MAR Oncology and Hematology (2024) 4:10

Research Article

An Independent Prediction of the effects of MFAP2 on Stomach Adenocarcinomas.

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Received: 04 Oct 2024

Published: 24 Oct 2024

DOI: https://doi.org/10.5281/zenodo.14044554

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MFAP2, an extracellular matrix protein, is elevated in squamous carcinoma of skin and neck, hepatocellular carcinoma, and stomach adenocarcinoma. Its molecular characteristics and prognostic usefulness in stomach adenocarcinoma (STAD) have not been documented. A study using Prognoscan, Ualcan, Kaplan-Meier Plotter, Linkedomics, GEPIA2, TIMER, and a timer portal and Spearman's correlation phase coefficient found that MFAP2 expression was increased and validated in TCGA-STAD tumor tissues. Higher MFAP2 terms were related to lower survival in TCGA and cohort. MFAP2 expression was found to be an independent risk factor for average survival, disease-specific survival, and progression-free survival in STAD. MFAP2 affects RNA transportation, oocyte meiosis, spliceosome, and ribosome biogenesis. It is also associated with B cells, CD4+ T cells, and neutrophils infiltration. B lymphocytes and dendritic cells predicted STAD prognosis. Closing the MFAP2 connection to macrophage marker genes is the immune response's fundamental goal, laying the groundwork for future studies on MFAP2's immunomodulatory role in STAD.

KEYWORDS: *MFAP2, prognosis, stomach cancer.*

Introduction

The most common type of gastric cancer is gastric adenocarcinoma (STAD) (1). Despite the increase in STAD diagnosis and treatment over the past few decades, STAD morbidity and mortality continue to increase due to the lack of early diagnostic procedures and intensive treatment (1). If STAD patients are diagnosed early and treated with endoscopy or surgery, the five-year rate should be greater than 90% (2). Direct estimation from STAD improves predictions. Therefore, finding new candidate genes that play an important role in the initiation and development of SATD is important for reducing mortality and improving prognosis. The benefits of continuous sequencing and high-throughput sequencing in biomicroarray are benefiting science (3-9). The Cancer Genome Atlas (TCGA) is a large database that makes genetic and clinical evidence of most cancers publicly available (10). Researchers can use this

repository to conduct in-depth and accurate studies on cancer and its pathophysiology (11). In addition, TCGA helps to predict cancer and individuality by discovering new candidate genes and information about most cancers (12). Network analysis is an effective method to construct scale-free gene co-expression networks (13). Weighted gene coexpression community assessment (WGCNA) has been widely used to examine the number and structure of associated genes (14). In addition, WGCNA has been used to evaluate genetic and scientific associations and has been established for various cancer types (15–18), prostate cancer (15), esophageal cancer (17), and most of the candidate cancer biomarkers (18). Therefore, WGCNA provides a good interpretation tool for most cancers and provides new insights into the molecular etiology and prognosis of cancer. To elucidate the underlying mechanisms of STAD and to identify the differences between predictive biomarkers and targeted therapy, microarray data from STAD patients were obtained together with sample size and gene expression. These genes discovered using the TCGA dataset may also act as oncogenes. MFAP2 has been shown to be a novel diagnostic and predictive biomarker that may provide additional information for the early detection and treatment of STAD patients.

Materials and Methods

The TCGA STAD gene expression statistics profiles and scientific data for patients, including age, gender, tumor stage, TNM classification, and survival status, are available for download via the TCGA portal. MFAP2 expression differs between individuals, and differential STAD mRNA in tumor and healthy tissues was used in the TCGA-STAD cohort. Oncomine, a microarray database of most cancers and data mining platforms, detected MFAP2 in STAD or normal tissues for its level of reproductive diversity mRNA expression.

The Kaplan-Meier and log-rank tests were used to examine the survival of MFAP2 in the TCGA-STAD cohort. The Kaplan-Meier Plotter is an Internet biomarker assessment tool for breast, ovarian, lung, stomach, and liver cancer, mostly based on meta-analysis. SurvMiner and the R Survival algorithms assessed TCGA-STAD and scanned prognostics. An connection between MFAP expression and DFS has been examined for belly adenocarcinoma and GEPIA.

Linkedemics is a network analysis that uses the LinkedOmics and GEPIA2 database to analyze the statistical properties of MFAP2 co-expression. The LinkInternet Interpreter module Linkedomics

(LinkInterpreters) is used to analyze the bio-process, gene-target enrichment, kinase-target enrichment, and transcription-target enrichment via gene-packet enhancement analysis (GSEA). The GEPIA2 database is an online service used to analyze RNA-sequencing data from 9,736 tumors and 8,587 daily TCGA and GTEX samples using advanced processing pipelines.

MFAP2 is linked to six different types of immune cells, and Timer's and Spearman's Tumor Association Correlations Module were used to investigate the relationship between MFAP2 expression and STAD abundance in B-cells, CD4+ T cells, CD8+ T cells, neutrophils, macrophages, and dendritic cells. A Kaplan-Meier analysis was used to analyze the predictive value of each immune invasion.

STRING is a database of recognized and predicted protein-protein interactions, consisting of direct and oblique associations resulting from calculational predictions and knowledge switch between organisms' primary databases.

Results

The MFAP2 mRNA in STAD samples is overexpressed, with higher levels found in tumor tissue than in daily tissues. The TCGA portal and FIREBROWSE were used to identify the expression stage of MFAP2 in tumor tissue. The UALCAN database showed that patients with high MFAP2 levels had shorter survival index (FP) and prognostic probability score (PPS) compared to those with low MFAP2 levels.

The clinical characteristics of STAD patients are linked to MFAP2 expression, but no research has found a link between MFAP2 expression and human STAD's scientific prediction. A Kaplan-Meier plotter tool was used to evaluate the influence of MFAP2 on the survival index. High MFAP2 levels were associated with shorter FP and PPS, and patients with high MFAP2 expression had shorter DFS in the GEPIA database.

String was used to achieve interaction between MFAP2 and various binding proteins, resulting in GO and KEGG pathway analysis to identify the organic properties of these co-DEGs. The study also investigated the relationship between MFAP2 expression and six key immune cells in STAD, finding that MFAP2 expression levels were related to B cells and CD8+ T cells.

The "LinkFinder" module of LinkedOmics was used to examine the MFAP2 co-expression sample for more organic recognition. The negative correlation of 6152 genes with MFAP2 was positive, while the positive correlation of 7399 genes was negative. Positive and negative MFAP2-related heatmaps of pinnacles of 50 genes.

Discussion

Our preliminary studies have shown that MFAP2 may function as a STAD proto-oncogene and serve as a regulatory biomarker in complementing population data. We examined the differential expression of STADs and found that their tissue significance in cancer is mainly through the formation of the STAD signaling pathway. According to the upcoming UALCAN and GEPIA databases, MFAP2 is mostly represented in STAD. Kaplan-Meier survival analysis showed that patients with high MFAP2 levels had lower OS and PPS. Furthermore, the amount of methylation in MFAP2 also affects the lower protein expression. Most patients with undiagnosed early-stage STAD are not candidates for treatment, which results in poor outcomes. (27) As a result, it is possible and effective. The use of diagnostic and therapeutic indicators is important. (26-28) Bioinformatic evaluation plays an important role in cancer research in general, and cancer evaluation using genetic information has been developed with bioinformatic systematic methods. In this study, we found MFAP2 expression in human gastric adenocarcinoma (STAD) and many other cancers. We found that MFAP2 is overexpressed in many malignancies. We found that MFAP2 was more abundant in STAD compared to normal tissues, which was associated with survival, OS, and DSS. In addition, to investigate whether MFAP2 silencing promotes tumor growth, we performed in vitro studies showing that MFAP2 transformation inhibits the proliferation and migration of ductal adenocarcinoma cells, which may be biomarkers for STAD. Several analyses of fibrillin-1 mutants and MAGP-1 (MFAP2)-deficient mice show similar characteristics. MFAP2 and fiberlin 1 overlap to regulate osteoclast differentiation and bone resorption. (28) According to the study, MFAP2 is not required for elastic fiber formation in mice but is required for various tissue homeostasis or different pathways. (30) Therefore, changes in fibrillin may alter the ability of fibrillin to bind to MFAP2 and often affect virus initiation and progression. Previous studies have identified a distinct, broad-spectrum proteoglycan matrix that binds to fibrillin-1, which plays an important role in cancer and metastasis. (29) Segade et al. The findings suggest that the early MFAP2-associated ECM signature and gene expression is a factor in the regulation of cell

adhesion, migration, and ECM deposition in human osteosarcoma. Our recent findings suggest that MFAP2 inhibition promotes migration and proliferation in vitro. MFAP2 may worsen and enhance STAD by interacting with mutant Fibrillin-1. Future studies should investigate whether fibrillin-1 interacts with MFAP2 in STAD cells. We then found that MFAP2 expression was used as a good histological level. MFAP2 was expressed at the highest concentrations; MFAp2 was most closely associated with STAD length, suggesting a link between MFAP2 expression and symptoms of STAD disease. Therefore, we performed a TCGA-STAD survival analysis, and the results showed that higher MFAP2 expression was associated with poor prognosis, which was also confirmed in several conflicting groups. Furthermore, Cox's analysis showed that MFAP2 was once a threat to STAD. Based on our findings, we can conclude that MFAP2 overexpression occurs in STAD, and a similar diagnosis is necessary based on accurate diagnosis and clinical manifestations. The amount of MFAP2 expression in the infiltrates was interdependent. In addition, subsequent Kaplan-Meier analysis showed that macrophages and dendritic cells could predict STAD outcome. According to Cox's analysis, macrophages and MFAP2 were statistically significant, and all variables were in equal proportion. These findings suggest that macrophages may be one of the most important determinants of MFAP2. On the other hand, human learning is affected by fundamental limitations. Most importantly, our research is mainly based on the analysis of biological data in addition to certain external experiments. Second, other important prognostic factors are needed to improve the accuracy of survival analysis. Furthermore, evidence on MFAP2 is important for many clinical studies and future research.

Conclusion

MFAP2 may also play an important role in the development of STAD. Thus, MFAP2 may become an important prognostic marker as well as the best immunological target in STAD.

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