Lipid and macromolecule suppression by double inversion recovery in metabolic mapping of the brain at 7T

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Target Audience:
Scientists with interest in MRS/MRSI sequence development at UHF

Purpose:
We present the use of double inversion recovery (DIR) pulses for lipid and macromolecule suppression in accelerated free induction decay (FID)[1,2,3] 2D-CSI of the brain at 7T. Contamination of metabolite signals, especially NAA, caused by the point-spread function, parallel imaging fold-in and B_0 inhomogeneities can in some cases pose a problem for metabolite quantification, especially for NAA. DIR-based lipid suppression reduces these artefacts, but also causes a loss of metabolite SNR that requires consideration. DIR was chosen as single IR would lead to further signal loss due to saturation effect at the TRs used.

Methods:
Our DIR MRSI sequence features two 10th-order WURST pulses with interleaved 4-pulse-WET water suppression (78 ms duration) (Fig.1). A DIR pulse duration of 80 ms was necessary to limit SAR, leading to a minimum possible TI_1 of 156 ms. After the TI_2, phase encoding and excitation with a 600 ms sinc pulse were followed by the signal acquisition after an acquisition delay of 1.3 ms. The DIR pulses used a bandwidth of 2000 Hz and a delta frequency of -1.7 ppm.
We conducted measurements of a healthy volunteer (male, 25 y) using a 7T Siemens Magnetom scanner (32 channel head coil in array coil mode, 64×64 matrix, elliptical weighting, FOV 220mm, 10 mm slice thickness). The DIR sequence used the shortest reasonable timing of$TR/TI_1/TI_2$ of 760/160/75 ms with 38:08 min total measurement time, a comparison measurement without DIR suppression used a TR of 600ms/30:07 min total measurement time. IR pulse voltage was set up to the maximum allowed by SAR limits. To simulate the effects of fold-in artefacts caused by parallel imaging, the fully acquired measurement data were under-sampled using 2D-GRAPPA[4] with an acceleration factor (R) of 4 and then combined with gradient echo image based coil combination[5]. The resulting spectra were processed with LCModel software.
For the calculation of tNAA SNR loss due to DIR, the same sequences were measured in a phantom containing brain metabolites in physiologic concentrations and with a T_1 similar to that of grey matter. This was necessary since a reliable SNR calculation of NAA in vivo may be complicated by lipid contamination that can artificially alter the computed SNR.

Fig.1: *Pulse sequence design composed of DIR, WS, and FID excitation*

Results:
SNR values in the phantom resulted in a ratio of 40% between DIR and no IR. In the volunteer, individual voxel spectra showed the lipid suppression in central and peripheral regions (Fig.2). A comparison of signal in the 1-4 ppm region over the whole slice (Fig.3) further demonstrates the DIR suppression efficiency.
NAA maps were created and interpolated to 128×128 for DIR and for no suppression with R1 and R4 (Fig.4). This maps show good comparability and a major reduction of ringing artefacts.Mean SNR for the tNAA signal in the DIR measurement was 9.95±2.48. Mean CRLB values were below 20, but increased from no IR to DIR from 3.8±2.1 to 6.1±4.2 for tNAA, 4.9±3.1 to 7.9±3.8 for tCr and 5.3±3.5 to 9.0±5.2 for tCho.

Discussion/Conclusion:
DIR-bases lipid and macromolecule suppression massively reduces artefacts in accelerated CSI at 7T, therefore enhancing the usability of the resulting metabolic maps. It faces restrictions primarily by SAR and available TIs at short TRs. The SNR loss for metabolites due to DIR further reduces the maximum acceleration factors and resolutions that allow metabolite quantification. Optimisation of these parameters may result in better suppression performance at higher metabolite SNRs.

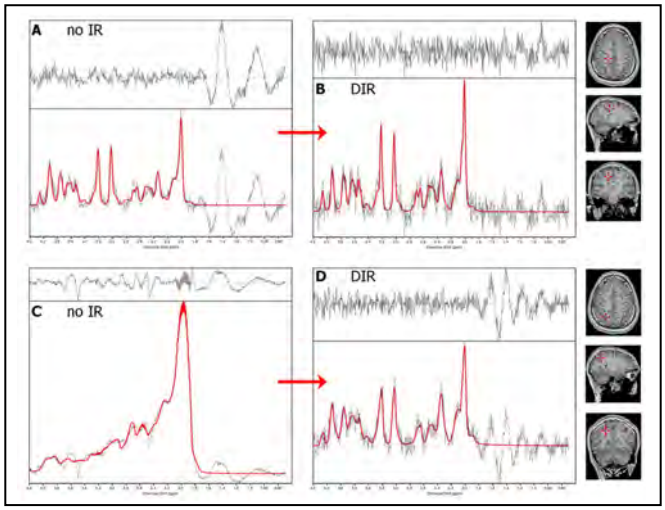

Fig.2: *Lipid signal reduction in example spectra;* ***A, B****: central WM voxel without and with DIR suppression;* ***C, D****: outer voxel without and with lipid suppression; [nominal voxel size: 3.4×3.4×10 mm]*

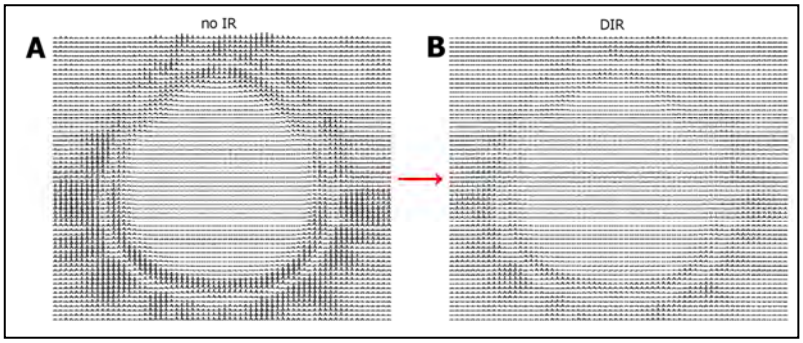

Fig.3: *Maps of the 0-3 ppm regions plotted over the whole slice;* ***A*** *without and* ***B*** *with DIR suppression; scaled to half the maximum value of signal in* ***A***

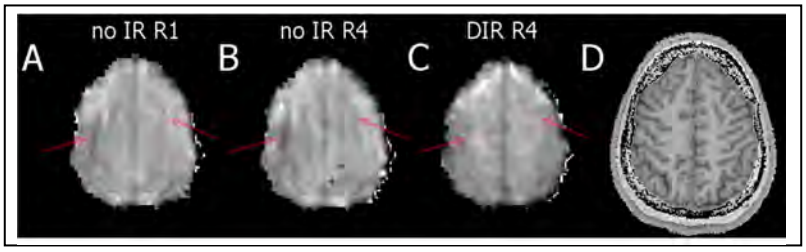

Fig.4: *tNAA maps for* ***A****: fully sampled without suppr.;****B****: R4 without suppr.;* ***C****: R4 with DIR suppr.;* ***D****: T_1-weighted reference; arrows indicate example regions of ringing artefacts*

References:
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