In Vivo Measurement of Relaxation Time of Water and N-acetyl in Intervertebral Disc Using MR Spectroscopy

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Introduction Intervertebral disc degeneration (IVDD) related back pain affects about 80% in the general population during the life-time. Traditional imaging techniques rely on disc morphology while actual disc degeneration begins with internal biochemical and biomechanical changes. Proton magnetic resonance spectroscopy (^{1}H-MRS) is a powerful non-invasive tool that has been used for the assessment of metabolites in tissues. Previously, ^{1}H-MRS on a clinical 3T magnetic resonance (MR) scanner has demonstrated the feasibility of using short-echo water suppressed point-resolved spectroscopy (PRESS) for evaluating biochemical changes in cadaveric bovine and human discs [1]. In these studies the degradation of bovine discs, induced by papain digestion, and the prevalent degeneration in cadaveric discs as assessed with Pfirrmann grading was correlated to spectra measures. In this study, we performed single voxel MRS technique in intervertebral discs from healthy volunteers and T1 and T2 relaxation times of water peak and N-acetyl peak of proteoglycan (PG) in the healthy discs were measured. As dehydration and loss of PG are the two primary consequences of disc degeneration, relaxation times may potentially change with degeneration, and quantification of relaxation times might provide valuable information related to disc degeneration.

Method Quantitative T1 and T2 measurements were performed on 3 healthy discs on 3 young volunteers (ages 26-28, 2 males and 1 female) using a 3 Tesla GE Excite Signa whole body MR scanner (General Electric Medical Systems, WI) using an 8-Channel CTL spine coil (GE). A single voxel point-resolved spectra selection (PRESS) sequence with a three-pulse chemical shift selective (CHESS) saturation for water suppression was chosen to acquire the spectra. A 5 × 20 × 18 mm^3 voxel was placed at the center of the disc and was adjusted according to the actual size of the disc. For T1 mapping, TE= 28ms, TR = 800/1000/1600/3200 ms; For T2 mapping, TR =1000ms, TE=28/56/84/112ms. The spectra were acquired with 1024 data points, 2000 Hz spectral width and 256 repetitions. Sixteen extra unsuppressed water spectra were acquired in each scan to obtain estimates of coil sensitivities and to calculate the relaxation time of water.

All post-processing was performed on a Sun workstation (Sun Microsystems, Palo Alto, CA). The acquired data were corrected with respect to phase and frequency using an internal water reference, and apodized with a 3-Hz Lorentzian function. Multiple channel data were then combined using the unsuppressed water signal if the individual channel had a signal larger than 3db. The data was then Fourier transformed to the frequency domain and baseline corrected. The unsuppressed water spectra were extracted to calculate the relaxation times of water. The N-acetyl region was identified between 1.90 and 2.10 ppm and measured based upon previous literature [1]. A peak-fitting program developed in-house [2] was then applied to provide robust and reliable estimation of the metabolite peak areas and peak heights. Peak area of the metabolite was considered as signal (S), the standard deviation of the last 200 points in the acquired spectrum was calculated as noise (N). The obtained SNRs, which were normalized signals, were then fitted to quantify the relaxation times. T1 relaxation times were calculated from data partial saturation using a two-parameter least-squares fitting routine to the equation $S/S_0 = 1\text{-}2*\exp[-(TR\text{-}TE/2)/T1]+\exp(-TR/T1)$ [3], where S is the actual normalized SNR, S_0 is the fully relaxed SNR. A Levenberg-Marquardt mono-exponential fitting algorithm was employed to calculate T2: $S(TE) \propto \exp(-TE/T2)$, where S is the normalized SNR.

Results Figure 1 shows representative MR spectrum (TE/TR=28/1000 ms) acquired from a healthy disc (corresponding T2-weighted fast spin echo image shown at the top left corner). The T1 mapping of N-acetyl (Fig. 2a) indicated an increase of SNR as TR increases, while a clear reduction of the N-acetyl peak heights can be observed as TE increases in the T2 mapping of N-acetyl (Fig. 2b). The calculated T1 of water and N-acetyl are and 1310±148 ms and 704± 122 ms, respectively; the calculated T2 of water and N-acetyl are 105± 12ms and 62±14 ms, respectively (Table 1).

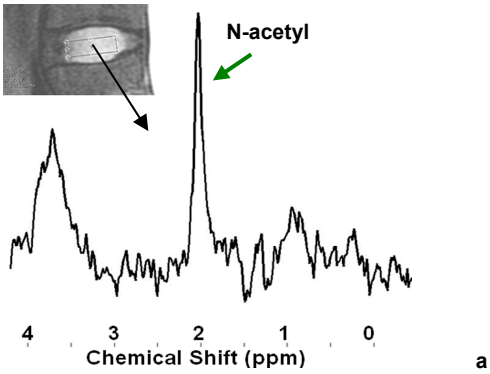

Fig.1 A MR spectrum acquired in a healthy disc.

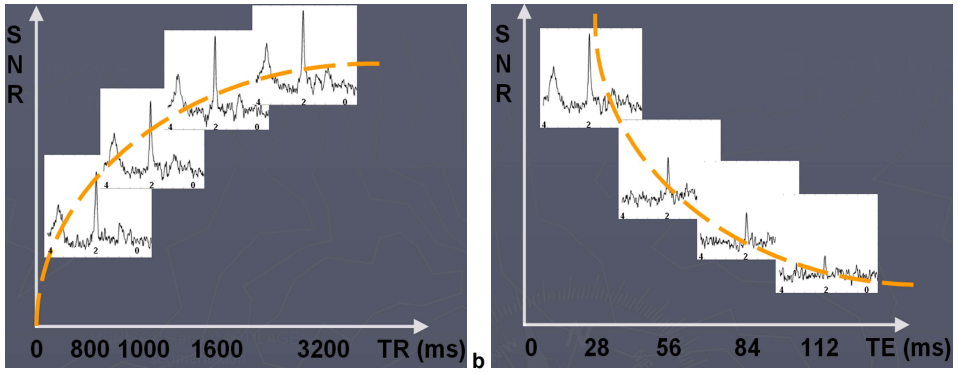

Fig. 2 Representative T1 mapping (**a**) and T2mapping (**b**) of N-acetyl.

Discussion This study assessed metabolites in intervertebral disc using a single-voxel MRS technique. Relaxation times of water and N-acetyl in healthy discs were also measured in the study. The acquired spectra with water suppression from a healthy disc showed a tall and clear depiction of N-acetyl peak, indicating a high concentration of PG. The spectra acquired without water suppression was used to calculate the relaxation times of water. The measured T1 and T2 of N-acetyl are in the same range as those measurements that were reported earlier in bovine discs [4]. Current measurements were made in healthy discs. As disc degeneration shortens the relaxation times, these values are expected to drop with IVDD. A more complete study should be accomplished with in vivo human discs with different grades of disc degeneration. Quantification of T1 and T2 with different status of disc degeneration may provide extra perspective to examine the correlation of these relaxation times with disease progression. The current study provided reference values to optimize future MRS studies. For example, the measurements of T1 indicated that the maximum signal to noise ratios (SNR) of N-acetyl could be achieved with a TR=750ms. Combining this information with scanner gradient limits, as well as the specific absorption rate (SAR) is essential to achieving an optimized SNR. Further in vivo studies are warranted to provide more information about the relationship between T1 and T2 of metabolites and disc degeneration.

	Water	N-acetyl
T1 (ms)	1310 ±148	704± 122
T2 (ms)	105± 12	62±14

Tab.1 Measured T1 and T2 for metabolites.

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[3] Young IR et al. J Comput Assist Tomogr 1982; 6:1-18. [4] Zuo J, et al. ISMRM 2009:2001.