A new 3D method for water and relaxation time mapping: comparison to the 2D “gold standard”

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Introduction

Water concentration is highly regulated in the healthy brain. Several pathologies - stroke, tumour, hepatic encephalopathy, to name a few - were shown to lead to either local or global disturbances in the water distribution and content [1,2]. The highly accurate water mapping methods developed in our group [2,3] were based on 2D acquisitions. However, several applications, such as quantitative VBM and quantitative imaging on small animals, require whole brain coverage with isotropic and high resolution. Here, we have developed a new 3D method for water content and relaxation time mapping in which the magnetisation density and longitudinal relaxation time are determined from a two-point fit to measured data sets including several corrections. The method is based on 3D multiple-echo gradient echo (meGRE) acquisitions, which also allow for accurate determination of the transversal relaxation time T₁*. We have applied this method at 3T to healthy volunteers. Multiple-echo GRE is the method of choice at very high fields due to its low SAR values and at any field it offers a very efficient read-out-time/TR ratio. Since the inhomogeneity of the RF field and the accuracy of its mapping are found to have a large effect on the precision of the method, already at 3T, we have compared the results of the new method to those obtained with a 2D method which combines aspects which can be largely considered to be a “gold standard”: B₁ mapping with the double-angle method and M₀ mapping from proton density images acquired at TR>5T, for the brain tissue. The accuracy of T₁ mapping has been investigated by comparison to results obtained with a fast, accurate, multi-slice Look-Locker sequence, TAPIR [4,5].

Materials and Methods

The basic ingredients of the 3D protocol are: a) two 3D multiple-echo spoiled gradient echo scans with TR=50ms and 12 echoes, b) B₁⁻¹ mapping using AFI [6] and c) B₁⁺ (receiver coil) calibration using GRE scans with short TR. Two reference probes filled with MnSO₄-doped water with T₁ values close to those of WM and GM and water content of 100 and 90% were included in the FOV. The temperature of one probe was continuously monitored during the measurements. The signal equation on which the fit of T₁ and M₀ is based is that of spoiled GRE, as described for example by [7]. Details of the general corrections required for accurate water mapping are given in [2,3]. The flip angles of the two TR=50ms acquisitions were determined based on Monte Carlo simulations such that the accuracy and precision of both M₀ and T₁ mapping were maximised. The optimal flip angles are 7 and 40deg and both the precision and accuracy of the method can be expected to be higher than 10% for T₁ and better than 5% for M₀. They both increase with increasing SNR. Results were obtained from five healthy volunteers (mean age 26y, from 24 to 27) scanned on a 3T TIM-Trio Siemens scanner equipped with a gradient system capable of 40mT/m; body coil (BC) transmit and 12 elements phased-array (PA) receive coil. Other parameters of the experimental 3D meGRE protocol were: FOV=200x162x5128mm³, matrix size=192x156x128, 12 echoes, TE₁=2.33ms, ΔTE=3.89ms; b) for AFI TR=90ms, alpha=60deg, n=5, FOV=same as meGRE, matrix size=192x156x64; for B₁; (receiver coil) calibration TR=7ms, alpha=10deg, FOV=same as meGRE, matrix size=208x256x128, 8avg(B/CA/PA) and 8avg(BC/BC). Slab selective pulses have been used throughout (and mapped with AFI). For the 2D acquisition, 2 sets of 5 slices of 2mm thickness with 1mm gap were acquired, with TR=10000ms and flip angles of 90 and 30deg. The signal intensity is thus purely M₀ and B₁-weighted, with no influence from T₂ effects (except a small factor for CSF) and no expected effects from possibly imperfect spoiling. The latter is a cause of concern for quantitative imaging using acquisitions with short TR [8]. An additional advantage of the very-long-TR data is that all the corrections to M₀ are multiplicative and can be eliminated by proper intensity inhomogeneity correction algorithms without being actually measured.

Results and Discussion

Phantom results obtained with the 3D method are compared in Fig. 1 to spectroscopic results for a range of T₁ and M₀ values relevant for the in vivo case. The agreement is within 5%. Representative M₀ (Fig. 2a) and T₁ (Fig. 2b) maps acquired with the 3D method from a healthy volunteer are compared to the M₀ map obtained with the 2D method for a similar slice (Fig. 2d) and a T₁ map obtained with TAPIR (Fig. 2a) on the same volunteer. The agreement is seen to be very good, and extends to comparison of the mean values and standard deviations of the centroids for M₀, T₁ for GM and WM for all five volunteers. The agreement with the 2D method is within 2% for M₀ and T₁ for T₁ and within 5% for T₁ comparison with TAPIR. We stress the fact that the 2D and 3D methods use very different B₀ fields (and T₂* versus 2D double-angle method) and that the 2-point fitting of the 3D method differs radically from the extensive multi-time-point acquisition of the inversion recovery of TAPIR. Agreement is, of course, expected for methods which are truly quantitative, expected for methods which are truly quantitative, but is seldom met in a survey of the literature regarding, for example T₁ mapping has been investigated by comparison to results obtained with the 3D method are compared to those obtained with a 2D method which combines aspects which can be largely considered to be a “gold standard”: B₁ mapping with the double-angle method and M₀ mapping from proton density images acquired at TR>5T, for the brain tissue. The accuracy of T₁ mapping has been investigated by comparison to results obtained with a fast, accurate, multi-slice Look-Locker sequence, TAPIR [4,5], expected for methods which are truly quantitative, but is seldom met in a survey of the literature regarding, for example T₁ mapping has been investigated by comparison to results obtained with the 3D method are compared to those obtained with a 2D method which combines aspects which can be largely considered to be a “gold standard”: B₁ mapping with the double-angle method and M₀ mapping from proton density images acquired at TR>5T, for the brain tissue. The accuracy of T₁ mapping has been investigated by comparison to results obtained with a fast, accurate, multi-slice Look-Locker sequence, TAPIR [4,5].

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