molecular prognostic factors. In the elderly group, however, there was no significant difference in OS according to MGMT status (methylated = 18.7 vs. unmethylated = 17.1, p = 0.3885) or triple CNA status (triple = 13.6 vs. non-triple = 19.6, p = 0.1784). On the other hand, statistical difference was observed according to NF1 status (del = 12.1 vs. non-del = 18.7, p = 0.0157)** even in the elderly cases. CONCLUSION: Prognostic effects of molecular factors might be attenuated in the elderly patients. Further investigation in a larger population is necessary.

MPC-04
UTILITY OF COMPREHENSIVE CANCER GENOME ANALYSIS FOR BRAIN TUMORS
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OBJECTIVE: Our hospital has been designated as a cancer genome medical cooperation hospital, and it is our responsibility to play a central role in cancer medicine. We were one of the first local hospitals to clinically apply cancer genome analysis, and in January 2019, we started PleSsion-Rapid testing as a clinical study without patient burden. This study examines data from patients with brain tumors, subjects it to cancer genome analysis, and reports on its utility and efficacy.

METHOD: Gene analysis was performed by PleSsion-Rapid examination for patients with brain tumors who underwent surgery between January 2019 and July 2020. Tissue DNA extracted from pathological specimens was used to perform next-generation sequencing (NGS) analysis. In the PleSsion-Rapid test, 160 genes are comprehensively analyzed, examined by genomics, and evaluated for the presence or absence of actionable and druggable mutations, and the mutation rate is determined.

RESULTS: There were 15 cases total. Histopathological diagnoses included glioblastoma (n=5), diffuse astrocytoma (n=1), metastatic brain tumor (n=4), meningioma (n=2), central nervous system primary malignant lymphoma (n=1), germinoma (n=1), and Langerhans cell histiocytosis (n=1). Of these 15 brain tumor cases, actionable mutations were detected in 80.0% of cases and druggable mutations in 66.6%. The average mutation rate was 8.29±5.32 (range, 1.3 to 22.8) per patient.

Conclusion: Although future improvements will be needed for cancer genome analysis in brain tumors, this strategy may be useful for the selection of molecularly targeted drugs with high antitumor efficacy. We will continue to accumulate and study such cases in the future.

MPC-06
CUTTING-EDGE OF CANCER GENOMIC MEDICINE FOR BRAIN TUMORS
Masahiro Mizoguchi1, Nobuhiro Hata1, Daikaku Kuga1, Ryusuke Hatae1, Yuhei Sangatsuda1, Yutaka Fujikota1, Kosuke Takigawa1, Yusuke Funakoshi1, Yuki Koga1; 1Department of Neurosurgery, Graduate School of Medical Sciences, Kyushu University, Japan

Kyushu University Hospital was designated a Cancer Genome Core Hospital in April 2018, and the multi-genie panel test has been introduced since August 2019. The expert panel has been held for 21 cases of the central nervous system (11 adult glioma, 5 pediatric brain tumors, 5 extramedullary tumors). Actionable gene abnormalities were newly detected in two cases. First case is epithelioid glioblastoma with BRAF V600E mutation, and second is embryonal tumor with VCL-ALK fusion.

For the first case, BRAF/MEK inhibitor can be used by the prospective trial of patient-proposed healthcare services with multiple targeted agent combination. For the second case, we are planning to introduce ALK inhibitor by indicator-initiated clinical trial while continuing ICI therapy. The current approved agents for tumor-agnostic treatment are immune checkpoint inhibitors for mismatch repair deficient (dMMR) cases and TRK inhibitors for NTRK fusion gene-positive cases. We selected microsatellite instability (MSI) test and immunostaining of MMR gene for the indication of immune checkpoint inhibitor for recurrent glioma and Lynch syndrome that require dMMR evaluation, but FoundationOne CDx (F1CDx) allows simultaneous evaluation of MSI and MMR gene abnormalities. Regarding the indication of TRK inhibitors, F1CDx assay is selected as a companion diagnosis for ALK, NTRK1/2/3 fusion gene analysis for pediatric cases. At present, the actionable gene abnormalities are detected by multi-genie panel tests in about 10% of brain tumors. Development of tumor-agnostic treatment will expand the molecular target therapy for brain tumor in the future. Based on the experience of different schemes for molecular targeted therapy, it became clear that it is necessary to establish a cancer genome medical system for prompt introduction of precision medicine for highly malignant brain tumors.

MPC-08
MOLECULAR RISK STRATIFICATION USING GENOM-WIDE DNA METHYLATION DATA OF STANDARD-RISK MEDULLOBLASTOMAS TREATED WITH 18-GY CRANIOSPINAL IRRADIATION
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A novel risk stratification of medulloblastoma has been proposed based on retrospective data from patients undergoing standard treatment. However, it remains unclear whether the classification is applicable to patients receiving reduced-dose craniospinal irradiation (CSI). We performed molecular diagnosis and copy number analysis using methylation array on patients with standard-risk medulloblastoma treated with 18 Gy CSI at our institution. Nine tumor samples were available for analysis from seven patients who had a median age of 7.4 years at disease onset and a median observation period of 73 months. Three patients had recurrence, and another patient developed radiation-induced glioblastoma. From the three recurrent cases, one was molecularly diagnosed as SHH subtype with MYCN amplification; another case was a Group 4 tumor without favorable prognostic chromosomal aberrations, and the remaining patient experienced a very late relapse despite low-risk stratification. Of the recurrence-free cases, one was classified as WNT subtype, and another was a Group 4 tumor with chromosome 7 gain, and loss of chromosomes 8 and 11, both of which were associated with good prognosis. Methylation analysis also unveiled the fact that the recurrent tumor diagnosed as relapsing medulloblastoma by conventional diagnostic tools was in fact a radiation-induced glioblastoma. Our data suggested that the new risk stratification may be useful for cases treated with CSI reduced to 18 Gy. However, due to the presence of the late-relapsed case stratified to low risk, further investigations with a larger cohort should be required to confirm the data.

MPC-11
COMPREHENSIVE GENE EXPRESSION ANALYSIS OF IDH-MUTATED ASTROCYTOMAS WITH 19Q-LOSS
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We previously reported that there was a subgroup of IDH-mutated astrocytomas, harboring only 19q-loss showing oligodendroglioma-like morphology and significantly longer overall survival (OS) compared with 19q-intact astrocytomas. To further explore the biological characteristics of this possible subgroup and obtain insight into the mechanism of their relatively benign clinical behavior, we compared gene expression patterns between five 19q-loss and five 19q-intact IDH-mutated astrocytomas by microarray analysis. By comparing expression levels of genes of 19q-loss astrocytomas to those of 19q-intact astrocytomas, 136 up-regulated genes and 203 down-regulated genes were extracted. Down-regulated genes in the 19q-loss astrocytomas were heavily clustered to 19q and 4p, and up-regulated genes to 4q. It was noted that fibroblast growth factor 1 associated with stem cell maintenance was down-regulated in 19q-loss astrocytomas. Genes associated with glioma progression were differentially expressed, these results were validated with the independent TCGA data set. On t-SNE analysis of the 19q-loss astrocytomas with other IDH-mutant glioma subgroups from the TCGA datasets, 19q-loss astrocytomas did not shift to oligodendrogliomas with 1p/19q codeletion but were a subgroup in astrocytomas. These results indicated that 19q-loss in astrocytomas is more likely to be an acquired event rather than early event in oncogenesis like 1p/19q codeletion in oligodendrogliomas, and the biological and morphological features of 19q-loss astrocytomas were possibly related to differentially expressed genes associated with stem cell maintenance and glioma progression.

NEUROIMAGING (NI)
NI-01
USEFULNESS OF PREOPERATIVE EVALUATION OF GLIOMA ELASTICITY BY THE MAGNETIC RESONANCE ELASTOGRAPHY
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INTRODUCTION: The elasticity of intracranial tumors is difficult to assess non-invasively because the lesion is surrounded by the skull. Therefore, intracranial tumors have not been verified before surgery in terms of elastic
modulus. Magnetic resonance elastography (MRE) is an epoch-making method capable of non-invasively imaging the elasticity of internal organs. We have examined the elasticity of meningiomas and pituitary adenomas and reported their usefulness. This time, we measured the glioma elasticity and verified usefulness of MRE.

METHOD: Twenty-four gliomas (mean age 51.8±15.7 years, male: female = 17: 7) who underwent tumor resection after MRE imaging from July 2017 to July 2020 were targeted. The average elasticity was measured as an evaluation of tumor elastic modulus by MRE. Gliomas were divided into a low-grade glioma group (LGG: Grade 1, 2) and a high-grade glioma group (HGG: Grade 3, 4). Then, a comparative statistical study was conducted.

RESULTS: The average values of the average elasticity of LGG group (WHO 2016 Grade: GII/III) were 1.8±0.8 kPa and 2.5±0.8 kPa, respectively. The average elasticity was significantly higher in the HGG group (p<0.023). In the ROC analysis, the cutoff value was 2.1 kPa (sensitivity 70%, specificity 70%). Therefore, it was suggested that the tumor is likely to be HGG when the average elasticity is 2.1 kPa or more.

DISCUSSION: The glioma elasticity by preoperative MRE was significantly higher in the HGG group. Based on actual surgical experience, the tumor seems to be hard in the HGG group, and it was judged to be consistent with this our MRE research. The preoperative evaluation of glioma elasticity by MRE was considered useful, and it might help in planning a surgical strategy considering malignant grade.

NI-09

AMIDE PROTON TRANSFER (APT) IMAGE IS USEFUL FOR DIAGNOSTIC IMAGING OF GLIOMA
Masami Shirota1, Masayuki Nitta2, Taichi Saitou3, Syunsuke Taduki4, Atsushi Fukui5, Souko Ikuta6, Katsumi Yoshida7, Katsuhiko Muragaki1, Takazaku Kawamata2, 3Tokyo Women’s Medical University Yachiyo Medical Center

INTRODUCTION: APT image(APT), which images the concentration of amide groups that increases in tumors, is expected to be applied clinically in diagnostic imaging of glioma. PURPOSE: APT was compared with MET-PET based on the pathological diagnosis results, and it was retrospectively verified that APT was useful for diagnostic imaging of glioma.

METHODS: A total of 46 cases with glioma (WHO 2016 Grade: II/III/IV) and Pseudoprogression were included. APT measured the APT measurement value by placing the region of interest in the tumor part. MET-PET was administered with 370MBq and the accumulation ratio(TNR) between the tumor part and the normal part was measured. RESULTS: The APT measurement value in all cases was 2.22±1.01 and the TNR was 2.85±1.50, and a correlation was observed between the APT measurement value and the TNR value (r=0.78, p<0.001).When the accuracy of discriminating GBM from IDH-mut, Codel and GBM, and IDH-wt and GBM were 3.61, 4.42, 3.92, and 7.56, respectively. The cutoff value was 2.1 kPa (sensitivity 70%, specificity 70%). Therefore, it was suggested that the tumor is likely to be HGG when the average elasticity is 2.1 kPa or more.

OBJECTIVE: Magnetic resonance imaging alone is not sufficient for the diagnosis and therapy outcomes in brain tumors. We herein examined the utility of positron emission tomography (PET) studies for diagnosis in brain tumors.

METHODS: Between April 2009 and June 2020, 320 patients with central nervous diseases, including 140, 65, 52, 52, and 11 patients with glioma, metastatic brain tumor, malignant lymphoma, meningoima, and demyelinating disease, respectively, underwent PET studies (FDG, MET, FLT, and FMISO) in our department. Lesion/normal (L/N) ratios for FDG, MET, and FLT were calculated to evaluate the uptake of the PET tracers. RESULTS: The L/N ratio of 2.10±0.49 in the glioma group and 1.60±0.32 in the metastatic brain tumor group were distinguishable by FDG, MET, and FLT L/N ratios of 2.29, 3.32, and 5.83, and FMISO L/B ratio of 1.68. CONCLUSION: Four PET tracers were required to differentiate glioma subtypes. FDG and MET were helpful for distinguishing GBM from metastatic brain tumor, malignant lymphoma, and meningoima, whereas accumulation was lower for all four PET tracers in demyelinating diseases than in GBM.

NI-09

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