

## Effect of J-coupling on lipid composition determination in vivo using proton MRS

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### Purpose:

The purpose of this educational abstract is to emphasize the significance of J-coupling effects when determining lipid compositions from spatially localized lipid proton magnetic resonance (MR) spectra.

### Outline of content:

Most lipid protons exhibit scalar coupling interactions rendering their response dependent on the *in-vivo* magnetic resonance spectroscopy (MRS) sequence being used. For example, it has been shown that  $T_2$  values of different lipid proton groups are lower when determined with PRESS (Point RESolved Spectroscopy) compared to with STEAM (Stimulated Echo Acquisition Mode) [1]. For spatially localized *in-vivo* measurements of lipids, often a PRESS sequence is employed. On a typical scanner, the shortest TE (echo time) attainable with PRESS is approximately 20 ms and all lipid resonances are modulated as a function of TE because of J-coupling evolution and transverse,  $T_2$ , relaxation effects. The different proton groups of a fatty acid are involved in scalar coupling interactions with their neighboring protons [2] and each has its own characteristic  $T_2$  constant. Knowledge of the  $T_2$  constants of the different proton groups is necessary for accurate lipid quantification, for example, when determining the ratio of the methylene peak area (at 1.3 ppm) to the methyl peak area (at 0.9 ppm) [3]. In addition, at higher field strengths such as 7 T or 9.4 T, the lipid peaks in a proton MR spectrum at 2.1 ppm (allylic protons), 2.3 ppm (alpha position protons with respect to the carbonyl group) and 2.8 ppm (diallylic protons) are well resolved enabling estimates of the amounts of saturated, monounsaturated, and diunsaturated fatty acids to be calculated (SFA, MUFA, and DUFA, respectively). The scalar coupling and transverse relaxation effects are superimposed making it difficult to separate their respective contributions, thereby resulting in quantification uncertainties for the various lipid peaks. A few studies have attempted to resolve this by acquiring lipid spectra at a few short-TE values in the approximate range of 10 – 70 ms and fitting the peak areas as a function of TE to monoexponentially decaying functions to extrapolate initial magnetizations [1, 4-6]. However, recent work [7] has shown that this technique can result in erroneous lipid compositions. The objective of the proposed educational e-poster is to discuss the following:

- The chemical shifts and J-coupling interactions of the relevant protons groups of a fatty acid molecule.
- The equations relating the 2.1, 2.3 and 2.8 ppm lipid resonance areas to the amount of SFA, MUFA and DUFA composing the lipid being studied.
- The errors introduced by J-coupling effects on  $T_2$  estimates of the different proton groups and consequently on the determined lipid composition.
- How the chemical shift displacement effect can be exploited to reduce J-coupling effects for weakly-coupled lipid protons.
- The negative consequence of fitting the response of a lipid resonance to PRESS as a function of TE, which is the product of scalar coupling modulation (sinusoidal in nature) and  $T_2$  relaxation, to a monoexponentially decaying function.

### Summary:

The presented educational abstract is intended to bring to attention the errors introduced to lipid composition estimates when J-coupling modulations of lipid resonances acquired by spatially localized MRS techniques such as PRESS are not corrected for or are compensated for incorrectly.

### References:

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