

"Genome Research in Hepatocellular Carcinoma"

by

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Abstract

Hepatocellular carcinoma (HCC) is a highly malignant tumor that is commonly fatal. Like other solid tumors, HCC is considered to develop through successive additions of genetic alterations. Despite much effort has been made to obtain a comprehensive picture on the genetic changes associated, information on molecular events that underpins the stepwise progression of HCC remained largely undefined. In an effort to simulate a tumor progression model for HCC, our group has previously attempted informatic analysis on the genome-wide aberrations of >150 HCC cases that were analyzed by chromosome-based comparative genomic hybridization (CGH). By the application of a self-organizing tree algorithm, specific regional chromosomal gains and losses were suggested in association with the initiation and progression of HCC. Significant CGH events identified were further used to construct an evolutionary tree that held inference for patient subgroups at differing degrees of tumor progression. Recent advances in the next generation sequencing technology have revolutionized gene discoveries in human cancers and promises to provide novel tumor biomarkers. By next generation sequencing, we deep sequenced primary HCC tumors and reference tissue from the same individual to explore nucleotide variants and other acquired somatic abnormalities that are tumor-specific. Chronic infection of the viral hepatitis B (HBV) is a major etiologic risk factor in the development of HCC. Despite viral DNA integration into the tumor genome is a common phenomenon, the role of HBV integrants in liver carcinogenesis remains unclear. We deployed RNA-seq data to study the effect of viral integrants on juxtapose cellular genes expression and showed a chimera read-through transcript holds function in predisposing to cancer risk. Our findings illustrate the potentials for next generation sequencings to provide novel insights into the mutational processes of HCC development.

About the Speaker

Prof. Nathalie Wong obtained her D.Phil. in Biochemistry from The University of Oxford, UK, and post-doctoral training at King's College School of Medicine and Dentistry, University of London, UK. She is now Professor at Dept of Anatomical and Cellular Pathology, The Chinese University of Hong Kong. Prof. Wong's research long focuses on understanding the molecular carcinogenesis of human hepatocellular carcinoma (HCC). Her group has previously studied the cytogenetic aberrations of HCC and defined a number of key genomic loci. Prof. Wong's current research includes whole genome and transcriptome sequencings of HCC, non-coding RNA analysis and functional characterization of somatic variants for cancer-causing effects in the development and progression of HCC. Their group has previously published in Cancer Cell, Gastroenterology and Hepatology.

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All are welcome