NIMG-15. 2-HYDROXYGLUTARATE MAGNETIC RESONANCE SPECTROSCOPY IN ADULT BRAINSTEM GLIOMA PATIENTS <u>Hiroaki Nagashima¹</u>, Kazuhiro Tanaka¹, Yuichi Fujita¹, Mitsuru Hashiguchi¹, Mashahiro Maeyama², Yuichiro Somiya³, Takanori Hirose³, Tomoo Itoh³, and Takashi Sasayama³; ¹Kobe University Hospital, Kobe, Hyogo, Japan, ²Yodogawa Christian Hospital, Osaka, Japan, ³Kobe University Graduate School of Medicine, Kobe, Hyogo, Japan

OBJECTIVE: The onco-metabolite, 2-Hydroxyglutarate (2HG), is non-invasive biomarker for detecting isocitrate dehydrogenase (IDH) mutant glioma by MR-Spectroscopy. Especially 2HG-MRS may be useful in patients with brainstem lesions, where surgical biopsy presents high risk of neurological injury. Here, we examined the utility of 2HG-MRS for diagnosis of IDH mutant adult brainstem glioma. METHODS: We conducted 3 tesla -MRS (3T-MRS) in 8 radiographically identified brainstem tumor (7 male and 1 female, median age 39). Single-voxel was localized from the T2-FLAIR using a 2HG-tailored MRS protocol (Philips, Achieva, PRESS, TE 35 ms). All patients underwent tumor biopsy using an intraoperative navigation system (Brain LABTM) or stereotactic biopsy system (Komai's CT-stereotactic frame) before initial treatment. IDH and H3K27M status were diagnosed by IHC and DNA sequence. RESULTS: 3 cases were H3K27M and 4 cases were IDH mutant (R132H 1 case, R132S 2 cases, and R132G 1 case). 1 case were neither H3K27M nor IDH mutant. H3-K27 and IDH1 mutations were mutually exclusive. All tumor located at pons. There were no significant radiological difference between H3K27M and IDH mutant in conventional MRI sequence. Pearson's chi-square test demonstrated that 2HG concentrations >1.5 mM were 100% sensitive and 75% specific for IDH mutant glioma (p = 0.0285). The median overall survival survival were 127 month in IDH mutant glioma (n=4) and 22.5 months in IDH wild-type glioma (n=4), respectively. CONCLUSIONS .: 2HG in adult brainstem glioma was detected by conventional 3T-MRS successfully. A noninvasive 2HG-MRS may be useful diagnostic modality for evaluating molecular status and prognosis in brainstem glioma noninvasively.

NIMG-16. DEEP LEARNING SUPER-RESOLUTION MR SPECTROSCOPIC IMAGING TO MAP TUMOR METABOLISM IN MUTANT IDH GLIOMA PATIENTS

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Metabolic imaging can map spatially abnormal molecular pathways with higher specificity for cancer compared to anatomical imaging. However, acquiring high resolution metabolic maps similar to anatomical MRI is challenging in patients due to low metabolite concentrations, and alternative approaches that increase resolution by post-acquisition image processing can mitigate this limitation. We developed deep learning super-resolution MR spectroscopic imaging (MRSI) to map tumor metabolism in patients with mutant IDH glioma. We used a generative adversarial network (GAN) architecture comprised of a UNet neural network as the generator network and a discriminator network for adversarial training. For initial training we simulated a large data set of 9600 images with realistic quality for acquired MRSI to effectively train the deep learning model to upsample by a factor of four. Two types of training were performed: 1) using only the MRSI data, and 2) using MRSI and prior information from anatomical MRI to further enhance structural details. The performance of super-resolution methods was evaluated by peak SNR (PSNR), structure similarity index (SSIM), and feature similarity index (FSIM). After training on simulations, GAN was evaluated on measured MRSI metabolic maps acquired with resolution $5.2 \times 5.2 \text{ mm}^2$ and upsampled to $1.3 \times 1.3 \text{ mm}^2$. The GAN trained only on MRSI achieved PSNR = 27.94, SSIM = 0.88, FSIM = 0.89. Using prior anatomical MRI improved GAN performance to PSNR = 30.75, SSIM = 0.90, FSIM = 0.92. In the patient measured data, GAN super-resolution metabolic images provided clearer tumor margins and made apparent the tumor metabolic heterogeneity. Compared to conventional image interpolation such as bicubic or total variation, deep learning methods provided sharper edges and less blurring of structural details. Our results indicate that the proposed deep learning method is effective in enhancing the spatial resolution of metabolite maps which may better guide treatment in mutant IDH glioma patients.

NIMG-17. SYSTEMATIC REVIEW OF LITERATURE EVALUATING MACHINE LEARNING ALGORITHMS TO DEVELOP OUTCOME PREDICTION MODELS IN GLIOMA USING MOLECULAR IMAGING WITH AMINO ACID PET

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PURPOSE: Machine learning (ML) algorithms demonstrate accurate prediction of tumor segmentation, molecular pathology, and outcomes in gliomas using MRI and recently application of ML tools has expanded into molecular imaging with PET. We performed a systematic review to evaluate the role and applications of ML in characterization of gliomas with PET. METHODS: Four databases were searched by medical school librarian and confirmed by an independent librarian: Ovid Embase, Ovid MEDLINE, Cochrane trials (CENTRAL), and Web of Science-Core Collection. The search strategy used keywords and controlled vocabulary combining the terms for: artificial intelligence, machine learning, deep learning, radiomics, magnetic resonance imaging, glioma, and related terms. All articles were reviewed by at least 2 independent reviewers at abstract screening, full text review, data extraction, and bias analysis using TRIPOD. RESULTS: An initial 11,727 publications were imported to Covidence for screening. After review, 1135 studies moved to full-text review and 715 articles were included. Twelve publications included PET imaging of gliomas. All publications used single-center databases (3-73 patients) with distribution of tracers being [18F]-FDG (1), [18F]-FET (6), [11C]-MET (3), [18F]-FDOPA (1), and [18F]-AMP (1). All but 2 papers used supervised machine learning algorithms. Number of features ranged from 4-19,284. Nine papers manually extracted semiquantitative features TBRmax, TBRmean, SUV, TTP, in addition to demographics. Study outcomes included prediction of treatment response, survival, molecular subtypes, tumor grade, segmentation, and accuracy of image fusion. Accuracy ranged from 0.64-0.95 with AUC 0.43-0.9. CONCLUSION: ML can be used on small datasets of PET imaging of brain tumors. While majority of the clinical scans are performed with FDG-PET, the machine learning approaches are being applied to mostly amino acid tracers. Extending ML approaches to FDG-PET, which is more common in clinical practice, is recommended. Overall, ML has potential as a useful tool for predicting patient outcomes and improving image postprocessing.

NIMG-18. [¹⁸F]FLUCICLOVINE PET TO DISTINGUISH PSEUDOPROGRESSION FROM TUMOR PROGRESSION IN POST-TREATMENT GLIOBLASTOMA

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Differentiation of true tumor progression (TP) from pseudoprogression (PsP) is a major unmet need in patients with glioblastoma. [18F]Fluciclovine is a synthetic amino acid PET radiotracer that is FDA-approved in biochemical recurrence in prostate cancer. The study aim was to assess the value of [18F] Fluciclovine PET in differentiation of histologically confirmed ("true") TP and PsP in post-treatment of glioblastoma. METHODS: 23 patients with glioblastoma with new contrast-enhancing lesions or lesions showing increased enhancement (> 25% increase) on standard MRI after completion of radi-ation underwent 60-minutes dynamic [18F]Fluciclovine PET imaging, Patients subsequently underwent resection of enhancing lesion and tumor percentage vs. treatment-related changes were quantified on histopathology. Patients were considered "true" TP if tumor represented ≥ 50% of the resected specimen, mixed TP-PsP if < 50% and > 10%, and PsP if tumor represented \leq 10%. Summed 30- to 40-minute post-injection PET images were used to measure SUV_{peak} and SUV_{max} (g/mL units). RESULTS: 15 patients with "true" TP, 3 with mixed TP-PsP, and 5 with PsP were included. There was a positive conrelation between SUV_{peak} by PET and tumor percentage by histology (Rho=0.56, p=0.006). Patients who demonstrated "true" TP had significantly higher compared to patients with histological PsP (4.8 ± 1.6 vs 2.9 ± 1.0 , p= SUV SUV_{peak} compared to patients with histological PsP (4.8±1.6 vs 2.9± 1.0, p= 0.02, AUC= 0.91, n=20). SUV_{peak} cut-off of 3.3 provided 93% sensitivity, 80% specificity, and 90% accuracy for differentiation of "true" TP from PsP. Paspecificity, and 90% accuracy for unrefermation of the Tr nominastration with "true" TP/mixed TP-PsP also had significantly higher SUV_{peak} than patients with PsP (4.6 \pm 1.5 vs 2.9 \pm 1.0, p= 0.03, AUC= 0.88, n=23). SUV_{max} and partial volume-corrected SUV_{peak} and SUV_{max} exhibited similar performance. CONCLUSION: Our results indicated that [¹⁸F]Fluciclovine PET imaging can accurately differentiate "true" TP from PsP. Further studies are required to confirm these promising early results and determine optimal criteria for interpreting [18F]Fluciclovine PET to distinguish PsP from TP.

NIMG-19. SYNTHETIC ISOCITRATE DEHYDROGENASE-MUTANT GLIOBLASTOMAS FROM GENERATIVE ADVERSARIAL NETWORK PROVIDE MORPHOLOGIC VARIABILITY AND DIAGNOSTIC PERFORMANCE SIMILAR TO REAL DATA: DEVELOPMENT AND VALIDATION

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