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Multi-voxel MR spectroscopic imaging of the brain: utility in clinical setting-initial results☆

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Abstract

Background and purpose: Compared to single voxel methods, MR spectroscopic imaging (MRSI) of the brain provides metabolic information with improved anatomical coverage and spectral resolution, but may be difficult to perform in the clinical setting. We evaluate the factors influencing spectral quality in MRSI using a semi-automated method, focussing on lipid contamination, and phase correction errors related to magnetic field inhomogeneity.
Methods: We retrospectively analysed MRSI studies planned by radiologists and radiographers. Two-dimensional MRSI studies using point-resolved spectroscopy (PRESS) localisation, at long echo time (135 or 144 ms) were acquired on a 1.5 T scanner. Studies that contained lipid contamination and abnormally inverted spectra were reviewed and the latter correlated with anatomic location at the base of skull, and with the area of the region of interest (ROI) studied.
Results: Of 128 consecutive MRSI studies, six showed abnormal inverted spectra, of which four were acquired at the base of skull. Multivariate logistic regression analysis showed that study location at the base of skull, but not larger ROI, was a significant predictor for the risk of being affected by inverted spectra (RR for base of skull: 11.76, 95% CI: 1.86–74.18, $P = 0.009$. RR for area of ROI: 3.68, 95% CI: 0.57–23.67, $P = 0.170$). Seven studies showed lipid contamination; all were in close proximity to the overlying scalp.
Conclusion: Using a semi-automated acquisition and post-processing method, MRSI can be successfully applied in the clinical setting. However, care should be taken to avoid regions of high magnetic field inhomogeneity at the base of skull, and lipid contamination in voxels prescribed near the scalp.

Keywords: Magnetic resonance imaging; Chemical shift imaging; Nuclear magnetic resonance; Spectroscopic imaging; Brain diseases; Brain metabolism

1. Introduction

Proton MR spectroscopy (MRS) provides metabolic information which is not available by conventional MR imaging. On many clinical MR scanners, it is now possible to acquire spectroscopic measurements as an additional pulse sequence, thus combining both morphological and metabolic information during the same study [1,2]. Single-voxel proton spectroscopy has been widely used for studying brain diseases, and has proven a reliable technique in clinical practice [2–4]. However, multi-voxel MR spectroscopic imaging (MRSI) [5–7] can potentially provide better spatial resolution and wider anatomical coverage, allowing areas of normal tissue to be included in a single study for comparison. Unfortunately, MRSI is technically more demanding in terms of acquisition and post-processing than single-voxel MR spectroscopy.

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Causes of sub-optimal MR spectroscopic examinations include poor spectral resolution, line width broadening, baseline distortion, phase correction errors, and lipid contamination; therefore some post-processing is often required before clinical interpretation. There are many encouraging reports of the usefulness of MRSI, but these tend to be performed at institutes with dedicated medical physicists and research departments [1,2,5–9]. And although it is well known in the MR spectroscopy community that spectra obtained at the skull base are distorted, there is no real study to highlight this point.

While single-voxel MRS is fully automated in the acquisition, processing and display of the single spectrum, the display of the processed MRSI spectra and images requires considerable user interaction. In our initial experience using a semi-automated method of acquiring and processing MRSI in a clinical setting, without sophisticated research and technical support, we found several studies affected by lipid contamination and abnormally inverted spectral peaks. Our hypothesis was that studies at the base of skull and with a larger region of interest were more likely to be affected by inverted spectra and that lipid contamination occurred in studies near the scalp. While there may be other reasons for unsatisfactory spectra (such as baseline distortions, spectral resolution and line width broadening), we focussed only on spectral inversion and lipid contamination in our current study.

2. Materials and methods

We retrospectively analysed all intracranial MRSI studies over the initial 9-month period after installation of scanning software. These were performed for a variety of non-haemorrhagic intracranial diseases, especially brain tumours. Two-dimensional MR spectroscopic imaging using point-resolved spectroscopy (PRESS) localisation (TR 1500 ms, TE 136 or 144 ms, FOV 24 cm, 16 × 16 or 24 × 24 phase encoding matrices, 1.0–1.5 cm section thickness) with automated shim and water suppression (PROBE-P, Version 8.3, GE Medical Systems, Milwaukee, WI) was acquired on a 1.5 T scanner. The localized region of interest (known as the PRESS ROI) was placed over the brain lesions by a neuroradiologist, or a radiology trainee. All studies were planned to include the abnormality visible on conventional MR imaging as well as areas of normal appearing brain parenchyma. Automatic prescan, which determines the center frequency, transmit and receive gains, optimizes the water suppression and homogeneity (shim) through the prescribed volume [10], was performed as recommended by the manufacturer. The MRSI scan was initiated if the line width reported by the prescan process was less than 6 Hz. If the line width was broader than 6 Hz, we prescribed these studies in different locations or planes. Each MRSI study lasted up to 15 min, including the prescan process.

Off-line spectral post-processing was carried out using semi-automated software (Probe 2000, Functool, Version 2.33, GE Medical Systems, Milwaukee, WI) [10]. Spectra were displayed as grids of nominal voxel size 1 cm × 1 cm and overlaid on the conventional MR image used to plan the study. Spectral peaks of the main metabolites—choline (Cho at 3.2 ppm), creatine (Cr at 3.0 ppm), *N*-acetyl aspartate (NAA at 2.0 ppm), lactate (Lac at 1.3 ppm) and lipid (Lip at 0.9 ppm), were visually analysed by two radiologists by consensus and the number of studies with sub-optimal spectra were counted. A MRSI study was considered sub-optimal if the normally positive spectral peaks (with the exception of lactate) were inverted below the baseline, or if there was lipid contamination, defined as an abnormally broad peak on the right side of the spectrum between 0.9 and 1.3 ppm. The anatomical site of ROI placement was recorded. A study was defined as located at the skull base if the following anatomical structures were seen in the image used to plan the PRESS ROI: orbits, sphenoid sinus/sella, inferior temporal fossa, clivus or the brainstem. Studies with lipid contamination were qualitatively assessed for their proximity to the subcutaneous tissue.

The data was analysed using SPSS statistical software (Version 11.0). Proportions (%) were used to describe categorical variables and χ^2-test and Fisher's exact test used to assess differences. Continuous variable (PRESS ROI area) was dichotomized due to data skewness, and cut off value set at 2500 mm^2 (i.e., values up to 2500 mm^2 were compared with those greater than 2500 mm^2). To predict the factors influencing the sub-optimal studies, bivariate and multivariate logistic regression was applied. Results were presented as relative risk (RR) with 95% confidence interval (95% CI). A *P*-value of 0.05 was taken as significant.

3. Results

We performed 128 consecutive MRSI studies in 102 patients: 92 studies for suspected brain tumours (Fig. 1) and 36

Table 1
Neurological conditions studied by MRSI

Pathology studied	Successful studies	Sub-optimal studies	Total
Primary tumor (excluding meningioma)	55	3	58
Secondary tumor	16	4	20
Meningioma	11	3	14
Infection	11	2	13
Other (normal, ischemia, trauma, etc.)	22	1	23
Total	115	13	128