



Value of magnetic resonance imaging in predicting BRAF mutation in craniopharyngiomas

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Craniopharyngiomas, according to the World Health Organization (WHO) definition, are benign, partially cystic epithelial tumors of the sellar region, presumably derived from Rathke pouch epithelium and designated as grade I lesion of the central nervous system. They have been described as histologically benign tumors that behaves in a malignant manner. This “malignancy” is due to the vicinity to highly eloquent brain structures, its unpredictable biologic behavior, and its high local recurrence rates.

There is a well-recognized bimodal age distribution, with the first peak occurring at school age (5–14 years) and a second occurring in middle to late adulthood (45–65 years). The histologic diagnosis also varies with age, with the papillary form of craniopharyngioma being seen almost exclusively in the adult group, whereas adamantinomatous tumors can be found in both groups. No environmental or genetic risk factors have been identified, and craniopharyngioma is best thought of as a sporadic condition.

The most useful imaging modality for the diagnosis of craniopharyngioma is magnetic resonance imaging (MRI), although computed tomography (CT) still has a role, particularly for assessing calcification (which can reliably differentiate craniopharyngioma from other suprasellar pathologies) and detailed evaluation of skull base anatomy for surgical planning. The MRI usually demonstrates a heterogeneous mass. Solid components are usually isointense in T1-weighted sequence and variable in T2-weighted sequence and enhance with gadolinium contrast. Cystic components often demonstrate ring enhancement, whereas the contents may vary in appearance depending on the protein or blood breakdown products. There may even be fluid levels within individual cysts or heterogeneity

in signal characteristics between different cysts in the same tumor.

The understanding of the molecular pathways involved in craniopharyngioma is still matter of study. Mutations of the *CTNNB1* gene, encoding b-catenin, have been described in adamantinomatous craniopharyngioma; accumulations of nuclear b-catenin, consistent with activation of the WNT pathway, are identified in scattered cells within this craniopharyngioma type (1). By contrast, the BRAF C600E mutation is found in up to 100% of papillary craniopharyngiomas (2).

In a recent publication (3), Dr. Yue and his colleagues analyzed retrospectively their cases of adult craniopharyngiomas with the aim to verify any possible correlation between the mutation of BRAF and MRI characteristics.

Fifty-two patients with craniopharyngioma were included in this retrospective study. In 8 of these 52 cases, laboratory histological examination has shown the BRAF V600E mutation. *CTNNB1* mutation, another common mutation in craniopharyngioma, was found in 25 tumors in the BRAF wild-type (WT) group.

A comparison of findings between the BRAF and WT group have showed some significant differences; among them we should outline that BRAF-mutated craniopharyngiomas tended to be suprasellar ($P < 0.001$), whereas BRAF WT present mainly intrasellar extension. Other important characteristics: BRAF mutated craniopharyngiomas are significantly spherical, predominantly solid, and homogeneously enhancing. It was also noticed that patients with these tumors tended to have a thickened pituitary stalk. In this study, authors concluded that when at least 3 of these 5 features were present a tumor might be identified as BRAF

mutated with a sensitivity of 1.00 and a specificity of 0.91.

Some observations about this study should be outlined, among them, we should underline that the number of BRAF mutated patients (8 cases) is small, but still, it begins a range of brilliant ideas for a non-invasive diagnosis of BRAF mutation in craniopharyngiomas, which should be further analyzed. Second point is that the population presented is composed only by adult; in light of the craniopharyngioma incidence peak in adolescence, there should be another study composed only of pediatric population, considering that they may have a different pattern. A limitation of the study is presented by the retrospective form; a prospective study could be performed to avoid some of the possible confounding factors. We found very interesting the findings of this clinical article and encouraging for further research. It could be fascinating to perform similar studies for other lesions which present a similar genetic pattern in term of mutation like pituitary adenoma, Rathke cleft cyst, and germ cell tumor.

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Footnote

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