Impact of parallel imaging acceleration on perfusion measurements of the rodent brain

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INTRODUCTION The feasibility of dynamic susceptibility contrast (DSC) MRI has been demonstrated to reveal pathological changes of brain perfusion in both humans and small animals [1-3]. In this technique the first passage of a contrast agent through the cerebral tissue is detected. For this purpose, high temporal resolution is required to densely sample this fast change of the signal time curve. In addition, a large coverage of the brain is desired to reveal perfusion changes in the different brain areas. Recently, the parallel imaging technique SENSitivity Encoding (SENSE) [4] has been applied in humans DSC studies to increase the temporal resolution. In this work the parallel imaging techniques SENSE and GRAPPA [5] are applied for accelerating data collection of the rat brain. Furthermore, computer simulations were carried out to investigate potential of acquiring multiple slices at preserved temporal resolutions. The effect of the accelerated data collection was investigated for perfusion parameters like relative cerebral blood volume, mean transit time and relative cerebral blood flow.

METHODS All *in vivo* experiments were carried out on a Bruker BioSpec 94/30 (Bruker BioSpin MRI, Ettlingen, Germany) small animal MR system operating at 400 MHz. A linear polarized volume resonator was used for excitation and a four element phased array surface coil for signal reception.

The experiments were performed on male Lewis rats (200-300g body weight) in strict adherence with the Swiss law for animal protection. In order to generate the susceptibility contrast, an intravascular contrast agent (CA) Endorem® was administered into the tail vein of the animals (dose: 30mg/kg) using an automated injector (injection rate: 0.6ml/s). DSC data were acquired using a gradient echo recalled sequence with the following acquisition parameters: FOV = 26x26 mm², matrix dimension = 200x55, slice thickness = 1.5 mm, pulse angle = 10°, TE = 5ms, TR = 18.2 ms. A series of 128 T2* weighted axial brain images with a temporal resolution of 1s (non-accelerated) were acquired in four animals. In further three rats data collection were accelerated using the parallel imaging technique GRAPPA resulting in a series of 200 T2* weighted images with a temporal resolution of 0.64s and a net acceleration of 1.6 (15 auto-calibration lines). In addition, data were SENSE reconstructed on a separate workstation using an in-house software written in IDL (RSI, Boulder, USA). Coil sensitivities were estimated from additional reference scans.

Computer simulations were carried out to investigate the feasibility of acquiring multiple slices at almost preserved temporal resolution. For this purpose, the time series of the non-accelerated acquisition was decimated by extracting every second and every third image, respectively. The GRAPPA/SENSE accelerated data were decimated by discarding every second image resulting in a temporal resolution comparable to the non-accelerated scans.

Concentration time curves were fitted for a region of interest (ROI) selected in the cortex of the rat brain. From the fitted curve different perfusion parameters such as relative cerebral blood volume (rCBV), mean transit time (MTT) and relative blood flow (rCBF) were derived using the Biomap software (4th version, M. Rausch, Novartis, Basel, Switzerland). The changes of the perfusion values derived from the simulated data were calculated with respect to those derived from the acquired data.

RESULTS For both accelerated and non-accelerated scans sufficient temporal resolution at reasonable signal to noise ratios was achieved to resolve the passage of the CA (Fig. 1). Perfusion values were comparable within the range of the physiological variability, rCBV / MTT / rCBF = 224±145 / 8.6±0.7 / 25.3±14.1 (non-accelerated), rCBV / MTT / rCBF = 198±84 / 8.1±0.8 / 24.3±8.8 (SENSE) and rCBV / MTT / rCBF = 213±79 / 8.2±0.8 / 26.1±8.1 (GRAPPA), respectively. Computer simulations revealed significant changes in the concentration time curve (Fig. 2a) and the derived perfusion parameters (Fig. 3a) for simulated two- and three-fold acceleration of the standard acquisition. In contrast, only minor deviations were found for the simulated acceleration of the SENSE and GRAPPA reconstructed scans (Fig. 2b,c and 3b,c).

DISCUSSION Dynamic contrast susceptibility imaging of the rat brain was successfully accelerated using both the parallel imaging techniques SENSE and GRAPPA. Computer simulations revealed the potential of the accelerated data collection to acquire multiple slices, while providing sufficient temporal resolution. In this work, a net acceleration factor of only 1.6 was achieved to facilitate both parallel imaging reconstructions, SENSE and GRAPPA. Higher acceleration factors are possible using the SENSE technique, if coil sensitivities are estimated from reference scans acquired previous to the time critical DSC scan. Furthermore, the rapid development of phased arrays with a large number of elements in the field of animal MRI might allow for even higher acceleration factors resulting in even larger volume coverage.

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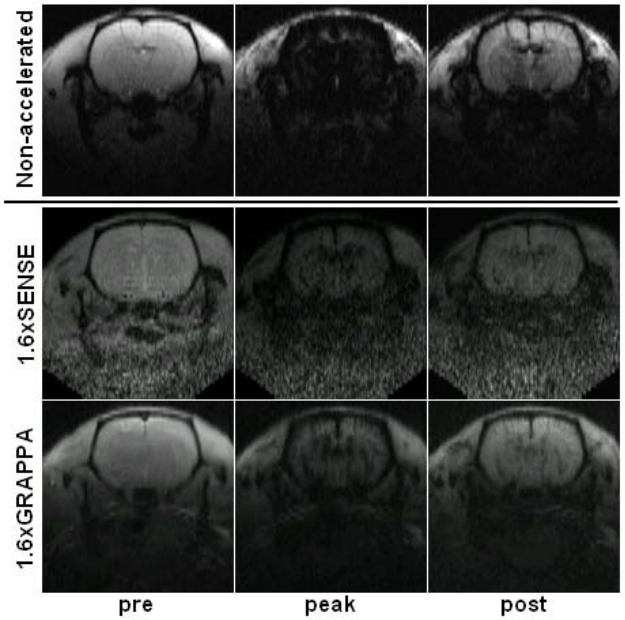

Fig.1: Axial images of the rat brain acquired previous (left), during (middle) and after (post) CA passage. Top row: non accelerated scan, Middle and bottom row: images from SENSE and GRAPPA reconstruction, respectively. Accelerated and non-accelerated images were acquired in two different animals.

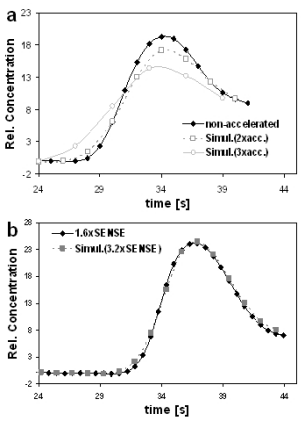

Fig.2: Relative CA concentration calculated from a non-accelerated acquisition and simulated two- and threefold accelerated data (a). Relative CA concentration calculated from SENSE (b) and GRAPPA (c) reconstructed data and corresponding simulations.

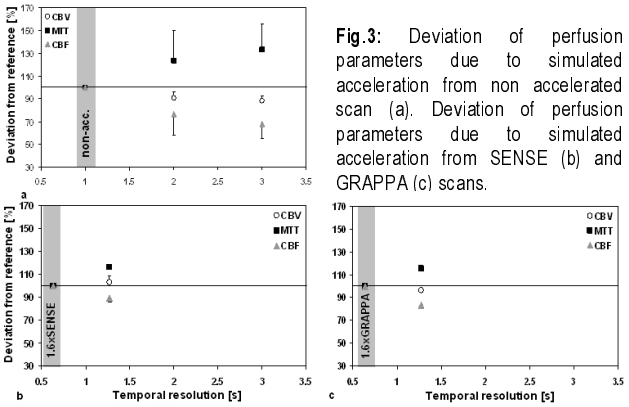

Fig.3: Deviation of perfusion parameters due to simulated acceleration from non accelerated scan (a). Deviation of perfusion parameters due to simulated acceleration from SENSE (b) and GRAPPA (c) scans.