WHOLE TRANSCRIPTOME SEQUENCING ANALYSIS OF PATIENTS WITH ESOPHAGEAL SQUAMOUS CELL CARCINOMA FROM KAZAKHSTAN

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Introduction: Esophageal cancer is the eighth most common cancer worldwide and sixth in Kazakhstan. Esophageal squamous cell carcinoma (ESCC) is the predominant histological subtype of esophageal cancer and diagnosed at late stage. The aim of the project was to identify genetic basis of ESCC by analyzing differentially expressed genes (DEGs) from whole-transcriptome sequencing of Kazakhstani patients.

Materials and Methods: Tissue samples were obtained from 25 ESCC-affected individuals immediately after Ivor-Lewis esophagectomy from Oncology Center in Nur-Sultan. Whole transcriptome sequencing was performed following the TruSeq RNA Protocol. STAR software and DESeq2package have been used for mapping and defining differentially expressed genes. Functional analysis of DEGs was performed using various R packages.

Results: The study sized 14 men and 11women, average age of patient 65.5±7.7 years 88% of the patients were diagnosed with advanced stages T3-T4. Analysis of tumor and normal esophageal tissues identified 7 DEGs, comprising 883 upregulated and 314 downregulated genes (with adjusted p-value <0.05). We found significant 4 up-regulated and 6 down-regulated KEGG pathways (p-value<0.05). Top 300 DEGs were mapped to PPI network and functional enrichment analysis was performed on identified three modules of closely connected nodes (genes).

Conclusion: ESCC with moderate dysplasia is the most common histologic subtype of esophageal cancer in our patients and is characterized by a poor prognosis.High-throughput sequencing approach allows identifying molecular pathways involved in esophageal carcinogenesis that could improve diagnosis and treatment strategies.

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