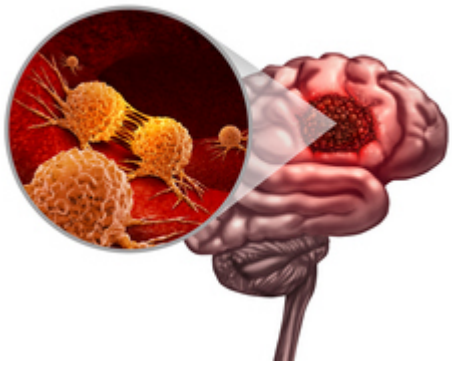
INNOVATION PARTNERSHIPS
UNIVERSITY OF MICHIGAN

Methods to quantify metabolic activity in human tissues

TECHNOLOGY NUMBER: 2023-133



OVERVIEW

Description of glioblastoma multiforme metabolic activity from a single measurement

- Machine learning that estimates tumor behavior from one 13C infusion measurement
- Provides a novel method to measure tumor behavior and treatment response

BACKGROUND

Glioblastoma multiforme (GBM) is the most common and lethal primary brain tumor in humans with a 5-year survival rate of less than 10%. The standard treatment for GBM involves surgical resection, when feasible, as well as temozolomide chemotherapy delivered concurrently with external beam radiotherapy (EBRT). The cellular makeup within GBM tumors shows heterogeneity that correlates with resistance to EBRT, with data revealing that radiation resistant GBM tumors exhibit higher levels of molecules that promote processes that allow cancer cells to adapt to changing microenvironments and to proliferate. The metabolic flux of cancerous tissue has historically been evaluated by mass spectrometry measurements of infused radioactive carbon isotopes such as carbon-13 (13C) to assess the effects of influence of these molecules. Given that existing measures are commonly limited in both number and time, a need exists for new methods to extrapolate the metabolic behavior of tumor cells from a limited number of data points.

INNOVATION

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Category

Diagnostics
Life Sciences

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Researchers at the University of Michigan have developed a method to utilize stable isotope infusions to quantify rates of metabolic activity from single measurements in mouse models of human brain tumors. While historical measures of tumor metabolic activity require multiple assessments over different timepoints, this invention employs machine learning models based on existing data that can determine metabolic activity from a single measurement. This invention can therefore measure the metabolic flux of tumors using 13C infusion and single time point analysis. Because most patient tumors can only provide a solitary metabolic measurement representing their activity at the time of biopsy or surgical resection, the development this model to estimate metabolic activity based on a single data point provides a novel means by which to assess tumor behavior. The information obtained from this approach can be used by clinicians when they choose which metabolic inhibitors to prescribe for their patients with glioblastoma multiforme, such as the delivery of agents which inhibit guanosine triphosphate and may therefore negate the radiation-resistant properties of tumors rich in this this nucleotide. The further study of this novel technique may provide a wealth of approaches for GBM treatment algorithms.