Can regional cerebral blood volume be extracted from T2-decay curves?

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INTRODUCTION

Regional cerebral blood volume (rCBV) is an important measure of brain function. Here, we investigate whether it is possible to extract the percent regional cerebral blood volume (rCBV) from accurate water T2-decay measurements performed for spectroscopic quantitation [1]. The T2-measurement of the unsuppressed water signal makes it possible to separate the contributions of cerebrospinal fluid (CSF) from that of brain tissue by means of their substantially different T2-values (≈ 70ms for brain tissue and ≈ 1,000 ms for CSF), and thereby eliminate the effects of water-T2 changes and volume-dilution due to CSF on metabolite concentrations. Since the T2-measurements are highly accurate (typical fitting errors < 1%), it might be feasible to further extract from the T2 signal-decay the contribution of blood, which has an intermediate T2-value of 250-300ms [2].

METHODS

T2-decay data sets from 40 subjects (21 HIV-positive and 19 HIV-negative) were analyzed. Unsuppressed water FIDs were acquired in 4 locations [frontal gray matter (GM) and white matter (WM), parietal gray matter, and basal ganglia, typical volume 6cc], using a single-voxel point-resolved spectroscopy (PRESS) sequence at 7 echo times (TE = 30, 50, 80, 120, 200, 500, 1000 ms). The in vivo data were fitted to a triple-exponential decay with 5 free parameters (S_{brain}, S_{CSF}, S_{blood}, $T2_{brain}$, and $T2_{CSF}$):

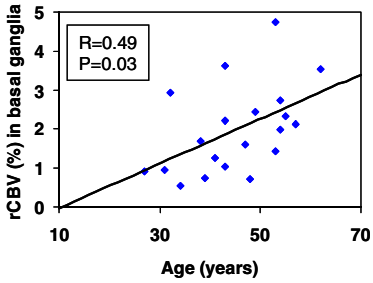
$$S(TE) = S_{brain} \cdot \exp(-TE/T2_{brain}) + S_{CSF} \cdot \exp(-TE/T2_{CSF}) + S_{blood} \cdot \exp(-TE/(275ms)) \quad [1]$$

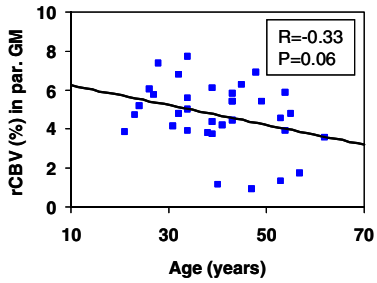
The blood T2-value was fixed at 275ms [2]. A Powell-algorithm was used to minimize the % squared sum between measured and fitted values, with additional cost terms to limit the range of T2 values for brain tissue (70ms±20%) and CSF (900ms±20%). Regional cerebral blood volume was calculated as $rCBV = S_{blood} / (S_{brain} + S_{CSF} + S_{blood})$; values < 0.5% were considered non-physiological and excluded.

RESULTS

rCBV in the cortical gray matter areas was ≈5%, while rCBV in the white matter and basal ganglia were ≈2% (Table). The differences in rCBV between cortical gray matter and the other two regions were highly significant (generally p<0.001), but no differences were found between HIV-positive and negative subjects. There was a correlation between rCBV and age in the basal ganglia (Figure center), and trends for inverse correlations in the parietal gray matter (Figure right) and the frontal gray matter (r = -0.29, p=0.1).

	HIV-negative (rCBV %)	HIV-positive (rCBV %)
Frontal GM	5.4 ± 0.74	6.3 ± 0.72
Parietal GM	4.8 ± 0.40	4.6 ± 0.42
Frontal WM	2.0 ± 0.25	2.1 ± 0.25
Basal ganglia	2.1 ± 0.40	1.8 ± 0.28





DISCUSSION

The white matter and cortical gray matter rCBV values obtained with the T2-decay method are very similar to those in prior studies (Kuppusamy et al: 2.0% and 4.8% [3]; Lu et al: 1.4% and 5.5% [4]). The basal ganglia rCBV in this study is lower than that in other studies [5], but this may be due to the inclusion of white matter in the relatively large MRS voxels. The decline in parietal gray matter rCBV (-10% / decade) is similar to that found in another study [6], but the reason for the increase in basal ganglia rCBV is unclear.

The proposed method for determining rCBV in MRS voxels is based on the differential T2-values of blood versus brain parenchyma and CSF. Advantages of this method include: 1) simultaneous acquisition with MRS data; 2) the ability to use existing T2-decay data; and 3) the method requires relatively few assumptions beyond a T2-value for blood. Accuracy might be improved by adding more TE-values or averaging, and using EKG-gating for acquisition to minimize variability in the rCBV.

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