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Research article

Development of metastasis-associated seven gene signature for predicting lung adenocarcinoma prognosis using single-cell RNA sequencing data

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Abstract: Metastasis is the primary cause of lung adenocarcinoma (LUAD)-related death. This study evaluated the metastasis-associated genes (MAGs) in single-cell RNA sequencing (scRNA-seq) data from LUAD tissues and developed a MAG signature to predict overall survival (OS) of LUAD patients. The LUAD scRNA-seq data was downloaded from the Gene Expression Omnibus (GEO) Database and MAGs were identified from LUAD scRNA-seq data. The LUAD transcriptomic and clinical data were obtained from The Cancer Genome Atlas (TCGA). Cox and LASSO regression analyses were performed to identify differentially expressed MAGs (DEMAGs) with prognostic value that were then used to construct a MAG signature and MAG-nomogram model. Finally, a functional enrichment analysis was performed via Gene Set Enrichment Analysis (GSEA). 414 MAGs and 22 prognostic DEMAGs were revealed in the study. Multivariate Cox proportional hazards regression analysis was utilized to construct a 7-MAG signature for predicting the OS of LUAD patients. Patients with high risk scores had a significantly worse OS than those with low risk scores in the training group (n = 236), and the 7-MAG signature was successfully confirmed in the testing group (n = 232) and the entire TCGA-LUAD cohort (n = 468). Furthermore, univariate and multivariate Cox regression suggested that the 7-MAG signature was an independent prognostic indicator. Additionally, based on the 7-MAG signature, a nomogram was established that could more intuitively help to predict the OS of LUAD patients. The GSEA revealed the underlying molecular mechanisms of the 7-MAG signature in LUAD metastasis. In conclusion, a 7-MAG signature was developed based on LUAD scRNA-seq data that could effectively predict LUAD patient prognosis and provide novel insights for therapeutic targets and the potential molecular mechanism of metastatic LUAD.

Keywords: lung cancer; metastasis; single-cell RNA sequencing; prognosis; gene signature



Supplementary

Figure S1. Prognostic significance of metastatic-associated genes (MAGs) in The Cancer Genome Atlas - Lung Adenocarcinoma (TCGA-LUAD) dataset. The univariate Cox regression analysis shows the 95% confidence interval (CI) and hazard ratio (HR) for each metastatic-associated gene.



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