

# Magnetization Transfer Profiles and T<sub>2</sub> Characterization of White Matter Tracts

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## Abstract

Magnetization Transfer (MT) is a unique MRI contrast revealing information on the macromolecular content of tissue. MT profiles and absolute T<sub>2</sub> maps were acquired for individual white matter tracts in the brainstem, as identified by diffusion tensor imaging (DTI). Based on MT analysis, the six delineated tracts could be separated in three different groups. Fibers with the largest MT effect, such as the cortical spinal tract, showed the shortest T<sub>2</sub>, in agreement with the concept that myelination reduces water T<sub>2</sub> and enhances the MT effect. The MT effect is more sensitive than T<sub>2</sub> for characterizing each fiber, due to a broader distribution range.

## Introduction

Magnetization Transfer Ratios (MTR) have been proven very useful in the early detection of white matter degeneration, such as in multiple sclerosis (MS) (1). MTR maps are derived on a voxel-by-voxel basis from MR images obtained with and without a single off-resonance saturation pulse. At present, the only possible approach is to assign a single MTR value to white matter lesions that may consist of multiple fiber bundles. One possible way to enhance the specificity of early changes would be to acquire MTR profiles for individual white matter tracts. If combined with measurement of relaxation times, this method would provide various parameters, such as the transfer rate or the relative size of the two pools (free water and bound macro-molecules) (2,3). As an initial study to test this approach, we used DTI to delineate different tracts in the brainstem of adult volunteers, and measured their complete MTR spectra and T<sub>2</sub> relaxation time to identify whether more specific characterization of their myelin content could be achieved.

## Methods

Informed consent was obtained from three healthy volunteers. All studies were performed using a 1.5-T Philips Intera-NT system (Philips Medical Systems, Best The Netherlands), equipped with high-performance gradients (22 mT/m). Diffusion-weighted imaging was accomplished using multi-slice segmented EPI sequence, with cardiac triggering and real-time navigator echo phase correction and a motion-based reacquisition scheme (4). Parameters were: matrix = 64x51 (128x128 reconstructed); FOV = 120 mm; EPI readout = 17 echoes / excitation; 40 slices; slice thickness = 3 mm; TE / TR = 92 ms / 5 heartbeats. Diffusion weighting ( $b = 600 \text{ s/mm}^2$ ) was performed along six independent axes, and combined with a reference image to calculate the diffusion tensor. Four averages were acquired to enhance signal-to-noise ratio.

An MP-RAGE scan was obtained for co-registration: TR / TE / flip angle ( $\alpha$ ) = 8 ms / 4 ms / 8°; Inter-shot time = 3 s; FOV = 240 mm, 51 (40 reconstructed) z-phase encoding steps, 3 mm slice thickness, TI = 748 ms, matrix = 256x179, rFOV = 70%, 2 NSA.

An 8-echo 3D-CPMG sequence was combined with a segmented EPI readout (13 echoes / excitation) to get absolute T<sub>2</sub> using the following parameters: TR / TEs /  $\alpha = 1 \text{ s} / 8 \times 26 \text{ ms} / 90^\circ$ , FOV = 120 mm, 51 (40 reconstructed) z-phase encoding steps, 3 mm slice thickness, matrix = 64 x 52 (128x128 reconstructed), rFOV = 100%.

Finally, two different MTR scans were then obtained using a RF-spoiled segmented 3D-GRE-EPI acquisition technique, and a sinc-shaped MT pre-pulse of 15 ms and  $\alpha = 640^\circ / 128^\circ$ , with 30 RF offsets logarithmically sampled between 100 Hz – 80 kHz, and a reference scan with a 0°-MT-prepulse (3). These two different MT irradiations allow measurement of both the direct RF saturation and the MT-profiles in each individual pixel. The other parameters were: TR / TE /  $\alpha = 32 \text{ ms} / 7 \text{ ms} / 25^\circ$ , FOV = 120 mm, 51 (40 reconstructed) z-phase encoding steps, with a linear profile acquisition order, 3 mm slice thickness, EPI shots = 4, matrix =

64x52 (zero-filled to 128x128), rFOV = 100%, 2 NSA, scan time per 3D-volume = 16 s.

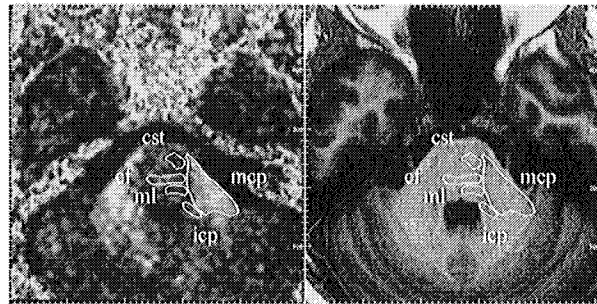


Figure 1: Axial cut of the DTI-calculated color map (A) and T<sub>1</sub>-weighted (MP-RAGE) image (B) through the brain stem at the pons level, showing the cortical spinal tract (cst), medial lemniscus (ml), crossing fibers (cf), inferior (icp) and middle cerebellar peduncle (mcp).

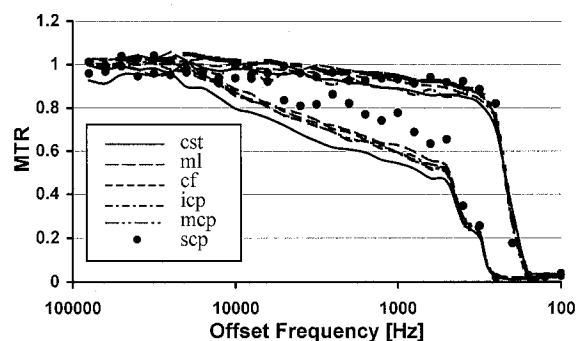


Figure 2: Direct saturation (upper curves) and MTR spectra (lower curves) from 6 large fiber bundles in the brain stem.

## Results and Discussion

Fig. 1 demonstrates the DTI-based delineation of various fibers of the brainstem at the pons level. Corresponding MTR spectra are represented for these 5 fibers plus the superior cerebellar peduncle (scp), not present at this slice level. One can see that different fibers demonstrate different MT profiles, possibly due to difference in the myelin content (5). The three groups of fibers (I: cst, ml, cf; II: icp, mcp; III: scp) have MT effects (area between the direct and MT curves) that are inversely proportional to their T<sub>2</sub> (Table). This trend is in agreement with the understanding that increased myelination corresponds to increased MTR and reduced T<sub>2</sub> (5).

	MT [au]	T <sub>2</sub> [ms]
Group I	6.9 ± 0.4	85 ± 10
Group II	5.9 ± 0.4	89 ± 8
Group III	4.4 ± 0.8	96 ± 10

In conclusion, this study shows that it is possible to derive MTR spectra of individual types of fiber bundles, which may help in the understanding of MTR changes across different brain areas, and therefore increase the specificity of MTR imaging in the early detection of micro-structural brain damages in WM diseases.

## References

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