

Summary

Introduction

Gliomas are the most common primary tumors of the central nervous system, characterized by significant histological and genetic heterogeneity. In recent years, genetic profiling has played an increasing role in the diagnosis and classification of these tumors, allowing for more precise disease prognosis and therapy selection. However, a full molecular analysis requires tissue material, which can be obtained through biopsy or neurosurgical intervention. These procedures can be risky and, in some cases, impossible to perform. Meanwhile, magnetic resonance imaging (MRI) is a standard non-invasive procedure performed on all patients suspected of having gliomas. Advanced MRI techniques, such as perfusion MRI (DSC-MRI) and diffusion-weighted imaging (DWI/ADC), can provide valuable information for predicting molecular characteristics. Identifying correlations between MRI parameters and genetic mutations presents a promising approach for supporting early diagnosis and personalized treatment.

Study Objective

This study aimed to assess the usefulness of MRI imaging parameters in predicting the genetic characteristics of gliomas, particularly *IDH1* mutation, *MGMT* methylation, *EGFR* amplification, *CDKN2A* deletion, and the presence of the pathogenic *TERT* variant.

Methodology

The analysis included data from three publications evaluating the correlations between perfusion and diffusion MRI parameters and the molecular status of gliomas. DSC-MRI was used to assess perfusion, while DWI/ADC was applied to analyze tumor cell density. MRI findings were compared with histopathological and genetic data obtained from tissue-based studies.

Results

Significant associations between imaging parameters and molecular features of gliomas were observed. IDH1-wildtype gliomas exhibited higher rCBV and rCBF values and lower ADC values, indicating increased cellular density and intense angiogenesis. The *IDH1* mutation and *MGMT* methylation were associated with lower perfusion values and higher ADC values. In contrast, *EGFR* amplification and *CDKN2A* deletion correlated with intense tumor vascularization, higher perfusion, and lower ADC values. The pathogenic *TERT* variant was linked to lower diffusion coefficient values and strong contrast enhancement, suggesting its role in the aggressive tumor phenotype.

Conclusions

Advanced MRI techniques may serve as valuable tools for the non-invasive assessment of glioma molecular characteristics. The correlation between perfusion and diffusion parameters and the tumor's genetic profile suggests the potential use of MRI as a method to support early diagnosis and personalized treatment for patients. In the future, further research in radiogenomics may enable even more accurate prediction of genetic mutations based on imaging, potentially reducing the need for invasive diagnostic procedures.