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

*IE Harmsen (Edmonton)* M Scherer (Toronto) N Samuel (Toronto) GJ Elias (Toronto) J Germann (Toronto) A Boutet (Toronto) P Giacobbe (Toronto) NC Rowland (Charleston) L Milosevic (Toronto) AM Lozano (Toronto)*

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

*AP Landry (Toronto)* V Patil (Toronto) JZ Wang (Toronto) F Nassiri (Toronto) G Zadeh (Toronto)*

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

*JZ Wang (Toronto)* V Patil (Toronto) AP Landry (Toronto) C Gui (Toronto) A Ajisebutu (Toronto) C Wilson (Tulsa) A Cohen Gadol (Bloomington) A Rebchuk (Vancouver) S Makarenko (Vancouver) S Yip (Vancouver) K Aldape (Bethesda) F Nassiri (Toronto) G Zadeh (Toronto)*

doi: 10.1017/cjn.2024.105

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

study, we prospectively validate the prognostic capabilities of a DNA methylation-based predictor and multiomic molecular groups (MG) of meningiomas. Methods: DNA methylation profiles were generated using the Illumina EPICarray. MG were assigned as previously published. Performance of our methylation-based predictor and MG were compared with WHO grade using generalized boosted regression modeling by generating time-dependent receiver operating characteristic (ROC) curves and computing area under the ROC curves (AUCs) along with their 95% confidence interval using bootstrap resampling. Results: 295 meningiomas treated from 2018-2021 were included. Methylation-defined high-risk meningiomas had significantly poorer PFS and OS compared to low-risk cases ($p<0.0001$). Methylation risk increased with higher WHO grade and MG. Higher methylome risk (HR 4.89, 95%CI 2.02-11.82) and proliferative MG (HR 4.11, 95%CI 1.29-13.06) were associated with significantly worse PFS independent of WHO grade, extent of resection, and adjuvant RT. Both methylome-risk and MG classification predicted 3- and 5-year PFS and OS more accurately than WHO grade alone ($\Delta AUC=0.10-0.23$). 42 cases were prescribed adjuvant RT prospectively although RT did not significantly improve PFS in high-risk cases ($p=0.41$). Conclusions: Molecular profiling outperforms conventional WHO grading for prognostication in an independent, prospectively collected cohort of meningiomas.

## F.4

### Anatomical assessment and comparative analysis of ventricular access points in pterional approach: a cadaveric study

*U Cikla (madison)* MK Baskaya (madison)*

doi: 10.1017/cjn.2024.106

Background: In early-stage transsylvian aneurysm surgery, achieving brain relaxation is crucial for the safe exposure of aneurysms; however, in cases of tight, hemorrhagic brains, ventricular drainage is often required. Although Paine/Samson initially proposed a ventricular access point in the frontal horn of the lateral ventricle, and numerous points and techniques have been described since, their consistency and success rates have not undergone rigorous evaluation through comparative cadaveric anatomical studies. Methods: We injected 2 cc agar-agar solutions with distinct colors into the lateral ventricles of twelve cadaveric brains, utilizing four described points, followed by refrigeration at 4°C for one hour for each injection. Next, the brains were sectioned in the coronal plane at 2 cm intervals for evaluation. We assessed the efficacy of the injections in reaching the ventricles and measured the ventricular dimensions, in addition to calculating the Evans' index for each brain. Results: Injections at Paine/Samson's point achieved a 100% success rate, followed by Hyunn's point with a 91.6% success rate. The success rates at Temporal point and Park point were 83.3% and 58.3%, respectively. Conclusions: We emphasize the significance of direct ventricle puncture technique and our findings indicate that the classical Paine/Samson point is the most reliable among the evaluated methods.

## F.5

### A neurotransmitter-dependent mechanism of ependymal cell activation: Insights into a novel therapeutic target for spinal cord injury

*LD Hachem (Toronto)* H Moradi (Toronto) G Balbinot (Toronto) AJ Mothe (Toronto) W Lu (Bethesda) T Valiante (Toronto) CH Tator (Toronto) MG Fehlings (Toronto)*

doi: 10.1017/cjn.2024.107

Background: The drivers that activate endogenous ependymal-derived neural stem/progenitor cells (epNSPCs) remain unknown. Understanding the mechanisms that govern the biology of these cells is critical in developing a therapeutic strategy to harness their regenerative potential after injury. Methods: FoxJ1-CreER-tdTomato reporter mice were used for epNSPC lineage tracing. A conditional genetic knock-out mouse line of glutamate-subtype AMPA receptor (AMPAR) subunits in epNSPCs was generated. Electrophysiological properties were assessed using single cell patch clamp and slice culture recordings. For in vivo studies, mice underwent cervical SCI. To examine the effect of positive modulation of AMPARs, mice received the ampakine CX546 or vehicle and underwent electrophysiological testing, behavioural assessment and spinal cord extraction. Results: Glutamate excitotoxicity, a hallmark in the pathogenesis of acute SCI, drives epNSPCs activation via AMPARs. Genetic knock-out of AMPARs in epNSPCs inhibits their activation following SCI. Positive pharmacological modulation of AMPARs after SCI enhances the migration and differentiation of epNSPCs, increases neuronal sparing and improves long-term locomotor/forelimb function. SCI decreases the excitability of corticospinal tract projections, which is improved with positive AMPAR modulation. Conclusions: Glutamatergic signaling via AMPARs is an important mediator of epNSPC activation after injury. Pharmacological targeting of this mechanism can be used to enhance endogenous regeneration and improve recovery post-SCI.

## F.6

### Opportunities for improvement: understanding drivers of emergency department visits within 90 days of posterior spinal decompression surgery

*J Smith-Forrester (Halifax)* J Douglas (Halifax) E Nemeth (Halifax) J Alant (Halifax) S Barry (Halifax) A Glennie (Halifax) W Oxner (Halifax) L Weise (Halifax) S Christie (Halifax)*

doi: 10.1017/cjn.2024.108

Background: Canadian Emergency Departments (EDs) are overburdened. Understanding the drivers for postoperative patients to attend the ED allows for targeted interventions thereby reducing demand. We sought to identify "bounce back" patterns for subsequent QI initiatives. Methods: From April 1, 2016 to March 31, 2022, all provincial ED datasets (EDIS, STAR, Meditech) identified patients presenting within 90 days post-spine surgery. Using Canadian Classification of Health