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Transcriptional activity of *PTX3* gene in diffuse gastric carcinoma subtype

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Introduction: Gastric cancer (GC) is the fifth most commonly diagnosed malignancy and the third leading cause of cancer-associated mortality worldwide. Based on its histological characteristics GC has been historically divided into three major subtypes: intestinal-, diffuse- and mixed-type GC. Among them, patients with diffuse-type gastric cancer (DGC) have a particularly poor prognosis that only marginally improved over the last decades, as conventional chemotherapies are frequently ineffective and specific therapies are unavailable. Up to now, the molecular mechanisms underlying the pathohistogenesis of DGC have not been fully elucidated.

Aim: This study aimed to explore the mRNA expression pattern of long pentraxin 3 (PTX3), an acute-phase protein, and a newly clarified mediator for innate immunity and inflammation in DGC tumor tissue samples and non-tumor gastric tissue controls.

Materials & Methods: *PTX3* mRNA expression levels were measured in 62 DGC tumor tissues and 62 normal gastric mucosal samples obtained from patients with non-malignant disease using quantitative real-time PCR (RT-qPCR). *In silico* analysis of *PTX3* mRNA levels in GC tissues and normal control samples based on publicly available RNA-sequencing data (UALCAN database) derived from the TCGA-STAD project was performed as well.

Results: qRT-PCR-results revealed no difference in *PTX3* mRNA expression between the DGC tumor tissues and normal non-malignant gastric mucosal samples. The obtained qRT-PCR results were further confirmed by in silico analysis of TCGA-STAD RNA-sequencing data. However, the data obtained by *in silico* analysis revealed a statistically significant difference in *PTX3* mRNA expression between the normal tissue samples and the intestinal-GC type and between the DGC and intestinal-GC subtype.

Conclusion: The present study's findings indicate the possible role of the *PTX3* gene in the pathogenesis of histologically different GC subtypes. However, elucidation of its role, if any, in DGC histological subtype requires further analysis.

Keywords: diffuse gastric carcinoma, PTX3, RNA-sequencing data, UALCAN database