Whole genome cell-free tumor DNA mutational signatures for noninvasive monitoring of pediatric brain cancers

Ivy Tran¹, Kristyn Galbraith¹, Guisheng Zhao², Robyn Borsuk², Joyce Varkey², Sharon Gardner², Jeffrey Allen², David Harter³, Jeffrey Wisoff³, Eveline Teresa Hidalgo³, Sunil Deochand⁴, Dillon Maloney⁴, Danielle Afterman⁴, Tomer Lauterman⁴, Noah Friedman⁴, Imane Bourzgui⁴, Nidhi Ramaraj⁴, Zohar Donenhirsh⁵, Ronel Veksler⁴, Jonathan Rosenfeld⁴, Ravi Kandasamy⁴, Iman Tavassoly⁴, Boris Oklander⁵, G. Praveen Raju⁶, Theodore Nicolaides², Asaf Zviran⁴, Matija Snuderl¹

¹Department of Pathology, NYU Grossman School of Medicine, ²Department of Pediatrics, ³Department of Neurosurgery, NYU Grossman School of Medicine, New York, NY, USA, ⁴C2i Genomics. INC, New York, NY, USA, ⁵C2i Genomics. LTD, Haifa, Israel, ¹Department of Neurology & Pediatrics, Icahn School of Medicine at Mount Sinai, New York, NY, USA

INTRODUCTION

Liquid biopsy offers a noninvasive approach to monitor cancer burden during therapy and surveillance period. However, in pediatric brain cancers, liquid biopsy methods from the blood have been unsuccessful due to a low tumor burden and low number of mutations in coding regions. We hypothesized that a whole genome sequencing (WGS)-derived patient specific mutational signature from a matched tumor-normal WGS can provide a sensitive and specific approach to detect mutations in circulating cell free tumor DNA (ctDNA) and provide blood-based monitoring in pediatric patients with brain tumor.

Corresponding author: matija.snuderl@nyulangone.org

May 2021

Blood sample #2

December 2021 Blood sample #3

Post chemotherapy – cycle 2 Post chemotherapy – at completion

April 2021

Blood sample #1

Post chemotherapy – cycle 1

Patient-specific tumor signature Identifying unique tumor mutations | Fireth fizzer | Fireth

brain tumors were analyzed and molecularly subclassified using whole genome DNA methylation profiling and AI classification. Tumor DNA was extracted from pathology tissue and normal germline DNA from the white blood cells, ctDNA was extracted from 1-2 mL of post-surgery blood samples for each patient at 1-3 available time points. The ctDNA Tumor Fraction (TF) was compared to the clinical status and imaging.

RESULTS

We profiled 7 pediatric brain tumors, including 2 medulloblastomas (one Group 3, one Group 4), 3 pediatric glioblastomas IDH wild-type, 1 ependymoma PFA subtype and one low grade ganglioglioma. Tumor specific signatures were identified and detected in the plasma of 5 patients with clinical disease with a TF range 0.02-0.0005 but not in 2 patients with no tumor at the time of blood collection. In two children with a medulloblastoma and glioblastoma, the decrease of tumor fraction in ctDNA over 2 (TF: 0.002 to 0.0009) and 3 time points (TF: 0.0005 to undetectable), respectively, correlated with response to therapy based on imaging.

CONCLUSIONS

Patient-specific WGS tumor signature in ctDNA from blood can be used for sensitive monitoring of children with brain tumors. Patient specific signatures could be established across various histologic subtypes and were present at the time of diagnosis. This blood based monitoring method is minimally-invasive compared to CSF liquid biopsy testing.







