Abstracts

**MPC-05**

**TUMOR RELATED EPILEPSY AND IDH MUTATIONS IN GLIOMAS**

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**OBJECTIVE:** Tumor related epilepsy (TRE) is an important complication in the treatment of brain tumors. In recent studies, it is assumed that isocitrate dehydrogenase (IDH) mutations are correlated with TRE. In the present study, we examined the association between IDH mutations and TRE in our cases.

**METHODS:** 115 patients who had a supratentorial glioma and were treated in our hospital from February 2009 to November 2018 were retrospectively assessed for IDH mutations and TRE. RESULTS: 14 patients (12.2%) were the IDH mutant group (16 females, mean age 43.7±12.9 years, mean follow-up time 44.0 months). 77 patients were the IDH wild group (35 females, mean age 61.6±16.6 years, mean follow-up time 18.1 months).

**CONCLUSION:** The incidence of seizures as presenting symptom was 20 patients (32.6%) in the IDH mutant group and 16 patients (20.8%) in the IDH wild group, and was significantly higher in the IDH mutant group (p<0.05). 27 patients (71.1%) in the IDH mutant group had TRE at least once during follow-up time and 39 patients (50.0%) in the IDH wild group (p=0.06). In addition, the median OS for the group with seizure onset (36 patients) was 69.2 months and the group with the other onset (79 patients) was 22.4 months. The seizure onset group had a significantly better prognosis (p<0.05). CONCLUSION: Gliomas with IDH mutations have a higher incidence of TRE. Although IDH mutations are considered to be a risk factor for TRE, which is consistent with previous studies, but it is suggested that differences in survival may have an effect on the incidence of TRE.

**MPC-06**

**LRG1 HAS MULTIPLE POTENTIAL FOR CLINICOPATHOLOGICAL BIOMARKER OF GLOBLASTOMA**

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**BACKGROUND AND AIM:** Leucine-rich α2-glycoprotein 1 (LRG1) is one of the candidate proteins as a diagnostic marker for glioblastoma. Although association with angiogenesis has been reported, it has been suggested that the role as a biomarker differs depending on the tumor types. The role of LRG1 as a biomarker in glioblastoma was examined clinicopathologically. **METHODS:** Tumors of 156 cases diagnosed as diffusely glioma (27 astrocytomas, 15 oligodendrogliomas, 114 glioblastomas) according to WHO 2016 classification at Kurume University from January 2001 to April 2019 were used. The immunohistochemical intensity and molecular markers were immunohistochemically assessed. RESULTS: The intensity was graded as 1+ (weak), 2+ (medium), 3+ (strong). LRG1 expression was defined as low expression and score 2–3 was defined as high expression. The role of LRG1 as a biomarker in glioblastoma was examined clinicopathologically. **RESULTS:** Low expression was observed in 17 cases (12%), 29 cases (22%), and 100 cases (76%) in grade I, II, and III, respectively. High expression was observed in 2 cases (1.3%), 10 cases (7.8%), and 12 cases (9.3%) in grade I, II, and III, respectively. LRG1 expression was significantly associated with lower-grade glioma (p = 0.0003). HIGH expression of LRG1 was an independent favorable prognostic factor (HR 0.41, 95% CI 0.18–0.86, p=0.019) in IDH-wildtype glioblastoma, and correlated with overall survival (p = 0.002) and the tumor location of the non-subventricular zone (SVZ) (p = 0.00007). **CONCLUSION:** LRG1 demonstrated multiple potential as diagnostic, prognostic, and regional biomarker for glioblastoma.

**MPC-07**

**MECHANISMS OF BETTER PROGNOSIS IN IDH-MUTATED ASTROCYTOMA WITH 19Q-LOSS**

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We previously reported that there was a subgroup of IDH-mutated astrocytomas harboring only 19q-los showing oligodendroglioma-like morphology and significantly longer overall survival (OS) compared with 19q-intact astrocytomas (Otani et al. Cancer Sci 2018). The purpose of the present study was to reveal how 19q-loss contributed to better prognosis and the morphology in the subgroup. We compared expression pattern between five 19q-loss and 19q-intact IDH-mutated astrocytomas by miRNA and mRNA analysis. 136 up-regulated genes and 203 down regulated genes were extracted in 19q-loss astrocytomas compared with 19q-intact astrocytoma. Significantly changed genes distributed throughout all chromosomes, but more down-regulated genes were on 19q and 4p, and more up-regulated genes were on 4q.

Genes associated with apoptosis, cell adhesion, and antigen presentation were up-regulated, and genes associated with Ras signaling pathway were down-regulated. These changes could result in better prognosis. By contrast, there was no expression change between gene associated with oligodendroglioma-like morphology although up-regulation of genes associated with axon guidance and down-regulation of genes associated with cell shape might result in the morphology or neuronal differentiation. Expression pattern of 19q-loss astrocytoma indicated no tendency of oligodendrogial differentiation.

Better prognosis of 19q-loss astrocytomas was derived from expression changes associated with tumor proliferation and tumor immunity.

**MPC-08**

**CLINICOPATHOLOGICAL ANALYSIS OF 12P GAIN IN INTRACRANIAL GERM CELL TUMORS**

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**BACKGROUND:** Gain of short arm of chromosome 12 (12p) is commonly observed in testicular germ cell tumors (gCTs). 12p gain is frequently seen in intracranial GCTs (iGCTs). However, little is known about the clinical significance of 12p gain in iGCTs. MATERIALS AND METHODS: We have collected over 200 fresh frozen tissue samples of GCTs from the Intracranial Germ Cell Tumor Genome Analyses Consortium in Japan. Firstly, we analyzed DNA methylation status in 83 GCTs, 3 seminomas and 6 normal control samples using Infinium Human Methylation 450K BeadChip array (Illumina, CA). Idat files were processed using R (Version 3.5.3) and minfi package (1.30.0) to generate copy number variations. Compared with 6 normal control samples using Infinium Human Methylation 450K BeadChip array (Illumina, CA), Idat files were processed using R (Version 3.5.3) and minfi package (1.30.0) to generate copy number variations. Compared with average genome-wide copy number level, 12p gain was determined. Then, 38 iGCTs with clinicopathological information were analyzed for progression-free survival (PFS) and overall survival (OS). **RESULTS:** Tumors that consist of only other germinal and/or mature teratoma components were classified as Favorable Histology (FH) and all the others that contains malignant histological components were classified as Unfavorable Histology (UH). 12p gain was observed in 100% (3/3) of seminoma, 13.6% (3/22) of germ cell tumor (GCT) and 16.7% (16/98) of mature teratoma, 25% (1/4) of immature teratoma, 55% (11/20) of mixed germ cell tumor, 100% (4/4) of yolk sac tumor, 100% (1/1) of embryonal carcinoma, and 100% (1/1) of choriocarcinoma. In total, 44.6% (37/83) of 41GCT showed 12p gain. Regarding histological classification, the 12p gain rate in UH (72%, 18/25) was significantly higher than that in FH (12.1%, 4/33, P<0.01). Both PFS and OS were significantly worse in 12p gain. Compared with average genome-wide copy number level, 12p gain was determined. Then, 38 iGCTs with clinicopathological information were analyzed for progression-free survival (PFS) and overall survival (OS). **DISCUSSION:** 12p gain can be a molecular marker to predict prognosis and histological malignancy in iGCTs.

**MPC-09**

**THE OPTIMIZATION OF TREATMENTS FOR SO-CALLED PRIMITIVE NEUROECTODERMAL TUMORS WITH MOLECULAR ANALYSIS**

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**INTRODUCTION:** In the previous WHO classification of central nervous system tumors, the supratentorial tumors comprise small round blue cells with aggressive clinical features had been defined as primitive neuroectodermal tumor (PNET). Recent molecular analysis revealed that they do not belong to a single entity, but they are re-classified as the tumors of other well-defined tumor subtypes and newly defined molecular subtypes were referred to the new classifications. While, there are few studies showed the