Chang is a professor in the college of Veterinary medicine, Cornell University, Ithaca, New York. Dr. Chang obtained his Veterinarian degree at the National Pin-Tung University of Science and Technology, Taiwan, MS in immunology at the University of Idaho, Moscow, Idaho, and Ph.D in Microbiology from the College of Veterinary medicine, at Texas A&M University, College Station, TX. He spent five years as postDoc in Medical Biochemistry and Biochemistry from the College of Medicine, Texas A&M University before moving to Cornell University as an assistant, associate and full professor. He is the author of 150+ peer-reviewed manuscripts and the inventor of several patents. He received a distinguish alumni award from the National Pin-Tung University of Science and Technology in 2006. He has served as editor of several Journals. His work has been supported by NIH, USDA, Research foundation and private sectors.

Contact

Ms Irene Wong (Tel: 3442-4707/ Email: irene.wong@cityu.edu.hk)

All are welcome