Introducing Dynamic Multi-exponential T2-Relaxation for Studying Muscle Pattern and Activation in the Human

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Introduction: MR Studies of skeletal muscle, their composition, physiological and patho-physiological responses to exercise have gained increased popularity with recent advances in MRI and have become an interesting complementary technique in addition to the direct measures of muscle activity, e.g. electromyography EMG. MRI is particularly useful for mapping spatial variations of anatomy and activity within a muscle that could remain completely undetected with EMG. The quite established technique of muscle functional imaging relies on the activity induced increase of T2 of muscle water. Because of its sensitivity T2-muscle mapping holds great potential for demonstrating patterns of muscle activation of normal and pathological or diseased states [1]. The early work of Bratton [2] explained the increase of T2 under muscle contraction by release of protein-bound water molecules in exchange with free water (two compartment model). For this model the underlying water exchange times have to be smaller than the time scale of the MR-experiment. Furthermore recent findings of Saab et al. [3] demonstrated multi-component T2 relaxation even in in-vivo tissue but their technique did not provide any spatially resolved data. With recent advancements in high precision multi-relaxation data acquisition techniques even on conventional whole body MRI-systems as demonstrated in [4], we introduce the ability of an in-vivo spatial and dynamic resolved multi-component relaxation technique for the human muscle anatomy. This technique could not be used until recently for this type of measurements in such problematic areas as the human muscle anatomy because of its inherent problem with generating slice excitation as well as refocusing patterns from inhomogenous RF that lead to contaminated T2-echo decay curve due to stimulated echoes and makes revealing multiple components impossible. With the use of a B1-NNLS correction technique, as originally proposed by Jones [5] and recently adopted in a clinical research study for myelin water imaging by Pasloski et al. [6], as well as the ability to control B1-homogeneity with a multi-transmit system, we could demonstrate the feasibility to decompose multiple relaxation compartments in the human calf-muscle with high spatial and sufficient dynamic resolution.

Methods: MR-relaxation measurements on the calf-muscle of 2 healthy volunteers were carried out with two approaches: 1. 3D-multi-echo accelerated GRASE with 32 echoes at TE=10ms spacing [4] and 2. a multi-echo MS-FSE sequence with TE=6.2ms on a 3T Philips Ingenia system with multi-transmit ability (RF-shimming) and using a dedicated small phased-array coil. For the static imaging of multi-compartment anatomy 5 slices were acquired in less than 5min. Additionally a dynamic multi-echo 2D-FSE was facilitated after calf-muscle exercise to monitor the various T2-components while returning into the muscle's rest state over a period of 20 min with a dynamic resolution of 1min.

Results: Fig.1 depicts the various anatomical compartments in the human calf based on their geometric mean T2, an average measure of relaxation based on multi-component T2-relaxation [7]. In fig.2 the gastrocnemius muscle was identified (blue) and a T2-deconvolution obtained from all data in the ROI (blue), revealing two components of intra-extracellular water. Additionally four other major muscle structures were investigated: the soleus, flexor digitorum longus, tibialis anterior and peroneus longus brevis muscle (ref. table 1).

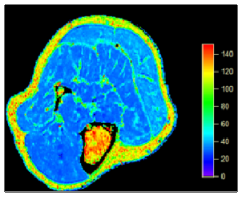


Fig.1: geometric mean T2-map

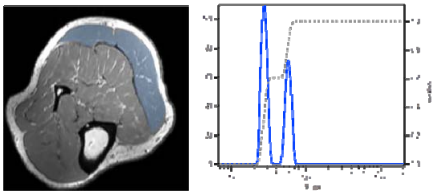


Fig.2: ROI-T2-NNLS analysis of the gastrocnemius medial and lateral muscle, identifying two T2-components at 30ms (60%) and 60ms (40%).

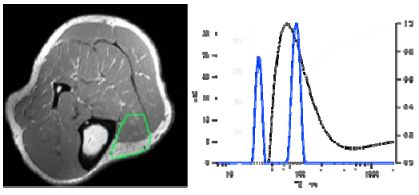


Fig.3: partial averaging of muscle and fatty tissue. Without B1-correction a distinct deconvolution of the components is impossible (dashed line).

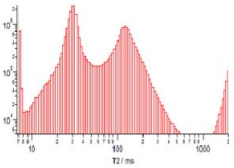
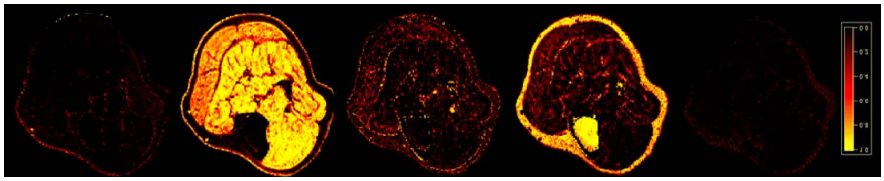


Fig.4: pixel-wise obtained histogram over all T2-distributions in the gastroc. muscle.



T2-range: 6-10ms restricted (bound) water | 10-40ms water1 | 40-80ms water2/fat | 90-500ms fat | 500-1000ms free water

Fig.5: partial T2-range integration maps from various compartments that could be identified from the overall histograms (cf. fig.4). While the separation between water and fat is obvious the distinct differentiation between water1 and water2/fat becomes ambiguous. The very short T2<10ms approaches the resolution limit for this sequence.

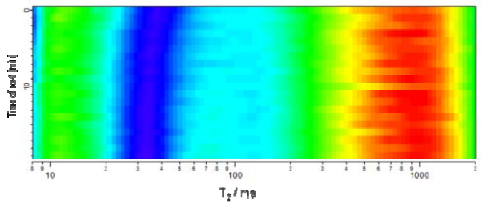


Fig.6: dynamic monitoring of the multi-compartment relaxation after muscle exercise. The downwards shift to lower T2-values is noticable for the water1 component, although the decrease in the short T2-amp. (T2<10ms) supporting the hypothesis of water exchange between those two pools.

Muscle	T2<10ms (A)	10<T2<40ms (B)	40<T2<90ms (C)	90<T2<500ms (D)	T2>500ms (E)
gastrocnemius muscle	0.005	0.63	0.27	0.065	0.002
soleus muscle	0.009	0.76	0.14	0.058	0.004
flexor digitorum longus muscle	0.016	0.76	0.16	0.030	0.002
tibialis anterior muscle	0.019	0.81	0.14	0.019	0.003
peroneus longus + brevis muscle	0.040	0.64	0.22	0.074	0.013

Table 1: The major lower leg muscles from common anatomy with their respective T2-fractions of the five distinguishable pools from multi-relaxation NNLS analysis. The T2-ranges correspond to the ones identified in fig.5.
While the short T2<10ms and the very long T2>500ms might be ambiguous and the accuracy of the fractions questionable because of hardware and SAR limitations (lowest TE, pulse aplitude and width), the three intermediate components can be robustly identified and measured. The distinct difference in water/fat content between the various muscle groups is reproducible and might be a valuable tool for diagnostic purposes.

Conclusion: We successfully demonstrated the ability of acquiring high resolution in-vivo T2-relaxation data for quantitative multi-component analysis in human muscle with adequate B1-correction techniques. The T2-components identified are in agreement with recent non-spatially resolved studies from high SNR single voxel T2-experiment [3]. The ability to monitor dynamic changes in muscle-compartmentalization might provide a powerful technique to assess the effectiveness of specific exercise and rehabilitation protocols and monitor treatment efficacy of interventions. All this information may proof very valuable to understand compensatory muscle activation in the healthy human subjects as well as patterns associated with injury and/or pathophysiology. Nevertheless more elaborate experiments and studies are required to better understand and identify the various compartments in the in-vivo human muscle.

[1] Ch. Patten et al. Sem. Muscul. Rad. 7 (2003), 297-305; CB Bratton et al. Science 147 (1965), 738-739; [3] G. Saab et al. MRM 42 (1999), 150-157; [4] B.Mädler et al. Proc. ISMRM (2007); [5] C. Jones et al. Proc. ISMRM (2003); [6] T. Prasloski et al. MRM (2011) in press ; [7] K.P.Whittall et al., MRM 37 (1997), 34-43;