CANCER SCIENCE INSTITUTE OF SINGAPORE

SEMINAR ANNOUNCEMENT

Technology-Driven Assay Development

Date: Tuesday, 19 April 2016
Time: 2pm - 4pm
Venue: #01-01A Learning Rm, Centre for Translational Medicine
(14 Medical Drive, Singapore 117599)
Modulator: Dr Edward Kai-Hua Chow

Michael Rhodes



Director, Collaboration and Applications Development
Nanostring Technologies

3D Biology: Simultaneous single-molecule quantification of DNA (SNPs), mRNA, and proteins using molecular barcodes.

Imagine what you could do with a revolutionary technology that enables you to analyse expression levels by counting RNA, DNA and Protein molecules. In this seminar we will discuss the basics of the technology developed by Nanostring that shows the power of a digital, non- enzymatic methodology, with no RT or polymerase and direct single molecule counting, which delivers low bias accurate counts over 5 logs of magnitude. The RNA application especially as it applies to hard to utilize samples such as FFPE samples will be highlighted. The ability to study expressed fusion genes as well two prebuilt fusion gene panels covering clinically relevant fusions in lung cancer and Leukemia will be described. The combined RNA-Protein analysis as enabled in the latest immune-oncology panel will be covered and finally an example of the RNA-Protein-SNP analysis will be given. These applications will summarize the revolutionary technology that offers the ability to digitally analyse expression levels of RNA, miRNA and Protein, quantify DNA copy number variations and measure SNPs. It is a powerful research tool that has also been used to develop an FDA cleared Assay Prosigna®.

Ruby Yun-Ju Huang



Principal Associate, CSI Singapore

EMT in Oncology Scoring (EpiMet-OS): From Genomics Data to A Clinical Assay

Epithelial-mesenchymal transition (EMT) describes how polarized epithelial cells convert into motile mesenchymal cells. Functional roles of EMT in carcinoma progression have been extensively demonstrated. Despite increasing understandings of how EMT contributes to the aggressiveness in cancer metastases and treatment resistance, translating these scientific evidences to clinical practice to improve oncology patient care is still unproven. We have adopted a gap-bridging translational approach by using a microarray-based Generic EMT Signature to assign the relative EMT scores to cancer cells and tumors. The significance of the EMT-scoring scheme has been shown in the pan-caner meta-analysis to prognosticate overall survival in ovarian, gastric, pancreatic cancers and glioblastoma. The technology barrier for further translating the finding to clinical application is the lack of cost-efficient yet robust EMT-scoring assays. This EpiMeT-OS platform provides a technological solution for the void of quantitative diagnostic test for EMT that can be applied in clinical samples.