

Differences in the Spatial Distribution of Paraspinal Muscle Fat Between T1-weighted and Water-Fat Sequences May Provide Insight Into Muscle Changes Associated With Chronic Low Back Pain

Lucas K Dziesinski¹, Jessica Ornowski¹, Karim Khattab¹, Jiamin Zhou¹, Noah B Bonheim¹, Aaron J Fields¹, Aseem Sharma², Jeannie F Bailey¹

¹Department of Orthopaedic Surgery, University of California, San Francisco, CA, ²Department of Radiology, Michigan Medicine, University of Michigan, Ann Arbor, MI

Lucas.Dziesinski@einsteinmed.edu

Disclosures: None of the authors disclose any relevant disclosures. A complete list of author disclosures can be taken from the online abstract system.

INTRODUCTION: Deficits in paraspinal muscle (PSM) quality are considered an important feature in chronic low back pain (cLBP). Muscle quality is often assessed by measuring muscle fat content, which can be accurately quantified using water-fat MRI. Additionally, thresholding approaches using T1- and/or T2-weighted images may also enable quantitative analysis of muscle fat; however, the accuracy of T1- and T2-weighted sequences commensurate with water-fat MRI is unclear, which limits the clinical utility of these sequences. Therefore, to explore the validity of estimating paraspinal muscle fat on T1-weighted images, we compared differences in fat quality and spatial distribution measured using water-fat MRI with thresholded T1-weighted images. We hypothesized there would be differences in the spatial distribution of fat between water-fat and T1-weighted images suggesting that 1) using T1-weighted images to estimate muscle fat fraction may be unreliable or prone to error; and 2) voxel signal intensities from T1-weighted images are sensitive to compositional factors beyond fat. This study provides a novel insight into the potential presence of other non-muscular/non-fatty tissues (i.e., fibrotic tissue, increased blood, etc.) within the PSMs of cLBP patients.

METHODS: Non-fat suppressed T1-weighted and fat fraction IDEAL (Iterative Decomposition of water and fat with Echo Asymmetry and Least-Squares Estimation) axial lumbar sequences were obtained from 51 patients with cLBP. Slice thickness for both sequences was 4 mm with a 1-mm interslice gap. T1-weighted sequences were pre-processed with N4 bias field correction and subsequently normalized to a 0-100 range based on the minimum pixel value for a given series and a maximum pixel value based on the average of the greatest five percent of pixels to account for the large pixel values of subcutaneous tissue. The multifidus (MF) muscles were segmented at two slices per disc level from L1 to S1 and the erector spinae (ES) muscles from L1 to L5, yielding ten segmented slices per patient. DICOM metadata for image position, image orientation, and pixel spacing was used to transform segmentations from IDEAL to T1-weighted sequences and manually adjusted as needed. The center of rotation (CoR) was approximated at each disc level at a position 12.5% from the posterior edge of the disc. Multiple circular regions of interest (ROI) with a thickness of two pixels were defined in increasing radii from the CoR until the superficial edge of each segmentation and the average pixel value in each ROI was computed. These non-normalized distances were linearly interpolated to a 0 to 100% range and statistical parametric mapping (SPM) two-tailed paired t-tests were used to compare fat fraction patterns for MF and ES muscles between T1-weighted and IDEAL sequences.

RESULTS: Mean fat fraction was significantly higher on T1-weighted images compared to the reference standard IDEAL images (mean difference = 8.1%, $p < 0.001$) at all levels and for both the MF and ES. Spatial distribution patterns differed significantly between T1-weighted and IDEAL sequence types at all levels and for both the MF and ES from a normalized distance of 0 to 3.4% ($p = 0.038$), 3.8 to 33.4% ($p < 0.001$) and 36.2 to 100% ($p < 0.001$) of muscle radii. This significance remained when analyzing each level individually. For example, when comparing T1-weighted to IDEAL sequences at L4L5 for the multifidus, we found a significant difference in spatial fat fraction from 0 to 3.4% ($p = 0.036$), 4.4 to 37.2% ($p < 0.001$), and 44.3 to 100% ($p < 0.001$) of the distribution (Figure 1). This trend of statistical significance in both deep and superficial regions continued across all levels (Figure 2).

DISCUSSION: We found differences in non-muscle composition patterns between T1-weighted and water-fat (IDEAL) sequences. This highlights the potential pitfalls in using clinical MR sequences to estimate fat with thresholding. Additionally, SPM analysis denoted that T1-weighted images underestimate fat content within the deep regions of the muscle and overestimate fat content within the superficial regions. For example, when analyzing a single muscle for a particular patient, the normalized heatmap denotes a similar pattern of fat (Figure 3, Left and Center). Upon looking at the difference in normalized pixel values (Figure 3, right) between these sequences, however, the heatmap denotes areas in the deep region of the muscle where IDEAL estimates greater fat than T1-weighted (purple) whereas T1-weighted estimates greater fat in the superficial regions (orange). These findings illuminate the potential presence of other T1 hyperintense pathologic tissue besides fat within the paraspinal muscles in patients with low back pain, which clinical sequences highlight that may have substantial impacts on PSM function. Further studies are needed to elucidate the nature of such additional pathologic changes as well as to explore how patterns in T1-weighted compare to IDEAL with respect to patient age and symptom severity.

SIGNIFICANCE: This study outlines a method to deduce the composition of other non-muscular/non-fatty tissue types affecting PSM health in cLBP patients.

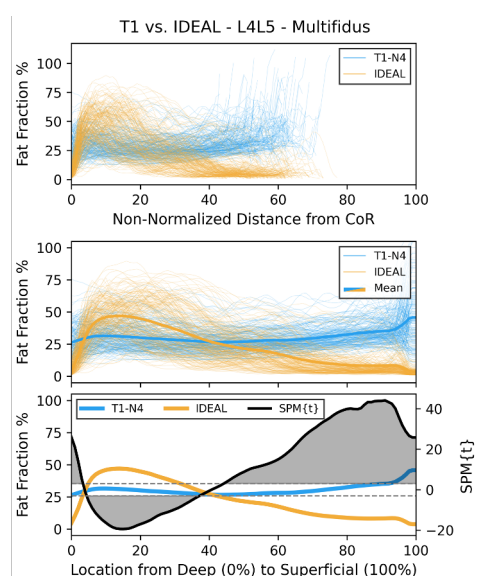


Figure 1. Top: Non-normalized individual radial distributions from deep to superficial regions of the muscle. **Middle:** Normalized individual muscle radial distributions. **Bottom:** SPM analysis denoting differences in fat fraction distribution between T1-weighted and IDEAL. Significance achieved if the SPM_t surpassed the critical threshold ($\alpha = 0.05$). Regions of significance are shaded for visualization.

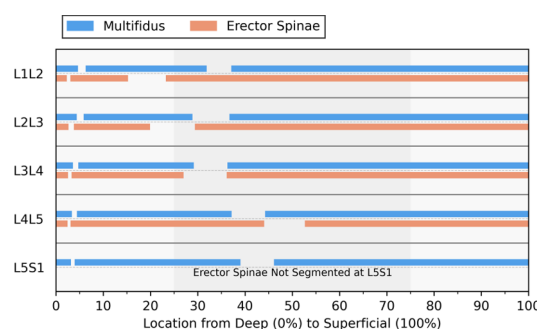


Figure 2. Cluster locations derived from SPM depicting regions of significant difference between T1-weighted and IDEAL sequence types.

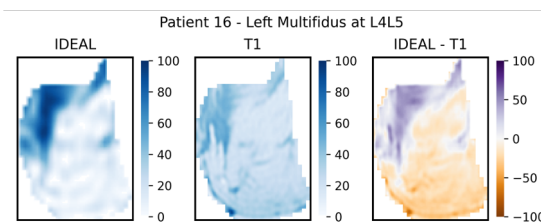


Figure 3. Axial heatmap depicting normalized pixel values of the multifidus for a single patient at L4L5 on IDEAL (left), T1-weighted (center), and difference between IDEAL and T1-weighted (right).