A temporal comparison of diffusion-weighted fMRI, NIRS and BOLD responses to visual stimuli in adult humans

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Introduction

Functional response of diffusion-weighted magnetic resonance imaging (DfMRI) at high b-value precedes that of blood oxygenation level dependent (BOLD) fMRI by several seconds. The evidence suggests a direct link of DfMRI signal to neuronal activation, such as cell swelling [1]. However, it was reported that total hemoglobin response measured with near-infrared spectroscopy (NIRS) also precedes BOLD response [2]. Here, we compared temporal dynamics of DfMRI, NIRS and BOLD response, by conducting simultaneous acquisition of those signals during visual stimulation.

Materials and Methods

Subjects and Equipments: Six male healthy volunteers gave written informed consent to participate in the present study (shaved hair: 5, not shaved hair: 1, age: 19-38). We used a 3T scanner (Trio, Siemens, Erlangen, Germany) equipped with a 8-channel phased-array coil for MRI data acquisition. We examined NIRS response using a multi-channel continuous-wave optical imager (NIRStation, Shimadzu, Kyoto, Japan) with three laser diodes of 780 nm, 805 nm and 830 nm. To record in MRI environment, four 8 m optical fiber cables were used for NIRS data acquisition.

Setting and Protocol: First, four source fibers and five detector fibers (12 channels) were placed in the occipital region of each volunteer to localize the area activated by visual stimulation. Then, for the combined NIRS/MRI acquisitions, two source fibers and two detector fibers (4 channels) were placed over the activated area. The distance between the source and detector pairs was 2.5 cm. Four E-vitamin capsules were placed at the midpoints of the source and detector pairs, as markers of NIRS channel positions (Fig.1). A custom-made cushion was used to set the optical fibers on the occipital area in the supine body position (Fig.2). We measured DfMRI, NIRS and BOLD response to visual stimulation of a flickering dartboard (frequency, 15 Hz) during 3 epochs of 10.5s separated by a 31.5s.

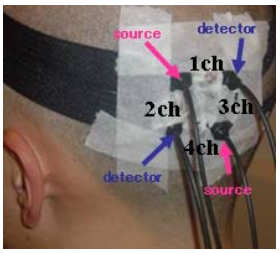

Fig.1. Placement for NIRS measurement. This probe consisted of 2 source and 2 detector positions. The source detector separation was 2.5 cm.

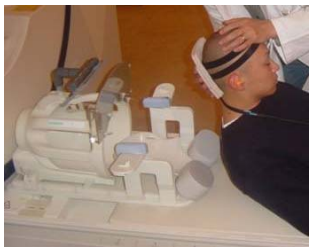

Fig.2. Preparation for simultaneous acquisition of the fMRI and NIRS, demonstrating the positioned probe on a MRI subject.

Acquisition: To minimize residual susceptibility effects DfMRI sequence consisted in a twice refocused spin-echo echo-planar imaging (EPI) sequence sensitized to diffusion by an interleaved pair of bipolar magnetic field gradient pulses [1,3]. Acquisition parameters were: matrix = 96x96x10, voxel size = 2x2x3 mm^2, TE = 89 ms, TR = 1.5 s. DfMRI sequences with Motion-Probing Gradient (b =1,800 s/mm^2) and without (SE-BOLD with b = 0 s/mm^2) were used. GE-BOLD fMRI images were acquired by using a gradient-echo EPI with same parameters (except TE = 30 ms). Temporal resolution of NIRS was 40 ms.

Data processing: We identified activation maps of MRI data using SPM5 software (included slice-timing correction and realignment). All MRI data were analyzed with a box car function to avoid any bias. For NIRS, we selected the channel with the largest changes for further analysis. To compare the temporal dynamics between NIRS and MRI signals, we drew a 30 mm (as well as 40 mm and 50 mm) half-sphere centered on the selected NIRS channel and extracted the raw signal time series from each mode (DfMRI, SE-BOLD, GE-BOLD). To decrease noise, Savitzky-Golay smoothing [4] was used as 3 points for MRI and 125 points for NIRS. Changes in oxygenated, deoxygenated and total hemoglobin concentrations were calculated using the Modified Beer-Lambert law with the extinction coefficients reported by Matcher et al. We used literature values of 5.92, 5.76 and 5.39 for the differential-pathlength-factor (DPF) at 780, 805 and 830 nm, respectively [5].

Results

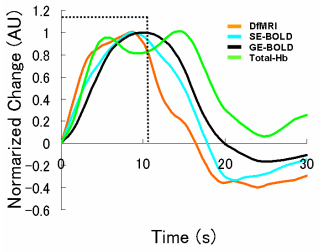

Fig.3. Normalized time courses of DfMRI, SE-BOLD, GE-BOLD and total hemoglobin for six averaged subjects.

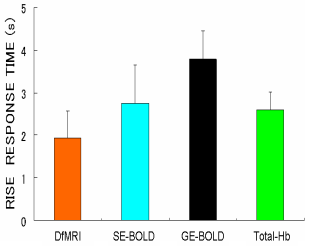

Fig.4. Rise response time in each method defined at 50% of maximal peak. The rise response time of DfMRI was faster than that of total-Hb (p=0.01: paired t-test).

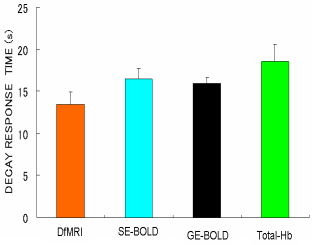

Fig.5. Decay response time in each method defined at 50% of maximal peak. The decay response time of DfMRI was faster than that of total-Hb (p=0.001: paired t-test).

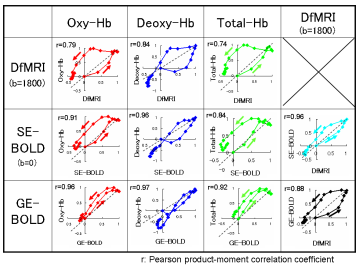

Fig.6. Correlation plots of three fMRI (DfMRI , SE-BOLD, GE-BOLD) time courses and the three hemodynamic time courses in Fig.3 (the arrows indicate the direction of time in the data).

All subjects showed significant activation (data not shown). Time series of 30mm, 40mm and 50mm half-sphere regions of interest (ROI) centering on the selected NIRS channel showed similar tendency (data not shown). Rise response time and decay response time defined as time points at 50% of maximal peak showed that DfMRI response was the fastest than total Hb, SE-BOLD and GE-BOLD (Fig.3, 4, 5). The correlation coefficients for DfMRI, SE-BOLD and GE-BOLD to total-Hb were 0.74. 0.84 and 0.92. The correlation coefficients for DfMRI, GE-BOLD and GE-BOLD to oxy-Hb were 0.79. 0.91 and 0.96. The correlation coefficients for DfMRI , SE-BOLD and GE-BOLD to deoxy-Hb were 0.84. 0.96 and 0.97 (Fig.6).

Discussion and conclusion

We observed clear differences both for the rise response time and decay response time among DfMRI, NIRS, SE-BOLD and GE-BOLD (Fig.4, 6). The rise response time of SE-BOLD and total-Hb were faster than GE-BOLD, in agreement with several previous works [2, 6]. However, we found that the rise response time of DfMRI was even faster than that of SE-BOLD and total-Hb. The decay response time of DfMRI was also the fastest. The correlation coefficients of oxy-Hb, deoxy-Hb and total-Hb signals were smaller with DfMRI than with SE-BOLD and BOLD. Those results strongly suggest that the DfMRI signal may originate from earlier (neuronal) events that precede the vascular response observed with NIRS hemoglobin and BOLD.

References

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