

GENE EXPRESSION PROFILE OF THE ABCA FAMILY IN GASTRIC CANCER: A STUDY USING RNA-SEQ

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Introduction: Gastric cancer (GC) is a leading cause of cancer-related death worldwide, with poor prognosis due to late diagnosis and limited treatment options. The ABCA family of transporters is involved in key cellular processes, including drug resistance and cancer progression. Alterations in the expression of ABCA genes may influence gastric cancer biology, making them potential targets for new diagnostic and therapeutic approaches.

Objectives: This study aims to evaluate the expression profile of ABCA transporters in gastric cancer tissues to better understand their role in disease progression.

Methods: We analyzed the expression of ABCA family genes in paired tumor and adjacent tissue samples from 42 patients (CAAE: 47580121.9.0000.5634). Total RNA was extracted using TRIzol® and evaluated for integrity using the 2200 TapeStation System (Agilent Technologies). RNA-seq was conducted on the NextSeq® platform (Illumina®, USA). The raw data was converted to FASTQ format using Reporter software, and the reads were mapped using the Salmon tool, with annotation based on the hg38 version of GENCODE.

The identified reads were quantified and imported into the R statistical environment via the tximport library, and the significance of differences was determined using the Wilcoxon-Mann-Whitney test.

Differential gene expression of all ABCA family genes between adjacent and cancer tissues was analyzed through RNA-Seq.

Results: The analysis revealed a significant increase in the expression of the *ABCA1* gene in cancerous tissue samples. On the other hand, genes *ABCA6*, *ABCA8*, and *ABCA9* showed reduced expression in comparison to non-neoplastic tissues.

No significant differences in expression were observed for *ABCA10*, *ABCA12*, *ABCA13*, *ABCA2*, *ABCA3*, *ABCA4*, *ABCA5*, and *ABCA7* between gastric cancer and adjacent tissues.

The Receiver Operating Characteristic (ROC) curve was generated for the genes *ABCA1*, *ABCA6*, *ABCA8*, and *ABCA9*, which showed significant differences in expression between cancerous and adjacent tissues.

The Area Under the Curve (AUC) values were 0.81 for *ABCA1*, 0.71 for *ABCA6*, 0.85 for *ABCA8*, and 0.70 for *ABCA9*.

Conclusion: The ABCA family genes are dysregulated in gastric cancer, exhibiting high expression of *ABCA1* and low expression of *ABCA6*, *ABCA8*, and *ABCA9*. These alterations may

contribute to the development and progression of gastric cancer, providing potential therapeutic targets for future interventions.

Keywords: Gastric cancer; *ABCA*; RNA-Seq;