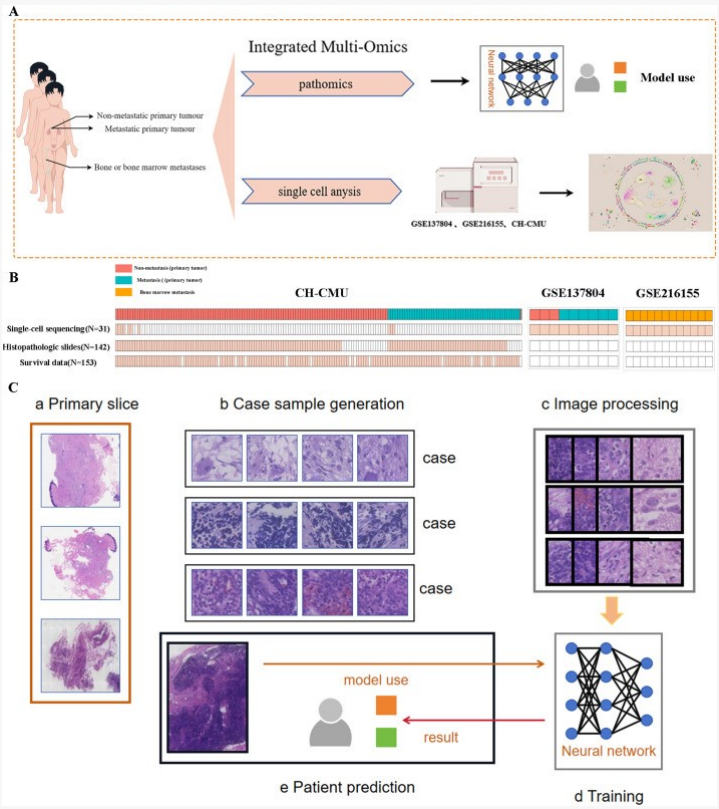
AI-Driven Advancements in Neuroblastoma Diagnosis and Bone/Bone Marrow Metastasis Prediction

Groundbreaking Study Unveils Key Mechanisms in Neuroblastoma Bone and Bone Marrow Metastasis

CHINA, March 11, 2025 /EINPresswire.com/ -- Neuroblastoma (NB), the most prevalent extracranial solid tumor among children, is characterized by a high rate of metastasis. The pathogenesis of NB with bone or bone marrow metastasis (NB-BBM) and its complex immune microenvironment remain poorly understood, posing challenges for effective risk prediction for BBM and limiting therapeutic strategies.



(A) Experimental scheme for investigating the mechanisms underlying NB-BBM. (B) The sample overviews available for single-cell, whole genome sequencing, pathohistological, and survival data. (C) Workflow of a deep learning model for a multi-instance learn

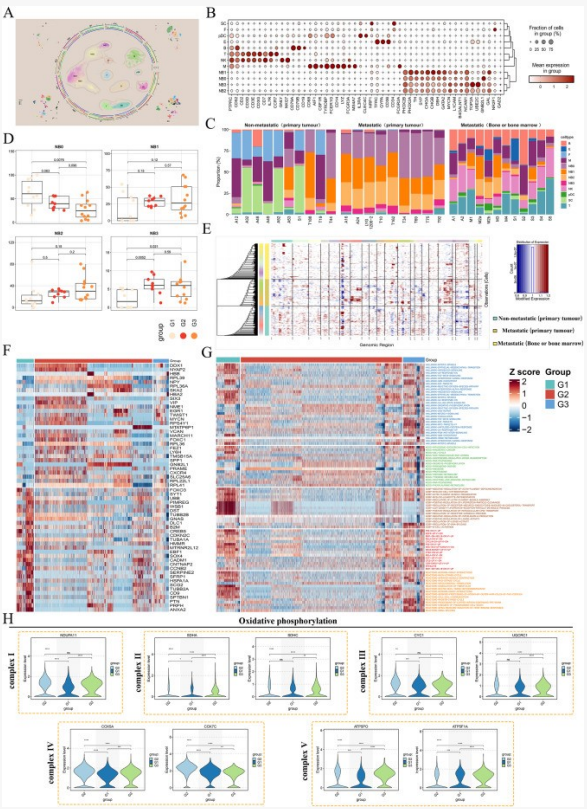
This research, published in the Genes & Diseases journal by a team from The Children's Hospital of Chongqing Medical University, highlights key genomic and single-cell transcriptomic alterations in NB-BBM, underscoring the significance of predictive pathology for NB-BBM and its role in understanding tumor onset, progression, and heterogeneity.

The researchers used a Swin-Transformer deep learning model to analyze 142 paraffin-embedded hematoxylin-eosin-stained tumor section images to predict NB-BBM occurrence, achieving a classification accuracy exceeding 85%. In parallel, single-cell transcriptomics identified a tumor cell subpopulation (NB3) and two tumor-associated macrophage (TAM) subpopulations (SPP1+ TAMs and IGHM+ TAMs) closely associated with BBM progression. Interestingly, findings reveal that oxidative phosphorylation (OXPHOS) also plays a crucial role in BBM development.

Additionally, this study highlighted transketolase (TKT) as a crucial metabolic molecule linked to BBM. The researchers showed that the TKT gene was strongly associated with the clinical features of NB patients, especially in the BBM group. Functional experiments validated TKT's involvement in malignant behavior, while pathway enrichment analysis showed correlations between high TKT expression and cell cycle activity.

Moreover, expression analysis of immune checkpoint genes CD274, LAG3, and TIGIT revealed their significant upregulation in NB-BBM, suggesting potential targets for antibody-based immunotherapies. Furthermore, immunohistochemical validation demonstrated a pronounced expression of PD-L1 in NB-BBM, indicating its potential as a biomarker.

Although this research provides a predictive model for NB-BBM risk assessment, it has certain limitations, including the need for multicenter validation of the predictive model and prospective studies to confirm clinical utility. Despite these challenges, this study offers a pathodiagnostic prediction for the risk of NB-BBM, enhances other imaging diagnoses, and elucidates the cellular heterogeneity of initial, progressive, and distant metastatic sites in NB.



(A) UMAP of single-cell RNA sequencing data for all cells from 31 neuroblastoma patients. (B) Expression of typical cell type marker genes in 12 clusters. (C) The percentage of each of the 12 cell subpopulations in the neuroblastoma patient samples. (D)

Reference

Title of the original paper - Integrated multi-omics characterization of neuroblastoma with bone or bone marrow metastasis

Journal: Genes & Diseases

Genes & Diseases is a journal for molecular and translational medicine. The journal primarily focuses on publishing investigations on the molecular bases and experimental therapeutics of human diseases. Publication formats include full length research article, review article, short communication, correspondence, perspectives, commentary, views on news, and research watch.

DOI: https://doi.org/10.1016/j.gendis.2024.101511

Funding Information:

Key Project of the National Key R&D Plan “Research on Prevention and Control of Major Chronic Non-Communicable Diseases” (China)
Ministry of Science and Technology of the People's Republic of China
National Key R&D Program of China (No. 2018YFC1313000, 2018YFC1313004)

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Scopus CiteScore: 7.3 | Impact Factor: 6.9

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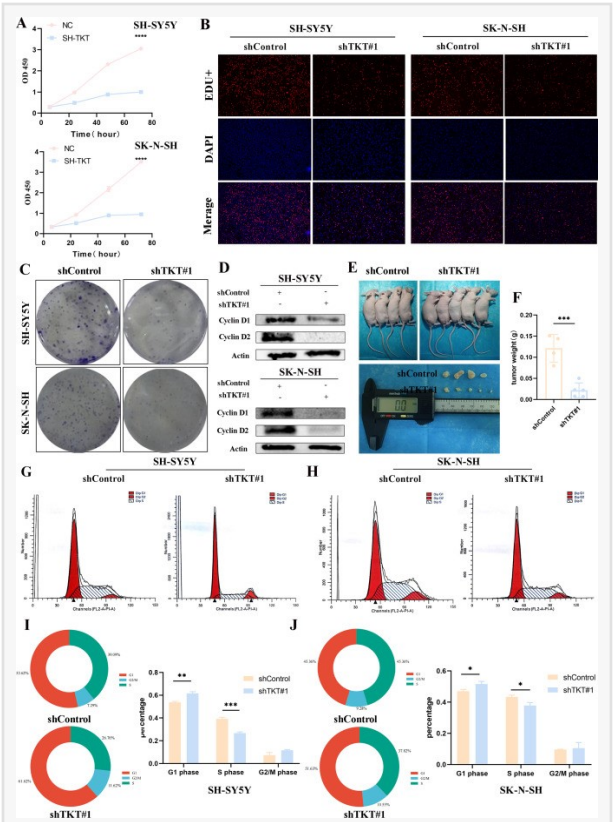

(A) The growth rate of neuroblastoma cells was significantly reduced after TKT knockdown as detected by the CCK-8 assay. (B) 5-Ethyl-2-deoxyuridine (EdU) assay showed that down-regulation of TKT reduced the growth of neuroblastoma cells. (C) Colony format

Print ISSN: 2352-4820
eISSN: 2352-3042
CN: 50-1221/R

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