

## **DIFFERENTIAL LONG NON-CODING RNA EXPRESSIONS IN GLIOMAS WITH EGFR ALTERATION**

*Karrie Mei-yee Kiang, Xiaoqin Zhang, Gilberto Ka-kit Leung*

Department of Surgery, Li Ka Shing Faculty of Medicine, The University of Hong Kong, Queen Mary Hospital, Hong Kong

**BACKGROUND:** Epidermal growth factor receptor (EGFR) is frequently overexpressed and mutated in various types of malignancies. In glioblastoma multiforme (GBM), the most aggressive form of brain tumor, EGFRvIII is the most common deletion mutant of EGFR that leads to its constant activation. Both EGFR amplification and EGFRvIII mutation have been associated with poorer prognosis in GBM patients, however, the downstream effects of this EGFR over-activity remains incompletely understood. Long non-coding RNAs (lncRNAs) are emerging as important regulators in different types of cancers. Given that we have previously identified a set of GBM-associated lncRNAs, its dysregulation is strongly implicated in gliomagenesis.

**METHODS:** To comprehensively identify the differences in long non-coding RNAs profile as a consequence of EGFR over-activation, we performed lncRNA profiling in two different public glioma microarray datasets by lncRNA mining approach established earlier in our lab. Gene expression comparison analysis were conducted between glioma samples with EGFR over-activation and EGFR wild-type.

**RESULTS AND CONCLUSION:** Differential expressions between two groups were observed for a subset of probesets, suggesting that these lncRNAs were associated with EGFR activation. Current study is ongoing, we believe our data will provide evidence the potential roles of certain lncRNA in gliomagenesis, and may help to understand the pathogenesis of gliomas through EGFR over-activation.