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Short Communication

Beyond Traditional Markers: Exploring a Groundbreaking Immune-Related lncRNA Model for Clear Cell Renal Cell Carcinoma Prognostication

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DESCRIPTION

The incidence and death rates of Clear Cell Renal Cell Carcinoma (ccRCC), which accounts for more than 75% of all kidney malignancies globally [1], are rising, and it is typically identified at an advanced stage [2]. The commonly used Tumor Node Metastasis (TNM) staging method, which estimates the outcomes of ccRCC, is shown to have insufficient predictive value [3]. This would most likely be the outcome of the tumor's heterogeneity and the aetiology' complexity [4].

It is now necessary to uncover appropriate and unique epigenetic variables because prognostic models that combine TNM stage with other values, such as pathogenic factors, clinical factors, and molecular markers, have generated a great deal of attention and been found to have greater predictive value [5]. Long Noncoding RNAs (lncRNAs) are a kind of RNA that are longer than 200 nucleotides but do not have the ability to code for proteins [6].

They often play a role in posttranscriptional regulation, epigenetic control, and the regulation of gene transcription. Growing evidence suggests that lncRNAs play important roles in tumour prognosis and oncogenesis. Immune-related lncRNAs, for example, exert their carcinogenic effects by altering immune responses, including immune activation, immune cell migration, differentiation, and differentiation of tumor-infiltrating immune cells. It has been shown to be related to numerous levels of gene expression in human tumours [7].

Immune cells that infiltrate tumours have recently come to light as a tumour prognostic factor that is related to ccRCC patient prognosis. A potential treatment approach to improve the prognosis of survival in ccRCC patients is immunotherapy. Nevertheless, not all patients respond to immunotherapy in the same way, and it has not yet realized its full potential. To evaluate the host antitumor immune response and investigate the potential mechanism underlying it, additional knowledge must be acquired. Hence, identifying the optimal immune-related lncRNAs as biomarkers for ccRCC patient prognosis prediction and offering hints to design unique immunological therapy regimens are vital and promising. In order to forecast the prognosis of ccRCC patients, a model made up of five immune-related prognostic lncRNAs and clinical factors was developed in this study. To find immune-related differentially expressed lncRNAs, The Cancer Genome Atlas (TCGA) high-throughput sequencing data of ccRCC were examined. After classifying the continuous expression of lncRNAs into categorical values, the prognostic value of lncRNAs for ccRCC was then investigated using univariate Cox proportional hazards regression analysis, Least Absolute Shrinkage and Selection Operator (LASSO) method, and multivariate Cox proportional hazards regression analysis. The categorical values of the expression of five genes were multiplied, along with the Cox coefficients, which were utilized to build a nomogram together with clinical factors, to determine the risk score. The nomogram was then evaluated using a calibration plot and a Time-Dependent Receiver Operating Characteristic (tROC) curve analysis. To increase the persuasive power of the forecast, internal and external validations were carried out. In order to further enhance the immune-related qualities of the optimal lncRNAs, functional enrichment analysis and coexpressed tumor-infiltrating immune cells were investigated. In order to offer a comprehensive perspective of potential transcriptional relationships and disclose a potential regulatory mechanism for the expression of lncRNAs, a regulatory relationship network made up of coexpressed TF genes and the optimal lncRNAs was built. The most prevalent form of kidney cancer is ccRCC, which accounts for 2% of all cancers worldwide and is becoming more common. It has been determined that immunotherapy, such as anti-CTLA-4 and anti-PD-1 antibodies, is a potential treatment for ccRCC.

Just a small percentage of patients, however, exhibit long-lasting improvements, suggesting that an additional mechanism limits the immune response and permits cancer to evade immunosurveillance. As they might control innate and adaptive immunity by modulating immune response genes, lncRNAs have been viewed as an essential component of cancer immunotherapy. The prognosis of cancer patients might be impacted by abnormal expression of lncRNAs, according to growing data. Dysregulated lncRNA expression would affect several biological processes, which would result in oncogenesis.

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CONCLUSION

Constructed a powerful five lncRNA based nomogram to predict 3, 5, and 7-year OS of ccRCC patients after identifying five novel prognostic immune-related lncRNAs through mining publicly available databases. This nomogram was likely used to direct clinicians in decisions regarding clinical diagnosis, prognosis, and treatment. Each lncRNA and the multi-lncRNA signature exhibit immune-related traits that may be used to inform immunotherapy for ccRCC. This information is revealed by functional enrichment analysis and its relationship to immune cells that have invaded the tumour.

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