From Diagnosis to Risk Stratification: Exploring the Dual Role of SSTR2A and p16 Immunohistochemistry in Meningiomas

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Abstract

Background: Meningiomas display considerable morphological diversity and a variable clinical course. With the increasing integration of ancillary techniques into neuropathology, immunohistochemical markers may provide information beyond conventional morphology. SSTR2A is characteristically expressed in meningiomas and can support meningothelial differentiation, while p16 is a cell-cycle regulatory protein encoded by *CDKN2A*, a gene implicated in aggressive meningioma biology. The present study assessed SSTR2A expression in meningiomas and explored the pattern of p16 expression across different CNS WHO grades.

Methods: This cross-sectional observational study comprised 50 histopathologically confirmed meningiomas. SSTR2A immunohistochemistry was evaluated in all cases and correlated with histological subtype and CNS WHO grade. Subsequently, p16 immunohistochemistry was performed in a selected subset of 17 tumours, including 10 grade 1 and 7 grade 2/3 meningiomas. Tumour-cell p16 expression was classified as retained or lost and compared between lower- and higher-grade tumours.

Results: The study included 40 (80%) grade 1, 8 (16%) grade 2 and 2 (4%) grade 3 meningiomas. High SSTR2A expression was identified in 37/50 (74%) cases, with no significant association with CNS WHO grade (p=0.424) or histological subtype (p=0.936). All 10 grade 1 tumours assessed for p16 demonstrated retained expression. In comparison, among the 7 grade 2/3 tumours, 3 (42.9%) retained p16 expression, whereas 4 (57.1%) showed loss of expression.

Conclusion: Frequent SSTR2A expression across meningiomas supports its application as an ancillary marker of meningothelial differentiation. In contrast, p16 loss was observed only among higher-grade tumours in the evaluated subset, suggesting an association with higher histological grade. These findings highlight complementary roles for SSTR2A and p16 in the diagnostic and biological characterization of meningiomas. Further studies incorporating *CDKN2A/B* molecular analysis and clinical outcome are required to establish the prognostic significance of p16 loss.

Keywords

Meningioma, SSTR2A, p16, *CDKN2A*, immunohistochemistry, CNS WHO grade.