

City University of Hong Kong  
Department of Biomedical Sciences  
presents a seminar



## “EPIGENOMIC STUDY OF NASOPHARYNGEAL CARCINOMA (NPC)”

*by*

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**Date : 11 March 2016**

**Time: 2.30pm to 4.00pm**

**Venue: G5-215 (green zone), 5/F, (near Lift 8), Academic 1 Building, CityU**

### **Abstract**

Carcinogenesis involves alterations of multiple cancer genes including the epigenetic inactivation of tumor suppressor genes (TSGs). NPC is a major tumor in Hong Kong, as the top cancer for males of 20-44 year-old. Current genomic sequencing studies found only rare mutations in this tumor, indicating a critical role of its epigenetic etiology. NPC is virtually 100% associated with the infection of a human herpesvirus Epstein-Barr virus (EBV), which is a strong epigenetic driver inducing more CpG methylation in infected cells. We have profiled the whole-genome CpG methylation (methylomes) of NPC and normal nasopharyngeal epithelial cells. We observed extensive, genome-wide methylation of cellular genes in this tumor, with methylation of multiple known and novel genes verified. We identified ~1000-2000 methylated genes with promoter CGIs in cell lines and primary tumors. Epigenetic disruption of key signaling pathways including Wnt, MAPK, TGF-beta, Hedgehog and ErbB signaling was detected. Frequent methylation of known and novel Wnt signaling regulators, including SFRPs, DACTs, WNT5A and ROR2, was detected in cell lines and primary tumors. Further functional studies showed that these genes are bona fide TSGs for NPC. TSG methylation could also be detected in nose swab and serum samples from NPC patients, hence of biomarker value. Thus, NPC methylome shows a special high-degree CpG methylation epigenotype, similar to the EBV-infected gastric cancer, indicating a critical role of epigenetic alterations in its pathogenesis.

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**All are welcome**