TO DIFFERENTIATE GLUTAMINE FROM GLUTAMATE IN HEPATIC ENCEPHALOPATHY BY TWO-DIMENSIONAL (2D) LOCALIZED CORRELATED SPECTROSCOPY (L-COSY) COMBINED WITH PROFIT QUANTITATION

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Purpose:

Hepatic encephalopathy (HE) is a problem with the brain that is caused by liver disease. The brain problem may be temporary or permanent. People with a liver disease called cirrhosis are most commonly affected. If the liver is not working properly, toxins can build up in the blood. The toxic blood travels to the brain, affecting the brain's ability to function. HE encompasses a wide spectrum of neuropsychiatric abnormalities and motor disturbances that range from mild cognitive impairment to coma and death (1-2). MR Spectroscopy has been used extensively as a noninvasive tool to examine the role of cerebral metabolites *in vivo* for the diagnosis of HE (3-4). In the previous studies, changes of (glutamine plus glutamate) have been reported instead of Glutamine (Gln) and Glutamate (Glu) separately. The purpose of the study is to demonstrate the role of two-dimensional (2D) localized correlated spectroscopy (L-COSY) combined with prior knowledge fitting (ProFit) algorithm (5-7) to differentiate glutamine from glutamate in addition to quantify more metabolites in Hepatic Encephalopathy.

Outline of Content:

Issues in 1D MRS: One-dimensional (1D) MR spectra suffer from overlapping resonances of several metabolites. As a result of this overlap, information from metabolically important or potentially diagnostic resonances can be obscured, affecting both peak assignment and accurate quantitation of metabolite levels.

Issues in spectral Editing technique: Selected metabolites, namely GABA and lactate, glutathione have been discriminated from the overlapping metabolites and lipids. A major drawback of the editing sequences is that only one metabolite can be detected per measurement. Also, when the J-coupled metabolites are not well separated, the editing sequences require longer spin selective RF pulses, minimizing the efficiency of the editing sequences dramatically. Hence, there is a need for a nonselective technique that can discriminate several metabolites from each other in a single measurement.

Advantage of 2D MRS: Two-dimensional (2D) L-COSY overcomes this problem by adding a second frequency dimension by acquiring multiple 1D spectra with incrementally longer TEs and applying double Fourier transform on the set of spectra to produce a 2D spectrum. Two-dimensional (2D) correlated spectroscopy (COSY) facilitates mapping the connectivity between different protons within brain metabolites. The 2D L-COSY MRS method allows the clear and unambiguous identification of several metabolites from a single measurement in vivo.

ProFit Quantitation: ProFit is based on a linear combination of the prior knowledge spectra. The optimization problem consists on identifying the best combination of the basis spectra that minimizes the error when compared with the original spectrum to be fitted. Combining 2D L-COSY with ProFit algorithm detect and quantify the following cerebral metabolites: creatine (Cr), N-acetylaspartate (NAA), glycerylphosphorylcholine (GPC), phosphorylcholine (PCh), free choline (Ch), alanine (Ala), aspartate (Asp), GABA, glucose (Glc), glutamine (Gln), glutamate (Glu), glycine (Gly), glutathione (GSH), lactate (Lac), threonine (Thr), myoinositol (mI), N-acetylaspartylglutamate (NAAG), phosphoethanolamine (PE), taurine (Tau), scyllo-inositol (Scy), and ascorbate (Asc).

The following figures (Fig.1 and 2) show the comparison of 1D and 2D MRS spectrum of hepatic Encephalopathy patients.

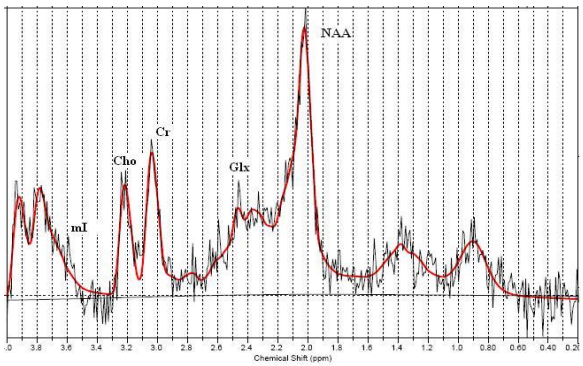

Fig.1. 1D MRS spectrum of 51 years old HE patient

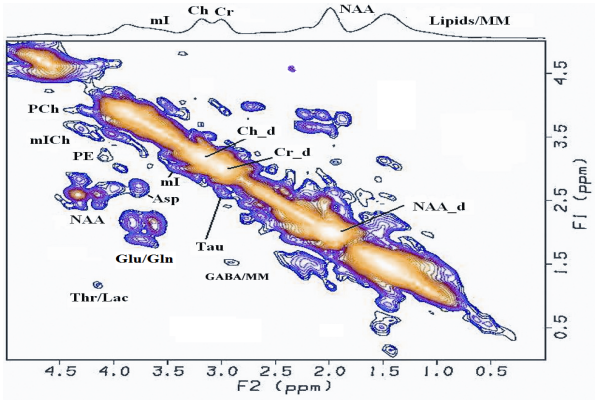

Fig.2. 2D L-COSY spectrum of 51 years old HE patient

Summary:

Prior-knowledge based metabolites quantitation using 2D MRS provides more metabolites than the conventional 1D MRS in addition to quantifying Glu and Gln separately. This differentiation would be quite useful in studying HE and other diseases and disorders since 1D MRS has been quite limited in its ability to separately quantify these overlapping metabolites.

References:

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