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 TUB3 expression increased in 1/3 (20%), 1/4 (25%) and 2/10 (20%) tumors while no decrease seen. Expression of PD-1, TOP2A, TOP2A and TSH showed both increase and decrease. 8 pairs had paired sequencing, acquisition of EGFR (V92L), FLT3 (D324N), NOTCH1 (G763R) 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 degree of genetic negative variation compared to the initial diagnosis. There was evidence 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.

PMTH-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 ethical committee approval, nine samples and four 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 performed by originally designed, dedicated analysis pipeline by ‘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, NFI 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. 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 underreporting of high grade gliomas caused by tumor heterogeneity.

PMTH-57. GENOTYPING OF GLIOMA INCLUDING 1p19q CODELETON 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, approximately 80% of gliomas have been classified. Liquid biopsy, which uses cell-free DNA (cfDNA) isolated from blood, has been used for detecting genetic biomarkers. In this study, we investigated the clinical significance of targetable mutations in glioma patients using targeted next-generation sequencing (NGS). We developed a method called Genomic Biomarker Analysis (GBA) to analyze the cfDNA in glioma patients. The GBA method was designed to detect genetic biomarkers that could be used as indicators of the optimal treatment for glioma patients. METHODS: We collected cfDNA from 15 glioma patients who were enrolled in the study. We used the GBA method to analyze the cfDNA samples, and we compared the results with those obtained using conventional methods, such as cytogenetic analysis and immunohistochemistry. We found that the GBA method was more sensitive and specific than the conventional methods. CONCLUSION: Our findings suggest that the GBA method can be used to identify targetable mutations in glioma patients, which could help in the development of more effective treatments for these patients.


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BACKGROUND: Fluoropyrimidines analogues, 5FU, Capecitabine and Pemetrexde, 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 metastasis remains unclear. METHODS: 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 meninapgia pts: SD for 2 mo (still on treatment) and 4 mo. Both pts also received concurrent cisplatin based on WHO C1 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. I chordoma pt involving cervical/skull base: SD for 11 month, metastatic/recurrent breast: SD for 12 mo. CONCLUSIONS: 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. Participation in the elderly population, in light of excellent toxicity, 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.