# J refocused coherence transfer spectroscopic imaging at 7T

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**Introduction:** The detection of amino acids at ultra high field is enhanced due to improved spectral resolution in comparison to 3T. However, due to J-modulation and T2 losses short spin echo acquisitions are typically used at 7T. Unfortunately, broad macromolecule resonances, visible at short TE, can make accurate detection of the metabolites difficult. J refocused coherence transfer spectroscopy is known to suppress J-modulation of coupled spin systems allowing echo times to be lengthened to suppress macromolecule signals. We describe simulation and implementation of a J-refocused transfer sequence for spectroscopic imaging of glutamate and glutamine in the human brain at 7T.

**Methods:** The J-refocused transfer sequence is a double echo sequence where J-modulation of spin coupled resonances is induced in the first echo, reciprocally transferred and rephased in the second echo. In this implementation, slice selective pulses are used for the excitation and transfer pulses. For water suppression, an optimized broad T1 inversion approach using three low power (narrow band) adiabatic inversion pulses and optimized delays was used to suppress water over a range of T1 values (400-5000ms). These pulses were applied using a "homogeneous" RF distribution (phases and amplitudes of the individual coils of the transceiver array optimized to maximize homogeneity over the entire slice), while a separate RF "ring" distribution (optimized for the scalp) was used for outer volume suppression (1).

A Varian DirectDrive head only 7T system with a gradient head insert and $1^{st}$-$3^{rd}$ order shims was used. An 8 element transceiver array was used for all studies with a CPC RF amplifier operating in 8x1kW mode. The two RF distributions (homogeneous and ring) were determined for each volunteer by $B_1$ mapping and RF shimming. Non-iterative Bo shimming was performed using $1^{st}$-$3^{rd}$ order shim corrections, resulting in σBo ~10Hz for the entire slice over the centrum seimovale. Phase encoding (24x24) was performed over 192x192 FOV, 10mm slice (voxel size 0.64cc), TR/TE 1500/34ms. The study duration was ~50min including $B_1$, Bo shimming, anatomical images and SI.

**Results:** Simulation (performed using the GAMMA C++ pulse library (2)) of 10 typical brain metabolites (NAA, cre, cho, glu, gln, asp, myo, tau, gaba, lac), shows that the J- refocused sequence provides improved retention and resolution of amino acids (Fig 1). In vivo, the J-refocused sequence shows outstanding water suppression and excellent distinction between Glu and Gln (Fig. 2). Macromolecules are suppressed although not wholly eliminated.

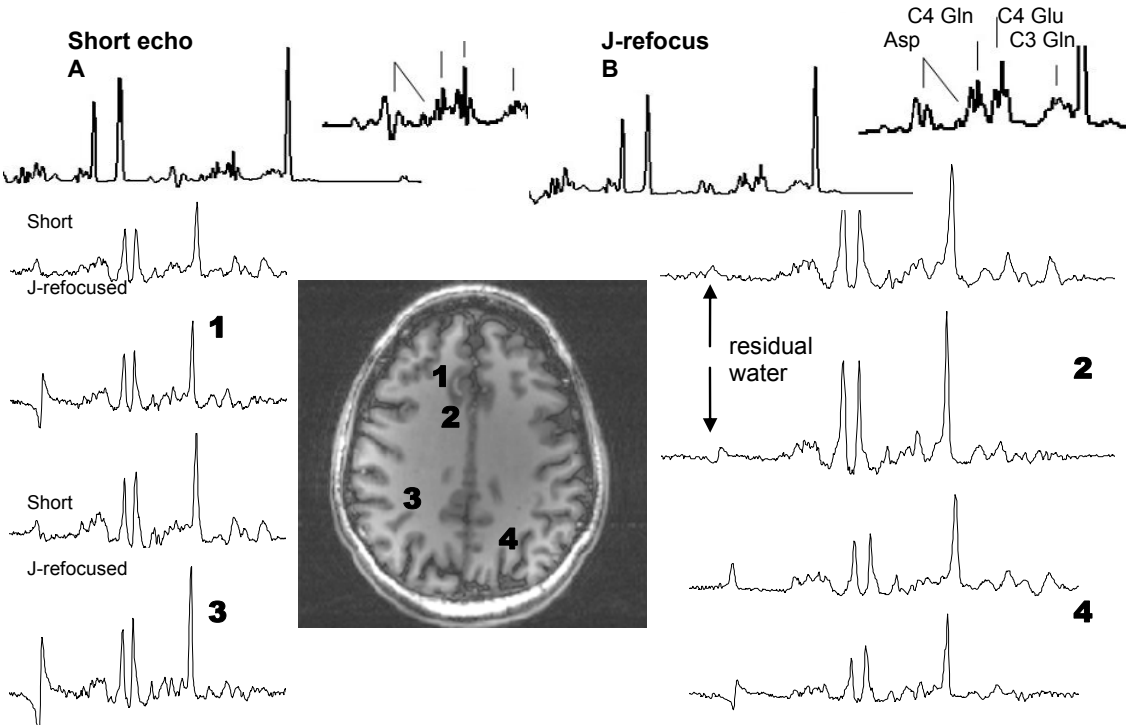


Figure 1. Simulation of short echo (A) and J-refocused (B) with insets showing a magnified view between 1.9 to 2.9ppm. The lines indicate areas of better resolution: between the C4s of glu, gln; the C3 of gln is better retained and the aspartyl resonances are absorptive.

Figure 2. Spectroscopic imaging data showing scout and spectra. For each identified location, the corresponding spectra are shown, with short echo 15ms (top) and J-refocused (bottom). The arrow displays the residual water.

**Conclusions:** The J-refocused coherence transfer sequence performs well in spectroscopic imaging format at 7T. The use of the dual RF distributions eliminated need for additional in-plane spatial localization. No adiabatic refocusing pulses are used, with the SAR well below FDA guidelines, and outstanding water suppression is achieved. In comparison to a TE15msec spectroscopic image, the J-refocused sequence retains much of the amino acids and singlet resonances, suggesting that the incremental T2 losses for TE34msec are not substantial.

Refs: (1) Avdievich et al 2009; (2) Smith et al 1994