FAST AND SIMPLE WATER SIGNAL ACQUISITION SEQUENCE FOR QUANTIFICATION OF ^{1}H METABOLITES IN THE BRAIN

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Target audience

The methods proposed by 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

The most common way of ^{1}H MRS metabolite quantification is scaling the spectra to additionally acquired water signal. However, traditional water spectroscopic measurements are sensitive to water T_2 (and sometimes T_1), which vary in many brain pathologies. In 2D or 3D spectroscopic imaging (CSI), water measurement becomes more time-consuming and T_1 weighted. The problem of water relaxation times has been solved for apparently healthy brain tissue by its segmentation[1], but the method has no solution in tumors or oedemas. In this work we introduce and test 3D FID (pulse-gradient-acquire) sequence for absolute water quantification, with identical geometry and resolution to metabolic 3D CSI, negligible T_2 or T_1 weighting and measurement time of less than 2 minutes.

Methods

Measurements were performed using a clinical 1.5 T scanner (Siemens Symphony) with whole-body excitation and an 8-element head array for reception. **1)** For proper ***in vitro*** quantification, we designed a 2-liter aqueous phantom containting NAA, Cre, Cho and lac in higher concentrations (<50 mmol/l). Short TE PRESS sequence was used to measure 3D CSI of metabolites (14x14x8, 30/1500 ms, 12 minutes). Following, water signal was acquired using our proposed 3-dimensional CSI FID sequence (pulse-phase_gradient-acquire) with identical slab orientation and resolution, short TE (2.3 ms) to avoid T2(*) weighting and 1-degree excitation pulses to prevent T1 weighting (TR 200 ms, 1.5 minutes). We measured again 3D PRESS sequence without water suppression ("RF off only") as a gold standard to quantify water signal in phantoms (15 minutes). **2)** The set of sequences was tested ***in vivo*** in 3 heatlhy volunteers and 3 patients with brain tumors. LCModel with water scaling[2] was used to quantify the data and jSIPRO[3] to visualize metabolic maps.

Results

With large field of view (14x14x9 cm) for PRESS excitation, metabolite maps showed pronounced inhomogeneities as expected from receiver coil construction (**Fig. 1a**). For statistical evaluation, we used a smaller ROI, avoiding the areas of improper excitation at PRESS box edges and phantom curvature. Within the ROI (5x12x4=240 voxels, **Fig. 1a$_2$**), we evaluated the standard deviation (SD) of the metabolite signals a) without water scaling, b) with water scaling using our proposed FID, and c) with water scaling to identical PRESS measurement with no water suppression. Moreover, d) the SDs of metabolic ratios of other metabolites to Cre was evaluated as a measure of inaccuracy of excitation and spectral fitting. The SDs were found in a range of a) 14-18%, b) 4-5%, c) 4-6% and d) 3-4%. As this was a homogeneous phantom, lower SD stands for more accurate concentration correction. **2)** In healthy volunteers, the improvement of the metabolic map consistency and uniformity after applying water scaling with our method was apparent. Water scaling correction factor for LCModel was determined using literature data for brain metabolite concentrations[4, 5]. Absolute metabolite values were calculated for brain tumor patients and corrected metabolic maps were plotted (**Fig. 2**).

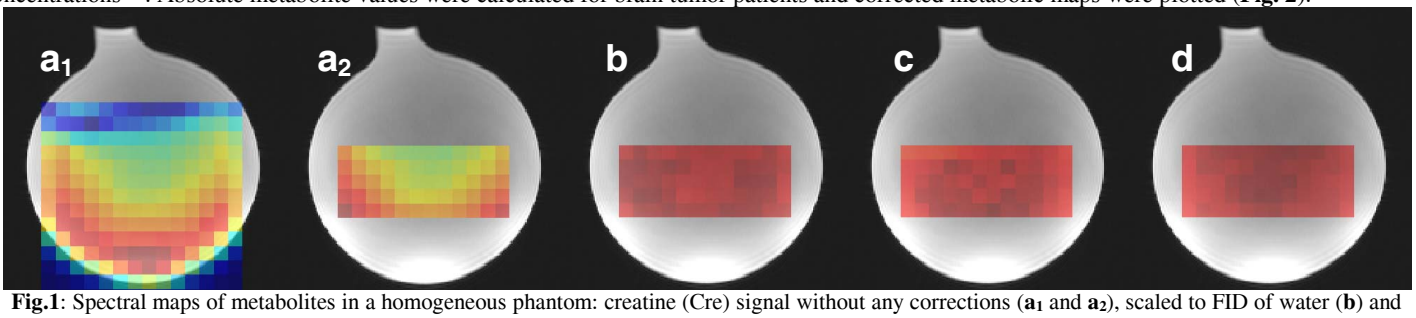

Fig.1: Spectral maps of metabolites in a homogeneous phantom: creatine (Cre) signal without any corrections (**a$_1$** and **a$_2$**), scaled to FID of water (**b**) and to PRESS CSI measurement without water suppression (**c**). Map of Cho:Cre ratio (**d**).

Discussion

Measurements in a homogeneous phantom suggest that our scaling method has a similar effect as scaling to Cre, or to water measured with PRESS. In vivo, moreover, the FID sequence benefits negligible T2 or T1 influence and short acquisition time, along with identical resolution and thus spatial point-spread function. Our volunteer and patient measurements suggest a potential for quantification and more accurate metabolite mapping *in vivo*, provided that the whole-body coil is used for excitation.

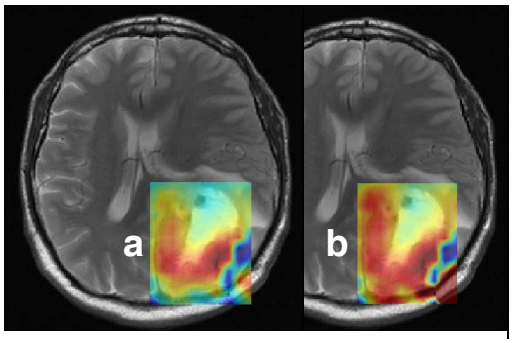

Fig.2: Map of the cholines in a patient with a tumor, without corrections (**a**) and with water scaling using 3D FID (**b**). Notice the visual improvement of the map consistency in the medial part of the cystic tumor.

References

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This work was supported by project "Increasing Opportunities for Career Growth in Research and Development in the Field of Medical Sciences", ITMS: 26110230067, co-funded from EU sources and European Social Fund