Rigshospitalet
Department of Oncology, Copenhagen

The DCCC Brain Tumor Center
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The Glioflow study. (1046)
Treatment evaluation by cfDNA/ctDNA through repetitive plasma samples in patients with newly diagnosed brain cancer

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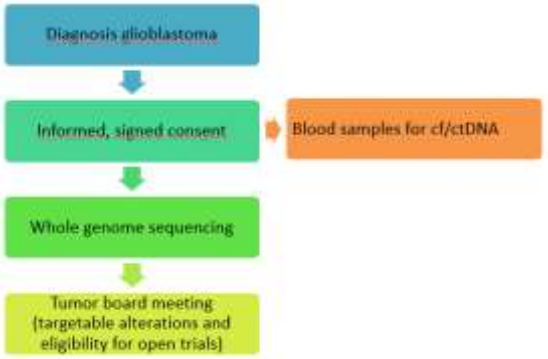
BACKGROUND

Glioblastoma (GBM) is an aggressive brain cancer with a median overall survival of 16-24 months. Better evaluation methods and better treatment is much warranted, and both are influenced by the blood-brain-barrier. We aim to improve these two factors by investigating the role of cfDNA/ctDNA in a large prospective cohort, included from our out-patient clinic through the Neurogenome protocol. Inclusion began June 2022.

THE NEUROGENOME PROTOCOL



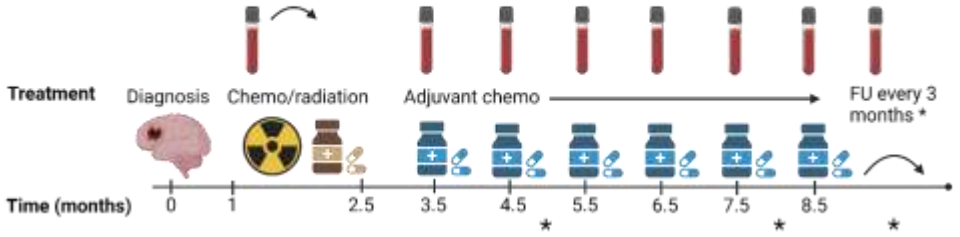


Figure 1: Workflow of the Glioflow study. Blood samples are taken at fixed time intervals. Treatment consists of radiation with 2 Gy x 30, 5F/W concurrent with Temozolomide and followed by adjuvant Temozolomide for 6 cycles. * indicates evaluation with MRI.

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CONCLUSION & FUTURE PERSPECTIVES

CfDNA concentrations could be quantified from plasma. As expected, they were lower than in other solid tumors. Surprisingly, no tumor-tissue specific variants were called with TSO500 ctDNA panel. We plan to investigate TSO500 raw data with the following in mind: input of cfDNA concentration, sequencing depth, clinical data (treatment, stable versus progressive disease and more). Inclusion will continue.

PATIENTS

Newly diagnosed patients with GBM, eligible for 1st line treatment
PS 0-1
Able to read and understand Danish

METHODS

Whole genome sequencing (WGS) is performed on tumor tissue. Peripheral blood is collected in STRECK tubes at fixed time points untill progression with an expected average of 10 samples per patient (figure 1). cfDNA will be quantified on a Qubit Fluorometer. Selected patients will be analysed either with the pancancer TSO500 ctDNA panel, covering 523 genes or with ctDNA analyses, guided by tissue-WGS from each patient. Results will be correlated to the clinical status of the patient

RESULTS

As of April 2023, we have included 55 patients and 15 patients have progressed.

Six patients have had one sample with cfDNA quantified with a median of 0.9 ng/µl (0.5-1.7). All samples were collected prior to progression. No known tumor variants from tissue-WGS were called with the TSO500 ctDNA panel.

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