Absolute quantification of cerebral blood flow in normal volunteers: Dynamic susceptibility contrast MRI compared with Xe-133-SPECT

L. Knutsson[1], S. Börjesson[2], E-M. Larsson[3], J. Risberg[2], L. Gustafsson[4], U. Passant[4], F. Ståhlberg[1,3], R. Wirestam[1]

[1]Department of Medical Radiation Physics, Lund, Sweden, [2]Department of Psychology, Lund, Sweden, [3]Department of Diagnostic Radiology, Lund, Sweden, [4]Department of Psychogeriatrics, Lund, Sweden

Introduction

Reproducible absolute quantification of cerebral blood flow (CBF) is desirable, for example, in therapy monitoring, in the assessment of ischemic threshold levels in acute stroke and when a global reduction of CBF can be expected as, for example, in patients with dementia. Studies investigating the quantitative accuracy of current EPI-based dynamic susceptibility contrast (DSC) MRI protocols are sparse, and the present comparison between absolute CBF estimates obtained by DSC-MRI and Xe-133-SPECT in a group of normal volunteers is therefore motivated.

Methods

Absolute CBF was measured in 20 healthy volunteers (45-80 years old) using DSC-MRI and Xe-133-SPECT on different occasions. In the Xe-133-SPECT experiment, xenon gas (500 MBq/L in air) was inhaled during 8 minutes and CBF was calculated using a bi-exponential analysis. In DSC-MRI, the first passage of the contrast-agent bolus was monitored using gradient-echo EPI (GRE-EPI) and CBF was calculated using Zierler's area-to-height relationship and the central volume principle [1]. The deconvolution was performed using a block-circulant singular value decomposition algorithm [2], and regional arterial input functions were retrieved using factor analysis of dynamic studies (FADS) [3]. Large-vessel identification by FADS was also employed for removal of large-vessel hyperintensity in the GRE-EPI-based CBF maps. For accurate absolute quantification of the DSC-MRI-based CBF estimates, a correction of the arterial concentration time integral was introduced (assuming that arterial and venous time integrals are identical). First, a signal curve in the sagittal sinus was selected manually. Typically, such a signal curve is distorted at peak concentration due to local geometric distortion and/or signal saturation. By selecting a small vein at another location, an approximation to the correct shape of the sagittal sinus concentration time curve can be acquired. This curve with correct shape was then time shifted (if necessary) and multiplied by an amplification factor so that the base and flanks of the sagittal sinus concentration time curve closely matched the corresponding parts of the curve from the smaller vein. A range of time shifts and amplification factors were investigated, allowing the sum of the squares of the differences between the included points to be minimized.

Results

DSC-MRI showed an average whole-brain CBF of 85 ± 23 ml/(min 100 g) and the Xe-133-SPECT measurement resulted in a corresponding average whole-brain CBF of 40 ± 8 ml/(min 100 g). Figure 1 shows the individual data points, displayed as CBF(MRI) versus CBF(SPECT). In Fig. 2, an example of CBF maps from DSC-MRI and Xe-133-SPECT is given.

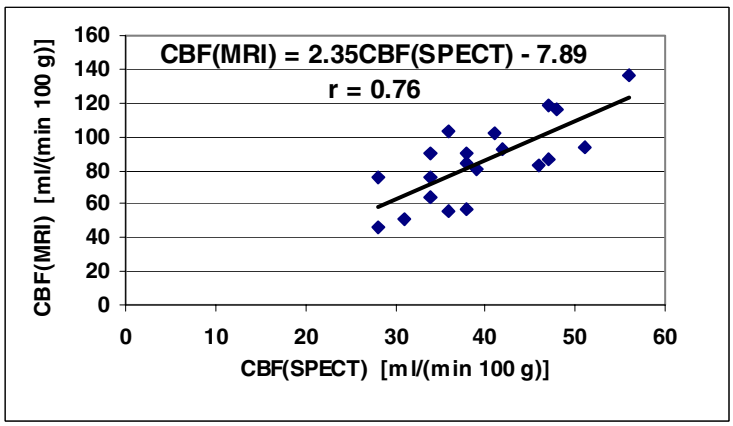
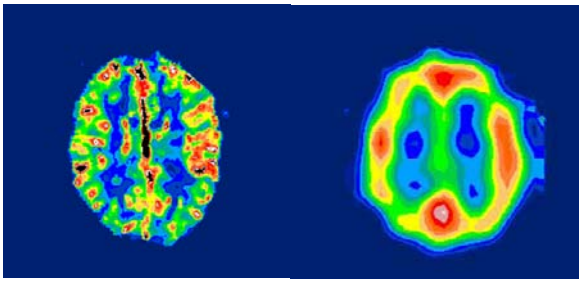


Figure 1. Cerebral blood flow in ml/(min 100g) obtained using Xe-133-SPECT and DSC-MRI in 20 healthy volunteers.



a b

Figure 2. Absolute CBF maps in a healthy volunteer measured by (a) DSC-MRI and (b) Xe-133-SPECT.

Discussion

The correlation between CBF estimates obtained by DSC-MRI and Xe-133-SPECT was quite reasonable (r=0.76), providing that a time-integral correction was performed. If proportionality between the DSC-MRI-based and SPECT-based CBF results is assumed, i.e. CBF(MRI)=k·CBF(SPECT), the present data indicates that k=2.16 (r=0.76). DSC-MRI shows, as in previous studies, overestimated CBF values, but the degree of correlation between the two modalities is indeed encouraging. Finally, the present results are consistent with an earlier CBF study [1], in which a previous-generation Xe-133-SPECT system was compared with DSC-MRI in single-slice mode using a conventional GRE pulse sequence.

References: [1] Wirestam et al., MAGMA 11, 2000, 96; [2] Wu et al., MRM 50, 2003, 164; [3] Knutsson et al., 21st ESMRMB, 2004, 187