Clinica Chimica Acta 578 (2026) 120568

Contents lists available at ScienceDirect

Clinica Chimica Acta

journal homepage: www.elsevier.com/locate/cca

Ganglioside profiling in neuroblastoma

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ARTICLE INFO

Keywords:
Analytical techniques
Biomarker discovery
Drug development
Gangliosides
Neuroblastoma
Omics integration

ABSTRACT

Gangliosides play important roles in neuroblastoma research through their functions in adhesion, proliferation, and signalling. Researchers have quantified neuroblastoma cells to understand their importance and identify potential diagnostic targets. This study analyses methods for neuroblastoma cell ganglioside quantification. Scientists use techniques including mass spectrometry (MS), nuclear magnetic resonance (NMR) spectroscopy, fluorescence imaging, immunoassays, and advanced approaches like multidimensional chromatography and imaging mass spectrometry. These advances have made ganglioside analysis more sensitive and comprehensive. Researchers perform ganglioside analysis for biomarker discovery, metabolism investigation, and therapeutic agent development. Although progress has been made, challenges remain in standardizing methods, resolving sample complexity, and integrating multi-omics data. Researchers must collaborate across disciplines to overcome these challenges. Ganglioside analysis provides insights into neuroblastoma biology. By leveraging analytical advancements and addressing limitations, researchers can improve pediatric cancer treatment.

1. Introduction

Neuroblastoma is an aggressive pediatric cancer that is difficult to manage [1,2]. Malignant neoplasms develop from the adrenal sympathetic ganglia, with diseases characterized as mysterious and capricious due to their clinical heterogeneity. After central neurocytoma, neuroblastoma is the second most common extracerebral malignant tumor in children from birth to six months [3–6]. About 10 per million children under 15 years are affected, mostly in children under two. Diagnosis typically occurs in the first year, with over 90 % of cases detected before age five [7,8]. Despite improved treatments, only 30–40 % of children with high-risk neuroblastoma survive long-term [9–13]. Studies are investigating innovative approaches targeting genetic and molecular abnormalities in neuroblastoma cells [14], aiming to enhance outcomes in high-risk patients [15]. The targeting of epigenetic regulators has gained attention, as most high-risk neuroblastomas remain therapy-resistant. Epigenetic changes influence neuroblastic tumor development, and this strategy aims to address aberrant gene expression in high-risk neuroblastoma [16,17]. The tumor develops from the neural crest-derived sympathetic nervous system, requiring individualized treatment approaches [18]. Despite treatment advances, the prognosis for high-risk neuroblastoma remains poor, necessitating further research into molecular pathways driving disease progression [19,20].

One such molecular component crucial in neuroblastoma

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https://doi.org/10.1016/j.cca.2025.120568
Received 6 June 2025; Received in revised form 20 August 2025; Accepted 21 August 2025
Available online 24 August 2025