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Development of Programmed Cell Death Protein 1 Pathway-Associated Prognostic Biomarkers for Bladder Cancer Using Transcriptomic Databases

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Abstract : The emergence of immune checkpoint inhibitors (ICIs) targeting proteins like PD-1 and PD-L1 has changed the treatment paradigm of bladder cancer. However, not all patients benefit from ICIs, with some experiencing early death. There's a significant need for biomarkers associated with the PD-1 pathway in bladder cancer. Current biomarkers focus on tumor PD-L1 expression, but a more comprehensive understanding of PD-1-related biology is needed. Our study has developed a seven-gene risk score panel, employing a comprehensive bioinformatics strategy, which could serve as a potential prognostic and predictive biomarker for bladder cancer. This panel incorporates the FYN, GRAP2, TRIB3, MAP3K8, AKT3, CD274, and CD80 genes. Additionally, we examined the relationship between this panel and immune cell function, utilizing validated tools such as ESTIMATE, TIDE, and CIBERSORT. Our seven-genes panel has been found to be significantly associated with bladder cancer survival in two independent cohorts. The panel was also significantly correlated with tumor infiltration lymphocytes, immune scores, and tumor purity. These factors have been previously reported to have clinical implications on ICIs. The findings suggest the potential of a PD-1 pathway-based transcriptomic panel as a prognostic and predictive biomarker in bladder cancer, which could help optimize treatment strategies and improve patient outcomes.

Keywords : bladder cancer, programmed cell death protein 1, prognostic biomarker, immune checkpoint inhibitors, predictive biomarker
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