Cross-relaxation imaging reveals detailed anatomy of white matter fiber tracts in the human brain

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Introduction

Cross-relaxation imaging (CRI) is a common term defining a new group of quantitative MRI methods (specifically, quantitative magnetization transfer (MT) (1,2), pulsed Z-spectroscopy (3)), which allow mapping of fundamental parameters determining the magnetization transfer effect in tissues. Recent time-efficient method of CRI (4) provides three-dimensional (3D) maps of the cross-relaxation rate constant (*k*) and bound pool fraction (*f*) in the entire brain with high spatial resolution and clinically acceptable scan time.

Purpose: to evaluate anatomic correlations of cross-relaxation parametric images in the normal brain.

Methods

Images were acquired on a 1.5 T whole-body MR scanner (GE Signa) using a 3D spoiled gradient-echo pulse sequence with an MT preparative pulse. Two series of 3D whole-brain datasets were obtained: 1) a series of four MT-weighted scans with TR/TE = 32/2.4 ms, flip angle $\alpha = 10°$, and variable offset frequency of a saturation pulse, Δ = 3, 6, 9, and 12 kHz and 2) a series for T_1 relaxometry (without MT preparation, used as a complementary dataset in processing algorithm) consisted of four scans with TR/TE = 20/2.4 ms and variable α = 4, 10, 20, and 30°. All data were acquired with actual resolution of 1.4x2.3x2.8 mm and were zero-interpolated before Fourier transform to obtain an isotropic voxel size of 1.4 mm. The scan time was 3 min for MT-weighted scans and 2 min for variable flip angle scans. The total examination time was about 30 min. The method was tested in three healthy volunteers (two male, one female, age range 25 to 32 years). Reconstruction of *k* and *f* maps was performed using an accurate model of pulsed MT effect, which relies on a two-pool model of MT (5) and treats the evolution of magnetization during actual time intervals of the pulse sequence (3,4). The model included superLorentzian line shape for bound proton fraction.

Results

The maps of bound fraction, *f*, demonstrated high heterogeneity of white matter within an overall range of *f*=9-15%. Lower *f* values were found in gray matter (6.5-8.5%) with the highest *f*=8.5% in the anterior thalamus. Areas of elevated *f* were unambiguously interpreted as the manifestation of compact fiber tracts. The following tracts were identified as zones of consistently increased *f* (to 12-15%) in the forebrain (Fig. 1): 1) commissurial tracts: corpus callosum, anterior commissure, posterior commissure; 2) projection tracts: optic radiations, auditory radiations, anterior thalamic radiations; 3) association tracts: cingulum, fornix, superior longitudinal fasciculus, superior fronto-occipital fasciculus, inferior longitudinal fasciculus, inferior fronto-occipital fasciculus, and uncinate fasciculus. Among the brain stem structures, an increased *f* was found in the middle cerebellar peduncle, decussation of superior cerebellar peduncle, medial lemniscus, and central tegmental tract.

Distribution of cross-relaxation rate constant, *k*, was relatively uniform in white matter, while this parameter produced sharp contrast between gray and white matter quantitatively characterized by the values ~1.6 and 3.3 s^{-1} respectively. The most marked specific feature of *k* maps is their ability to visualize the corticospinal tract (CST) (Fig. 2). The course of CST can be seen on all levels, including the brain stem, cerebral peduncle, posterior limb of internal capsule, corona radiata, and centrum semiovale. Quantitatively, CST is characterized by elevated *k* ranged from 3.4 to 3.8 s^{-1}. At the same time, CST was invisible on *f* maps.

Discussion

An increased *f* in a majority of compact fiber tracts well correlates with myelination of these structures (6). Specific appearance of CST on *k* maps is likely related to the presence of heavily myelinated axons with thick myelin sheaths, which may facilitate a faster exchange between water and macromolecular protons. The absence of an increase of *f* in CST can be explained by the relatively large interstitial spaces (7) resulting in effective averaging of the macromolecular proton content.

Conclusions

Cross-relaxation parametric maps provide new types of tissue contrast specifically highlighting compact fiber tracts in white matter.

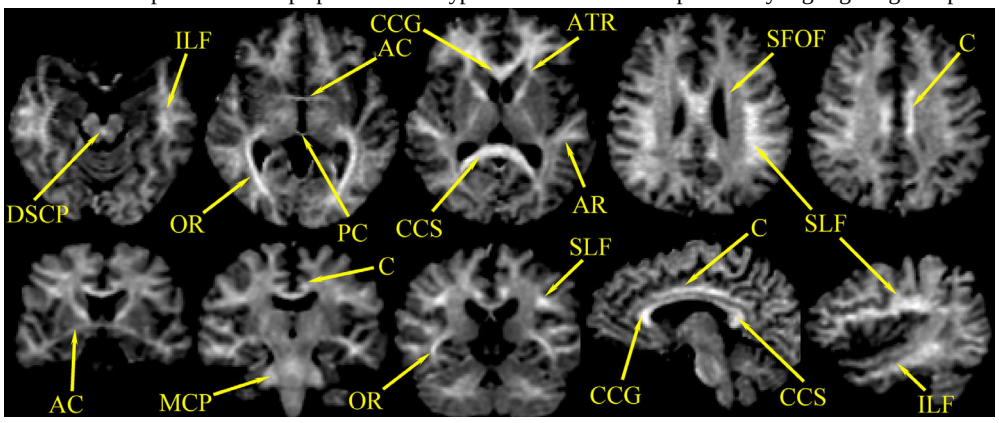

Fig. 1. Anatomy of major fiber tracts on 3D bound pool fraction (*f*) maps. The following structures are labeled: corpus callosum, genu (CCG) and splenium (CCS); anterior commissure (AC); posterior commissure (PC); optic radiations (OR); auditory radiations (AR); anterior thalamic radiations (ATR); cingulum (C); superior longitudinal fasciculus (SLF); superior fronto-occipital fasciculus (SFOF); inferior longitudinal fasciculus (ILF); middle cerebellar peduncle (MCP); decussation of superior cerebellar peduncle (DSCP).

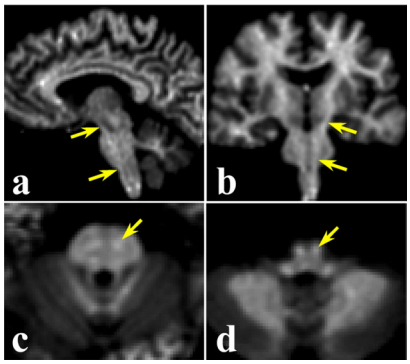

Fig. 2. Anatomy of the corticospinal tract (arrows) on 3D cross-relaxation rate constant (*k*) maps reformatted in parasagittal (**a**), coronal (**b**), and axial (**c**,**d**) planes. The axial images correspond to levels of midpons (**c**) and upper medulla (**d**).

References: 1) Sled JG, Pike GB. *MRM* 2001;46:923. 2) Tozer D et al. *MRM* 2003;50:83. 3) Yarnykh VL. *MRM* 2002;47 929. 4) Yarnykh VL, Yuan C. *Proc. ISMRM* 2003, p.1105. 5) Morrison C, Henkelman RM. *MRM* 1995;33:475. 6) Curnes JT et al. *AJNR* 1988;9:1061. 7) Yagishita A et al. *Radiology* 1994;191:455.