

Correlation Time Diffusion MRI of Mouse Liver at 11.7T: Magnetization Transfer Effects

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Purpose: To develop a technique for mapping the correlation time diffusion coefficient (CT-D) of *ex vivo* liver samples imaged at 11.7T and to compare results quantitatively vs. the standard pulsed-field gradient (PFG-D) diffusion MRI.

Theory: The binary spin bath Bloch equation for the liquid pool (A) is (Ref. 1):

$$\frac{\partial M_z^{(A)}}{\partial t} = -2\pi\gamma \text{Im}\{B_{1T}^{(\text{Exp})} m^{(A)}\} + \left[\frac{1}{T_1^{(A)}} \right]_{(\text{kin})} + RM_z^{(B-\text{eq})} \left(M_z^{(A-\text{eq})} - M_z^{(A)} \right) + \text{Constant} \quad \text{Eq. 1}$$

From which the total or observed T1 relaxation rate is the sum of a kinetic term and a magnetization exchange term.

$$\frac{1}{T_1^{(A)}} = \left[\frac{1}{T_1^{(A)}} \right]_{(\text{kin})} + RM_z^{(B-\text{eq})} \quad \text{Eq. 2}$$

These two relaxation terms can be modeled as functions of the rotational and translational correlation times using the BPP theory:

$$\left[\frac{1}{T_1^{(A)}} \right]_{(\text{kin})} = \left[\frac{1}{(1 + \omega_0^2 \tau_{(\text{rot})}^2)} + \frac{4}{(1 + 4\omega_0^2 \tau_{(\text{rot})}^2)} \right] \lambda_0 \tau_{(\text{rot})} + \left[\frac{1}{(1 + \omega_0^2 \tau_{(\text{trans})}^2)} + \frac{2}{(4 + \omega_0^2 \tau_{(\text{trans})}^2)} \right] PD^{(\text{norm})} \lambda_1 \tau_{(\text{trans})} \quad \text{Eq. 3}$$

and phenomenologically as function of the binary spin bath parameters for the semisolid pool, specifically:

$$RM_0^B = \eta \left(\frac{1}{T_1^{(A)}} - \frac{1}{T_1^{(B)}} \right) \left(\frac{PD^{(\text{water})} - PD}{PD^{(\text{water})}} \right) \quad \text{Eq. 4}$$

where η is a dimensionless MT coupling constant and $T_1^{(B)}$ is the longitudinal relaxation time of the semisolid pool.

Experimental Methods: A previously described (Ref. 2) CT-D algorithm based on the theory above was adapted to hepatic tissue and used with water normalized proton density (PD) and T1 maps obtained with the Tandem-TSE pulse sequence, which is qMRI multispectral in T1, T2, and PD: key parameters: 35 slices/voxel size 0.1x0.1x0.6mm³/400TI/9.7,23ms TE1,2 / 4000, 4400msTR1,2. CT-D algorithm was programmed in MathCAD (PTC, Needham, MA). For PFG diffusion weighted MRI (DWI), a multi-slice spin echo image pulsed field gradient acquisition (10msTE /2000msTR) was used with three b-values of 21, 301, and 601 s/mm². All images of a vial containing the mouse liver (C57BL/6, male) sample in a bath of phosphate buffered saline (PBS) were acquired using a Bruker 11.7T scanner (BioSpinTM, Ultra Shield 500MHz) NMR spectrometer with imaging capabilities and temperature control: 23.5°C was used.

Results: Selected diffusion coefficient maps are shown in Fig. 1: CT-D map (top left, obtained with $\eta=1.75$ and $T_1^{(B)}=444\text{ms}$), PFG-D map (middle left), and vanishingly small difference map (bottom left). The quantitative diffusion coefficient distribution agreement obtained with the two techniques is further evidenced by the near perfect match between the whole-liver histograms on the right hand side. We note that the CT-D histogram is approximately five fold narrower than the D-PFG histogram and also, that excellent quantitative agreement is obtained (see Fig. 1) for the PBS liquid bath with the known value for water at 23.5°C ($D=2,350 \cdot 10^{-6} \text{mm}^2/\text{s}$).

Conclusion: A correlation time diffusion coefficient mapping technique that includes the effects of magnetization transfer in hepatic tissue has been developed and tested with a mouse liver sample at 11.7T. Excellent quantitative agreement was found between this non-PFG diffusion technique, which produces substantially improved SNR, vs. the standard PFG diffusion technique. In summary, CT-D diffusion MRI could be a viable alternative to standard PFG-diffusion MRI with higher SNR and is less demanding on the imaging gradients.

References

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