Evaluation of a multiparamteric qBOLD approach in patients with brain tumors

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Introduction

In clinical monitoring of brain tumors, Perfusion Weigthed Imaging (PWI) contributes to tumor grading and to assess the response to treatment, as early as possible [1]. Beyond tumor perfusion, tumor hypoxia has been shown to determine the reponse of various therapeutic approaches including radiotherapy. The aim of this study is to evaluate in patients how tissular oxygen saturation (StO_2), assessed with a multiparametric qBOLD approach [2], could contribute to characterize brain tumors using a model-based cluster approach.

Materials and Methods

Groups. Thirteen subjects (7 males/6 females) with untreated brain tumor were examined after written informed consent was obtained (approved by local IRB). Group was composed of 5 glioblastomas, 2 metastases, 1 meningioma, 2 astrocytomas, 1 gliomatosis, 1 ependymoma, 1 oligodendroglioma.

Acquisition. The imaging protocol was carried out on a 3T TX Achieva MR scanner (Philips Healthcare®) using a whole-body RF transmit and 8-channel head receive coils. Three sequences were acquired with a FOV of 224x20x184mm: a 3D multi gradient echo (GE) sequence to obtain a T_2* estimate; a multiple spin-echo experiment for T_2 mapping; a perfusion sequence with injection of a bolus of Gadolinium-DOTA (0.1mmol/kg, Guerbet, France) to map cerebral blood volume (CBV) cerebral blood flow (CBF) and mean transit time (MTT). The final spatial resolution was 2*2*4mm.

Data Analysis. As described in the literature [2], StO_2 maps were obtained pixelwise from a combination of CBV and T_2' where $1/T_2' = 1/T_2^* - 1/T_2$ and using a hematocrit of 0.4; T_2 and T_2* maps were calculated by fitting a monoexponential decay to the corresponding MR images. A map of Cerebral Metabolic Rate of oxygen ($CMRO_2$) was computed using $CMRO_2$ = CBF x (1-StO_2/100). Eventually, a model-based cluster analysis was performed on voxels obtained from the 13 patients in all the brain parenchyma. Normal mixture modeling was performed on voxel data using Expectation-Maximization algorithms implemented in the R package mclust [3]. Model choice and the optimal number of clusters (k=7 clusters) were determined with a Bayesian information criterion [3].

Results

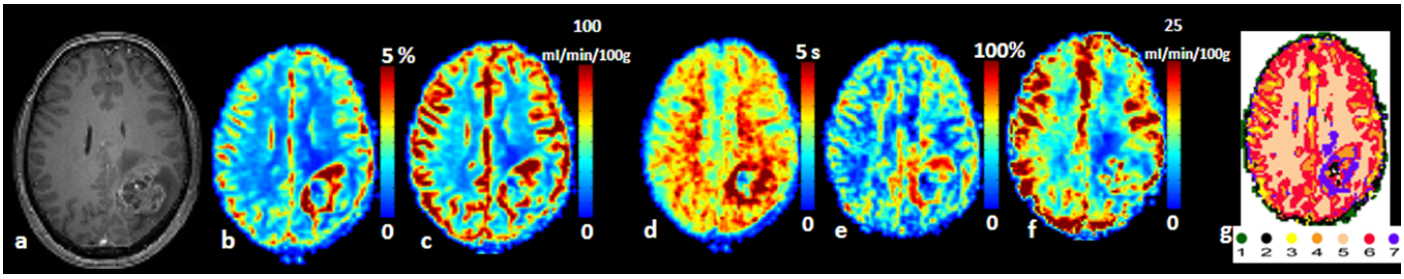

Figure 1. 3DT_1 Gd (**a**). CBV (**b**), CBF (**c**), MTT (**d**) StO2 **(e)** $CMRO_2$ maps **(f)** and model-based cluster analysis **(g)** from one patient with glioblastoma.

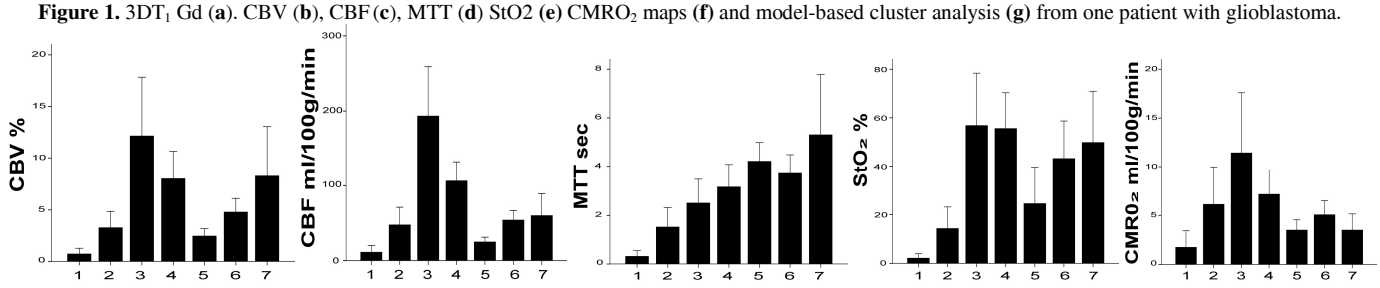

Figure 2. CBV, CBF, MTT, StO_2 and $CMRO_2$ in the 7 clusters (mean ± SD across the patients).

Fig. 1 shows representative parametric maps obtained from one patient. The model-based cluster analysis (**Fig.1g**) of 7 clusters shows that white matter composed of the same cluster (pink), which can thus be related to "healthy" voxels. All the parameters in the clusters 1 and 2 are lower than other clusters and correspond to cerebrospinal fluid except in the tumor or it's probably necrosis. The yellow cluster is similar to the orange cluster but has higher CBV, CBF and$CMRO_2$ (**Fig 2**). The red cluster corresponds to gray matter component.

Tumor is heterogeneously composed of 4 clusters (black, orange, purple and red) but mainly composed of the purple cluster for which the mean transit time is increased. A gadolinium-enhanced scan (**Fig 1a**) shows active lesion, meaning that there is a degradation of the vascular wall integrity explaining the increase in the mean transit time.

Discussion / Conclusion

This study on brain tumor oxygenation is the first report of StO_2 obtained with MRI. StO_2 and $CMRO_2$ seem to provide new information that could contribute to tumor grading and tumor hypoxia evaluation. Cluster analysis can be used to structure the wealth of information gathered with multiparametric microvascular MRI. The cluster-based analysis highlights several types of physiological behavior, which could correspond to different level of the tumor evolution. A cluster-based analysis of the tumor microvascular characteristic has a great potential to ease tumor diagnosis, prognosis, and treatment follow-up.

References

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