seen. EGFRvIII and 1p19q co-deletion were lost over time in 1/5(20%) and 1/6(17%), respectively. In contrast, cMET expression, amplification, and TUBB3 expression increased in 1/5(20%), 1/4(25%) and 2/10(20%) tumors while no decrease seen. Expression of PD-1, TOP2A, TOPO1 and TS showed both increase and decrease. 8 pairs had paired sequencing, acquisition of EGFR(V292L), FLT3(D324N), NOTCH1(G736R) and RB1 (E746fs) were seen in one case each. In 8 pairs of MGMT methylation, two samples showed decreased MGMT methylation. CONCLUSIONS: Although cohort is small, we show dynamic changes in recurrent malignant gliomas with high discordance rate of 29% compared to the first test. There was greater loss of targetable-biomarkers than gains over time which could impact the selection of treatment options (p=0.015). Reanalyzing the most current tissue prior to making a decision on the next line of treatment should be considered.

MPTH-56. ALGORITHM BASED LIQUID BIOPSY FOR THE DIAGNOSIS OF GLIOBLASTOMA

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AIM: The aim of this study was to develop an algorithm that would accurately diagnose, offer therapy management options and help in the monitoring of recurrence in patients with glioblastoma. METHODS: In a prospective study, after ethics committee approval, ninety samples and fifty controls were collected from Apollo Hospitals. All patients had lesions that had the radiological appearance of a high grade glioma. All patients had attempted radical resections. Blood samples were drawn after written consent either on the day or on the day before surgery. Pathological diagnosis was considered to be the gold standard. Liquid biopsy was performed using the 'Next Gen Sequencing' platform. Analysis was based on the data obtained from analysis of exosomal RNA, cell free DNA and micro RNA. The lab was blinded to the results of the biopsy till the entire study was completed. RESULTS: Big data analysis revealed 19 different markers that can help in the diagnosis, pathway analysis and recurrence monitoring of glioblastoma. This included EGFR amplification, PDGFR amplification, NF1 mutation, TP53 mutation, PTEN mutation etc and microRNAs miR-27a, 210, 124, 210 etc. 48 tumors were diagnosed to be GBMs by the pathologists. All 48 were diagnosed on liquid biopsy as well. 27 tumors were diagnosed as grade 3. Liquid biopsy identified 24 as grade 3 and 3 as GBMs. The rest were Grade 2 according to pathology. Of these, there were 15 tumors. However, 3 were classified as GBMs and 4 were thought to be grade 3 tumors. All control samples were negative. CONCLUSION: Liquid biopsy can play an important role in the diagnosis of patients with gliomas and reduce the under reporting of high grade gliomas caused by tumor heterogeneity.

MPTH-57. GENOTYPING OF GLIOMA INCLUDING 1p19q CODELETION BY TARGETED SEQUENCING

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BACKGROUND: Gliomas are the most common primary brain tumors, accounting for about 25% of all intracranial tumors. To date, detailed genotyping for glioma detecting the mutation in IDH1/2, ATRX, p53, TERT promoter region in addition to 1p19q codeletion is mandatory for final diagnosis especially for selecting the treatment after surgery. Currently, the practical genotyping methods for glioma are still discordant i.e., Sanger sequence for each genes and FISH for codeletion, nevertheless of recent development of next generation sequencer. Here we established rapid and valuable targeted sequence pipeline for glioma genotyping for not only SNV detection but also 1p19q codeleiton. METHODS: Surgically resected glioma samples were fixed with PAXgene Tissue System (QIAGEN) and embedded in paraffin (PFPE). Capture sequencing panel targeted 16 genes including ATRX,IDH1,IDH2, TP53,TERT were designed by SeqCap EZ target enrichment system (Roche). Genomic DNA was extracted from PFPE tissues and the libraries were sequenced by the MiSeq (Illumina). The raw read data obtained from amplicon sequencing were processed by originally designed, dedicated analysis pipeline by Genome Jack (Mitsubishi Space Software Inc.) RESULTS: We detected IDH1 R132H mutation in 3 out of 7 high grade gliomas. In addition, 1p19q codeletion was identified in these 3 cases by out sequence pipeline and also FISH. Moreover, we successfully detected LOH of PTEN and amplification of EGFR and MET. CONCLUSIONS: Here we established the rapid clinical sequence system for glioma by targeted sequencing using a desktop sequencer Miseq. Our workflow can be finished within 7 working days with reasonable cost, offering a practical laboratory developed test for glioma genotyping.

MPTH-58. PEMETREXED: A POTENTIAL NEW THERAPEUTIC OPTION FOR THE TREATMENT OF THYMIDYLATE SYNTHASE (TS) NEGATIVE RECURRENT PRIMARY AND SYSTEMIC MALIGNANCIES WITH CNS METASTASIS

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BACKGROUND: Fluoropyrimidine analogues, 5FU, Capecitabine and Pemetrexate, inhibit thymidylate synthase and they have been widely used for the treatment of systemic malignancies. Capecitabine can penetrate CNS and has shown some efficacy in the treatment of breast cancers with CNS metastasis. The role of Pemetrexed in the treatment of recurrent primary and systemic malignancies with CNS metastsis is not known. METHOD: We have treated 33 pts with previously heavily-treated recurrent primary and systemic malignancies with CNS metastasis based on the results of the molecular profiling. 16/33 pts were found to have TS-negative and 9/16 TS-negative patients were treated with Pemetrexed. MRI was performed every 2-3 months for tumor evaluation. RESULTS: Total pts: 9. M:F 5:4, Age: 48-88 yo. Median age 70.7 yo. Treatment period: 7/14 - 6/16. 1/1 GBM pt: SD for 4 mo. 1/2 anaplastic astrocytoma pts: SD for 4 mo. 1 Gr. II astrocytoma pt: SD for 7 mo. 2/2 meningioma pts: SD for 2 mo (still on treatment) and 4 mo. Both pts also received concurrent cisplatin based on ERCC1 and BRCA1 markers. 2/2 pts with squamous cell Ca of skin with skull base/brain metastasis: 1 PR for 24 mo, 1 SD for 18 mo respectively and still receiving treatment. 1 chordoma pt involving cervical/skull base: SD for 11 mo: still receiving treatment. Toxicities were very mild except 2 meningioma pts (Gr. 3-4) who also received cisplatin. CONCLUSIONS: Pemetrexed treatment for TS-negative recurrent primary and systemic malignancies with CNS metastasis demonstrated an excellent response rate of 89% (PR:1, SD:7, TP:1). Toxicities were minimal and tumor responses were durable. Particularly in the elderly population, in light of excellent toxicity profile, Pemetrexed should be considered as a part of the first treatment options for TS-negative CNS malignancies. A TS directed trial for pts with TS-negative recurrent CNS malignancies is warranted.

MPTH-59. ANAPLASTIC PLEOMORPHIC XANTHOASTROCYTOMAS: A CLINICOPATHOLOGIC AND MOLECULAR PROFILE

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Pleomorphic xanthoastrocytomas (PXAs) are grade II neoplasms according to the 2007 WHO classification. The diagnosis is made predominantly on the basis of histology and immunohistochemistry. The diagnosis "PXA with anaplastic features" (aPXA) is rendered when increased mitotic activity and/or necrosis are recognized. The presence of BRAF V600E point mutation is characteristic but only present in approximately 50% of PXAs. We evaluated 23 tumors (5 PXAs and 18 aPXAs), comparing morphology and immunophenotype. DNA was isolated from tissue and genome-wide methylation array profiling was performed on a subset of tumors. Methylation profiles were compared to a reference cohort of PXA samples. All 21 tumors for which GFAP was evaluated were immunoreactive for GFAP. 2 PXAs and 6 aPXAs harbored BRAF V600E point mutations. The remaining PXAs were not evaluated for BRAF V600E point mutations; 6 aPXAs were negative for this mutation. 75% of evaluated PXAs and 86% of evaluated aPXAs demonstrated CDKN2A/B loss. 68% of evaluated tumors displayed abnormal copy number profiles, with more complex copy number profiles associated with anaplastic histology. Alterations of BRAF V600E and CDKN2A/B were seen in a similar proportion of PXA and aPXA. Although neither of these changes correlated with anaplastic behavior, CDKN2A/B may be a useful molecular diagnostic marker for PXA in general. Progression-free survival time was not statistically different for patients with aPXA compared to those with PXA in our small sample. However, 39% of aPXAs progressed to higher-grade tumors in our series, while no PXAs did. Overall survival was also similar between the two groups during our follow-up period, which ranged from 1-132 months, but the 4 patients in our study who died were all aPXAs. All of the PXA patients were treated with surgery alone, while aPXA patients all received adjuvant chemotherapy, radiation therapy, or both, resulting in many favorable outcomes.