BRAF V600E MUTANT OLIGODENDROGLIOMA-LIKE TUMORS WITH CHROMOSOMAL INSTABILITY IN ADOLESCENTS AND YOUNG ADULTS
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We performed genome-wide methylation analysis on 136 pediatric low grade gliomas to identify a molecular subtype cluster consisting of oligodendroglioma-like BRAF V600E mutant tumors with Recurrent gain of Chromosome 7 and loss of Chromosome 10 (OLIVER). Hierarchical clustering and t-stochastic neighbor embedding analyses cluster them with previously described pediatric-type low grade gliomas, separate from adult gliomas. OLIVER exhibits distinct clinical behavior as temporal lobe lesions in adolescents and young adults, prolonged history of seizures and all are alive with no recurrence (follow-up 3.2 to 13.2 years). Morphologically, all showed oligodendroglioma-like features, including round nuclei, perinuclear halos, a chicken-wire pattern of branching capillaries and microcalcification. None showed astrocytic features or characteristics suggestive of high-grade tumors including necrosis or mitotic figures. All tumors harbored multiple chromosomal copy number abnormalities (more than 10 chromosomes per OLIVER), but none showed 1p/19q co-deletion or IDH1 mutation. Interestingly, one tumor showed a TERT promoter mutation. Although the series is small, OLIVER may represent a new category of IDH wild-type low grade gliomas which may be confused with molecular GBM. Further, they highlight the heterogeneity of IDH wild-type gliomas and the relatively indolent behavior of pediatric-type gliomas.

MPC-15
FEASIBILITY OF GLIOMA SPECIFIC ONCPANEL IN THE DIAGNOSIS OF GLIOMA
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AIM: Molecular classification of glioma is a mandatory in the diagnosis of glioma according to the WHO 2016 classification of tumors of the central nervous system. However, WHO does not indicate the molecular methodology to be integrated, and the versatility and cost-effectiveness of molecular diagnosis is a concern. In this study, we evaluate the feasibility of a glioma specific tailored NGS panel where driver gene mutation and molecular diagnosis is a concern. In this study, we evaluate the feasibility of a glioma specific tailored NGS panel.

METHODS: We developed a glioma specific tailored NGS panel consisting of 48 genes including IDH1/2, TP53, PTEN, EGF, PDGFR, NFI, RB1, CDKN2A, and the TERT promoter. DNA was extracted from FFPE tumor tissues histologically identified by a pathologist, and from patient-derived blood to serve as a control. In this system, gene mutations and copy number alterations can be precisely characterized, thus 1p/19q co-deletion can also be evaluated. We have analyzed 106 glioma patients (Grade II: 19 cases, Grade III: 23 cases, Grade IV: 64 cases) using this system.

RESULTS: From these 106 cases, IDH1 and TERT promoter mutations were detected in 33 cases (28%) and 55 cases (52%), respectively. 1p/19q co-deletion was detected in 19 cases (18%), with IDH1 mutations in all cases. In 57 Grade IV cases, TP53, PTEN, RB1, NFI, PDGFR mutations were detected in 25 cases (43%), 24 cases (41%), 10 cases (17%), 8 cases (14%) and 6 cases (10%). Although EGFR mutation frequency was low (3%), amplification was detected in 14 cases (24%). As for deletion, PTEN and CDKN2A loci were deleted in 36 cases (62%) and 30 cases (52%), respectively. To note, MET alterations were detected in 2 cases. The cases in which histopathological diagnosis is difficult to make have a tendency to show atypical genetic alterations.

CONCLUSION: Diagnosis of glioma patients with this glioma-specific tailored NGS panel is feasible.