N6-Methyladenosine

Epigenetic regulations of immune responses are essential for cancer development and growth. As a critical step, comprehensive and rigorous explorations of m6A methylation are important to determine its prognostic significance, tumor microenvironment (TME) infiltration characteristics and underlying relationship with glioblastoma (GBM).

Methods: To evaluate m6A modification patterns in GBM, we conducted unsupervised clustering to determine the expression levels of GBM-related m6A regulatory factors and performed differential analysis to obtain m6A-related genes. Consistent clustering was used to generate m6A regulators cluster A and B. Machine learning algorithms were implemented for identifying TME features and predicting the response of GBM patients receiving immunotherapy.

Results: It is found that the m6A regulatory factor significantly regulates the mutation of GBM and TME. Based on Europe, America, and China data, we established m6Ascore through the m6A model. The model accurately predicted the results of 1206 GBM patients from the discovery cohort. Additionally, a high m6A score was associated with poor prognoses. Significant TME features were found among the different m6A score groups, which demonstrated positive correlations with biological functions (i.e., EMT2) and immune checkpoints.

Conclusions: m6A modification was important to characterize the tumorigenesis and TME infiltration in GBM. The m6Ascore provided GBM patients with valuable and accurate prognosis and prediction of clinical response to various treatment modalities, which could be useful to guide patient treatments [1)].

N6-methyladenosine (m6A) and Long non-coding RNAs (lncRNAs) conduct important biological functions in patients' survival status and the immunotherapeutic response. Here, m6A-related lncRNAs were identified by a co-expression method. Univariate and multivariate Cox regression together with LASSO were applied to establish the risk model. Kaplan-Meier and ROC analysis was applied to evaluate the prediction power of this risk model. Finally, the related immune profiling and chemical sensitivity targets were also investigated. The risk model holding three m6A-related lncRNAs was confirmed as an independent predictor for the prognosis. Furthermore, we found the risk model based on m6A-related lncRNAs is associated with the immune status, immunosuppressive biomarkers, and chemo-sensitivity in Glioblastoma patients. The RP11-552D4.1 is found to facilitate neuronal proliferation. This risk model consisted of m6A-related lncRNAs may be available for clinical interventions in Glioblastoma patients [2)].

1)
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2)
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