

Measurement of Short and Ultra-short T_2 Components Using Progressive Binomial RF Saturation

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Introduction:

T_2 relaxation analysis is commonly accepted as a promising tool to study the microstructural characteristics of tissue. Traditionally, T_2 measurements are done by acquiring images at multiple echo times and by applying a fitting technique such as the non-negative least squares (NNLS) algorithm (1). Using this technique, several distinct T_2 components have been detected in various tissues. However, despite recent advances the robust and accurate quantitation of T_2 components smaller than 20ms is still not fully resolved. This is primarily because it is difficult to satisfy the criteria for the acquisition of multi-component T_2 data in vivo in terms of SNR, echo spacing, and total number of echoes (2). We here present a non-CPMG method that allows to measure T_2 components down to the range of microseconds.

Theory:

From numerical simulations of the coupled Bloch equations we found that the saturation function of a single binomial $1\perp$ RF pulse, i.e. the remaining longitudinal magnetization as a function of T_2 , can be modelled with a simple peak function. On a logarithmic T_2 scale, the $1\perp$ saturation function can be modelled best with a pseudo-Voigt function, however, a Gaussian function also provides a reasonable approximation (Figure 1). The most important feature of the $1\perp$ pulse is that T_2^0 , i.e. the T_2 value where the saturation function has a minimum, is linearly proportional to the pulse duration δ provided that the flip angle remains constant. However, resonance offsets can distort this relationship. This means that the saturation function can be shifted along a logarithmic T_2 scale with essentially the same shape just by changing δ (Figure 2). It can be shown that a saturation spectrum, obtained from a series of measurements where δ is slightly altered over subsequent repetitions, is simply a convolution of the logarithmic T_2 -spectrum with the saturation function. For simplicity we assume that we have a number of discrete T_2 components with a Gaussian distribution function rather than a continuous spectrum. Then, as the convolution of two Gaussians is another Gaussian, the saturation spectrum is given by:

$$1 - \frac{S(T_2^{0\ln})}{S_0} = \sum_{i=1}^n \frac{m_i m_{\text{sat}}}{\sqrt{2\pi(\sigma_{\text{sat}}^2 + \sigma_i^2)}} \exp\left(-\frac{(T_2^{0\ln} - T_{2i}^{0\ln})^2}{2(\sigma_{\text{sat}}^2 + \sigma_i^2)}\right) \quad [1]$$

where m_{sat} and σ_{sat} are the amplitude and standard deviation of the saturation function, respectively. Equation [1] means that n individual T_2 components, defined by m_i , $T_{2i}^{0\ln}$, and σ_i can simply be determined by fitting multiple Gaussian functions into a data set obtained with progressive binomial saturation.

Material and Methods:

To validate the method experimentally, we implemented a HASTE sequence with binomial pre-saturation on a Philips Intera 1.5 T scanner (Philips Medical Systems, Best, The Netherlands). Additionally, a 32 echo CPMG sequence (interecho spacing 4,6 ms) for providing reference T_2 measurements and a dual echo gradient echo sequence for B_0 mapping were used. Five samples of pig liver served as a model for multiexponential T_2 relaxation. These were mounted in a 17 cm circularly polarized receive coil. RF excitation was performed with a volume coil that enabled B_1 amplitudes up to 27 μT . The measurements started with the modified HASTE sequence and were performed without binomial saturation and with 50 – 60 different saturation pulses with a duration between 300 μs and 100 ms. To achieve a constant flip angle of 120° the amplitude of the binomial pulse was adjusted accordingly for each step. The progressive saturation experiments were followed by B_0 mapping and by the multiecho sequence. Using the B_0 maps as reference, T_2 analysis was done in the regions with the lowest B_0 error. To identify the number of T_2 components and their intrinsic T_2 values the CPMG data was analyzed with the NNLS algorithm proposed by Lawson and Hanson (3). The dataset with progressive binomial saturation was analyzed as follows: First, a series of signal attenuation and corresponding T_2^0 values were created. The T_2^0 values were calculated from the individual pulse duration and flip angle of the saturation pulse neglecting possible B_0 errors. Then, two and three Gaussian functions were fitted into the T_2^0 spectrum according to Eq. 1 using a non-linear least square technique. To obtain a stable fit, all T_2 components were assumed to have the same σ .

Results

The NNLS analysis of the liver samples revealed three distinct T_2 -components, a short component with approximately 11 ms, a long component between 33 ms and 47 ms, and an additional component with a T_2 longer than 110 ms. As a rule, the T_2 spectra obtained with the progressive saturation technique could always be fitted best with two Gaussian functions (Figure 3). The analysis of the T_2^0 spectra revealed an ultra-short component with approximately 1 ms and a short component between 14 and 28 ms. However, a closer inspection suggested that both the short and the long T_2 components observed by the NNLS analysis presented as a single peak in the saturation spectrum. In accordance with numerical simulations, this seems to be a B_0 effect which shifts T_2 peaks to the left. However, the ultra-short component at 1 ms was not influenced by this effect.

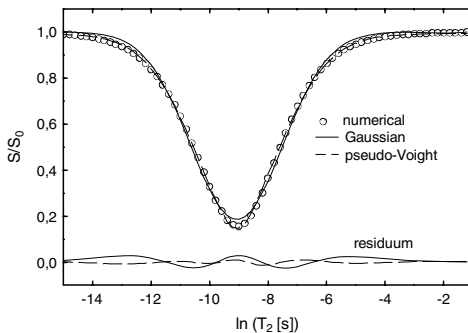


Fig.1. Saturation function of single $1\perp$ -Pulse

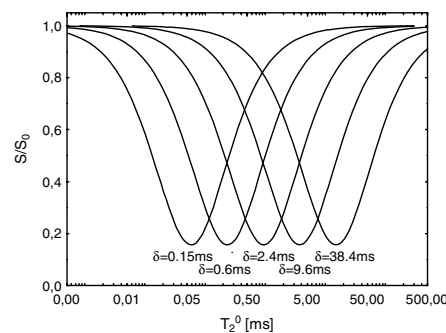


Fig.2. Saturation function for a FA of 120°

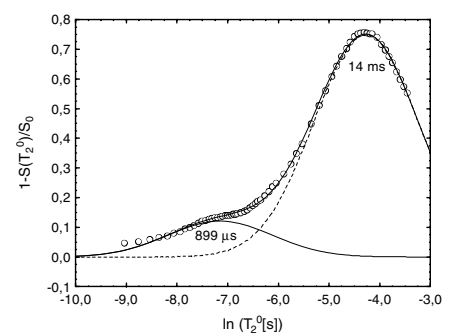


Fig.3. Fitted T_2 -spectrum of pork liver

Conclusion:

We have developed a new method for measuring different T_2 components in biologic tissues. Compared with conventional multi-echo T_2 measurements, the proposed method has no echo time constraints and allows to probe ultra-short T_2 components smaller than 1 ms. Inhomogeneities of the B_0 field may significantly distort the T_2 spectrum and therefore require further attention.

References:

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- (3) Lawson CL, Hanson RJ. Solving. Englewood Cliffs, NJ:Prentice-Hall; 1974.