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

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Introduction: Esophageal cancer is the sixth most common cancer in Kazakhstan, and usually not detected until it has progressed to an advanced incurable stage. The predominant histological subtype of esophageal cancer in Kazakhstan is esophageal squamous cell carcinoma (ESCC). The purpose of the project was to identify genetic basis of ESCC by analysing 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 Multidisciplinary Medical Center. Normal esophageal tissue sample were extracted from Atlas of RNA sequencing profiles. Whole transcriptome sequencing was prepared and performed following the TruSeq RNA Protocol. STAR software and DESeq2package have been used for mapping and identifying differentially expressed genes (DEGs). 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. Bioinformatics analysis of tumor and normal esophageal tissues identified 34 DEGs (adj. p-value <0.05). We found ten significantly upregulated and two significantly downregulated KEGG pathways (p-value <0.05). Top 300 DEGs were mapped to PPI network and three modules of closely connected nodes were identified. Functional enrichment analysis of these modules showed that “module 1” is significantly associated with immune response, “module 2” is linked with histone functions, and “module 3” is associated with mitotic division and checkpoint.

Conclusion: Most patients diagnosed with late stages T3-T4 with moderate dysplasia, which was the most common histologic subtype of esophageal cancer in Kazakhstani patients High-throughput sequencing approach allows the comprehensive understanding of molecular pathways involved in esophageal carcinogenesis that could improve diagnosis and treatment strategies.

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