Single versus double inversion recovery techniques for nulling of low molecular weight metabolites in in vivo 1H MRS of the brain in 1.5 and 3.0 T magnetic fields

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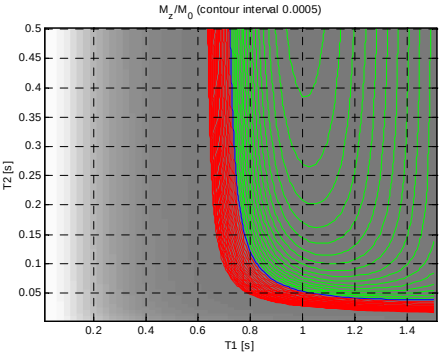
Abstract

Adequate measurement of in vivo ^{1}H MR spectra of macromolecules (proteins, lipids) in the brain requires effective suppression of considerably stronger signals of low molecular weight metabolites, whose T_1 and T_2 relaxation times are fairly inhomogeneous. Schemes with single or double inversion recovery are most often employed for this purpose, exploiting the differences of T_1 relaxation times of macromolecules and metabolites. In this paper, comparison of some properties of these schemes is presented, mainly with respect to the efficiency of metabolite suppression and macromolecule detection. Additionally, problems of incorporating highly effective B_1-, T_1- and B_0-insensitive water suppression into the inversion recovery schemes are dealt with.

Introduction

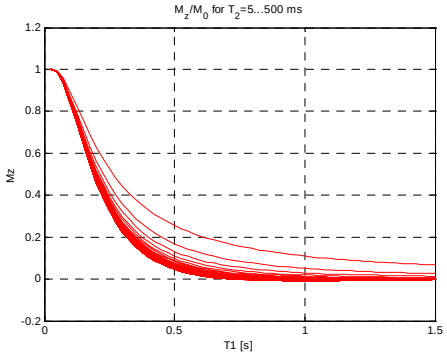
In short echo time (TE) ^{1}H MRS of the normal brain, broad resonances of macromolecules appear, which have been, in part, tentatively assigned to methyl and methylene protons of amino acids in proteins. Macromolecular proteins share the same frequency range with mobile lipids, which appear in the brain as a result of different diseases, including brain tumors, inflammatory and ischemic diseases, multiple sclerosis, injuries, etc. (1-5). These resonances are, therefore, of growing clinical interest, and methods for their accurate and reliable detection and evaluation are investigated. So far the best resolved macromolecule spectra were reproducibly obtained at 9.4 T from the rat brain (6,7). These spectra are in excellent agreement with spectra acquired from human cerebral cytosol (3) at similar B_0. Sufficiently accurate and reliable detection of macromolecules and their differentiation is a complicated task. Enormous attention must be paid to the suppression of all artifacts, such as those originating at short TE from insufficient suppression of the water signal, and of lipid signals from outside the volume of interest. Outstanding suppression of much stronger signals of low molecular weight metabolites must be performed without diminishing substantially the efficiency of macromolecule detection. Differentiation between protein and lipid resonances is very difficult, especially at low magnetic fields providing spectra with poor resolution and low sensitivity.



Methods

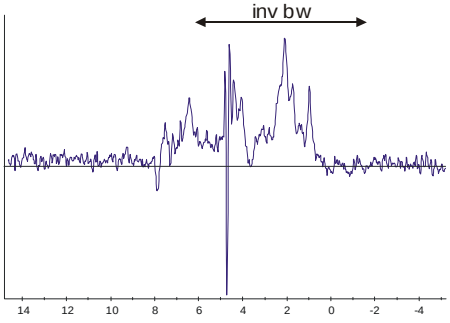
For the design and evaluation of the inversion recovery sequences (SIR and DIR), numerical integration of the Bloch equations has been employed, taking into account the T_1 and T_2 relaxation of metabolites and macromolecules, characteristic for 1.5 and 3.0 T magnetic fields. The IR schemes tested were optimized for an efficient suppression of metabolites as well as of water. Special sequences were developed for simultaneous B_1, T_1, and B_0 insensitive water suppression consisting of up to 5 selective asymmetric RF pulses with properly chosen frequency profiles to attain a broad flat suppression plateau.

Experiments were performed on a 3T Medspec system (Bruker Medical Inc., Ettlingen, Germany) and on a 1.5T Symphony system (Siemens, Erlangen). STEAM and PRESS sequences were used to localize a volume (mostly 2×2×3 cm^3) in healthy subjects, NA=128. Written informed consent was obtained prior to measurements. Volume head coils were used for signal detection.



Results

Simulations show that the use of DIR schemes provides far better suppression efficiency (more than one order) of low molecular weight metabolites than SIR techniques can. E.g., DIR scheme 510ms-Pi-670ms-Pi-240ms-Loc-Acq with 40-ms adiabatic inversion pulses Pi (HS20) is capable of 100-fold suppression of metabolite signals along with >200-fold of water in the whole range of the respective relaxation times, in practice adjustable to 2500-fold suppression. Fig. 1 shows the simulated T_1- and T_2-dependence of the resulting excitation M_z/M_0 prior to the localization module (Loc), with a contour interval of 0.0005 (red for M_z>0, green <0, blue=0). The macromolecule signal is suppressed 5× (see Fig. 2). To eliminate water signal artifacts, additional suppression may be needed, such as a CHESS pulse in TM of STEAM (Fig. 3, 3×3×3 cm^3, occipital GM; processing: gaussian apodization 5 Hz, signal rotation, FT, 0-order phase correction). Sequences with CHESS pulses before and between the inversion pulses are the other option studied.



Conclusions

Simulations show that the use of DIR schemes provides far better suppression efficiency (more than one order) of low molecular weight metabolites than SIR techniques. A DIR alone can provide water suppression that may be sufficient in some systems, which would be a benefit for the application in spectroscopic imaging, where the efficiency of the CHESS approach suffers from B_0 inhomogeneity. However, because of the very low intensity of macromolecule signals, very efficient elimination of all contaminating signals (residual water, lipids outside the volume of interest) is absolutely necessary. The optimization of sequences, especially for 1.5 T, must take also T_2 relaxation in account (see Fig. 1).

Acknowledgements

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References

[1] Behar KL et al., Magn. Reson. Med. 32, 294-302 (1994).
[2] Mader I et al., Brain 124, 953-961 (2001).
[3] Mader I et al., J. Magn. Reson. Imaging 16, 160-167 (2002).
[4] Star-Lack JM et al., Magn. Reson. Med. 43, 325-330 (2000).
[5] Auer DP et al., Magn. Reson. Med. 46, 615-618 (200-1).
[6] Starcuk Z et al., 7th Annual Meeting of ISMRM 1999, p.1582.
[7] Pfeuffer J et al., J. Magn. Reson. 141, 104-120 (1999).