Using edited MRS to reveal extra metabolites

Who will benefit from this information?

This lecture will describe a group of methods that allow the information content of MR spectra to be 'edited'. The description will be conceptual and equation-free, and will be accessible to all ISMRM members, whether they have technical or clinical in interests. MRS researchers will benefit from an improved understanding of the conceptual framework of editing experiments and access to a potential new tool to apply. MRI researchers with an interest in MRS will benefit from improved knowledge of the range of MRS techniques that are available. Clinical and non-clinical researchers for whom MR is one tool among many to address scientific questions will be be made aware of an exciting new class of metabolite species that can be measured with edited MRS, and which will answer important questions about normal and abnormal brain function.

How was a problem determined?

In *in vivo* MR spectroscopy, signals from different metabolites are separated on the basis of differing chemical shifts; that is, the frequency of the signals is shifted depending on the chemical environment of the nucleus, allowing different chemical species to be distinguished. Thus the MR spectrum consists of a number of peaks each associate with different chemical species. One limitation to the utility of *in vivo* ^{1}H-MRS is the fact that the chemical shift range over which signals are spread is relatively modest (~5 ppm) compared to the width of signals (typically ~0.1 ppm). Thus, although the MR spectrum contains signals from all the metabolites in the brain, the number of chemical species that can be differentiated and measured is fundamentally limited (and it is the most concentrated species and those that give the strongest signals that predominate).

Edited MRS responds to this problem of "too much information spread over too small a range", by reducing the information content of the spectrum, preferentially detecting signals of interest based on prior knowledge and careful experimental design. In this lecture, we will look at how some signals can be separated from stronger overlying signals in this way.

Examples of how this issue has been addressed

Examples covered will include three main classes of editing experiment: J-difference, multiple-quantum filtered and asymmetric editing. We will discuss how each method allows signals in the MR spectrum to be separates, the strengths and weaknesses of each approach, and the effort involved to implement each method. Experimental strategies that are alternatives to editing, for example localized two-dimensional J-resolved spectroscopy (J-PRESS), will be briefly mentioned.

We will discuss various editing target molecules, including GABA (γ-aminobutyric acid), lactate, glutathione (GSH), ascorbate (Vitamin C), N-acetyl aspartyl glutamate (NAAG), 2-hydroxyglutatarate (2HG) and others. These target metabolites have wide-ranging functional significance, from neurotransmitters and neuromodulators (GABA and NAAG), to antioxidants (GSH and ascorbate), to oncometabolites (2HG). A number of published studies in which editing methods have been applied to answer research questions will be presented.

What will learners be able to do differently because of this information?

This lecture will give learners:

1. a thorough overview of how editing methods work, including practical knowledge on how to set up and implement editing methods;

2. a summary of what new chemical species can be investigated with MRS beyond the historical triad of NAA, Creatine and Choline;
3. references to appropriate literature for further reading, and online resources to obtain relevant experimental and post-procesing tools.