Quantification and Mapping of T_1 Relaxation Time in the Tongue

I. E. Evangelou[1], G. Chi-Fishman[1]

[1]Physical Disabilities Branch, Clinical Center Rehabilitation Medicine Dept. & NICHD, National Institutes of Health, Bethesda, MD, United States

Introduction

Contrast between different tissues in MR images depends primarily on the tissue's proton density as well as its intrinsic T_1 and T_2 parameters. T_1 relaxation is related to tissue macromolecular structure, water binding and water content [1] providing a means for MRI-based quantitative tissue characterization, distinguishing between normal and pathologic tissues and tracking the progression of disease [2]. Furthermore, accurate determination of T_1 relaxation enables optimization and design of pulse sequences yielding maximum contrast between different tissues for better tissue delineation and selective tissue imaging. As an important initial step toward quantitative lingual tissue characterization, we measured and mapped T_1 values of *in vivo* human lingual tissue in 3.0T. For methodology optimization and comparison, we also made measurements using an ex vivo animal model in 1.5T and 3.0T.

Methods

Preliminary experiments: Three formalin-preserved calf tongues (status post preservation 402±51.5 days) and 1 fresh calf tongue (within 1 hour of slaughter), excised en bloc, were used in preliminary experiments to determine and optimize imaging parameters and analysis methods. Specimens were imaged in 3.0T and 1.5T GE whole body scanners using a 4-channel NVPA coil and a 4-channel CTL coil, respectively, and an FSE-IR pulse sequence (TE = 12 ms, TR = 3000/5000/8000 ms, RBw = 15.63 KHz, FOV = 18x18 cm, Acq Matrix = 192x192). To avoid intersection modulation effects, we chose a single-slice approach and imaged a coronal slice (5-mm thick) through the center of the tongue core at different inversion times (TI), range = 50-4000 ms. To avoid the order effect, the TIs were completely randomized. Both linear and geometric time spacing schemes [3] were tested at 12 and 6 TIs, respectively, within the specified range. The preliminary experiments identified geometric time spacing and TR=5000ms to be optimal for clinical application, as the former reduced scan time by a factor of 2 at no loss of fitting accuracy, and the latter provided adequate relaxation (3-5 times the maximum T_1 of the tissue and larger than the highest TI value) within clinically acceptable imaging time constraints.

Human studies: Our human subjects included 4 male and 2 female healthy volunteers (mean age 25.6 yrs). MRI studies were performed in a 3.0T scanner using the optimal parameters described above. Three equidistant slices, normalized in inter-slice distances to the midsagittal length of the individual tongue, were identified to represent the anterior, mid and posterior tongue regions.

Post-processing: All image post-processing and analysis were performed using MATLAB. For each slice, an ROI was defined that included the overall tongue (visible regions occupied by intrinsic and extrinsic lingual muscles). T_1 measurements were made using a 3-parameter exponential fit on each voxel as follows:

$$M_z(TI) = M_0 \cdot \left[1 - 2 \cdot \alpha \cdot e^{-TI/T_1} + e^{-TR/T_1}\right]$$

where M_z is the longitudinal magnetization (signal intensity), M_0 is the maximum observable signal intensity, and α is the spin-density factor corrected for T_2 losses. The factor of 2 makes it possible to find a finite value of T_1 where the signal is zero. The 3-parameter fit is preferred over a 2-parameter fit since it accounts for imperfect flip angles and slice profiles [4]. Using initial estimates for M_0 and T_1, the fitting procedure returned three parameters in each voxel: M_0, α and T_1. Based on a nonlinear minimization using the Nelder-Mead simplex direct search algorithm [5], T_1 values within the defined tongue ROI were calculated by curve-fitting the relaxation equation to the modulus of the measured signal intensity. The calculated T_1 values were then used to produce a pseudocolor parametric T_1 map overlaid on the anatomical image, in which the voxel color value represented the absolute T_1 relaxation time of each tissue. Statistical analysis, where indicated, was performed with alpha = 0.05.

Results

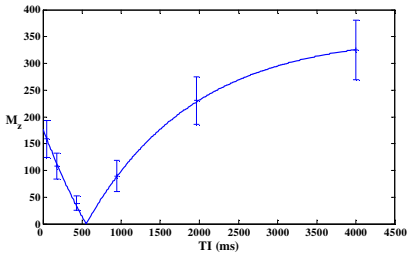
As shown in the tables below, the T_1 values of human tongues were considerably greater than those of the fresh calf tongue, and preserved-aged specimens had the lowest T_1 values. Magnetic field strength had a significant effect ($p = 0.0051$) on calf tongue T_1 measurements in that the values increased from 1.5T to 3.0T.

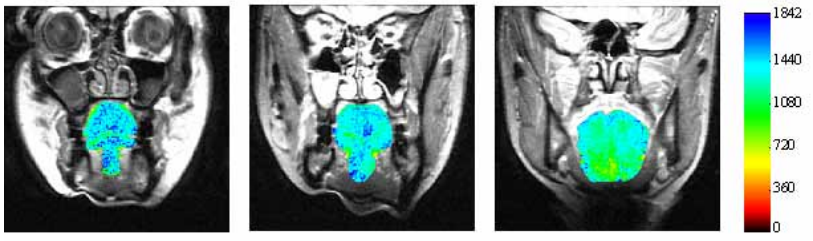
Human (pooled)	Fresh calf
1306.76 ± 218.41	809.5 ± 228.59

Fresh calf	Aged calf (pooled)
809.5 ± 228.59	373.91 ± 59.27

Spacing	1.5 T	3.0 T
Linear	326.42 ± 37.03	374.89 ± 26.97
Geometric	297.97 ± 6.59	364.96 ± 24.64

Our most salient finding was that T_1 measurements were sensitive enough to identify inter-region differences in the human tongue. Specifically, mean T_1 values of the posterior tongue slice were significantly lower than those of the anterior tongue slice ($p < 0.01$) and those of the mid tongue slice ($p < 0.05$). Gender was not a significant factor, nor did it affect inter-region differences in T_1 values. For every subject, our curve-fitting produced nearly perfect results (see representative plot below; fitting error = 0.18%), and the parametric maps for each region adequately represented the anatomy and illustrated the range of absolute T_1 values per voxel of tissues present throughout the different regional tongue slices (see representative images below).





Discussion & Conclusion

This study is the first to report quantitative T_1 data for lingual tissue both in vivo and ex vivo in current clinical magnetic field strengths. From the range of T_1 values in our parametric maps, the tongue of young healthy volunteers can be seen as a highly muscular organ rich in water content with minor fat infiltrations. Significant inter-region differences in T_1 relaxation time suggest regional specificity in lingual tissue distribution; the posterior tongue slice in our sampled subjects appeared to have more infiltration of other tissue types into the muscles than the other regions. Further parsing of the parametric maps into constituent tissues (e.g., muscular, adipose, connective) is needed and will enable detailed, image-based, quantitative characterization of lingual tissue for a better understanding of the distribution and anatomical interaction of different tissue types in the tongue. Our research includes multiexponential T_2 measurements that are not reported here. Further augmentation by other quantitative imaging methods (e.g., MRS for metabolite concentrations, DWI for water mobility in tissue, PWI for blood delivery to tissue) will provide a more comprehensive quantitative investigation of changes in lingual tissue composition due to disease, aging and exercise.

References

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