Excitation and preparation pulses affect UTE bi-component analysis of bound and free water in cortical bone

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INTRODUCTION

Biological tissues frequently contain distinct water compartments with different transverse relaxation times. Multi-component fitting techniques are important for realistic analysis of T2 relaxation curves (1-3). For cortical bone it is impractical to generate T2 relaxation curves using whole-body clinical MR systems due to the relatively long minimum TEs of spin echo sequences. It is much easier to generate T2* relaxation curves which potentially can be used to separate bound water with a shorter T2* from free water with a longer T2* (4-6). However, bound and free water T2*s and the relative fractions are affected by multiple factors including excitation and preparation pulses. In this study we investigated the effect of excitation pulse shape, fat saturation pulse, long T2 saturation pulse and adiabatic inversion pulse on ultrashort echo time (UTE) bi-component analysis of bound and free water in bovine and human cortical bone samples.

MATERIALS AND METHODS

Three bovine cortical bone samples （length×width×height~10×10×10 mm^3 ） and three cross-sectional human tibial midshaft samples （thickness~20-30 mm） were harvested from cadaveric leg specimens which had been cleared of external muscle and soft tissues. The bovine and human cortical bone samples were subject to non-slice selective 2D UTE imaging using a 3 T GE whole-body scanner. **Figure 1** shows the pulses sequences, including the basic 2D UTE sequence with a short rectangular pulse (duration = 32 μs) or a short half pulse (duration = 477 μs) for signal excitation, and their combination with a chemical shift based fat saturation (FS) pulse, a long T2 saturation (SAT) pulse (8 ms Gaussian pulse) or an adiabatic inversion recovery (IR) pulse (duration = 8.6 ms). The basic 2D UTE imaging protocol used the following parameters: TR = 300 ms, field of view (FOV) = 8 cm, matrix = 256×256, band width = 125 kHz, 20 TEs (0.01, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6. 0.8, 1.0, 1.2, 1.4, 1.6, 2, 2.5, 3, 4, 5, 6, 7, 8 ms), 2 minutes per image. A home-built birdcage coil (~2.5 cm in diameter) was used for signal excitation and reception. Each bone sample was placed in a 30 ml syringe filled with perfluorooctyl bromide (PFOB) during MR imaging to maintain hydration and minimize susceptibility effects at air-bone junctions.

A semi-automated matlab program was developed for UTE bi-component analysis, where three fitting parameters (bound water T2*, free water T2*, bound or free water fraction) were subject to non-negative least-square curve fitting with background noise automatically estimated based on maximum likelihood estimation (MLE) distribution fitting of a partial histogram (4). The bound and free water T2*s as well as their relative fractions for all six cortical bone samples were compared for each of the eight acquisition modes.

RESULTS and DISCUSSION

Two distinct T2* components were detected in cortical bone as demonstrated in **Figure 2.** Significant errors (residual > 10%) were seen with single-component fitting. Excellent fitting (residual < 1%) was achieved with the bi-component model, suggesting the existence of two distinct components (bound vs free water) in bone.

Figure 3 shows representative bi-component curves fitting of UTE images of a bovine cortical bone sample acquired with rectangular and half sinc pulse excitations, fat suppression, long T2 saturation as well as adiabatic inversion, respectively. Significant errors were seen with single-component fitting (not shown). Excellent fitting was achieved with the bi-component model.

Figure 4 shows average (over all five bovine bone samples) of bound and free water T2*s and their relative fractions derived from the eight UTE acquisition modes. Bound water T2* ranged from 0.28 to 0.32 ms. Free water T2* ranged from 1.92 to 2.02 ms. Bound water fraction ranged from 62% to 100%. Similar trends were found for the five human cortical bone samples.

Bound water fraction is slightly higher with rectangular pulse excitation due to more efficient excitation of shorter T2* tissues with a short hard pulse. Fat saturation leads to reduced bound water fraction due to direct saturation effect. Long T2 saturation leads to increased bound water fraction since free water signal is suppressed. IR pulse tends to invert and null free water. Only bound water is detected with this sequence.

CONCLUSIONS

UTE bi-component analysis provides information on T2*s and fractions of bound and free water in cortical bone. It is affected by pulse shape and preparation pulses.

REFERENCES

1. Reiter DA, MRM 2009.
2. Horch RA, MRM 2010.
3. Nyman JS, Bone 2008.
4. Du J, et al, MRM 2011.
5. Bae W, JBMR 2012.
6. Biswas R, Bone 2011.

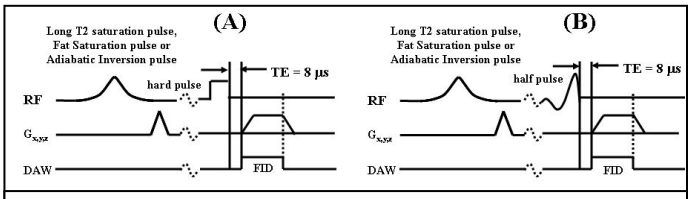

Fig 1 *2D non-selective UTE imaging with rectangular (A) or half (B) pulse excitation The basic UTE sequences can be preceded by long T2 saturation, fat saturation or adiabatic inversion pulse for UTE imaging of bone with bi-component analysis.*

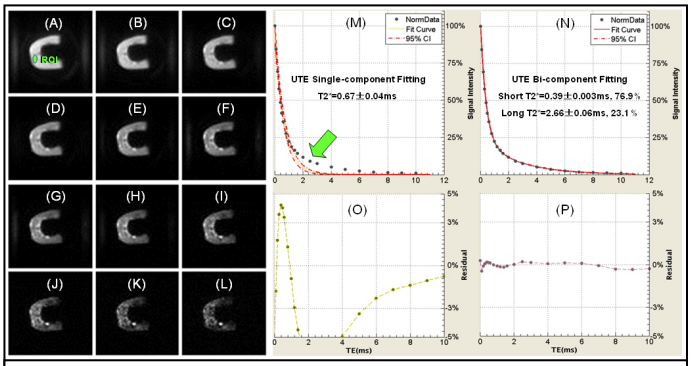

Fig 2 *Selected UTE imaging of a human cortical bone sample with TEs of 10 μs (A), 0.2 ms (B), 0.4 ms (C), 0.6 ms (D), 0.8 ms (E), 1.2 ms (F), 1.6 ms (G), 2.0 ms (H), 3.0 ms (I), 4.0 ms (J), 5.0 ms (K), and 6.0 ms (L), single- (M) and bi-component (N) fitting and the corresponding fitting residuals (O, P). Single-component fitting shows significant residual signal (> 10%). The residual signal is reduced to less than 0.5% by bi-component fitting, which shows a shorter T2* of 0.39 ms and a longer T2* of 2.66 ms with respective fractions of 76.9% and 23.1% by volume.*

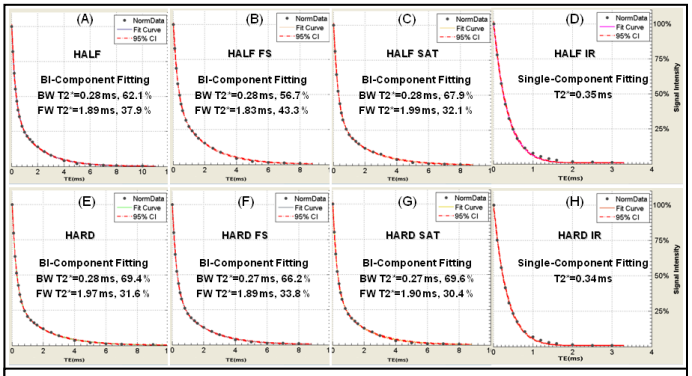

Fig 3 *Bi-component analysis of UTE images of a bovine bone acquired with a rectangular pulse (1st row) and a half-pulse (2nd row) without prep pulses (A, E), with a fat sat pulse (B, F), a long T2 sat pulse (C, G) or an adiabatic IR pulse (D, H).*

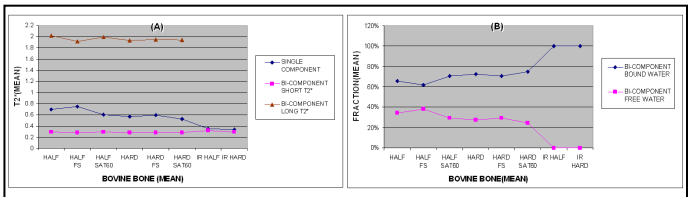

Fig 4 *Summary of bound water T2*s (A) as well as bound and free water fractions (B) from bi-component analysis of the 8 acquisition modes shown above. Bound water fraction is higher with rectangular pulse excitation. Fat sat leads to reduced bound water fraction. Long T2 sat pulse leads to increased bound water fraction. IR pulse tends to null free water, leading to selective imaging of bound water in bone.*