PATH-37. LIQUID BIOPSY FOR IDENTIFICATION OF NEWLY DIAGNOSED GLIOMA

Ian Lee[1], Lisa Scarpace [2], Kevin Nelson[1], Darshana Patil[3], Vineet Datta[3], Dadasaheb Akolkar[3], Sachin Apurva[3], Pooja Fulmali[3], Sneha Puranik[3], James Snyder[1], Houtan Noushmehr[1], Pradeep Devhare[3], Ana deCarvalho[1], Rajan Datar[3], Tobias Walbert[4] and Steven Kalkanis[2]; [1]Henry Ford Health System, Detroit, MI, USA, [2]Department of Neurosurgery, Henry Ford Health System, Detroit, MI, USA, [3]Datar Genetics, Nashik, Maharashtra, India, [4]Henry Ford Hospital, Detroit, MI, USA

INTRODUCTION: In patients with newly diagnosed intracerebral lesions based on MRI, gliomas are often suspected, but MRI is rarely definitive thus necessitating biopsy. For non-enhancing lesions involving eloquent or deep-seated structures, diagnosis can be especially challenging as biopsy may be relatively risky or undesirable to the patient. In this study, analysis of plasma isolated cell-free DNA and exosome mRNA and miRNA from newly diagnosed glioma patients and from cancer-free volunteers was used to predict disease. METHODS: Blood was drawn from 40 patients with newly diagnosed gliomas (28 high grade glioma (HGG), 12 low grade (LGG)) and 10 healthy volunteers without documented history of cancer. High quality DNA and RNA was isolated and sequenced using Next Generation Sequencing and Digital Droplet PCR was used for detection and verification of trace molecular artefacts. Multianalyte processing yielded data that was harmonized and interpreted through an Artificial Intelligence based algorithm to assess for possible glioma and to assign grade. EGFRviii and IDH1 mutations were also analyzed and compared to molecular testing from tumor specimens. RESULTS: 97.5% (39 of 40) of glioma patients were deemed to have gliomas by plasma testing. 96% of HGG patients and 67% of the LGG patients were correctly graded. Of the 10 healthy controls, 8 were concluded to be cancer-free. Two of the patients were suspicious for malignancy, of which one was possible glioma. IDH1 and EGFRviii mutation had concordance at 74 % (26/35) and 59% (12/16), respectively. CONCLUSIONS: Analysis of plasma cell free tumor derived DNA and RNA was highly sensitive for detecting glioma with high agreement in grading as well. In patients with newly diagnosed intracerebral lesions, this may be a useful screening test to determine the need for more invasive testing, i.e. biopsy/resection. Further testing in blinded samples from brain tumor patients and healthy subjects will follow.