Systematic analysis of the prognostic value and immunological function of LTBR in cancer

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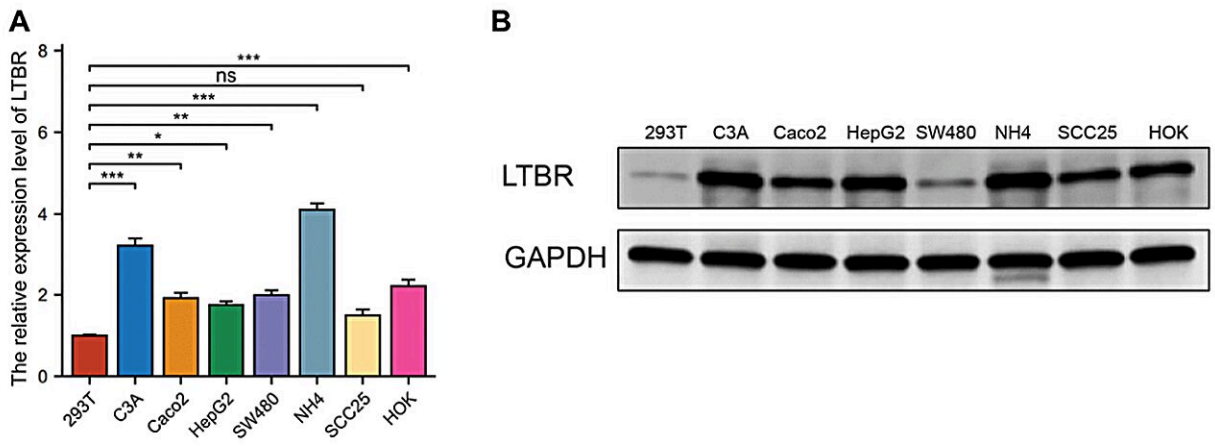

Validation of expression of the LTBR gene. Credit: *Aging* (2024). DOI: 10.18632/aging.205356

A new research paper titled "Systematic analysis of the prognostic value and immunological function of LTBR in human cancer" has been published in *Aging*.

Lymphotoxin beta receptor (LTBR) is a positive T cell proliferation regulator gene. It is closely associated with the tumor immune microenvironment. However, its role in cancer and immunotherapy is unclear.

In this new study, researchers Yinteng Wu, Shijian Zhao, Wenliang Guo, Ying Liu, Marìa Del Mar Requena Mullor, Raquel Alarcòn Rodrìguez, and Ruqiong Wei from The First Affiliated Hospital of Guangxi Medical University, The Eighth Affiliated Hospital of Guangxi Medical University and the University of Almerìa first analyzed the expression level and prognostic value of LTBR in clinical stages, immune subtypes, and molecular subtypes.

Then they examined the correlation between LTBR and immune regulatory genes, immune checkpoint genes, and RNA modification genes. Correlations between LTBR and immune cells, scores, cancer-related functional status, tumor stemness index, mismatch repair (MMR) genes, and DNA methyltransferase were also assessed.

In addition, the team looked at the role of LTBR in DNA methylation, mutational status, tumor mutation burden (TMB), and microsatellite instability (MSI). Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG), and Gene Set Enrichment Analysis (GSEA) were used to explore the role of LTBR in pan-cancer. Finally, they investigated the drugs associated with LTBR.

"In this work, we looked into the expression of LTBR at multiple levels," they summarize.

The expression of LTBR was confirmed using quantitative real-time PCR and Western blot. LTBR is significantly overexpressed in most cancers and is associated with low patient survival. In addition, LTBR expression was strongly correlated with immune cells, score, cancer-

related functional status, tumor stemness index, MMR genes, DNA methyltransferase, DNA methylation, mutational status, TMB, and MSI.

Enrichment analysis revealed that LTBR was associated with apoptosis, necroptosis, and immune-related pathways. Finally, multiple drugs targeting LTBR were identified. LTBR is overexpressed in several tumors and is associated with a poor prognosis. It is related to immune-related genes and immune cell infiltration.

The team concludes, "Notably, we identified LTBR as a potential target for cancer immunotherapy and a marker of immune infiltration and poor prognosis. This study offers new possibilities for the diagnosis and treatment of cancer patients, instilling hope for improved outcomes."

More information: Yinteng Wu et al, Systematic analysis of the prognostic value and immunological function of LTBR in human cancer, *Aging* (2024). DOI: 10.18632/aging.205356

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