**INTRODUCTION:** MRI-occult pathology in Multiple Sclerosis (MS) is detectable with proton MR spectroscopy (1H-MRS), but unlike conventional (qualitative) MRI, 1H-MRS needs to account for parameters that affect its quantitative assessment. At intermediate- and long-echo times (TE) the molecular environment factors require knowledge of the local transverse, T2, relaxation time. To our knowledge, brain metabolites T2s have not been thoroughly characterized in MS patients, forcing two implicit assumptions on 1H-MRS: that the same global T2 can be used (i) anywhere in the brain (ii) for all MS subjects. While recently substantiated in healthy individuals (1-2), these assumptions require validation in MS, given its well documented focal and diffuse pathology and different clinical course. Specifically, three scenarios can be envisioned (from best to worst): (i) regional inter- and intra-patient T2S are indistinguishable from controls, incurring no bias; (ii) similar inter- and intra-patient T2s differ significantly from controls*, requiring one set of T2 corrections; (iii) significant regional intra- and inter-patient variations, requiring individual regional T2 correction. Our aim, therefore, was to obtain the T2 distributions of N-acetylaspartate (NAA), choline (Cho) and creatinine (Cr) at 3 T in the most common (85%) relapsing-remitting (RR) phenotype of MS and assess any bias incurred by differences in inter- and intra-patient T2s. This was done using 1 cm3 spatial resolution three-dimensional 1H-MRS in a two-point protocol optimized for T2-precision per unit time (3).

**METHODS:** Seven patients (42±13 years old, 3 women, 4 men) with clinically definite RR MS (mean disease duration 3 years, range 1-7) and mean EDSS of 3 (range 0.0-5.0) were scanned at 3 Tesla. MP-RAGE and T2-weighted FLAIR MRI guided a PRESS 10x10x10 cm3 volume of interest (VOI) with TR=1,26 s. The two-point T2 estimation paradigm (3) optimized the two TES, and the number of averages (N1 and N2) to T2E=35 ms (N=1) and T2E=200 ms (N=3). The VOI was encoded with Hadamard spectroscopic imaging into 4 (IS) slices, each partitioned with 16x16 CSI over a 16x16 cm2 region of interest (VOI) with a spatial resolution three-dimensional 1H-MRS in a two-point protocol optimized for T2-precision per unit time (3).

**RESULTS:** Histograms of T2S from all voxels of each patient revealed inter- and intra-subject similarity similar to age-matched controls' (Fig. 2). The T2S (average±standard error) in GM, WM and lesions were: NAA: 307±21, 354±16 and 358±72 ms; Cr: 174±2, 181±15 and 184±18 ms; and Cho: 252±19, 259±10 and 226±12 ms. Compared to average T2S of controls, this amounted to differences of only 4% for NAA, and 3% for Cr and Cho.

**CONCLUSION:** Based on these results we can conjecture that for metabolic quantification in MS: (i) obtaining T2 values for each patient is unnecessary; and (ii) for TEs under 100 ms a global average T2 value per metabolite suffices, therefore, (iii) obtaining regional brain and lesion T2S is also not needed.

**REFERENCES:**
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