## Quantitative fast T1 mapping at 7 Tesla: Initial results in Multiple Sclerosis patients and healthy controls

W. L. de Graaf¹, J. M. Hoogduin², F. Visser².³, P. Pouwels⁴, H. Vrenken⁴, C. H. Polman⁵, F. Barkhof¹, P. R. Luijten², and J. A. Castelijns¹¹Radiology, VU University Medical Center, Amsterdam, Netherlands, ²Image Science Institute, University Medical Center Utrecht, Utrecht, Netherlands, ³PHILIPS Healthcare, ⁴Physics and Medical Technology, VU University Medical Center, Amsterdam, Netherlands, ⁵Neurology, VU University Medical Center, Amsterdam, Netherlands

**Introduction:** It has been shown that normal appearing white (NAWM) and grey matter (NAGM) in the brain of Multiple Sclerosis patients as seen with conventional qualitative MR imaging is different from healthy controls when observed by T1 relaxation time mapping [1]. As these changes are subtle at lower field (1.5 T and 3.0 T), they are expected to become much more pronounced at high field (7 T) as T1 relaxation times increase with field strength. In this study, whole brain T1 maps of MS patients as well as healthy controls were made at 7 T within 4.5 minutes by use of a sequence which is a variation on the work by Clare & Jezzard [2,3]. Whole brain T1 relaxation time histograms and measurements of specific regions were compared between patients and controls.

Methods: 6 MS patients (mainly PP-MS) as well as 5 healthy volunteers were examined at 7 T. The protocol consisted of a PD/T2 (TSE factor: 8, TR/TE1/TE2: 4969/21/80 ms, FOV: 230x200x89 mm, slice thickness: 2 mm, matrix: 328x196) and a quantitative T1 mapping sequence. Details of the T1 sequence can be found in [3]. In short: after a non-selective adiabatic inversion pulse the inversion recovery curve is sampled by a multi slice EPI readout covering a large part of the brain with 46 slices of 1.5mm thickness. This measurement is repeated 23 times. Each time the readout order of the slices is changed, giving a different TI for every slice after each inversion. The odd slices were sampled at T1=20+n\*222 ms while the even slices were sampled at T1=131+n\*222 ms (n=0-22). Other scan parameters were: EPI factor: 65, TR /TE: 10000/9.4 ms, FOV: 224x224, in plane resolution 1x1 mm², SENSE factor 3.6, T1 values were calculated on a pixel-by-pixel basis with a 3-parameter fit. Besides the T1 inversion time this fit includes the fully relaxed magnetization and the inversion efficiency of the adiabatic pulse. The Pd/T2 weighted sequence was used to determine lesion locations and areas with normal appearing white matter. The duration of the protocol (Pd/T2 and T1-mapping) was about 20 minutes. After brain extraction, histograms of T1 values over the whole brain were made and specific regions (NAWM, GM, lesions) were outlined for which average T1 values were calculated.

#### Results:

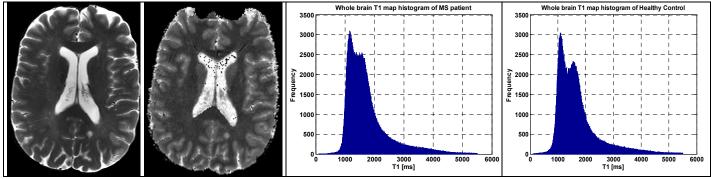


Figure 1: a) T2w image, b) T1 relaxation map, c) whole brain histogram MS patient and d) healthy control

A T2 weighted image of a patient, used as reference, is shown in figure 1a. A calculated T1 map of the same patient is shown in figure 1b. Note the geometric distortions in the frontal area, which is a result of the EPI acquisition. Whole brain histograms of T1 values are shown in figure 1c and d. The left peak originates mainly from white matter and the right peak from cortex. The right shoulder represents cerebral spinal fluid inside the sulci and ventricles. As lesions are included in the histograms, peak shifting and broadening is observed in patients. Table 1 shows T1 values per subject of specific brain areas: NAWM, NAGM, peri-ventricular lesions (PV), deep white matter lesions (DWM) and mixed grey matter/white matter lesions (Mixed). ROI's were drawn inside the structures to prevent partial volume effects.

Table 1. T1 relaxation times of brain areas in MS patients and controls.

Table 1, 11 relaxation times of brain areas in MS patients and controls					
Subject	NAWM	NAGM	PV Lesion	DWM lesion	Mixed Lesion
_	T1 (sd) [ms]				
Patient 1	1009 (121)	1533 (155)	2784 (393)	1492 (167)	2688 (264)
Patient 2	1193 (97)	1907 (302)	2300 (268)	1954 (250)	NA*
Patient 3	1191 (103)	1673 (103)	2284 (200)	1448 (147)	2627 (518)
Patient 4	1009 (116)	1711 (173)	NA*	NA*	NA*
Patient 5	1032 (72)	1578 (117)	2063 (206)	1660 (168)	1980 (136)
Patient 6	1073 (82)	1745 (110)	1909 (221)	2192 (214)	1763 (114)
Mean Pat.	1085 (100)	1691 (132)	2500 (640)	1749 (317)	2265 (463)
Control 1	980 (73)	1705 (93)	NA*	NA*	NA*
Control 2	1077 (72)	1867 (124)	NA*	NA*	NA*
Control 3	1094 (80)	1877 (108)	NA*	NA*	NA*
Control 4	1025 (55)	1668 (93)	NA*	NA*	NA*
Control 5	1037 (45)	1903 (82)	NA*	NA*	NA*
Mean Ctrl.	1043 (45)	1804 (109)			

# NA: not applicable (no lesions)

### Discussion

Changes in normal appearing grey and white matter T1 values are observed in MS patients. Whole brain T1 relaxation histograms showed shifting and broadening of the peaks of white and grey matter, partly due to the presence of brain lesions. For the specific brain areas there seems to be a tendency of lower grey matter T1 values in patients compared to controls at 7 Tesla. This result differs from the study of PP-MS patients at 1.5 T of Vrenken et al. [1], where no change in NAGM values was observed. However, no conclusions can yet be drawn with this small group of subjects. By increasing the number of subjects and the use of segmenting techniques more conclusive information may be found to assess the sensitivity of the method for differentiating *normal* from *normal appearing* grey and white matter in MS.

### Conclusions

This initial study shows that at 7 T fast quantitative T1 mapping can be performed with a  $1x1mm^2$  in plane resolution and a small slice thickness of 1.5 mm. This fast sequence can easily be added to other protocols as T1-mapping takes only 4.5 minutes. This can help to differentiate normal from normal appearing brain tissue and to define characteristics of lesions found with other sequences.

Ref: [1] Vrenken et al. Radiology 2006, [2] Clare, Jezzard, MRM 2002, [3] de Smit, Hoogduin, ISMRM Conf. Proceedings 2006.