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Expression, Prognostic Value, and Pro-Oncogenic Mechanism of TARBP1 in Prostate Cancer

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Abstract: Prostate cancer (PCa) is one of the most common malignancies in men worldwide, and current tools for diagnosis and prognosis remain limited. This study aimed to investigate the expression, prognostic value, and biological function of the nucleotide metabolism-related gene TARBP1 in prostate cancer. Through bioinformatics analysis of the TCGA and GEO databases, five key genes associated with biochemical recurrence (BCR) were identified (RGS11, KAT2A, MXD3, TARBP1, WFIKKN), and a prognostic risk model was constructed. The model showed good predictive performance in both the training set (TCGA) and the validation set (GSE70769) (AUC > 0.7). Experimentally, immunohistochemistry confirmed that TARBP1 was highly expressed in PCa tissues and positively correlated with Gleason score, clinical stage, and metastatic risk. In vitro, knockdown of TARBP1 significantly inhibited the proliferation and migration of LNCaP cells. Animal experiments further demonstrated that TARBP1 knockdown suppressed tumor growth in nude mouse xenografts and down-regulated the expression of metabolism-related genes such as HPRT1 and B2M. Additionally, tumor microenvironment analysis indicated that low-risk patients had higher immune cell infiltration and immune scores. Drug sensitivity analysis identified potential therapeutic agents including KU-55933. This study systematically reveals the pro-oncogenic role of TARBP1 in PCa for the first time and establishes a prognostic model based on nucleotide metabolism-related genes, providing novel biomarkers and therapeutic targets for the precision diagnosis and treatment of prostate cancer.

Keywords: prostate cancer; TARBP1; prognostic model; nucleotide metabolism; gene knockdown; nude mouse model

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1. Introduction

Epidemiology and current diagnostic challenges of prostate cancer
Role of nucleotide metabolism and RNA-binding proteins in cancer
Research background of TARBP1 and its unknown role in PCa
Objectives and novelty of the present study

2. Materials and Methods

Data sources: TCGA-PRAD, GSE70769
Bioinformatics: Differential expression analysis, WGCNA, prognostic model construction, immune infiltration analysis, etc.

Experimental validation: Immunohistochemistry, cell culture and viral infection, qPCR/WB, nude mouse xenograft assay

3. Results

Identification of five key prognostic genes and construction of a risk model

Good performance of the model in internal and external validation

High expression of TARBP1 in cancer tissues and its association with clinicopathological features

Knockdown of TARBP1 inhibits cell proliferation, migration, and in vivo tumor growth

Tumor microenvironment and drug sensitivity analysis

4. Discussion

Significance of TARBP1 as a potential biomarker and therapeutic target in PCa

Clinical translational value of the prognostic model

Limitations and future directions

5. Conclusion

TARBP1 is highly expressed in PCa and promotes tumor progression

The nucleotide metabolism-based prognostic model exhibits good predictive ability

TARBP1 may serve as a novel therapeutic target for prostate cancer

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