High-resolution quantitative magnetization transfer imaging of post-mortem marmoset brain

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Target audience. Researchers interested in MR contrast mechanisms, quantitative brain imaging, qMTI, and MR microscopy.

Purpose. Quantitative magnetization transfer imaging (qMTI) provides information on otherwise MR-invisible macromolecules via cross relaxation or proton exchange with water molecules. In cerebral white matter (WM), qMT parameters are assumed to be related to myelination and have been used as markers of WM pathology [1]. This is particularly true for the macromolecular pool-size fraction, M_{0b}. In this abstract, we investigate whether high-resolution (200 µm isotropic) qMTI at 3 T can visualize indicators of myelination well in a *post-mortem* marmoset brain. We compare our findings with T_1 mapping in the same brain at 7 T, since T_1-weighted imaging is more commonly used for visualizing neuroanatomy.

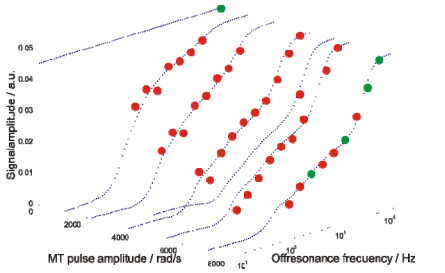

Fig. 1. *Z*-spectrum from a WM voxel (dotted lines: fitting results to the full data set; green circles: data points selected for accelerated parameter estimation by ANNs.

Methods. qMTI data were acquired at room temperature from a *post-mortem* marmoset brain (male animal, 7.6 years; perfusion fixation by 4% formalin in PBS, storage in PBS/NaN_3 for 17 months) on a 3T MedSpec 30/100 scanner (Bruker, Ettlingen, Germany) with a custom-made transceiver brain-specimen coil [2]. 45 image volumes (200µm nominal isotropic resolution) were recorded with a 3D FLASH sequence (TR 32 ms, TE 8.2 ms, α 10°) and pulsed off-resonance saturation (10 ms Gaussian pulse; 7 different pulse amplitudes with γB_1 between 0.6 and 7068 rad/s; 11 logarithmically distributed offset frequencies with $\Omega/2\pi$ between 250 and 50000 Hz). The qMT parameters from selected slices were obtained by non-linear least-squares fitting with a matrix-exponential algorithm [3] to solve the Bloch-McConnell equations for the binary spin-bath model [4]. Subsequently, these data were used to train an artificial neural network (ANN) algorithm [5] for accelerated parameter estimation of the full 3D data set. High-resolution T_1 maps were also recorded at 7 T (MAGNETOM 7T, Siemens, Erlangen, Germany) with an MP2RAGE sequence. FSL 5.0.5 was used for registration and segmentation of qMTI and T_1 maps for voxel-wise correlation of imaging results.

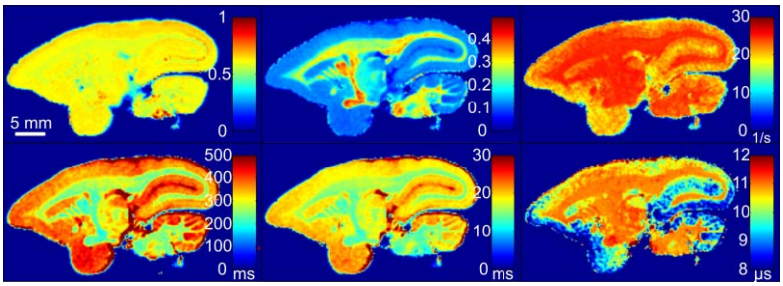

Fig. 2. qMT parameter maps (ANN results); top row: σM_{0a} (liquid pool size with scaling factor), M_{0b} (relative semi-solid pool size), R (exchange rate constant); bottom row: T_{1a} (liquid pool longitudinal relaxation time), T_{2a} (liquid pool transverse relaxation time), T_{2b} (semi-solid pool transverse relaxation time).

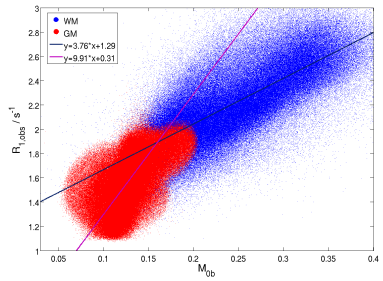

Fig. 3. Plot of $R_{1,obs}$(7 T) vs. M_{0b}. Separate analyses of segmented GM and WM data yielded a steeper increase of $R_{1,obs}$ with increasing M_{0b} in GM.

Results and Discussion. Representative Z-spectra and fitted parameter maps are shown in Figs. 1 and 2. Figure 3 presents a plot of $1/T_{1obs}$ recorded at 7T vs. M_{0b} from the qMT fitting, both parameters assumed to reflect myelination. Both measures were highly correlated, yielding reduced $1/T_{1obs}$ and M_{0b} values in voxels with predominantly gray matter (GM) as compared to voxels with predominantly white matter (WM). However, the slope obtained by linear regression from GM voxels was different from that obtained from WM voxels. This seems to suggest that myelination affects both contrast parameters in slightly different ways in the different tissues. Alternatively, other factors showing significant variation between GM and WM (for example iron content) might contribute to this result.

Figure 4 presents zoomed M_{0b} and T_{1obs} maps along with signal profiles recorded in the occipital lobe. With the achieved image resolution, both contrasts permit visualization of cortical layering, in particular the stria of Gennari, which is approximately 400 µm thick and known to be heavily myelinated. The combined results from the different imaging modalities may lead to better understanding of the particular contrast mechanisms and their relation to tissue microstructure.

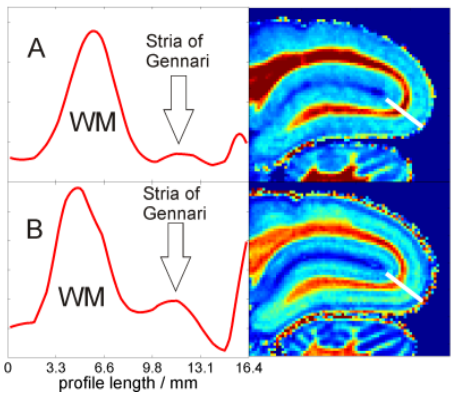

Fig. 4. High-resolution maps of M_{0b} **(A)** and T_{1obs} **(B)** and profiles of the parameter values along the white line in the occipital lobe.

Conclusion. High-resolution qMTI parameter maps permitted visualization of cortical substructures in the post-mortem marmoset brain.

References. [1] K. Schmierer, *J. Magn. Reson. Imaging* 26:41-51, 2007. [2] R. Müller, *Proc. ISMRM* 21:4366, 2013. [3] D.K. Müller, *J. Magn. Reson.* 230:88-97, 2013. [4] R.M. Henkelman, Magn. Reson. Med. 29: 759-765 (1993). [5] H. Marschner, *Proc. ISMRM* 21:4239, 2013.

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