Calibration of fMRI BOLD Signal: A New Approach

N. Fujita[1], T. Enoki[2], K. Matsumoto[2], H. Tanaka[1], Y. Watanabe[1], H. Nakamura[1], K. Murase[2]

[1]Radiology, Osaka Univ. Graduate School of Medicine, Suita, Osaka, Japan, [2]Allied Health Sciences, Osaka Univ. Graduate School of Medicine, Suita, Osaka, Japan

Synopsis

In the context of quantitative fMRI, baseline deoxyhemoglobin (dHb) content or its equivalent quantity needs to be evaluated in order to calibrate stimulation-induced BOLD signal. This quantity has been indirectly estimated by use of physiologic perturbation such as respiratory CO_2 challenge. Using a direct quantification of dHb-induced R_2', we propose a new approach for calibrating BOLD signal.

Introduction

BOLD contrast reflects the difference in dHb content between task and resting states, which predominantly results in a change in the reversible transverse relaxation rate (R_2') rather than that in the irreversible contribution (R_2) (1). Therefore, the BOLD signal in terms of relaxation rate ($-\Delta S/S/TE$: TE; echo time) corresponds to a change of dHb-induced R_2' ($R_{2'dHb}$), i.e., $\Delta R_{2'dHb}$ In quantitative fMRI, it is well recognised that the measured BOLD response, $\Delta R_{2'dHb}$ needs to be calibrated by baseline dHb content as represented by $R_{2'dHb}$. This quantity has been evaluated from independent measurements of BOLD and CBF under the condition of respiratory CO_2 challenge (2-4). The quantification relies on the relationship: $R_{2'dHb} = \Delta R_{2'dHb} / [(1+\Delta CBF/CBF)^{-(\beta-\alpha)} - 1)]$, where the following conditions are assumed: $\Delta CMRO_2=0$, v (venous fraction of CBV)~ $(CBF)^{\alpha}$, and $R_{2'dHb} \sim$ v (oxygen extraction)$^{\beta}$. In this study, baseline $R_{2'dHb}$ is directly measured in the human visual cortical areas at 1.5 T. The results are compared with those calculated from previous measurements based on the physiologic perturbation and assumptions.

Methods

To evaluate $R_{2'dHb}$, a direct approach based on R_2' quantification was employed under the assumption of a linear relationship between R_2' and dHb content. The details of the method are described (5), but a brief description is as follows. The R_2' measurement was based on a time efficient measurement of R_2^* using a modified GESFIDE sequence (6), and a correction of static field inhomogeneities. The presence of multi-exponential R_2 was found to introduce a substantial bias in the R_2' estimates, and this effect was corrected by means of an additional acquisition using a CPMG sequence.

All experiments were performed using a 1.5T MR system (Siemens, Vision). Eight normal volunteers gave written informed consent prior to participating. Baseline $R_{2'dHb}$ was evaluated using the above-mentioned method (single slice parallel to the calcarine fissure), and a conventional BOLD fMRI experiment (GE-EPI; TE=50 ms) was subsequently performed using photic stimulation (8Hz flicker). Activated voxels for the visual cortical areas were identified ($P<0.001$), and the baseline $R_{2'dHb}$ as well as the BOLD signal change were measured on those voxels.

Results and Discussion

Fig. 1 shows BOLD signal map and corresponding baseline $R_{2'dHb}$ map for a representative subject. The measured $R_{2'dHb}$ values for the activated voxels were summarized in Fig 2, which also shows calculated results from CBF and BOLD data in previous studies at 1.5T by use of respiratory CO_2 challenge. The calculated $R_{2'dHb}$ values, which depended on the assumed values of α and β, overlapped among those studies, but they were significantly different from each other. This might represent technical difficulties inherent to the indirect method. In our study, the average $R_{2'dHb}$ value was 2.64 ± 0.56 (1/s), which was in the intermediate range compared with the previous results. The measured BOLD signal was 1.74 ± 0.41%, and the calibrated BOLD signal, i.e., $\Delta R_{2'dHb} / R_{2'dH}$ was calculated to be -14.1 ± 3.6%. The calibrated BOLD signal represents the relative change of dHb content and, if the change in venous fraction of CBV is assumed to be small, it corresponds to the relative decrease in oxygen extraction.

Conclusion

The results showed that the method proposed here provided a good estimate for baseline $R_{2'dHb}$ without any physiologic perturbation or any physiologic assumption. Combined with fMRI techniques for BOLD as well as CBF measurements, this method will provide a simple and straightforward approach for quantitative fMRI linking the BOLD signal change with the change in physiological parameters such as $CMRO_2$.

References

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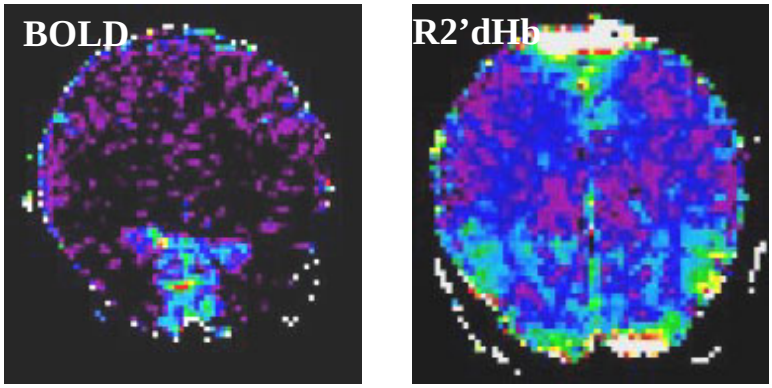

Figure 1

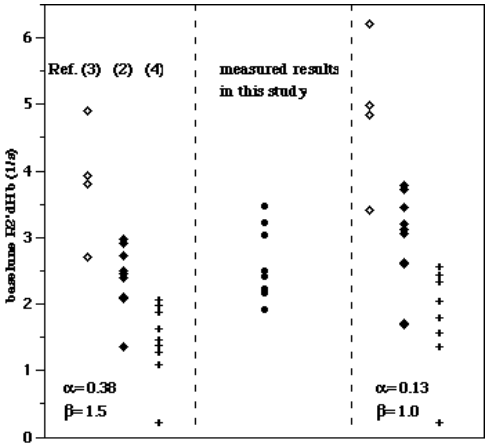

Figure 2