received adjuvant chemotherapy and/or immunotherapy, specifically ipilimumab and nivolumab (n=6) and temozolomide (n=1). Radiographic recurrence was observed in 7 (63.6%) cases at a median 11 (IQR: 3.5-14) months postoperatively. Median survival was 24 months (IQR: 4-103). Conclusions: Findins from this case series will assist in prognostication for PMN-CNS. Further multicenter international case series are needed to better understand these very rare neoplasms.

P.139

Predicting pituitary gland location during endoscopic endonasal surgery using machine learning model

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Background: Identifying the pituitary gland during surgery for pituitary neuroendocrine tumors (PitNET) is crucial for preserving gland tissue and reducing postoperative hormonal dysfunction. This study aimed to develop and validate a machine learning (ML) tool to identify the pituitary gland during endoscopic endonasal surgery. Methods: Anonymized surgical videos from PitNET resections were trimmed to key phases, starting after dura opening and ending before skull base reconstruction. Frames were manually annotated to delineate the pituitary gland's location. The ML model's performance was evaluated using a single hold-out set method. Results: A total of 2316 frames from 52 videos were annotated, with 60%, 20%, and 20% allocated to training, validating, and testing the ML model, respectively. Performance metrics were as follows: accuracy of 97.8%, specificity of 98.7%, recall of 27%, precision of 18.6%, and an F1-score of 0.22. Conclusions: This study highlights the feasibility of using ML to identify the pituitary gland in PitNET surgeries. While the model is highly accurate in distinguishing gland from non-gland tissue, its low precision indicates a propensity to misclassify adjacent background tissue as pituitary gland.Further refinements could enhance its precision, making it a valuable tool for improving intraoperative anatomical recognition and postoperative hormonal outcomes.

P.141

Spontaneous resolution of a left temporal extra-axial lesion: case report

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Background: Meningiomas are the most common intracranial extra-axial lesion. Reports of meningioma regression exist, often in the context of known hormonal or vascular fluctuations, though very few describe complete resolution. Though rare, extra-axial mimics such as lymphoma and chloroma may also spontaneously regress. Methods: Electronic medical records were used to access patient information in accordance with our local ethics review board. Results: A 29-year-old male presenting with new onset seizures was found to have a 22.7 x 26.6 mm left temporal extra-axial lesion, radiologically consistent with meningioma. Due to wait times and patient preference, repeat preoperative imaging was not available prior to surgical resection 13 months later, though an interim CT had confirmed persistence of the tumour's size 1 month after diagnosis. Decision was made to proceed with resection; however, intraoperatively, no lesion was identified. Post-operative imaging demonstrated complete disappearance of the lesion, and follow-up imaging has shown no recurrence. Conclusions: This case highlights the possibility of spontaneous resolution of extra-axial lesions and emphasizes the importance of serial imaging prior to resection.

P.142

Development and validation of a molecular classifier of meningiomas

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Background: Meningiomas exhibit considerable heterogeneity. We previously identified four distinct molecular groups (*immunogenic, NF2-wildtype, hypermetabolic, proliferative)* which address much of this heterogeneity. Despite their utility, the stochasticity of clustering methods and the requirement of multi-omics data limits the potential for classifying cases in the clinical setting. Methods: Using an international cohort of 1698 meningiomas, we constructed and validated a machine learning-based molecular classifier using DNA methylation alone. Original and newly-predicted molecular groups were compared using DNA methylation, RNA sequencing, whole exome sequencing, and clinical outcomes. Results: Group-specific outcomes in the validation cohort were nearly identical to those originally described, with median PFS of 7.4 (4.9-Inf) years in *hypermetabolic* tumors and 2.5 (2.3-5.3) years in *proliferative* tumors (not reached in the other groups). Predicted *NF2-wildtype* cases had no *NF2* mutations, and 51.4% had others mutations previously described in this group. RNA pathway analysis revealed upregulation of immune-related pathways in the *immunogenic* group, metabolic pathways in the *hypermetabolic* group and cell-cycle programs in the *proliferative* group. Bulk deconvolution similarly revealed enrichment of macrophages in *immunogenic* tumours and neoplastic cells in *hypermetabolic/proliferative* tumours. Conclusions: Our DNA methylation-based classifier faithfully recapitulates the biology and outcomes of the original molecular groups allowing for their widespread clinical implementation.

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