Accuracy of T_1 and equilibrium magnetization maps using a spoiled gradient-recalled echo sequence with variable flip angles at 4.7 T, 7 T, and 9.4 T: A gadolinium-doped gel phantom study.

H. Kuribayashi[1], T. Minowa[2], Y. Maitani[2], M. Sekino[3], H. Ohsaki[3], M. Ueda[4], and Y. Katayama[4]

[1]Varian Inc., Minato-ku, Tokyo, Japan, [2]Hoshi University, Shinagawa-ku, Tokyo, Japan, [3]The University of Tokyo, Kashiwa, Chiba, Japan, [4]Nippon Medical School, Bunkyo-ku, Tokyo, Japan

INTRODUCTION

A T_1map is required for some quantitative MR imaging applications. In dynamic contrast-enhanced (DCE) MRI, a T_1map obtained before contrast agent administration allows us to convert image intensity into gadolinium concentration. Spoiled gradient-recalled echo (SPGR) sequence with variable flip angle (VFA) method has been widely used to construct T_1map. However, in our mouse DCE-MRI experiments at 9.4 T, we observed shorter T_1 values in gadolinium-doped agar gel phantoms alongside the animal from the SPGR-VFA approach compared to the corresponding T_1s measured separately by inversion recovery (IR) 1D NMR spectroscopy. Thus, we investigated the T_1map accuracy of the SPGR-VFA approach. Because the 9.4 T is classified as high field in MR and T_1 has magnetic field dependence, the examination was also carried out at 4.7 and 7 T using the same set of the phantoms. In addition to T_1map, an equilibrium magnetization (Mo) map, which could be obtained together with T_1map calculation, is also used to quantify the gadolinium concentration in DCE-MRI. Therefore, Momap accuracy was also examined.

METHODS

Agar gels (4 % w/w, Agarose S, Nippon Gene) doped with various Gd-DTPA (Magnevist, Bayer) concentrations, giving different relaxation times, were prepared in 5-mm NMR test tubes. Each T_1 and T_2 was measured separately using IR and Carr-Purcell Meiboom-Gill 1D NMR spectroscopy, respectively. The relaxation times and MR images of the phantoms were acquired at room temperature using a 4.7 T and a 7 T horizontal MRI (UNITYINOVA, Varian) and a 9.4 T vertical MRI (Varian MRI System, Varian). The 4 tube phantoms were placed parallel to the main field inside the magnet and scanned as a single slice axial 2D image. In the SPGR-VFA sequence, the flip angles (α) were 2^o, 5^o, 10^o, 20^o, and 30^o. TR of 7.8 ms was chosen to give 1-s imaging temporal resolution in the DCE-MRI application with 64-phase-encoding steps and 2-averages. Four different TRs (7.8 (tr), 39.0 (5tr), 78.1 (10tr), 117.2 (15tr) ms) were also examined. Steady-state pulses were applied for longer than 15 s. IR-prepared SPGR sequence was also used to obtain T_1map for comparison. The IR was performed using a 180^o hard RF pulse followed by a gradient crusher pulse. Inversion times (TI) were 0.01, 0.03, 0.05, 0.1, 0.3, 0.5, 1, 3, 5, 10 s. A full k-space of the following SPGR was sequentially filled with a centric-ordered k-trajectory and $\alpha = 10^o$. The repetition of the IR pulses was 15 s. The other MRI parameters were: TE = 3 ms, FOV = 30 × 30 mm, slice thickness = 4 mm, matrix size = 64 × 64. Both RF and gradient spoilers were applied. As additional information, T_2*maps were also obtained using SPGR with 12 different TEs (3-36 ms) and TR = 50 ms.

Pixel-by-pixel T_1 and Momaps from SPGR-VFA data were calculated using MATLAB (MathWorks). The fitting equation was a linear form of the SPGR steady-state signal intensity (Si): $Si/\sin\alpha = Si\exp(-TR/T_1)/\tan\alpha + Mo(1-\exp(-TR/T_1))$. The maps from IR-SPGR data and the T_2* maps were calculated using VnmrJ Math Fit Program (Varian) with fitting equations of $Si = |(S(0) - Mo)\exp(-TI/T_1) + Mo|$, where S(0) is the calculated signal intensity at TI = 0 s, and of $Si = Mo(1-\exp(-TE/T_2^*))$, respectively. T_1 and T_2* of these phantoms were measured as the mean intensity in a square region of 5×5-pixels placed on the centre of each phantom image.

RESULTS

Fig. 1 (top) shows the T_1s of the 0 mM Gd-DTPA-doped agar gel measured using the VFA with tr, 5tr, 10tr, 15tr (dark blue-to-yellow), the IR-SPGR (orange) and IR 1D NMR methods (dark red) at the 3 different field strengths. The T_1s measured using the VFA method with TR = 7.8 ms were much shorter than those from the IR-SPGR and the IR 1D NMR, which were in close agreement. Moreover the shortened T_1s from the VFA method showed a recovery profile with increasing TR. The recovery profiles without the shortest T_1 were fit with a single exponential function against TR. Fig. 1 (bottom) shows the T_1s of the 0.5 mM Gd-DTPA-doped agar gel. The severity of shortening T_1 measured using the VFA method at 4.7 T and 7 T was diminished compared with that of the longer T_1 gel phantom. The recovery profile including the shortest T_1 at 4.7 and 7 T was fit with a single exponential. The T_1s of all phantoms (0-1 mM [Gd]) from the VFA at 9.4 T was much shorter than those from the other approaches. T_2* didn't show gadolinium concentration dependence. However, the averaged T_2* among all of the phantoms decreased suddenly from 4.7 T (60.4 ± 27.6 ms) to 7 T (18.7 ± 7.4 ms) and did slightly to 9.4 T (14.8 ± 5.9 ms). Interestingly, Momaps from the VFA method showed consistent Mo values among the variable TRs (Fig. 2) in contrast to the shown recovery profile of T_1 with increasing TR (Fig. 1).

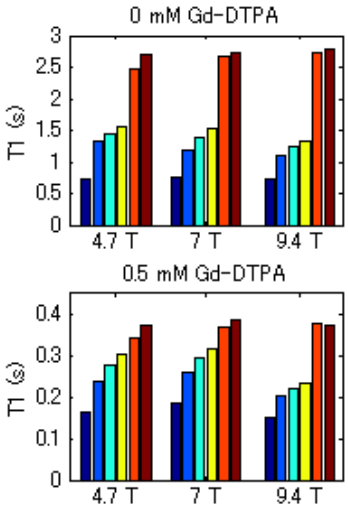

Fig. 1 T_1 of 0 mM (top) and 0.5 mM (bottom) Gd-DTPA-doped agar gel.

DISCUSSION

We demonstrated that the T_1 obtained using the SPGR-VFA method with short TR was underestimated. As Ref. (1) reported, The T_1 at 4.7 T and 7 T might be corrected with variable TR data except for that of TR = 7.8 ms, even though such short TR has been frequently used especially for 3D MRI studies. With TR = 7.8 ms, noise bias and spoiling imperfection (2) might increase apparent signal intensity and underestimate the T_1. The short T_2* won't be the main reason of the shortening T_1 from the SPGR-VFA at 9.4 T. Constant Mo with different TRs will be an important key for a further investigation of T_1map accuracy of the SPGR-VFA method. The IR-prepared SPGR should be a chosen T_1map method especially for long T_1 and/or at high field MR.

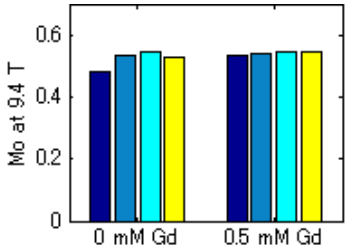

Fig. 2 Mo of 0 and 0.5 mM [Gd] gel from the VFA method with tr, 5tr, 10tr, and 15tr (left-to-right) at 9.4 T.

REFERENCES

1. Fleysher R et al., *ISMRM 2008* p. 1406. 2. Yarnykh V L., *ISMRM 2008* p. 234.