Bi-component analysis of UTE images: a feasibility study

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INTRODUCTION

Biological tissues commonly contain distinct water compartments and display multiple T2 relaxation behavior (1-3). It is of great interest to measure T2 and fractions of these components. Current standard techniques are based on multi-component fitting of multiple spin-echo images acquired with CPMG sequences, which on clinical scanners typically have echo times (TEs) > 10 milliseconds, thus rather too long to detect the short T2 components. In fact there are a group of musculoskeletal (MSK) tissues such as menisci, ligaments, tendons and cortical bone which show little or no signal with clinical CPMG or gradient echo sequences. Both free water and water bound to the collagen fibers are typically 'invisible', and therefore their T2 values and fractions are virtually unknown. Here we propose a bi-component T2* analysis of images acquired with an ultrashort TE (UTE) sequence with a minimum TE of 8 μs to quantify the free and bound water components (4).

MATERIALS AND METHODS

A 2D UTE sequence with a minimum TE of 8 μs was implemented on a clinical GE 3T scanner.

$$SI(t) = M_{z0,b} \times e^{-t/T_{2b}^*} + M_{z0,f} \times e^{-t/T_{2f}^*} + \text{noise} \quad [1]$$

T2* and fractions of the multi-components can be measured through exponential fitting of UTE images. Considering that multi-component fitting is sensitive to SNR, number of components, and the separation of the T2 values, the following steps were employed to minimize fitting errors. Firstly, only two components, namely free water (T^*_{2f}, $M_{z0,f}$) with longer T2*, and bound water (T^*_{2b}, $M_{z0,b}$) with much shorter T2*, were assumed for bi-exponential fitting. Under this model, the UTE signal is given by equation [1]. Secondly, background noise was estimated through a comprehensive four-step noise estimation algorithm, where maximum likelihood (MLE) distribution fitting of a partial histogram was used to robustly estimate noise. Thirdly, the UTE signal with a near zero TE of 8 μs was normalized. The sum of the amplitude of the two components should equal 1, thus another degree of freedom was regained. The above three procedures reduced the fitting parameters down to only three parameters ($T2^*_b$, $T2^*_f$, $M_{z0,b}$ or $M_{z0,f}$), thus is expected to greatly improve the robustness of the fitting.

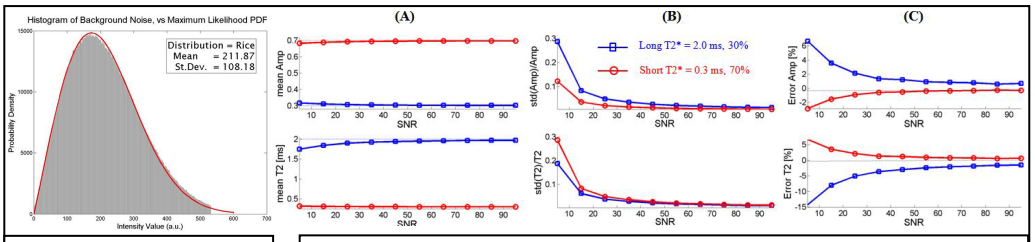

Fig 1 *Noise estimation based on MLE histogram fitting.*

Fig 2 *Numerical simulation on the modified bi-component model: the estimated T2* and fractions (A), standard errors (B) and relative errors (C) as a function of SNR.*

Simulation, phantom and in vitro specimens were performed for this feasibility study. Numerical simulation was performed on a two-component model where a longer T2* of 10 ms with a fraction of 30%, and a shorter T2* of 1 ms with a fraction of 70% were assumed. The bi-component model was further validated on a phantom with 50% long T2* (~10.5 ms) and 50% short T2* (~1.0 ms) by doping different levels of $MnCl_2$ solution in distilled water. The model was finally applied to the following in vitro specimens: goat PCL (n = 3), bovine tendons (n = 3), cadaveric human menisci (n = 3), and bovine cortical bone (n = 5). Typical imaging parameters included: TR = 200 ms, FOV = 10 cm, reconstruction matrix = 256 to 512, 355 half projections, slice thickness = 2 to 5 mm, 10 to 34 TEs. Since these cadaveric specimens varied greatly in T2* and fraction values for the free and bound water components, we did not intend to optimize the imaging parameters which were determined empirically for this feasibility study.

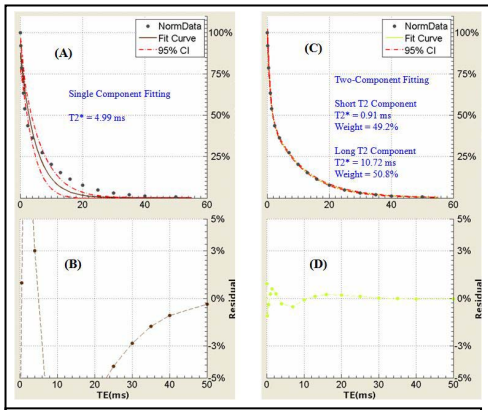

Fig 3 *Bi-component phantom study: single-component fitting (A, B) show significant error, bi-component fitting (C, D) accurately predicts T2* and fractions.*

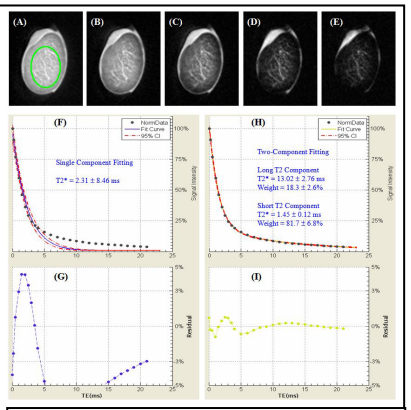

Fig 4 *UTE imaging of a goat PCL (A-E), single (F, G) and bi-component (H, I) fitting with residuals, T2* and fractions shown.*

RESULTS and DISCUSSION

Fig 1 shows an example on background noise estimation where a Rician distribution has been fitted to the signal histogram to estimate background noise. Simulation results based on the modified bi-component fitting model were shown in Fig 2, demonstrating that the new model can accurately estimate T2* and fractions of the two components with a clinically achievable SNR of around 50, with fitting error less than 3%. The results on phantom study were shown in Fig 3, where both single-component and bi-component T2* fitting of UTE images with 12 echoes were performed for comparison. Fig 4 shows selected UTE images of a goat ligament sample, as well as single and bi-component fitting. Two-component fitting significantly reduces the residual signals and shows a short T2* of 1.45 ± 0.12 ms and long T2* of 13.02 ± 2.76 ms with a fraction of 81.7% and 18.3%, respectively. Figure 5 shows selected UTE images of a bovine cortical bone and a two-component curve fitting, demonstrating excellent fitting with a bound water T2* of 271 μs and fraction of 75%, and free water T2* of 3004 μs and fraction of 25%. T2* is known to be sensitive to local field inhomogeneity. However, for short T2 species, T2* approximates T2 and local field inhomogeneities play a much reduced role, thus the robustness of bi-component analysis is improved. The relatively long quantification time may limit its potential clinical application. UTE spectroscopic imaging (UTESI) is able to provide UTE images in a very time efficient way, thus potential for clinical UTE T2* bi-component analysis in vivo (5).

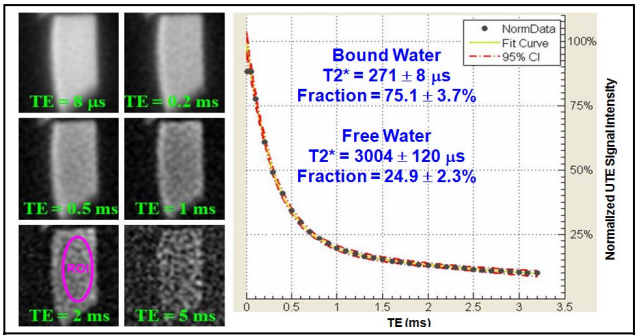

Fig 5 Selected UTE images of a bovine cortical bone and a two-component curve fitting of signal from an ROI, demonstrating a bound water T2* of 271 μs and fraction of 75%, and free water T2* of 3004 μs and fraction of 25%.

CONCLUSIONS This study demonstrates that the 2D UTE bi-component T2* analysis is able to quantify T2* and fractions of the free and bound water components in short T2 MSK tissues such as menisci, ligaments, tendons and cortical bone in vitro using a clinical 3T MR system.

REFERENCES 1. Whittall KP al., MRM 1989. 2. Reiter DA, MRM 2009. 3. Qian Y, et. al., ISMRM 2010. 4. Du, et al., MRM 2007; 5. Du, et al., JMRI 2008.