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LETTER TO THE EDITOR

New perspectives in prognostication of hepatocellular carcinoma: The role and clinical implications of transient receptor potential family genes

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Abstract

The study titled "Transient receptor potential-related risk model predicts prognosis of hepatocellular carcinoma patients" is a significant contribution to hepatocellular carcinoma (HCC) research, highlighting the role of transient receptor potential (*TRP*) family genes in the disease's progression and prognosis. Utilizing data from The Cancer Genome Atlas database, it establishes a new risk assessment model, emphasizing the interaction of *TRP* genes with tumor proliferation pathways, key metabolic reactions like retinol metabolism, and the tumor immune microenvironment. Notably, the overexpression of the *TRPC1* gene in HCC correlates with poorer patient survival outcomes, suggesting its potential as a prognostic biomarker and a target for personalized therapy, particularly in strategies combining immunotherapy and anti-TRP agents.

Key Words: Hepatocellular carcinoma; Transient receptor potential channels; *TRPC1* gene; Tumor immune microenvironment; Cancer prognosis; Bioinformatics in cancer research

Core Tip: This pivotal study unveils a novel risk assessment model based on transient receptor potential (*TRP*) family genes, offering significant advancements in the prognostication and personalized treatment of hepatocellular carcinoma (HCC). It highlights the crucial role of *TRPC1* gene expression as a prognostic marker linked to patient survival and disease progression, potentially reshaping HCC therapeutic strategies. The findings underscore the importance of *TRP* genes in cancer biology, particularly their integration with tumor immune responses, paving the way for innovative treatments that combine immunotherapy with targeted *TRP* gene inhibition.

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TO THE EDITOR

The study titled "Transient receptor potential-related risk model predicts prognosis of hepatocellular carcinoma patients" marks a significant contribution to the field of hepatocellular carcinoma (HCC) research[1]. Focusing on the role of transient receptor potential (*TRP*) family genes in HCC, it addresses a gap in this area of study. The research introduces a new risk assessment model that not only explores the role of these genes in the prognosis of HCC patients but also emphasizes their interaction with the tumor immune microenvironment, crucial for the early diagnosis and treatment of HCC.

Data from the well-recognized The Cancer Genome Atlas database were used, ensuring the reliability of the study's findings. The application of rigorous statistical methods and bioinformatics tools further enhances the accuracy and validity of the results. By identifying *TRP* genes significantly associated with the prognosis of HCC, the study offers new biomarkers for clinicians, aiding in personalized treatment of the disease.

Notably, the expression of the *TRPC1* gene in HCC is closely linked to reduced overall survival and shorter life expectancy in patients. TRPC1 may promote the onset of liver cancer by modulating tumor proliferation signaling pathways and key metabolic reactions, such as retinol metabolism. Additionally, TRPC1 might further advance liver cancer development by affecting the expression of genes like *ABI2*, *MAPRE1*, *YEATS2*, *MTA3*, *TMEM237*, *MTMR2*, *CCDC6*, *AC069544.2*, and *NCBP2*[2].

The role of TRP family genes in various cancers, particularly their functions in cell signaling, survival, and apoptosis, is garnering increasing attention[3,4]. In liver cancer research, the expression of *TRP* genes is closely related to disease progression and prognosis. Although this study is limited by its retrospective nature using database data, future research could further validate these findings through prospective clinical trials and explore more genes and molecular mechanisms related to HCC.

In summary, this research not only enhances our understanding of HCC but may also facilitate the development of new treatment, especially in the combination of immunotherapy and anti-TRP drugs. The association of *TRP* genes with the tumor immune microenvironment paves the way for future research and may aid in developing novel therapeutic strategies against these molecular targets.

FOOTNOTES

Author contributions: Guan SH and Hu WJ jointly contributed as co-first authors in the analysis and manuscript writing; Wang XY and Gu YX provided critical revisions of the manuscript; Zhou DH conceptualized and supervised the article's development, also contributing to its critical revision; and all authors have read and endorsed the final version of the manuscript.

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