An Objective Diagnostic Biomarker for Myofascial Pain Syndrome Using Low-Field NMR

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BACKGROUND

Myofascial pain syndrome (MPS) is characterized by regional pain and palpable taut bands or "trigger points," yet diagnosis remains largely dependent on physical examination and manual palpation. There is currently no objective, noninvasive method for quantifying the underlying tissue changes associated with fascial densification and fibrosis.

Fascia is challenging to characterize with conventional imaging. Collagen-rich fascia exhibits rapid transverse relaxation, making it difficult to capture with conventional MRI echo times. Specialized ultrashort-echo-time approaches can improve visualization, but quantitative characterization of fascial composition and densification remains challenging.

Ultrasound can measure fascial morphology and thickness, but the structural changes associated with densification may be subtle. Human ultrasound studies have demonstrated differences in thoracolumbar fascia thickness and remodeling between individuals with and without chronic low-back pain, highlighting the clinical relevance of quantitative fascial measurements.

A clinically useful biomarker should therefore provide a **quantitative, tissue-sensitive measurement** that can be acquired rapidly and repeatedly.

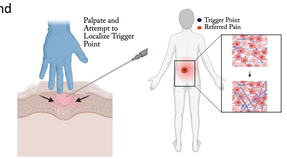


Figure 1. Clinical presentation of myofascial pain syndrome.

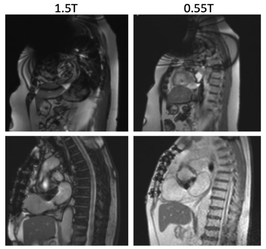


Figure 2. Magnetic field strength MRI comparisons of artifacts in tissue imaging.[6]

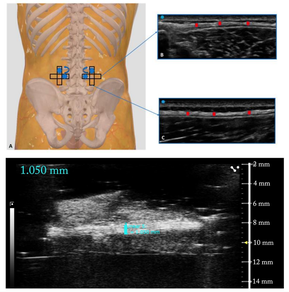


Figure 3. Ultrasound visualization of thoracolumbar fascia. (A) Representative human ultrasound demonstrating visualization and measurement of thoracolumbar fascia [5]. (B) Representative porcine ultrasound image from the experimental model. Ultrasound provides structural information about fascial thickness, but a quantitative tissue-composition biomarker could provide complementary information.

METHODS

Human Cadaveric Model
Bilateral lumbar tissue specimens containing epidermis through muscle were obtained from human cadavers through the Tulane Center for Anatomical and Movement Sciences (CAMS). Specimens were positioned against the NMR-MOUSE sensor and sampled across approximately 25–27 mm of tissue depth.

NMR Acquisition
Using the same NMR-MOUSE platform and acquisition strategy developed in the porcine model, depth-dependent **T_1 and T_2 relaxation profiles** were acquired. T_1 acquisition was prioritized based on the porcine LDA results, which identified T_1-family parameters as dominant discriminators of fascia.

Data Processing
Relaxation curves at each depth were fit using exponential recovery/decay models. Anatomical layers were manually assigned to facilitate qualitative comparison of relaxation profiles across skin, adipose, fascia, and muscle.

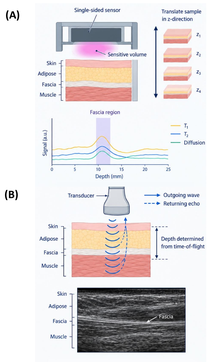


Figure 4. (Right) Comparison of depth localization with single-sided NMR (A) and ultrasound (B).

RESULTS

Established Porcine Model

Layer-resolved LDA identified **T_1-family parameter**s as among the strongest discriminators of fascia across all analyzed samples. A T_1-family parameter ranked first in 4 of 5 samples and accounted for approximately **20–33% of total discriminant weight.**
When considering grouped LDA sampling from a **leave out analysis**, diffusion became most discriminant of the fascia with up to **63% specificity and 100% sensitivity.**

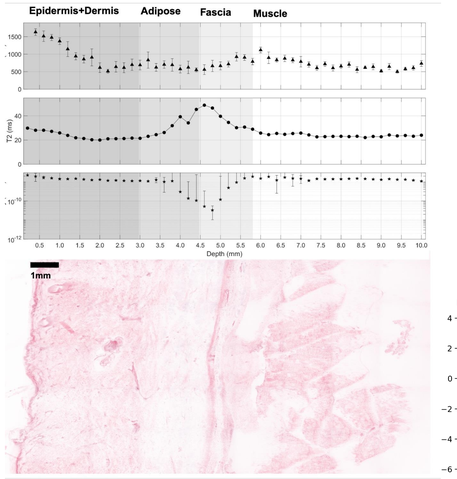


Figure 5. Depth-dependent NMR profiles and anatomical validation in porcine tissue.

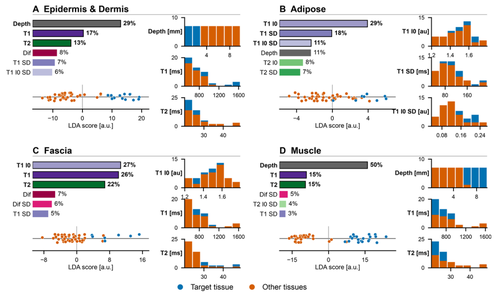


Figure 6. Layer-specific linear discriminant analysis of porcine NMR features.

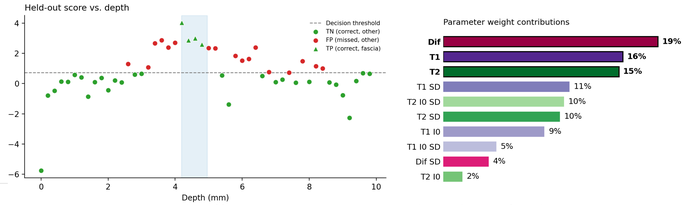


Figure 7. Leave out analysis of fascia in one representative porcine sample trained on rest of samples.

Human Cadaveric Tissue — Preliminary Work

The same acquisition strategy and anatomical layer convention were applied to human lumbar cadaveric specimens. A localized change in T_1 near the expected fascia depth qualitatively resembles the porcine pattern, while T_2 demonstrates more subtle depth dependence without a consistently defined fascia signature. These preliminary data demonstrate the feasibility of obtaining depth-dependent relaxation measurements through human lumbar tissue while highlighting the greater variability and noise observed in human specimens.

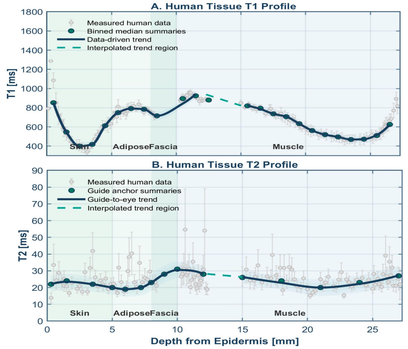


Figure 8. Preliminary depth-dependent relaxation profiles in cadaveric human thoracolumbar tissue.

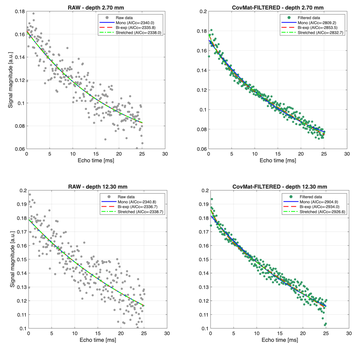


Figure 9. Noise reduction method of cadaveric depth-resolved NMR data.

DISCUSSION

Clinical Translation
A compact, single-sided low-field NMR sensor could provide a quantitative measurement of fascial tissue properties at the point of care. If the porcine T_1 signature is reproduced in human tissue, the approach could complement palpation by providing an objective, repeatable fascia-associated measurement.

Potential Clinical Applications
- **Objective diagnosis**
  Quantify tissue properties associated with fascial densification alongside clinical assessment of trigger points.
- **Treatment monitoring**
  Repeated measurements could providae a quantitative readout of tissue response following interventions such as dry needling, trigger-point injection, or manual therapy.
- **Point-of-care implementation**
  The small, single-sided geometry provides a potential route toward localized measurements outside conventional MRI environments.

Current Limitations & Next Steps
- **Human sample size**
  Preliminary human data are currently limited to a small number of cadaveric specimens; additional specimens are needed to assess reproducibility.
- **Ground truth**
  Human layer boundaries are currently based on manual anatomical measurements rather than optical/histological validation.
- **Biomarker validation**
  The porcine T_1-family biomarker has not yet been formally validated with LDA in human tissue.

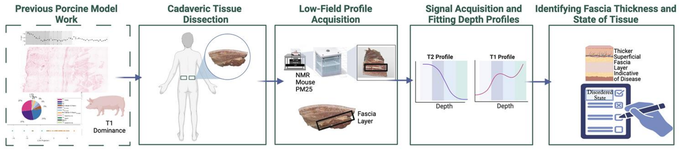


Figure 10. Workflow pipeline for future clinical translation feasibility.

CONCLUSION

Low-field, single-sided NMR provides depth-resolved relaxation measurements across human lumbar tissue and detects qualitative T_1 variation near the expected fascia region.
In the established porcine model, **T_1-family parameters were consistently among the strongest discriminators of fascia,**for single sample analysis providing a rationale for prioritizing T_1 during human translation.
Apparent Diffusion Coefficient values were found to have **high sensititivty and specificity** in identifying the fascaia region in grouped, leave out analysis.
These preliminary human results motivate continued development toward an **objective, quantitative, point-of-care biomarker for MPS**, with expanded specimen sampling, optical ground truth, and formal human LDA validation as the next steps.

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