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S100A4 and ERBB2 as Co-Factors in Pancreatic Cancer

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Abstract

Background: Pancreatic ductal adenocarcinoma (PDAC) remains one of the most aggressive tumors with dismal prognosis and survival rates. Identifying early molecular diagnostic markers could contribute in improving survival in this intractable disease. Chromosomal rearrangements and altered expression of the gene have been implicated in PDAC progression to metastasis. S100A4 protein promotes invasion and metastasis by binding to several intracellular target proteins and modulating their function. ERBB2 is marker of poor prognosis in multiple cancer types. This study examined the potential clinical significance of S100A4 and ERBB2 expression in PDAC.

Materials and methods: Pairs of non-tumoral and tumoral tissues from a total of 73 patients with PDAC were included in our study to assess the gene expression of S100A4 by two-step qPCR using TaqMan hydrolysis probes. ERBB2 gene expression was assessed by SYBR Green chemistry. S100A4 protein expression was evaluated by immunohistochemistry.

Results: Gene expression of S100A4 was increased at advances stages of PDAC (p-value=0.02) and with tumor grading. Kaplan-Meier survival distributions showed a significant difference in patient's survival outcome according to their S100A4 expression by immunohistochemistry (lower or higher than 10%. p-value=0.043). Multi-variate Log Rank (Mantel-Cox) test confirmed that resection type and S100A4 protein expression has a significant value in correlation with PDAC. Similarly, significant correlations were observed between ERBB2 gene expression and TNM tumor stage (p-value= 0.0048) and tumor grading (p-value=0.048). Additional analysis showed a statistically significant correlation between S100A4 and ERBB2 gene expression levels (p-value=0.0094).

Conclusions: Our results showed that both S100A4 and ERBB2 are associated with poor outcomes in PDAC, and might be valuable prognostic biomarkers.

Key words: PDAC, S100A4, ERBB2