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Upregulation of long non-coding RNA *RAB1A-2* induces FGF1 expression worsening lung cancer prognosis

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Abstract

The chromosomal locations of lncRNAs (long non-coding RNAs, lncRNAs) infer their biological functions in cancer. *Lnc-RAB1A-2*, a Ras-related protein Rab-1A (RAB1A) upstream lncRNA, was chosen for assessment of its impact on lung cancer prognosis in a case-based analysis and investigation of its biological function though a series of functional assays. *Lnc-RAB1A-2* was significantly upregulated in 276 lung cancer tissues compared with corresponding non-tumor tissues, and its expression level was significantly correlated with clinical stage and metastasis status in lung cancer patients. Patients with high expression levels of this lncRNA had a shorter median survival time (16.0 months vs. 23.0 months, P = 011 in southern samples; 8.0 months vs. 19.0 months, P=0.020 in eastern samples; 13.0 months vs. 19.0 months, P=0.002 in merged samples) and a higher risk of death than those with lower levels (HR=1.52; 95% CI=1.01-2.26, in merged samples). Additionally, overexpression of *lnc-RAB1A-2* significantly promoted lung cancer cell proliferation *in vitro* and *in vivo*. Further analyses using digital gene expression tag profiling revealed that *lnc-RAB1A-2* could affect the expression of fibroblast growth factor 1 (FGF1), a gene involved in the PI3K/AKT/mTOR pathway that is largely activated by RAB1A. *FGF1* was confirmed to be a down-stream gene of *lnc-RAB1A-2*. Collectively, our study demonstrated that *lnc-RAB1A-2* is associated with poor lung cancer prognosis by promoting lung cancer development.