**Synopsis**

At short echo times (TE = 2.8 ms), 1H MR spectra contain the contribution of mobile macromolecules (MM), i.e., broader resonances characterized by shorter relaxation times ($T_2$) than under the narrower peaks of metabolites. There are only a few studies assessing $T_2$ relaxation times, with only one study reporting $T_2$ of individual MM peaks in the full $T_2$ range (4–9 T). Unfortunately, only the peaks 1, 3, 4, 5, 6, 7, 10, 12, 20, 24, 26, 28, 30, 34, 40, and 46 ms were identified. Relaxation estimates, B) The MM spectra with marked components for which the relaxation times were estimated (up) and a 2 ms non-selective hyperbolic secant inversion pulse, applied at an $s$, since measuring $T_2$ and $T_0$. There are very few studies assessing $T_2$ relaxation times for 7 MM components in the rat brain at 9.4 T.

**Methods**

For measuring the in vivo spectrum of macromolecules, the SLC28 sequence was extended with a 2 ms non-selective hyperbolic secant inversion pulse, applied at an $s$, since measuring $T_2$ and $T_0$. There are very few studies assessing $T_2$ relaxation times for 7 MM components in the rat brain at 9.4 T. The described method also provides an efficient tool for a potential parametrization of individual MM. The information obtained by parametrization can be further used as an individual MM basis set for spectral quantification and detection of individual MM changes in pathologies.

**Results and discussion**

The excellent quality of the in vivo acquired MM is shown in Figure 1. All acquired spectra showed excellent SNR. The proposed post-processing method was efficient and provided very good quality of the metadate and macrodata providing some MM spectra for quantification and further analysis. All the components were quantified using AMARES. The results of $T_2$ relaxation times for all individual MM are not straightforward due to the overlapping metabolites and requires more complex and sophisticated approaches. In this work we present in new approach: single inversion recovery with an optimized TI and TE, which underlie the narrower peaks of metabolites. There are very few studies assessing $T_2$ relaxation times for 7 MM components in the rat brain at 9.4 T.

**Conclusions**

This study proposed a novel methodological approach allowing reliable post-processing and quantification of the MM spectra, together with $T_2$ relaxation time estimates of all individual MM components in the full $T_2$ range at 9.4 T. The described method also provides an efficient tool for a potential parametrization of individual MM. The information obtained by parametrization can be further used as an individual MM basis set for spectral quantification and detection of individual MM changes in pathologies. Furthermore, this approach can also characterize the MM spectra in different TIs and regions and this can provide comprehensive set of information necessary in a MM dimension for MR fingerprinting.

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**References**


**Figures**

Figure 1: A) in vivo series of IR spectra with TI ranging from 420 to 1000 ms revealing the evolution of metabolite intensities over a series of different TIs (acquisition parameters TE/TE/TE/TE/TE=2.8/2.8/2.8/2.8/2.8 ms); 5) Spectra acquired with a selected TI=750 ms and TE=2.8 ms as well as with TE=40 ms (5x magnified); 7) Original spectra acquired at TI=750 ms and TE=2.8 ms (shown in black), estimated fits of the residual metabolites using AMARES (shown in red) and the residue obtained after subtraction of the estimated metabolite signals remaining from the original spectrum (shown in blue).

Figure 2: Table showing the estimation error for AMARES quantification in frequency, number of peaks, linewidth and the shape of the metabolite residuals.