

A Novel Defined Lactate-related Gene Signature For Predicting The Prognosis Of Liver Cancer

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Background : The large amount of lactic acid produced by glycolysis in the tumor microenvironment was previously thought to be merely a metabolic waste product. However, more and more studies have shown that lactic acid can play a role in promoting tumor progression.

Methods : In this study, We obtained liver cancer data from The Cancer Genome Atlas (TCGA) database and identified 50 lactate-related genes that were differentially expressed between liver cancer and normal liver tissues. Based on these differentially expressed genes (DEGs), all liver cancer cases could be divided into two subtypes

Results : The prognostic value of each Lactate-related gene for survival was evaluated to construct a multigene signature using TCGA cohort. By applying the least absolute shrinkage and selection operator (LASSO) Cox regression method, a 2- gene signature was built and classified all liver cancer patients in the TCGA cohort into a low- or high-risk group. Liver cancer patients in the low-risk group showed significantly higher survival possibilities than those in the high-risk group ($P < 0.001$). Utilizing the median risk score from the TCGA cohort, Liver cancer patients from a Gene Expression Omnibus (GEO) cohort were divided into two risk subgroups, and the low-risk group had increased overall survival (OS) time. Combined with the clinical characteristics, the risk score was found to be an independent factor for predicting the OS of liver cancer patients

Conclusions : lactate-related genes play an important role in tumor progression and can be used to predict the prognosis of HCC patients

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