Correlation between Expression of EZH2 and p16 in Glial Tumours: A Cross-Sectional Observational Study

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Abstract

Background: Gliomas are among the most common primary malignant CNS tumours, with WHO 2021 classification shifting diagnosis toward integrated molecular criteria. EZH2, a chromatin-modifying oncogenic protein, epigenetically silences p16 (CDKN2A), a key tumour suppressor, however their combined expression across glial tumour subtypes remains underexplored. This study assessed EZH2 and p16 immunohistochemical expression in glial tumours and their correlation with clinicopathological parameters at a tertiary care centre.

Methods: This hospital-based cross-sectional study included 57 histopathologically confirmed glioma cases. Immunohistochemistry for EZH2 and p16 was performed and correlated with age, sex, histological subtype, WHO grade, and overall survival.

Results: Mean age was 42.6±15.6 years with male predominance (1.6:1). Glioblastoma was the most common (54.4%). High EZH2 expression was seen in 28.1% of cases, of cases, while p16 loss was observed in 63.2%. Both markers correlated significantly with histological subtype and grade (p=0.006/0.029 for diagnosis; p=0.007/0.011 for grade). Neither marker showed a significant association with age or gender. EZH2 and p16 showed weak positive correlation (ρ=0.234, p=0.079). High EZH2 was associated with poorer overall survival (p=0.007); p16 loss showed inferior median survival (10 months).

Conclusion: EZH2 overexpression and p16 loss were associated with higher tumour grade, aggressive clinicopathological features, and poorer survival outcomes in glial tumours. Together, these markers hold promise as complementary adjuncts in glioma diagnosis, grading, and prognostication, particularly in resource-limited settings where access to molecular testing is limited.

Keywords

Central nervous system, glioma, p16, ezh2, immunohistochemistry.