Impact of acquisition orientation on whole brain metabolite maps obtained by short echo time Echo Planar Spectroscopy Imaging (EPSI)

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Target audience: MR spectroscopy community and people interested in using whole brain MRSI in clinical research protocol

Purpose: High quality whole brain metabolite maps are mandatory to help magnetic resonance spectroscopic imaging to bridge the gap from a research tool to a real clinical imaging modality. One major limitation is the artifact related to magnetic susceptibility effects leading to metabolite map distortions and signal drop out. The use of a short echo time helps to reduce signal loss and minimize phase differences, but the susceptibility artifact could also be minimized by the choice of the MRSI data orientation. We aimed here to evaluate the impact of MRSI orientation on quality of whole brain N-Acetyl-Aspartate (NAA), Choline (Cho) and Creatine (Cre) maps between acquisitions performed along the anterior commissure posterior commissure (AC-PC) line and along a tilted orientation of 15° with respect to the AC-PC line using a recent whole brain MRSI sequence called Echo Planar Spectroscopy Imaging (EPSI) [1] with short echo time (20ms).

Methods: Five young healthy subjects (mean age=24±1.4, age range = [22-26], 3 women and 2 men) gave written and informed consent before participating to the protocol. All MR data were acquired on a 3T MR system (Siemens, Verio system) with a 32-channel receiver head coil. The imaging protocol included two 3D EPSI sequence[1] with different angulations (the first aligned along the AC-PC line and the second aligned along the AC-PC line tilted by an additional angulation of 15°) and two T1-weighted magnetization prepared rapid gradient echo (MPRAGE) with orientation similar to those prescribed for the EPSI. ***EPSI*** was performed with TR/TE=1710/20ms, a covered region of 280x280x180 mm^3, a matrix of 50x50x32. EPSI sequences included an interleaved water reference realized with a 10° excitation angle and TE=6.3ms. The sequence used oversampling to improve spatial coverage in the presence of inhomogeneities at the expense of SNR [2].

After processing data in the Midas software package [3], water-reference images derived from EPSI sequence were normalized on T1-template on SPM8 with the VBM8 toolbox. The transformation matrix was then applied on EPSI signal normalized metabolites images. Using the data from all subjects, voxel-wise mean signal normalized maps and voxel-wise normalized standard deviation maps defined as $nSD=\frac{\sigma}{mean}$ with $\sigma=\sqrt{variance}$, were computed for each major metabolites, NAA, Cho and Cre. In order to remove outlier pixels from metabolite maps, we selected pixels showing nSD values below 1 for each metabolite map obtained with the two orientations. After segmentation of normalized T1 images, we applied the corresponding gray matter and white matter masks (threshold 75%) to obtain GM and WM metabolite maps for the two orientations. Mean values and SD were extracted from these maps. Finally, statistical mapping analysis (paired t-test, $p<0.05$) was performed on NAA maps to evaluate the differences in metabolite concentrations (arbitrary units) obtained in the same subjects between acquisitions performed in the AC-PC plane and in the AC-PC+15° plane.

Results: 1- Table.1 showed metabolite values obtained in whole brain gray matter and white matter with acquisitions performed in the AC-PC and the AC-PC+15° planes. Similar values were obtained while mean inter-subject standard deviation was 6.3 % of the mean with a maximum of 10% for NAA values in the white matter AC-PC+15° acquisition.

orientation	AC-PC			AC-PC + 15°		
Institutional unit(IU)	**NAA**	**Cho**	**Cre**	**NAA**	**Cho**	**Cre**
Whole brain GM	12.1±0.9	2.3±0.1	10.1±0.4	12.7±1.0	2.2±0.1	10.4±0.5
Whole brain WM	13.2±1.0	2.4±0.1	9.8±0.5	14.1±1.4	2.3±0.2	9.7±0.7

Table.1 Average metabolite values and standard deviations (in Institutional Unit) over all subjects, for gray and white matters.

2- At the regional scale, figure.1 showed nSD maps (thresholded at 1) derived from NAA maps from the 5 volunteers acquired in the AC-PC plane (Figure.1.A) and in the AC-PC+15° plane (Figure.1.B). Most of the brain can be observed. The largest standard deviations were found in the cerebellum and the orbitofrontal region in the AC-PC plane while in the AC-PC+15° plane the largest standard deviations were observed in the upper slices. Accordingly, statistical map showing the comparison of NAA values between the two orientations (Figure.1.C) showed significant NAA signal drop out in the cerebellum and the prefrontal cortex for the AC-PC acquisition (blue) while the AC-PC+15° acquisition showed significant signal drop out in the frontal and parietal areas, especially in the upper slices (red).

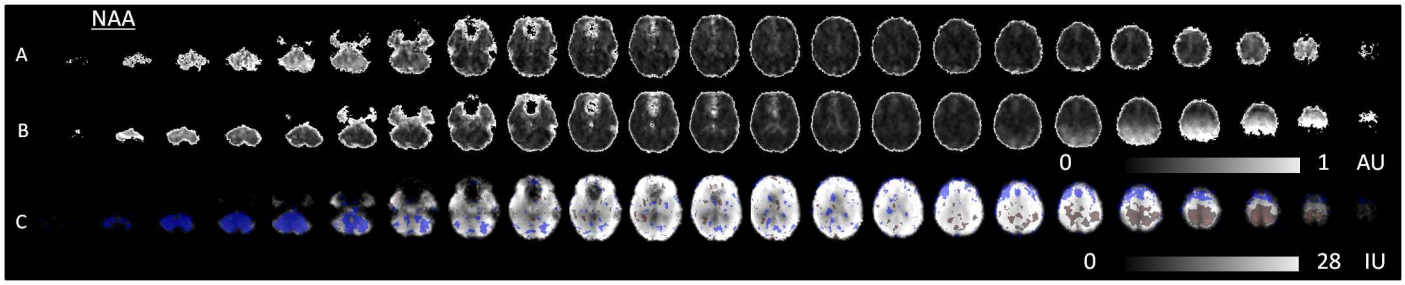

Figure.1 Threshold NAA normalized standard deviations (arbitrary units AU) maps over the brain for 2 orientations: (A) AC-PC and (B) AC-PC+15° and (C) mean NAA (IU) with regions where AC-PC values are higher (in red) and lower (in blue) than AC-PC+15° values

Conclusion: This work showed the impact of MRSI orientation on quality of metabolite maps. Whole brain NAA, Cre and Cho values appeared similar in controls whatever the orientation. Nevertheless, a spatial dependence was observed concerning NAA values relative to MRSI orientation. The AC-PC plane appeared more reliable for the upper slices while the AC-PC+15° plane was more robust for the cerebellum but suffered from reliability in the upper slices. According to the pathology studied, orientation has to be defined in lights of these results. In addition, procedures to limit susceptibility artifacts and others confounding factors, might help to minimize these differences and to really obtain accurate metabolic templates to be used to perform statistical mapping analysis on short TE MRSI data.

References: [1] Ebel and al, MRM, 53: 465-469 (2005) [2] Ebel et al. Magn. Reson. Imag. 21: 113-120 (2003) [3] Maudsley et al, NMR Biomed, 19:492-503 (2006)