ADVANCED BI-EXPONENTIAL ANALYSIS OF T2* IN THE ACHILLES TENDON OF PRE- AND POST-OPERATIVE PATIENTS USING A VARIABLE ECHO TIME SEQUENCE AT 3T

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Target audience

Musculoskeletal radiologists, physicists developing sequences for imaging of fast relaxing tissues

Introduction

The Achilles tendon (AT) is highly an organized tissue characterized by very short relaxation times on MRI (1). A novel multi-echo, variable echo time sequence (VTE) with sequentially shifted echo times enables quantitative MR imaging of the AT (and other fast-relaxing tissue) with very low echo times(2). The purpose of this study was to compare the mono- and bi-exponential curve-fitting performance for T2*-relaxation time calculation compared to clinical scoring in patients with an AT injury and in healthy volunteers at 3T.

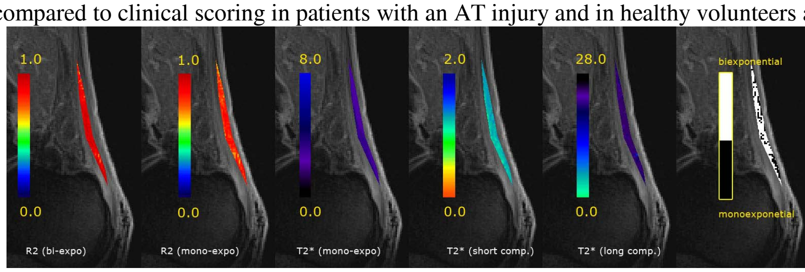

Figure 1. Example of T2 maps from a 23-year-old healthy volunteer.*

Materials and Methods

Institutional Review Board approval and written, informed consent were obtained. Ten patients (mean age, 43.9 ± 13.4 years) with a painful AT and ten age-matched, healthy volunteers (mean age, 43.7 ± 11.2 years) were examined with a 3T whole-body system, using an 8-channel knee coil. For quantitative bi-exponential T2* assessment, a multi-echo, variable echo time (me-vTE) sequence was performed. This sequence is based on 3D Cartesian spoiled gradient echo (SPGR) for sub-millisecond echo times using a variable duration phase and slice encoding gradient. The center of the k-space is sampled with a much shorter echo time compared to the outer areas; this results in a sub-millisecond effective echo time. Twenty echo times were used: TE = 0.8, 2.218, 3.126, 4.124, 5.122, 6.12, 7.118, 8.116, 9.114, 10.112, 11.1, 12.098, 13.096, 14.094, 15.092, 16.08, 17.078, 18.076, 19.074, 20.072 ms. Other parameters were set as follows: field of view, 118 x 180 mm; matrix, 168 x 256; section/slice – thickness, 0.7 mm, 320 Hz/pixel bandwidth; 144 sections; with a total acquisition time of 12.16 min. Mono- and bi-exponential pixel-wise fitting was performed using the following functions: SI=S0*exp(-TE/T2*) and SI = S0 * [exp(-TE/T2*s) + exp(-TE/T2*l)]. Pixels in which the ratio between the long and short T2* components was higher than five were considered bi-exponential, otherwise mono-exponential. T2* values were calculated using a manually drawn ROI analysis for the most severe pathology in patients and for the distal two-thirds of the AT in volunteers. All subjects were rated according to the Achilles tendon Total Rupture Score (ATRS; 0-100 points)(3). Statistical measures included an analysis of variance and Pearson correlation coefficient(r). We compared healthy volunteers with patients using these parameters: T_2*mono; T_2*short; and T_2*long.

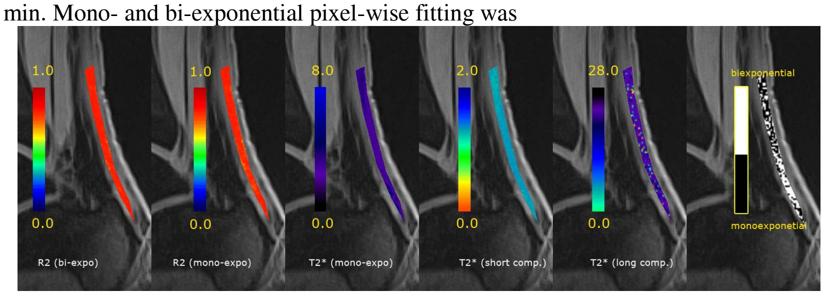

Figure 2. Example of T2 maps from a 64-year-old patient with an ATRS of 45. Note the higher diversity of the long T2* component as well as bi-exponential pixels.*

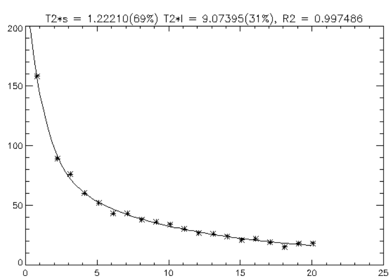

Figure 3. Example of bi-exponential fitting curve of the pixel in AT

Results

In volunteers, the mean T2*mono was 1.39±0.59 ms, T2*short was 0.56±0.31, and T2*long was 24.88±6.52 (Fig. 1). In patients, the mean T2*mono was 2.13±0.91 ms, T2*short was 1.37±0.87, and T2*long was 24.35±14.32 (Fig. 2). Respective T2* values for patients and volunteers were statistically significantly different, except for T2*long. Mean ATRS for patients was 56.30±24.94. A strong correlation was found between the ATRS and mean T2*mono (r=-0.793,R2=0.629,P<0.001), as well as for T2*short (r=-0.861, R2=0.432, P<0.001). No correlation was found for T2*long and ATRS (r=0.079,R2=0.013,P<0.001).

Discussion

Mono-exponential curve-fitting for T2* calculation in AT can lead to misinterpretation of the results. The suggested algorithm for bi-exponential T2* fitting enables T2* to be a robust parameter that correlates with the actual clinical condition of the patient's tendon. T2* short may be a predictive marker for the probability of an AT rupture, as well as for a re-rupture after surgery.

Conclusion

Bi-exponential fitting, although it is computationally more demanding, is also more precise and also allows distinguishing between bound and free water molecules.

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