contrast from hemorrhage. We sought to align the post EVT imaging practices with those after intravenous thrombolysis Methods: We reviewed the EMR records for all EVT patients from Jan 1, 2019 to Dec 31, 2021. We assessed quantity of CT within 24h of EVT, quantity of MRIs performed, and indications listed. We then undertook an educational program targeting stakeholders. The objective was to transition to MRI at 24h for imaging post EVT. Exceptions included neurologic change, need for antiplatelet infusion, or intraoperative complications. Results: Post intervention, a significant reduction in CT within 24h (-28%, P=0.01) and increase in MRIs (+42%, P<0.00). CT within 24h per patient dropped by 50% (1.12 pre vs 0.57 post). Radiation dose per patient dropped by 49%. Average imaging costs increased by 17%, and the number of transfers off unit for imaging increased by 11%. Good functional outcome dropped from 44% preintervention to 34% postintervention (P=0.06). Conclusions: This represents the first systematic evaluation of post EVT imaging in a single center. We demonstrate successful behavior changes for post EVT imaging.

NEUROSURGERY (CNSS)

F.1

Oscillatory network markers of subcallosal cingulate deep brain stimulation for depression

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doi: 10.1017/cjn.2024.103

Background: Identifying functional biomarkers related to treatment success can aid in optimizing therapy and provide a better understanding of the neural mechanisms of treatment-resistant depression (TRD) and subcallosal cingulate deep brain stimulation (SCC-DBS). Methods: Magnetoencephalography data were obtained from 16 individuals with SCC-DBS for TRD and 25 healthy subjects. We identified region-specific oscillatory modulations that both (i) discriminate individuals with TRD (SCC-DBS OFF) from healthy controls and (ii) discriminate responders from non-responders (SCC-DBS ON). The effects of stimulation intensity and frequency were also explored. Results: Discriminative regions that differentiated responders from non-responders based on modulations of increased alpha (8-12 Hz) and decreased gamma (32-116 Hz) power included nodes of the default mode, central executive, and somatomotor networks, Broca's area, and lingual gyrus. Furthermore, low stimulation frequency had stronger effects on oscillatory modulation. Conclusions: The identified functional biomarkers implicate modulations of TRD-related activity in brain regions involved in emotional control/processing, motor control, and interactions between speech, vision, and memory – all implicated in depression. These electrophysiological biomarkers have the potential to be used as functional proxies for therapy optimization. Additional stimulation parameter analyses revealed that oscillatory modulations are strengthened by increasing stimulation intensity or reducing frequency, which may benefit SCC-DBS non-responders.

F.2

Comprehensively mapping transcriptionally relevant histone modifications in aggressive meningioma leads to novel biologic insights and therapeutic vulnerabilities

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doi: 10.1017/cjn.2024.104

Background: We recently identified four molecular subgroups of meningioma with distinct biology and outcomes. While two (MG3/MG4) are associated with poor outcome, they display divergent transcriptional profiles (enriched in metabolic and cell cycling pathways, respectively) and therapeutic vulnerabilities (MG3 has no clear treatment target). We sought to understand drivers of these key differences at a chromatin level. Methods: We profiled MG3/MG4 meningiomas for common histone marks H3K27me3, H3K27Ac, H3K4me1, H3K4me3, H3K9me3, and H3K36me3. Multiple computational approaches were used to compare MG3 and MG4 tumours including superenhancer ranking, differential binding analysis, and unsupervised clustering. Results: Our cohort includes 11-20 meningiomas per histone mark. Clustering revealed striking separation of subgroups based on multiple histone marks, particularly H3K36me3. FOXC1, a known driver of the epithelial to mesenchymal transition, was identified as a recurrent superenhancer in both groups, whereas MG3-specific superenhancers mapped to immune regulatory networks. Integrated differential binding analysis confirmed an immune-rich microenvironment in MG3 tumours driven by multiple histone marks, suggesting a role for targeting novel immune checkpoint genes CD84 and CD48. Conclusions: This study is the first to apply integrated analysis of multiple histone modifications to aggressive meningioma. We further characterize MG3 tumours by identifying an epigenetically-driven immune phenotype and propose novel treatment targets.

F.3

Multicentre prospective validation of integrated molecular classification of meningiomas and prediction of recurrence risk using DNA methylation

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doi: 10.1017/cjn.2024.105

Background: Meningiomas have significant heterogeneity between patients, making prognostication challenging. For this