Review Cell Signal. 2024 Sep 3:124:111380. doi: 10.1016/j.cellsig.2024.111380.

Online ahead of print.

Unveiling the role of RNA methylation in glioma: Mechanisms, prognostic biomarkers, and therapeutic targets

Qichen Xu [1], Chunsong Yang [1], Liyun Wang [1], Jing Zhou [2]

Affiliations

PMID: 39236835 DOI: 10.1016/j.cellsig.2024.111380

Abstract

Gliomas, the most prevalent malignant brain tumors in the central nervous system, are marked by rapid growth, high recurrence rates, and poor prognosis. Glioblastoma (GBM) stands out as the most aggressive subtype, characterized by significant heterogeneity. The etiology of gliomas remains elusive. RNA modifications, particularly reversible methylation, play a crucial role in regulating transcription and translation throughout the RNA lifecycle. Increasing evidence highlights the prevalence of RNA methylation in primary central nervous system malignancies, underscoring its pivotal role in glioma pathogenesis. This review focuses on recent findings regarding changes in RNA methylation expression and their effects on glioma development and progression, including N6-methyladenosine (m6A), 5-methylcytosine (m5C), N1-methyladenosine (m1A), and N7-methylguanosine (m7G). Given the extensive roles of RNA methylation in gliomas, the potential of RNA methylation-related regulators as prognostic markers and therapeutic targets was also explored, aiming to enhance clinical management and improve patient outcomes.

Keywords: Clinical applications; Expression; Glioma; Mechanisms; RNA methylation.