Absolute Quantification of T1, T2, PD and B1 on Patients with Multiple Sclerosis, Covering the Brain in 5 Minutes.

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Introduction. Rapid quantification of MR parameters such as the longitudinal T1 relaxation time, the transverse T2 relaxation time and the proton density has been the subject of active research over the recent years. Tissue characterization using a single quantification scan may lead to an absolute assessment of diseases that cannot be obtained by conventional contrast imaging. The main challenge with this approach, however, is to decrease the required scan time to clinically acceptable times.

An imaging method called QRAPMASTER, '*Quantification of Relaxation times and Proton density by Multi-echo Acquisition of Saturation recovery with TSE Read-out*', allows the quantification of spatially resolved absolute T1 relaxation, T2 relaxation, proton density and the local B1 field with high resolution, covering the brain in only 5 minutes.
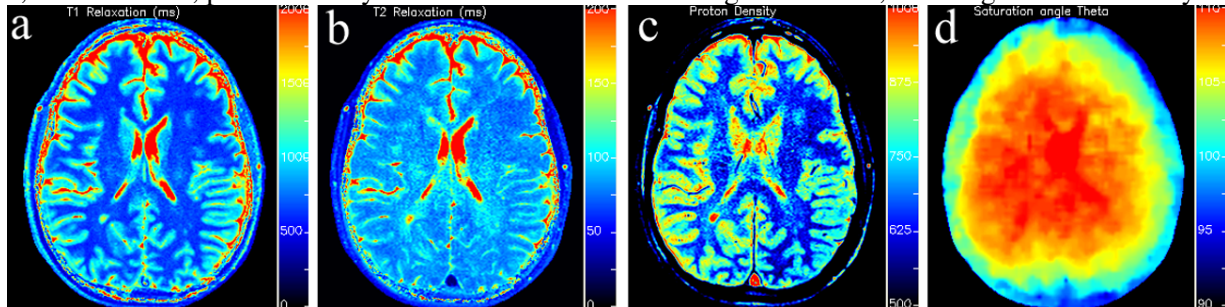

Fig. 1. Example of a QRAPMASTER measurement on a brain of a patient diagnosed with Clinically Definite Multiple Sclerosis (CDMS). A single axial slice is shown out of the 20 that were acquired (scan time 5:04 min, in-plane resolution 0.8 mm^2, thickness 5 mm): **a**. Absolute T1 (scale 0-2000 ms), **b**. Absolute T2 (scale 0-200 ms), **c**. Absolute proton density (scale 500 – 1000, where 1000 corresponds to pure water at 37 °C) and **d**. the B1 field (scale 90-110%)

Method. The multi-slice sequence consists of a saturation pulse that acts on a slice *m*, followed by a multi-echo TSE acquisition of slice *n*. By shifting the order of *m* and *n* any delay time can be chosen for a particular slice. Multiple scans with different delay times provides T1, the multi-echo acquisition provides T2. From the same data, the spatial distribution of B1 can also be estimated. Based on T1, T2 and B1, the PD is retrieved. The scanner used for the measurements was a 1.5 T Achieva (Philips Medical Systems, Best, the Netherlands)

Results. In Fig. 1, quantification data are shown for a single axial slice of the brain of a patient with CDMS, out of the 20 slices that were acquired (scan time 5:04 minutes). These absolute tissue parameters were used as coordinates in a R1-R2-PD space where the relaxation rates were defined as R1 = 1/T1 and R2 = 1/T2. In Fig. 2 the projection of this space onto the R1-R2 plane is shown for a ROI in the slice in Fig. 1. Additionally a comparable slice is shown of a healthy volunteer. It is clear that MS has completely different tissue characteristics than normal appearing, healthy white matter. Based on the R1-R2-PD parameters partial tissue volume per voxel can be calculated. Integration of partial volume over the whole brain results in an accurate quantification of the total volume of pure MS lesion in the brain.

Fig. 2. Quantification results of a healthy volunteer (**left**) compared to a patient with CDMS (**right**) in a small region of interest in the brain. Only the projection of the R1-R2-PD space onto the R1-R2 plane is shown (where R1 = 1/T1 and R2 = 1/T2). The healthy volunteer shows clusters of white matter, cortex and CSF as well as voxels with partial tissue volumes in between. The patient also had these three clusters, but in addition two distinct phases of a different tissue was observed, attributed to MS lesions. The first phase consists mostly of a reduction in R2, the second phase is a dramatic reduction in both R1 and R2. The hyper-intense focal lesions in a T2W image correspond to the second phase. The first phase shows up only as a slight intensity increase in the T2W image.