DREAM - A Novel Approach for Robust, Ultra-Fast, Multi-Slice B_1 Mapping

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Introduction

Fast and robust in vivo B_1 mapping is an essential prerequisite for quantitative MRI or multi-element transmit applications (1-3) like RF-shimming or accelerated multi-dimensional RF pulses. However, especially at higher field strength, the acquisition speed of current B_1-mapping approaches is typically limited by SAR constraints, T_1 relaxation times, or characteristic sequence properties, which makes a multi-transmit element B_1 calibration scan rather time consuming. Moreover, existing B_1 mapping approaches are typically prone to motion, since the flip angle is calculated from two or more acquisitions separated in time. In this work, a novel multi-slice B_1 mapping approach dubbed DREAM (Dual Refocusing Echo Acquisition Mode) is proposed, which derives a 2D B_1 map from a single, ultra-short acquisition of about 130 ms duration, which is more than an order of magnitude faster than most existing B_1 mapping techniques. Moreover, the transceive phase and B_0 are delivered in addition and for free. The performance of the approach is demonstrated in vivo by B_1 mapping experiments in the abdomen at 3T.

Theory

The DREAM method employs a STEAM (Stimulated Echo Acquisition Mode) preparation sequence (4) followed by a tailored single-shot low-angle gradient echo train (Fig.1). In contrast to existing rapid STEAM B_1 mapping techniques (5), both, the free induction decay (FID) and the stimulated echo (STE), are refocused quasi-simultaneously as gradient-recalled echoes I_1 and I_2, and their ratio is used to derive the actual flip angle of the STEAM preparation pulse sequence by a simple analytical expression (Eq.[1-3]). The small delay ΔT between the two echoes I_1 and I_2 is determined by the gradient-time area A_{mc2} of the STEAM dephaser gradient G_{mc2} and the readout gradient strength G_m (Eq.[4]). Moreover, the interval T_S between the STEAM pulses can be chosen to have equal, but *inverted* static dephasing (i.e. T_2*) times for I_1 and I_2 (Eq.[5]). Hence, apart from the actual STEAM flip angle α, the off-resonance phase ϕ_{B0} and the transceive phase ϕ_{B1} can be determined from a single DREAM experiment (Eq.[6-7]).

$$I_1 = \sin(\beta)\cos^2(\alpha)\cdot M_0 \quad [1]$$

$$I_2 = \tfrac{1}{2}\sin(\beta)\sin^2(\alpha)\cdot M_0 \quad [2]$$

$$\alpha = \arctan\sqrt{2I_2/I_1} \quad [3]$$

$$\Delta T = A_{mc2}/G_m \quad [4]$$

$$T_S = 2T_{E1} + \Delta T \quad [5]$$

$$\phi_{B_0} = \arg(I_1 \cdot I_2^*)/2 \quad [6]$$

$$\phi_{B_1} = \arg(I_1 \cdot I_2)/2 \quad [7]$$

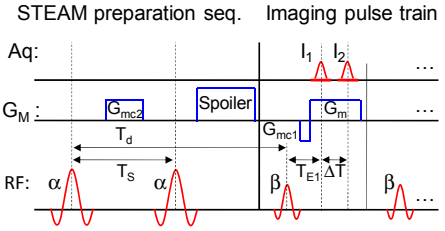

FIG. 1. **DREAM B_1 mapping sequence.** For clarity, the employed slice-selection and phase-encoding gradients have been omitted in this diagram.

Methods

Phantom and in vivo experiments were performed on a 3T MRI system (Philips Healthcare, Best, The Netherlands) equipped with an eight-channel parallel transmit extension (6). The accuracy of the DREAM approach was validated in simulations and phantom experiments, where the DREAM approach was compared with the AFI sequence (7) chosen as a reference. In vivo experiments were performed in the abdomen for five healthy volunteers. Written consent was obtained according to the rules of the institution. Transversal maps were acquired in Multi-2D acquisition (8 slices with FOV= 450×270 mm^2, scan matrix= 64×38, imaging slice thickness = 15 mm, STEAM slice thickness = 45 mm, slice gap = 30 mm, nominal STEAM flip angle α= 70°, nominal imaging flip angle β= 15°, TE_1=2.3 ms, ΔT =-0.6 ms, T_S = 4 ms, T_d =9 ms, TR= 3.2 ms, profiles per shot = 38, total scan duration 1.1 s for 8 slices). The chosen echo timing scheme resulted in fat-water in-phase signals for both echoes, with the stimulated echo acquired first (cf. Eq.[5]). The STEAM slice thickness was chosen larger than the imaging slice thickness to avoid signal contaminations due to slice profile imperfections. Moreover, the slices were acquired in "first odd, then even" acquisition order to avoid slice cross-talk effects. To minimize T_1 effects, no startup echoes were acquired, and a low-high profile order was used. The eight-channel body coil (8) was used in quadrature mode for both, signal transmission and reception. The magnitude of B_1 was derived according to Eq.[3]. In addition, maps of the B_0 field and the B_1 phase were determined according to Eq.[6] and Eq.[7], respectively. The FID signal was also used for masking the B_1 maps by applying a simple signal threshold.

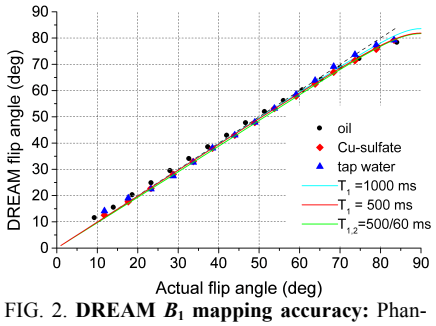

FIG. 2. **DREAM B_1 mapping accuracy:** Phantom experiments (filled symbols) and simulations (curves) are shown. The experimental values are plotted against corresponding AFI measurements, which were chosen as reference.

Results

Both, simulations and phantom experiments show a relatively good accuracy of the DREAM approach for STEAM flip angles from 10° to 70° with absolute deviations smaller than 2° for a broad range of T_1 and T_2 values (Fig.2). Figure 3 shows DREAM B_1 and B_0 maps of the abdomen along with the underlying FID and STE images. The dielectric shortening of the wavelength leads to typical standing wave patterns and inhomogeneous B_1, which are visible in the phase and magnitude maps of B_1, respectively. The slice through the pelvis partly exceeds the homogeneity sphere of the magnet, which is nicely depicted by the corresponding B_0 map (cf. Fig.3 right bottom).

Discussion

The DREAM approach offers some very favourable properties: The two signals, from which the flip angle is derived, are generated by a single RF pulse. Moreover, the B_1 mapping sequence is divided into a preparation sequence for B_1 encoding and an imaging sequence for spatial encoding. This results in an extremely short acquisition time and a rather low SAR burden. Furthermore, motion is efficiently frozen due to the short acquisition duration per slice. Finally, the transceive phase is delivered, facilitating advanced applications like local SAR determination via B_1 mapping (9).

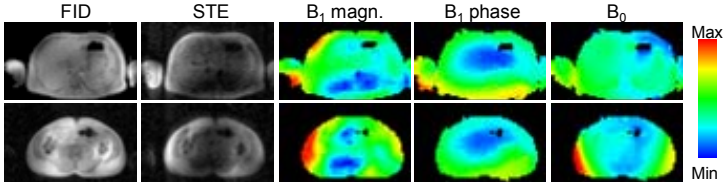

FIG. 3. **DREAM in vivo experiments:** Two selected slices are shown from the eight-slice data set measured in 1.1s (top: liver, bottom: pelvis).

References

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