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Functional and mechanistic analysis of long non-coding RNAs in lung cancer

Lung cancer is a molecularly-heterogenous disease and the leading cause of cancer mortality. The molecular basis for this clinical heterogeneity remains incompletely understood. Increasing appreciation of the role of long non-coding RNAs (lncRNAs) in cancer progression has led to the identification of these molecules as a largely uncharacterized aspect of disease biology and novel prognostic/diagnostic biomarkers. We recently generated transcriptome data using next-generation RNA sequencing (RNA-Seq) to reveal lncRNA expression patterns in lung cancer. Preliminary studies have identified several novel lncRNAs which were dysregulated in lung cancer. *LINC00857*, as one of the top dysregulated lncRNAs, was highly expressed in lung cancer and significantly related to poor survival in patients with lung adenocarcinomas. This was verified by several lung data sets and confirmed by RT-PCR in an independent data set. Functional studies of *in vitro* and *in vivo* models indicated that *LINC00857* plays an important role in lung cancer proliferation, invasion and cell cycle regulation. Mechanistic studies indicated that *LINC00857* mediated tumor growth potentially through regulation of autophagy via YBX1-MET/AMPKα axis in lung cancer cell lines. The study provided a comprehensive analysis of lncRNAs in lung adenocarcinomas. It established the role of *LINC00857* as a potential driver of lung cancer pathogenesis and a potentially as a new diagnostic/prognostic biomarker. Importantly this study may help identify new molecular targets or a predictive marker for lung cancer treatment in tumors with *TP53*, *KRAS* or *EGFR* mutations, as well as *ALK* fusion.

Biography

Guoan Chen is a Research Assistant Professor in the Section of Thoracic Surgery at the University of Michigan Medical School. He completed his PhD from Peking Union Medical College in 1999 and Post-doctoral training in tumor molecular biology at the University of Michigan in 2003. He has over 15 years of research experience in identification and characterization of molecular genetic alterations including protein profiles, autoantibody profiles, gene mutations, DNA copy number changes by SNP, DNA methylation, gene signatures by mRNAs, microRNA profiles, circRNAs and long non-coding RNAs in lung cancer using functional genomic, proteomics and bioinformatics approaches with more than 80 papers in reputed journals.

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