INTEGRATIVE ANALYSIS OF LNCRNA-MIRNA-MRNA EXPRESSION PROFILES IN ESOPHAGEAL SQUAMOUS CELL CARCINOMA TISSUES

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Background: Each year, more than 600,000 new cases of esophageal cancer are registered worldwide, and about 85-90% of these cases are esophageal squamous cell carcinoma (ESCC). The incidence and mortality rates of ESCC vary across countries, and it has been observed that Central Asia has a high incidence. Despite its prevalence, esophageal cancer remains significantly understudied compared to other common tumor types, and no specific risk factors have been identified to explain susceptibility to this disease in Central Asia.

Materials and methods: In this study, tumor tissues of 16 patients diagnosed with ESCC were collected for study. Tumor specimens were obtained from patients who had undergone Ivor-Lewis esophagectomy without receiving prior chemotherapy and radiotherapy. Small RNAs were isolated using the mirVana miRNA Isolation Kit and sequenced on the NovaSeq platform (NETFLEX Small RNA-Seq Kit). Total RNA was extracted from approximately 60 mg of tissue for each of the 16 tumor samples using the RNAiso Plus (Takara) and purified using DNase I kit (QIAGEN) based on manufacturer instructions.

Results: In this study, we performed integrative analysis of miRNA, lncRNA, and mRNA sequencing data from 16 ESCC patients in Kazakhstan. Differentially expressed miRNAs, lncRNAs, and mRNAs were identified in tumor tissues, and their putative targets were predicted using miRTarBase and ENCORI databases. Subsequently, a comprehensive lncRNA–miRNA– mRNA regulatory network was constructed to elucidate key molecular processes implicated in ESCC progression. Notably, we identified several miRNAs with robust overexpression ($log2FC > 4$, $padj < 0.05$) that have not been previously associated with ESCC. Furthermore, commonly dysregulated lncRNAs, miRNAs, and mRNAs were evaluated for their prognostic relevance using the TCGA ESCC cohort.

Conclusion: Our findings provide novel insights into the molecular landscape of ESCC in a Central Asian population and highlight candidate regulatory RNAs with potential diagnostic and therapeutic relevance.

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