Simultaneous acquisition of short and long echo time spectra of the mouse brain using proton magnetic resonance spectroscopic imaging at 11.75 T

P. Larvaron[1], Y. Le Fur[1], S. Confort-Gouny[1], P. Cozzone[1], and A. Viola[1]

[1]Faculté de Médecine, Université de la Méditerranée, Centre de Résonance Magnétique Biologique et Médicale, UMR CNRS 6612, Marseille, France

Introduction

The increasing number of genetically modified mice necessitates the development of new analytical tools to investigate the resulting phenotypes. MR techniques may provide alternative and versatile approaches to neurohistochemistry for defining the metabolic cerebral phenotype associated with a given genotype and allow longitudinal studies. Spectroscopic imaging techniques such as 2D-CSI enable to map out the regional localization of great number of brain metabolites, by acquiring a vast array of voxels at the same time. Here, we demonstrate the feasibility of simultaneously obtaining spectra at short and long echo times (6 ms and 135 ms respectively), a technique allowing at high field to considerably reduce the acquisition time, which was divided by a factor two.

Methods

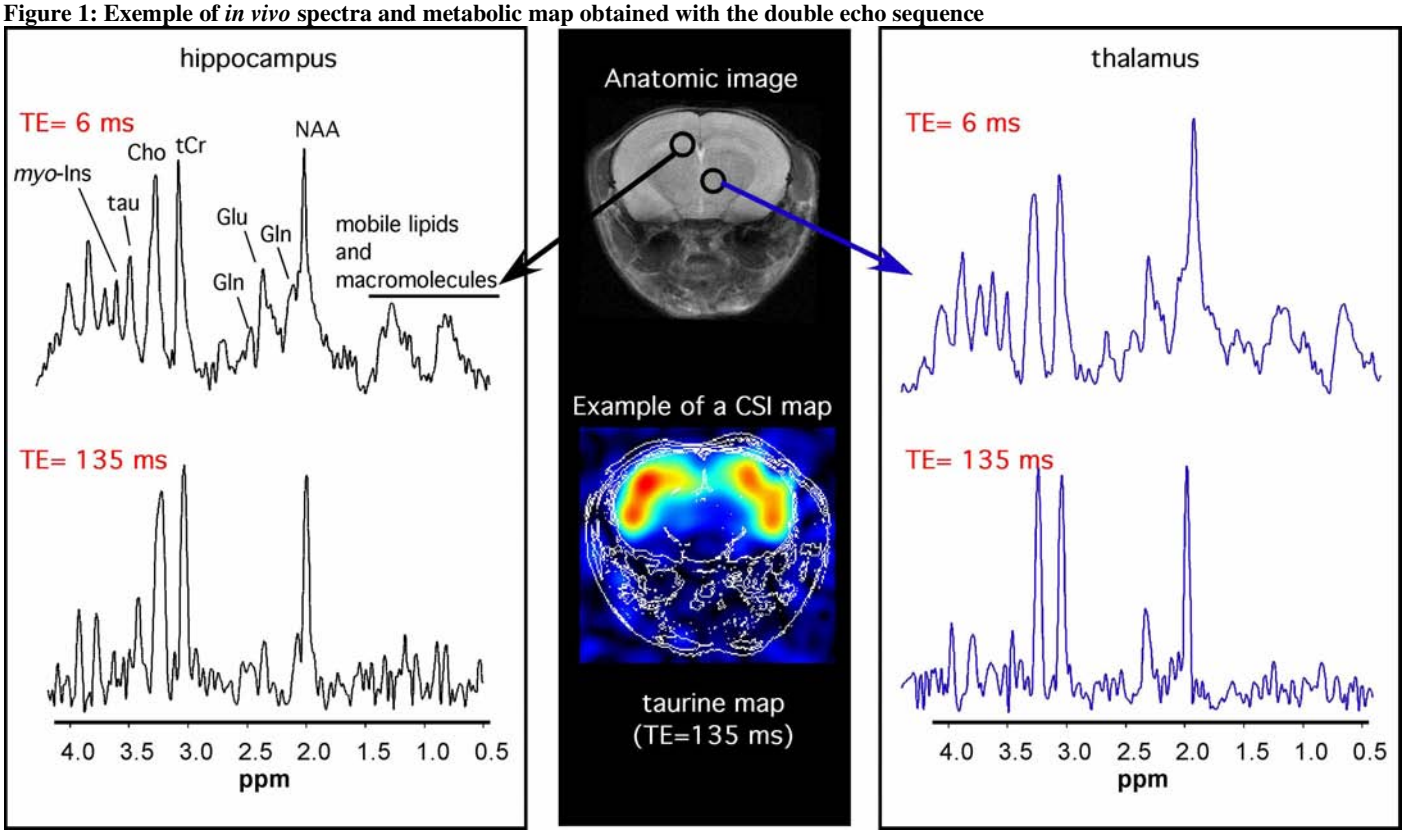
Isoflurane anesthetized C57Bl6 mice (6 week old) were explored on a 11.75 T vertical Bruker AVANCE 500WB wide-bore MR system and a transmitting and receiving head resonator.

Fastmap (voxel size 5^3 mm^3) was used for shimming. The CSI data were obtained by using a modified method based on the standard Bruker one. Encoding steps (15x15) with a field of view of 2^2 cm^2 were used resulting in a nominal spatial resolution of 1.33 mm. The data were acquired with the following parameters (TR: 3000; TE: 6 and 135 ms; slice thickness: 2 mm; 943 scans; total acquisition time: 47 min). The slice position was mid-axial. Water suppression was achieved using VAPOR scheme. Six outer volume suppression slices surrounding the skull were positioned for lipid suppression. The chemical shift of spectra was referenced to creatine (3.04 p.p.m.). Data were processed with a home-developed software developed under IDL environment (Interactive Data Language Research System, Boulder, Colorado).

Results

Figure 1 shows examples of *in vivo* high-resolution spectra routinely obtained from the mouse brain with the double sequence. The spectra shown here were from the hippocampus and thalamus. Note the high resolution of the spectra. The CSI map presented was obtained from the data acquired at long echo time.

Figure 1: Exemple of *in vivo* spectra and metabolic map obtained with the double echo sequence



Legend: anatomic MRI: spin echo sequence (TE, 9.1 ms; TR, 5 s; RARE factor 8; 2 averages) and the same geometrical parameters as for CSI.
Assignments: Cho, choline; tCr, total creatine; Gln, glutamine; Glu, glutamate; *s*-Ins, *myo*-inositol; NAA, *N*-acetylaspartate; tau, taurine.

Discussion

This new method will enable to map out spatial localization of a wide range of metabolites. Metabolic information is more important in spectra obtained at short echo time, with a higher number of signals that can be detected when compared to long echo time spectra. However, at short echo time some macromolecules signals superimpose with those of major brain metabolites. The possibility to acquire both short and long echo time spectra in a reasonable time is of special interest for estimating more precisely levels of brain metabolites by eliminating the contribution of macromolecule signals at long echo time. From a physiopathological standpoint, this double echo sequence should be of interest to assign doublets from small molecules such as lactate or aminoacids, which may be present in high quantity in models showing defective glycolysis or perturbations of aminoacid metabolism.