^{31}P 3D k-space weighted MRSI with adiabatic excitation: 3D absolute quantification of phosphorus metabolites in human liver

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Purpose/Introduction

MR spectroscopy allows us to measure hepatic concentration of phosphorus (^{31}P) rich metabolites and hence to assess the energetic status of the liver. Current methods for absolute quantification of MR-visible ^{31}P compounds in human liver employing localization by spectroscopic imaging suffer from B_1 field inhomogeneity, time demanding pulse adjustment and low spatial resolution, which enabled quantification of usually just one voxel per subject's liver [1],[2],[3].

The purpose of this study was to design, implement and test a protocol for absolute quantification of in vivo ^{31}P hepatic metabolites by employing high resolution 3D k-space weighted spectroscopic imaging with B_1 insensitive adiabatic excitation and a commercially available ^{1}H/^{31}P surface coil.

Subjects and Methods

Group of young volunteers (n=9) were positioned prone in a 3-T Medspec system S300 DBX (Bruker Biospin, Ettlingen, Germany) with the right lobe of the liver on the top of the 10-cm ^{1}H /^{31}P surface coil. A reference standard (triphenyl phosphate V=1 ml, c=1 mol/l) was attached to the center of the surface coil. MRI Flash images (15 slices, FOV 20x20cm, acq.15s) were acquired during one breath-hold.

A 3D k-space weighted SI localization technique with adiabatic excitation, (Matrix: 13x13x13; FOV 20x20x20 cm; nominal resolution = 3.65ml; TR = 1 s, 2.5ms sin/cos modulated AHP pulse ; 1024 points, hamming weighted acquisition, measurement time = 34min) was used. For quantification calibration data set was acquired using the phantom replacement technique (cylinder KH_2PO_4 solution doped with gadolinium, V=5 l, c= 50 mmol/l, T_1=2.27s).

In lab developed software package was used to preprocess data [4]. Absolute concentrations of each voxel were calculated according to (1) where I_{met} and I_{phan} are patient and phantom measurement's signals from the same location of voxels, $I_{ref.phan}/I_{ref.met.}$ summed signals from reference phantom and S_{met} and S_{phan} are saturation effect correction factors. T_1 relaxation times for saturation effect correction were used according to [5]. Up to 86 spectra per volunteer (mean=61.44) were quantified in jMRUI software package (Fig.1). Protocol reproducibility was measured on phantom with known concentration c=20mmol/l, and T_1 = 2.88s by three consecutive measurements with complete repositioning of phantom (Fig.2).

$$c_{met.} = c_{phan.} \frac{I_{met.}}{I_{phan.}} \frac{I_{ref.phan.}}{I_{ref.met.}} \frac{S_{phan.}}{S_{met.}} \quad (1)$$

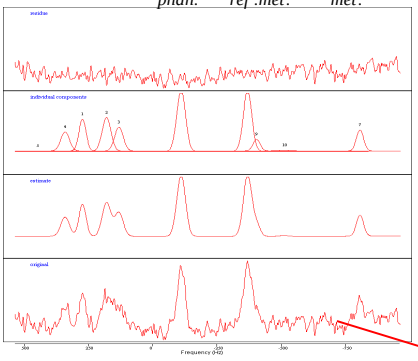

Fig.1 Example spectrum

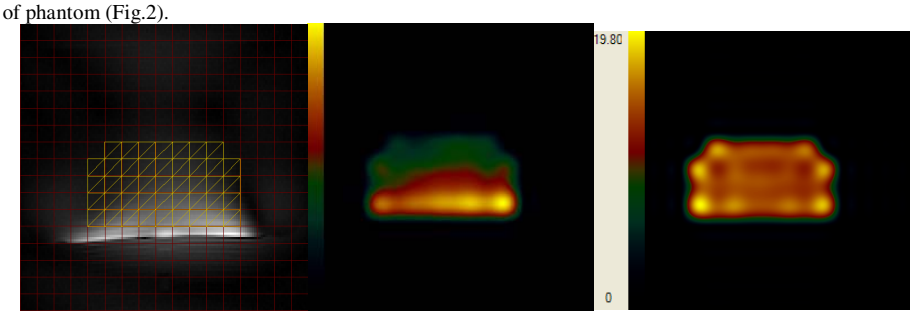

Fig.2 ^{31}P 3D SI of a phantom with concentration c=20mmol/l : ^{1}H image (a), ^{31}P signal image (b), ^{31}P absolute concentration image (c) of voxels in central slice selected according the image

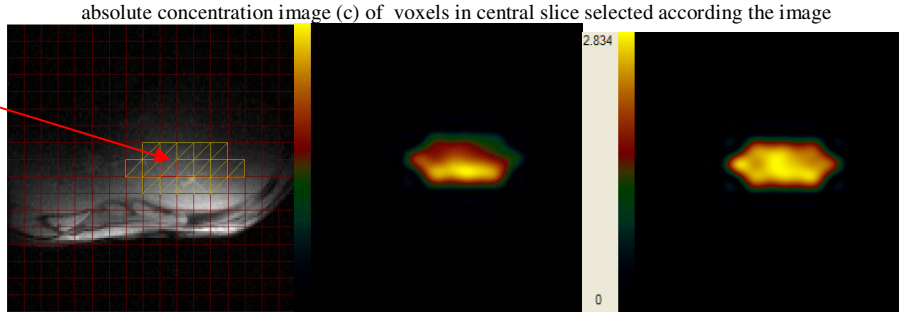

Fig.3 ^{31}P 3D SI of a volunteer's liver: ^{1}H image (a), γ-ATP signal image (b), ^{31}P absolute concentration image (c) of voxels in central slice selected according the image

Results

Results are based on weighted mean of quantified voxels (Phantom n=385 voxels, volunteers mean=61.44; weighting factor was S/N ratios of quantified signals). Phantom concentration was evaluated as: mean c=19.50mmol/l, coefficient of variation was 1.64%.

The ATP, PDE and PME in vivo concentrations (Table 1) are in the range of already published reports of ^{31}P spectroscopy in human liver [2,6-10]. Pi concentration is lower in our study. The difference in Pi concentrations could be explained by lower spectral resolution of PME-Pi-PDE complex (1.5T vs 3T and biger voxel volumes) in previous studies. This could leed to overestimation of Pi.

Table 1 Absolute values of ^{31}P metabolites in human liver (n=9,mean± sd)

Metabolite	γ -ATP	P_i	PDE	PME
c [mmol/l]	**2.10 ± 0.40**	**1.14 ± 0.28**	**7.58 ± 2.00**	**1.63 ± 0.41**
Published values [2,6-10]	**1.6-3.8**	**1.4-2.8**	**3.5-12.5**	**0.7-3.8**

Discussion/Conclusion

Compared to excitation pulses used in previous studies [1,2,3] robust adiabatic pulses used here do not need exact pulse calibration. In addition k-space weighted acquisition and 3T B_0 field lead to relative high spatially resolved spectra (3.65ml vs. 26-36ml[1,2,3]) in a reasonable measurement time. The processing tool allows data processing and quantifying of tens of spectra per patient which cover different parts of the liver. Metabolite concentration distribution can be visualized through absolute metabolic maps and potentially can visualize local differences of concentrations in focal pathologies. The described protocol shows potential for future utilization in monitoring pathological changes in phosphorus metabolites in the human liver, muscle and brain.

References

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