

ABSTRACT

Oral Squamous Cell Carcinoma (OSCC) is one of the leading malignant tumors worldwide. The oncogenic long non-coding RNA (lncRNA), LncX, was reported to play a critical role in OSCC progression. To further identify and characterize the key pathways and genes downstream of LncX, we will integrate online datasets and bioinformatic analysis to investigate the expression pattern of LncX in OSCC and identify gene signatures and pathways downstream of LncX to elucidate potential mechanisms due to its capabilities in mitigating laboratory cost and provide precise prediction toward biological studies. These analyses are correlation analysis, gene expression analysis, overall survivability analysis, expression level with LncX-KD treatment analysis, protein-protein interaction and pathway enrichment analysis from certain bioinformatic tools such as UALCAN, cBioPortal, GEO NCBI, KM-Plotter, DAVID, STRING, Metascape utilizing TCGA, WikiPathways, KEGG pathway, Reactome Pathway, GO Biological Processes, Canonical Pathway, and Reactome Gene sets databases. In protein-protein interaction analysis, 11 gene candidates have been identified and 3 have been selected for further investigation which are VEGFC, PLAU, and SLC7A5 gene due to its coexpression with the LncX. Not only that, there are 3 major pathway analyses for VEGFC, PLAU, and SLC7A5 genes to be involved in OSCC progression such as hemostasis, pleural mesothelioma, tissue morphogenesis, chemotaxis, and gland development which appeared to be disrupted in patients with OSCC development. Collectively, this project will provide fundamental and novel knowledge about the LncX-mediated downstream gene network regulation and its functional role in oral cancer progression.

Keywords: OSCC, LncRNA, LncX, Gene Candidates, Protein-Protein interactions, Pathway