T_2' relaxometry of the human lung at 1.5 and 3 Tesla

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Introduction

Lung diseases, such as chronic obstructive pulmonary disease or fibrosis, become manifest in changes of tissue structure. The relaxation time T_2' is sensitive to the underlying tissue structure and therefore, this parameter is currently under investigation as a promising biomarker for lung diseases [1, 2]. However, a fundamental problem is the precise measurement of the relaxation time due to low signal-to-noise ratio (SNR) and its extremely short duration at 1.5T and higher field strengths. Relaxation time measurements are presently acquired with ultra-short echo time (UTE) imaging sequences having the benefit of spatial coverage. But UTE imaging allows only a limited number of samples for measuring the relaxation with sufficient SNR at reasonable acquisition times. Therefore, the aim of this work is to increase the precision of relaxation time measurements in the human lung using a point resolved spectroscopy (PRESS) [3] sequence. PRESS allows for a sufficient sampling of the relaxation and represents a complementary approach with focus on temporal coverage of the relaxation. Furthermore, we show a comparison between the commonly used linear exponential model for the pulmonary relaxation and a quadratic exponential (Gaussian) model, which can be motivated by a theoretical framework describing transverse relaxation in the presence of magnetic field inhomogeneities at short time scales [4]. We also validate our findings in human lungs with a thorax phantom containing a preserved porcine lung.

Materials and Methods

Measurements were performed on a 1.5 and 3T MR system (Magnetom Avanto and Trio, Siemens Healthcare, Erlangen, Germany) with manufacturer provided thorax/spine coils as receiver. A PRESS pulse sequence [3] with the following parameters was used for acquisition: voxel volume V = 10×10×20 mm^3, TE = 27 msec, TR = 300 msec, FA = 90 deg, BW = 10 kHz, number of repetitions for averaging N = 500. In total 48 measurements were conducted, at each field strength 12 with healthy volunteers and for comparison 12 with a preserved porcine lung (Lung Demonstration Model R10060, Erler-Zimmer GmbH & Co. KG, Lauf, Germany) inside a thorax phantom (ArtiCHEST, PROdesign GmbH, Heiligkreuzsteinach, Germany) [5]. In each of the 2 volunteers, 6 measurements (ID #1-6 and #7-12) were conducted at different regions of interest (ROIs). The ROIs were evenly distributed, apart from larger vessels, on the right and left side in the upper lobes, where little motion is expected, in order to avoid motion artifacts during free-breathing. To obtain relaxation times, the following models were fitted to the acquired data around the spin echo in the so-called short-time regime:

1 Linear Exp. model $S(t) = a_1 \cdot e^{-\frac{|t|}{b_1}}$ 2 Gaussian model $S(t) = a_2 \cdot e^{-\left(\frac{t}{b_2}\right)^2}$ where the fit parameters a_1, a_2 denote the spin echo magnitude S(t = 0) in each case and b_1, b_2 are the relaxation times T_2', $T_2'_{,G}$, respectively.

The goodness of fit is evaluated using χ^2_{red}. The errors in the fit parameters are given in each case by the 95% confidence interval.

Results and Discussion

For the healthy volunteers, the Gaussian model results in lower χ^2_{red} values on average (2.2 ± 1.0 and 3.3 ± 2.9 at 1.5 and 3T, respectively) compared to the commonly used linear exponential model (5.5 ± 5.1 and 10.2 ± 15.3 at 1.5 and 3T, respectively). The χ^2_{red} values of the preserved porcine lung confirm this finding (Gaussian: 1.9 ± 0.5 and 2.6 ± 1.4 versus Linear Exp.: 7.7 ± 4.7 and 9.2 ± 9.8 at 1.5 and 3T, respectively). Out of 48 cases, only one case at 1.5T and two cases at 3T for human lungs and one case at 3T for the porcine lung showed lower χ^2_{red} with the linear exponential model, which on average indicates an enhanced description of lung data using the Gaussian model. Fig.1 shows a fit comparison for the measurements in a human lung with highest SNR. Fig.2a illustrates the relaxation times T_2' resulting from the linear exponential model, whereas in Fig.2b, the relaxation times $T_2'_{,G}$ resulting from the Gaussian model are plotted. In human lungs, the mean and standard deviation of T_2' is (3.70 ± 1.23) msec and (1.72 ± 1.17) msec at 1.5 and 3T, respectively. Whereas using the Gaussian model results in smaller mean and standard deviation values $T_2'_{,G}$ of (1.95 ± 0.32) msec and (0.96 ± 0.29) msec at 1.5 and 3T, respectively. This behavior is confirmed in the preserved porcine lung having T_2' values of (2.03 ± 0.18) msec and (1.09 ± 0.30) msec and $T_2'_{,G}$ values of (1.44 ± 0.07) msec and (0.75 ± 0.13) msec at 1.5 and 3T, respectively. Fig.3 shows a comparison between the relative error in relaxation time using the linear exponential and the Gaussian model. In human lungs, the relative errors are reduced on average by similar factors of (3.2 ± 1.5) and (3.2 ± 1.6) at 1.5 and 3T, respectively. In the porcine lung, the relative errors are slightly more reduced by similar factors of (3.8 ± 1.1) and (3.5 ± 1.5) at 1.5 and 3T, respectively. For all lung data, the Gaussian fit shows consistently lower relative errors compared to the linear exponential fit.

Summary and Conclusion

The PRESS sequence enables a comprehensive temporal sampling of the pulmonary relaxation. Compared to the commonly used linear exponential model, the Gaussian model provides an enhanced description of lung data. Strong effects of respiratory motion, pulsation and spurious chest wall signals on the measurements can be excluded due to the validation with a thorax phantom. For human lungs, average relaxation times of the Gaussian model $T_2'_{,G}$ result in (1.95 ± 0.32) msec and (0.96 ± 0.29) msec at 1.5 and 3T, respectively. Furthermore, the Gaussian model significantly reduces the relative error in relaxation time of the human lung by a factor of 3 on average. Hence, the relaxation time $T_2'_{,G}$ of the Gaussian model is a promising biomarker for investigations of lung diseases with increased precision.

References

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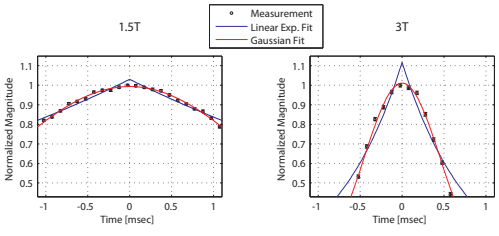

***Fig.1**: Fit comparison in human lungs at 1.5 and 3T in the short-time regime. The Gaussian model provides an enhanced description of the data.*

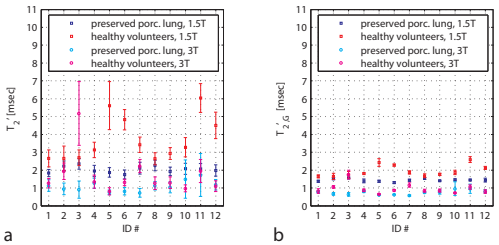

***Fig.2**: Relaxation times measured in a preserved porcine lung and in healthy volunteers at 1.5 and 3T. Comparison of (a) the relaxation times T_2' using the linear exponential model and (b) the relaxation times $T_2'_{,G}$ using the Gaussian model for given measurement IDs.*

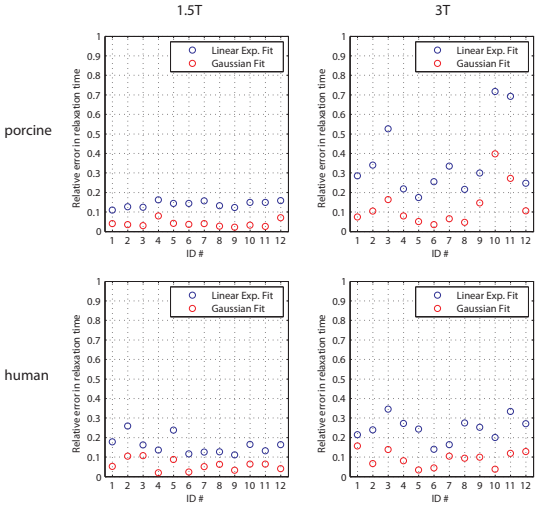

***Fig.3**: Relative error in relaxation time in a preserved porcine lung and in healthy volunteers at 1.5 and 3T. Comparison between the relative error in relaxation time using the linear exponential model and the Gaussian model for given measurement IDs.*