High-resolution 3D T1 and T2 Mapping of the Brain in a Clinically Acceptable Time with DESPOT1 and DESPOT2

S. C. Deoni[1], T. M. Peters[1], B. K. Rutt[1]

[1]Advanced Imaging Labs, Robarts Research Intitute, London, Ontario, Canada

Introduction:

Previous investigations[1-5] have associated changes in the longitudinal and/or transverse relaxation times (T1 and T2) within specific brain regions with a number of neurological and central nervous system disorders, including autism, schizophrenia, Parkinson's and Alzheimer's. Despite this, volumetric relaxometry has not become part of routine clinical evaluation. This is likely due to the low-resolution, limited volume coverage and lengthy acquisition and post-processing times associated with conventional methods. These restrictions have hindered the study of variations in both T1 and T2 at fine detail in normal and diseased states. Further, while these studies found T1 and T2 differences between patient and control groups, comparisons were limited to mean relaxometry values averaged over large anatomical regions, i.e. white matter, etc. Averaging over large regions masks localized T1 and T2 changes, limiting our ability to distinguish subtle variations and hindering our study of pathology at high levels of detail.

In this study the clinical feasibility of performing high-resolution T1 and T2 mapping of the brain with the DESPOT1 and DESPOT2 relaxometry methods[6] was examined. The DESPOT1 and DESPOT2 methods extract T1 and T2 information from multiple SPGR and fully-balanced SSFP acquisitions using constant TR and varied flip angle (FA). In addition to rapid 3D acquisition, the DESPOT methods also offer speedy processing[6]. Here we present the first matched full-brain (1mm isotropic resolution) T1 and T2 maps and the first sub-millimeter (0.7mm isotropic) T1 and T2 maps of the deep brain and basal ganglia and, in doing so, illustrate the potential of DESPOT1 and DESPOT2 in the study of neurological disease.

Methods:

Full-Brain Imaging: In the first part of this study, full brain T1 and T2 maps were acquired using the DESPOT1 and DESPOT2 methods. Sagittally oriented, full brain (25cm x 25cm x 13cm) volumes were acquired at the two ideal flip angles[6] with $1mm^3$ isotropic voxels and the following parameters, DESPOT1: FA = 3° and 12°, TR/TE = 5.3/1.9ms and acquisition time for both flip angle volumes (T_{acq}) = 5:47. DESPOT2: FA = 15° and 70°, TR/TE = 4.2/2.1ms, T_{acq} = 5:16.

Deep-Brain Imaging: In the second part of the study, we focused specifically on the deep brain, i.e. thalamus and surrounding area, as this region contains many of the structures suspected to be associated with neurological disease. Here, axially oriented data (18cm x 18cm x 9cm) with 0.7mm isotropic voxels were acquired with: DESPOT1: FA = 4° and 15°, TR/TE = 13.4/2.9ms and T_{acq} = 14:44. DESPOT2: FA = 15° and 70°, TR/TE = 5.6/2.8ms and T_{acq} = 6:07. To reduce patient motion between acquisitions, head fixation via a chinstrap and foam padding were used in all scans. To increase the signal-to-noise ratio of the images, in both the full-brain and deep-brain experiments two sets of DESPOT1 and DESPOT2 data were acquired and averaged.

Results:

Representative slices through the full and deep-brain T1 and T2 maps are shown in Figs. 1 and 2 and demonstrate the high quality and detail of the acquired maps. Average T1:T2 values (with standard deviations shown in brackets) corresponding to frontal white and grey matter, globus pallidus and putamen were: 606(27):63(4.3), 1245(59):105(8.9), 783(34):68(5.1) and 976(47):79(6.8) from the full brain maps and 613(54):61(6.1), 1278(115):98(10.5), 792(59):63(8.2) and 981(81):73(8.8) from the deep brain maps. Further increases in image quality and T1 and T2 precision could be realized by averaging multiple maps. The rapid acquisition speed (~12 and 20 minutes for single averages of the full and deep-brain maps) makes this possible without requiring excessively long exam times. The ability to acquire large volume maps provides a major advantage for elucidating disease processes that involve anatomically connected, but spatially separated brain regions.

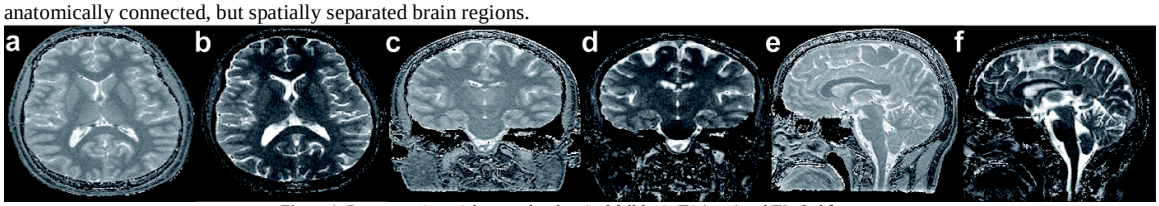

Figure 1: Representative axial, coronal and sagittal full-brain T1 (a,c,e) and T2 (b,d,f) maps.

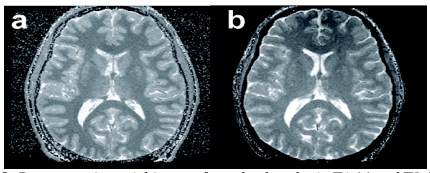

Figure 2: Representative axial images from the deep-brain T1 (a) and T2 (b) map.

Within the deep-brain T2 maps, a region of reduced signal (due to the off-resonance SSFP banding artifact) is seen in the frontal lobe region. This artifact can be eliminated by either further minimizing TR or by using a phase-cycled SSFP [7]sequence for DESPOT2. In the deep-brain images, our primary focus was the thalamus and surrounding area and thus the bands, which were primarily localized to the frontal lobe region, were not a concern.

Discussion and Conclusions:

The value of quantitative relaxometry in studying neuropathology has been well established. Unfortunately, the lack of a rapid, accurate and precise method for whole-brain, high-resolution, T1 and T2 mapping has hindered clinical adoption. In this study we have demonstrated the ability to perform high-resolution relaxometry studies in a clinically feasible time with DESPOT1 and DESPOT2. The ability to map T1 and T2 at the resolution demonstrated permits focused studies of localized changes with disease progression. Such studies will enable a more complete characterization of tissues and structures of interest and, therefore, have tremendous potential in the study, understanding and monitoring of disease processes.

References:

[1] Bartozokis G et al. Arch. Gen. Psych. 57:47-53, 2000. [2] Friedman SD et al. Neurology. 60:100-107, 2003. [3] Pitkamen A et al. Neurology. 46:1720-1730, 1996. [4] Vymazal J et al. Radiology. 211:489-495,1999. [5] Williamson P et al. Am. J. Psych. 149:549-551, 1992. [6] Deoni SCL et al. MRM 49:515-526, 2003. [7] Zur Y et al. Magn. Reson. Med. 16:444-459, 1990.