

FAST AND ROBUST T1 MAPPING OF THE HUMAN LUNG AT DIFFERENT SITES

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Introduction:

The complex nature of COPD requires a precise characterization of COPD on a regional basis for better diagnosis, therapy decision and monitoring. Therefore the goal of this project was the development of a robust, standardized and quantitative proton-based MRI method for the in vivo determination of the lung T_1 relaxation time. This would allow for an improved lung tissue characterization and for the functional assessment of the human lung (via oxygen enhancement), with the ultimate goal to establish a uniform standard for acquiring longitudinal MRI data on patients with COPD.

In the following, we present the first results obtained from our “multi-center study” conducted at different hospitals with identical MR systems demonstrating that the fast and reproducible T_1 mapping of the lung is indeed feasible.

Methods:

Phantom and in-vivo measurements were performed on clinical 1.5 Tesla scanners of the same model and vendor, located at three different hospital sites (named A, B, C). A phantom consisting of various containers filled with Gd-DTPA doped water (concentrations of Gd-DTPA ranging from 0.0 mmol/l to 0.2 mmol/l) was constructed to simulate the spectrum of T_1 -values of the lung. To model the short T_2^* (approx. 1 ms[1]) of the lung, glass beads with diameters of 0.5mm and 0.1mm were added. Additionally 20% vol. D_2O was added to adjust the proton density values according to the lung proton density values. In addition to the phantoms a healthy volunteer was examined at all three sites.

Relaxation time T_1 was measured using an IR-Snapshot FLASH sequence [2] ($TE/TR/\alpha = 0.75ms/3ms/8^\circ$, asymmetric echo, 15mm slice thickness, coronary slices, matrix: 64×128 , zero-filled to 256×256 , $FOV = 500 \times 500 \text{ mm}^2$). This method allows T_1 quantification with a single inversion pulse. A series of 32 Snapshot FLASH images was acquired after a non-selective inversion pulse. Total acquisition time was 6.2s. A POCS algorithm was used to restore parts of k-space lost due to the asymmetric echo. To reduce Gibbs artifacts, data filtering was performed using a Hanning filter function. Data was phase corrected using the phase information from the first image. A 3 parameter mono exponential model was fitted to the data on a pixel by pixel basis allowing the extraction of T_1 and M_0 [3]. All presented values are mean and standard deviation of a ROI. At each site the experiment was repeated ten times with the phantom and two times for three different slices with the volunteer to show the reproducibility of the results.

Results:

In Figure 1 the mean T_1 values of 10 experiments with the phantom are presented. The values range from approximately 640ms to 1700ms. Variation in relaxation times for each sample at different sites is below 4%. The small error bars demonstrate a good reproducibility of the results at each site. Figure 2 shows in vivo T_1 maps of a healthy volunteer at the end of inspiration. For the right lung the mean values are $1193ms \pm 51ms$, $1203ms \pm 64ms$, $1226 \pm 61 \text{ ms}$ at site A, B and C respectively. The left lung shows values from $1187ms \pm 54ms$, $1234ms \pm 32ms$, $1253ms \pm 38ms$ at site A, B and C respectively.

Discussion:

Relaxation times were acquired in a single shot experiment with a high accuracy. Phantom experiments show a very good reproducibility of T_1 values at different sites using an IR-Snapshot FLASH sequence. This demonstrates the robustness of the method. Comparison of in vivo results from different experiments is non-trivial, because it is difficult to choose exact the same slices and there are changes in positioning of the volunteer. Nevertheless the experiments show a high agreement in the relaxation values. The results are comparable to previous experiments [4]. Testing will be extended to a wider range of different scanners and manufacturers to see if an identical accuracy and reproducibility is possible.

Acknowledgements:

The authors would like to thank PD Dr. Sebastian Ley (University Hospital Heidelberg, Germany) and Julien Rivoire (University Hospital Mainz, Germany) for their support.

This work was funded by the BMBF as a part of AsCoNet.

References

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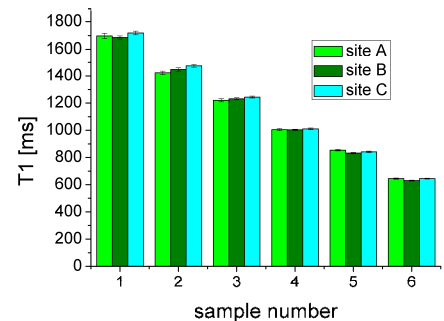


Fig. 1: Mean T_1 values of all samples measured at different sites.

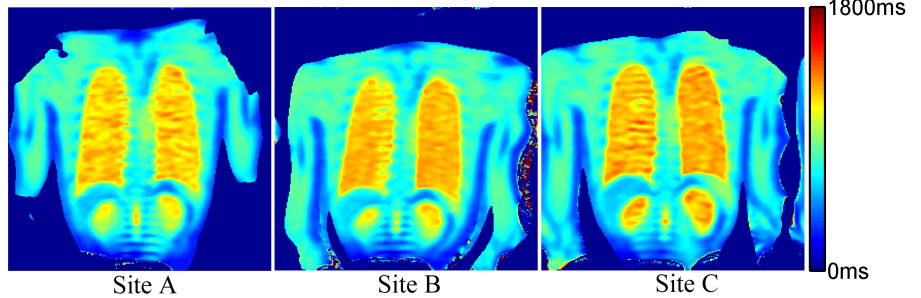


Fig. 2: In vivo T_1 -maps of a healthy volunteer from three different scanners