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The performance of Machine Learning for prediction of H3K27M Mutation in Midline Gliomas; A Systematic Review and Meta-Analysis

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Abstract

Background: Diffuse midline gliomas (DMGs) encompass a set of tumors, and those tumors with H3K27M mutation carry a poor prognosis. In recent years, machine learning (ML)-based radiomics have shown promising results in predicting gene mutation status non-invasively. Therefore, this study aims to comprehensively evaluate the diagnostic performance of ML-based magnetic resonance imaging (MRI) radiomics in predicting H3K27M mutation status in DMG patients.

Methods: A systematic search was conducted using relevant keywords in PubMed/Medline, Scopus, Embase, and Web of Science from inception to May 2023. Original studies evaluating the diagnostic performance of ML models in predicting H3K27M mutation status in DMGs were enrolled. Quality assessment of the enrolled studies was conducted using QUADAS-2. Data were analyzed using STATA version 17.0 to calculate pooled sensitivity, specificity, positive (PLR) and negative likelihood ratio (NLR), diagnostic score, and diagnostic odds ratio (DOR).

Results: A total of 13 studies, including 12 retrospectives and one both retrospective and prospective study, enrolled 1510 (male=777) DMG patients. Six studies underwent meta-analysis which showed a pooled sensitivity, specificity, PLR, NLR, diagnostic score, and DOR of 0.91 (95% CI 0.77-0.97), 0.81 (95% CI 0.73-0.88), 4.86 (95% CI 3.25-7.24), 0.11 (95% CI 0.04-0.29), 3.75 (95% CI 2.62-4.88), and 42.61 (95% CI 13.77-131.87), respectively.

Conclusion: Non-invasive prediction of H3K27M mutation status in patients with DMGs using MRI radiomics is a promising tool with good diagnostic performance. However, the pooled metrics had a wide confidence interval, which required further studies to enhance ML algorithms' accuracy and facilitate their integration into daily clinical practice.

Keywords: Glioma; Machine learning; Magnetic resonance imaging; Prognosis.

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