EXPRESSION ANALYSIS OF THE *CTCFL/BORIS* GENE IN GASTRIC CANCER PATIENTS FROM THE STATE OF PARÁ

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Introduction: Gastric cancer (GC) is a global public health challenge, ranking as the fifth most common cancer and the fourth leading cause of cancer-related deaths worldwide. Its high lethality is mainly attributed to late diagnosis and tumor heterogeneity, which limit therapeutic options and reduce patient survival. In this context, the identification of diagnostic, prognostic, and therapeutic biomarkers for GC becomes essential. CTCFL (also known as BORIS) belongs to the cancer-testis antigen (CTA) family, typically restricted to testicular tissue, but frequently overexpressed in various malignant tumors. Its high immunogenic potential makes it a promising candidate for immunotherapy. Therefore, investigating the tissue expression pattern of the *CTCFL* gene in GC patients is crucial to assess its clinical relevance in this malignancy. **Objective:** To analyze *CTCFL* gene expression in gastric adenocarcinoma (GA) samples from the state of Pará, Brazil. **Methods:** A total of 124 tumor tissue samples and 62 adjacent non-tumoral tissue (ADJ) samples from GA patients (CAAE: 47580121.9.0000.5634) were collected and subjected to total RNA sequencing. Based on the obtained reads, a comparative analysis of *CTCFL* expression levels between tumor and ADJ tissues was performed. Additionally, the association of *CTCFL* expression with: i) pathological variables: EBV and *H. pylori* status, histological subtypes, and overall survival (OS); and ii) clinical and epidemiological characteristics: gender and use of neoadjuvant chemotherapy, were evaluated. Group comparisons were performed using the Wilcoxon test with normalized expression data. Statistical significance was set at $p<0.05$. Data visualization was conducted through graphical analyses using R software. **Results:** The *CTCFL* gene showed significantly higher expression in tumor tissues compared to ADJ tissues ($p= 0.00782$). Gene expression analysis based on pathological features revealed a slight increase in *CTCFL* expression in EBV positive patients, although not statistically significant ($p= 0.33561$). Conversely, a significantly higher expression of *CTCFL* was observed in *H. pylori*-positive patients ($p = 0.0004$). Regarding histological subtypes (diffuse, intestinal, and mixed), expression levels were similar, with no statistically significant differences ($p= 0.16665$). Notably, elevated *CTCFL* expression was associated with increased overall survival (OS), reaching statistical significance ($p= 0.0039$), suggesting a better prognosis. No significant differences in gene expression were found between patients who underwent neoadjuvant therapy and

those who did not (p= 0.97131), nor between sexes (p= 0.48847). **Conclusion:** The results indicate that *CTCFL* is differentially expressed in gastric adenocarcinoma, with a significant association with *H. pylori* infection and impact on overall patient survival. These findings highlight the potential of *CTCFL* as a prognostic biomarker and a therapeutic target in gastric cancer. Further studies are needed to validate its immunogenicity and support the development of effective immunotherapeutic strategies.

Keywords: Gastric neoplasms; biomarkers; transcriptome.