EASILY IMPLEMENTABLE WATER SIGNAL SCALING FOR 3D ^{1}H MR SPECTROSCOPIC IMAGING IN THE HUMAN BRAIN

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Target audience

The results of this work are intended to be easily implemented by clinicians or physicists working with MR spectroscopic imaging who have the need of spatial and patient-to-patient quantification of ^{1}H metabolite signals under various pathologic brain conditions.

Purpose

Out of the few recent papers dealing with ^{1}H MRSI water scaling, many use very sophisticated measuring sequences[1] or complicated algorithms based upon brain segmentation, excluding their use for abnormal tissues such as tumors[2]. Our aim was to create a simple and clinically implementable 3D water scaling method based on traditional measurement protocols and overriding numerous pre-assumptions. It should be applicable in the most pathologic conditions of the human brain and allow the use of array coils with non-homogeneous sensitivity profiles.

Methods

The main idea to fulfill this aim was implementing a simple 3D "pulse-phase_gradient-acquire" (or "FID") sequence for water quantification with its voxels corresponding to the metabolic voxels, very small flip angle and short TR to provide quantitative properties within a reasonable measurement time. Our study was performed using a 1.5 T Siemens clinical MR scanner applying only the manufacturer-supplied basic spectroscopic sequences, with an 8-channel phased array head coil. 1) The in vivo 3D MRSI sequences (PRESS spin echo with TE 30 and 135 ms), used in our clinic for patient brain metabolite mapping, were tested in a spherical 2-liter **aqueous phantom containing four main brain metabolites** (NAA, creatine, choline and lactate) in higher concentrations (50-150 mmol/l). For the purpose of consistent water scaling, a geometrically identical 3D FID sequence (time-to-sample=2ms, TR=200 ms) with a large field of view was tested with a range of fields of view (FoV), spatial and spectral resolutions and flip angles. The main criterion for the optimal FID sequence was the spatial homogeneity of the metabolite signals measured with PRESS SE sequence after correction for water concentration using the 3D FID measurement. Data were processed using LCModel, manipulated only using a shareware program, Total Commander and a free tool jSIPRO[3], which was also used for anatomic visualization of metabolite maps. Subsequently, the feasibility of the optimized protocol was 2) tested in **three healthy volunteers** and 3) used for data quantification of 1H spectroscopic data in **ten patients with brain lesions.**

Results

As to the phantom optimization of the water quantifying FID sequence: 1) Optimal FoV was found to be equal or a double of the metabolic CSI FoV for easy reconstruction of water signal at identical voxels. 2) Optimal bandwidth for LCmodel water quantification was found to be as low as possible 3) Measuring the FID with a lower real resolution implied rapid shortening of the acquisition time. However, upon doing so, the quantitation failed i) at voxels whose point-spread function (PSF) extended away from the volume containing measurable water, and ii) at the places where the gradient of the coil sensitivity was non-linear. 4) A minimum flip angle of 1 degree was used to minimize any influence of water transverse relaxation; however, no apparent difference was found upon increasing it up to 5 degrees. The measurement time of the FID with a reasonable resolution could be completed in three minutes (Fig. 1).

The measurements in healthy volunteers have demonstrated the functionality of this method in different brain areas with homogeneous and inhomogeneous coil sensitivity. Measurements in the areas of brain lesions have shown improved consistency of the metabolic maps (Fig. 2).

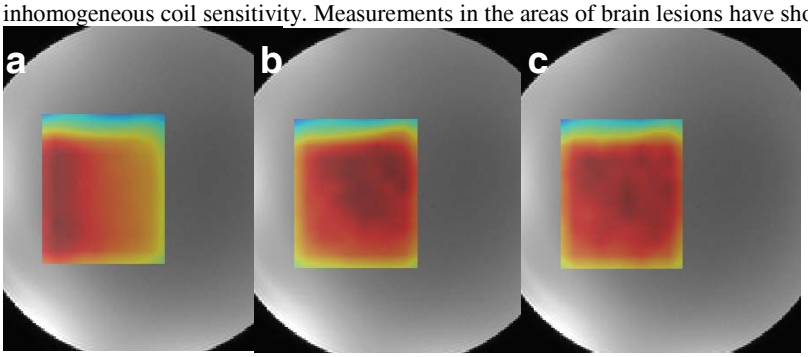

Fig.1: Spectral map of NAA in a homogeneous phantom without any corrections (**a**, SD of the NAA signal in the area being 15% of the average), corrected using a 1.5-minute very low resolution water 3D FID (**b**, SD=7%) and relatively higher-resolution 3-minute 3D FID (**c**, SD=5%).

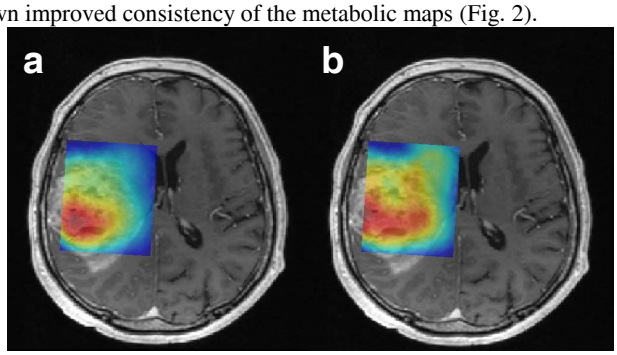

Fig.2: An example of a map of the cholines in a patient with a tumor, without any corrections (**a**) and with a correction using a 3D FID of water (**b**). Notice the visual improvement of the map consistency in the medial part of the tumor. The ventral area of relatively lower cholines is supposed to contain necrosis, which was confirmed by the distribution of lactate.

Discussion

Our results show that this method enables robust water scaling of 3D (or 2D) ^{1}H MRSI metabolites without the need for corrections of water relaxation times. The method enabled us to compare metabolite concentrations between patients and between different brain areas including tumors, where a referencing ^{1}H metabolite does not exist. It was easily implemented in our clinical environment using downloadable software (as an alternative to LCModel, jMRUI may be used). However, we have to be aware of the principal drawbacks of water scaling[4, 5].

References

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