3D T_2 mapping of human brain with high accuracy by 3D Turbo-Flash imaging prepared by multiecho adiabatic spin echo

Hidehiro Watanabe[1], Nobuhiro Takaya[1], and Fumiyuki Mitsumori[1]
[1]*Center for Environmental Measurement and Analysis, National Institute for Environmental Studies, Tsukuba, Ibaraki, Japan*

Introduction

An intrinsic parameter of T_2 reflects microscopic characteristics of the *in vivo* water molecule, such as its mobility and magnetic environment. Thus, T_2-weighted imaging is routinely used for diagnosing various diseases. In contrast, quantitative T_2 mapping has been pursued to a limited extent, due in part to obstacles in obtaining accurate T_2 values with slice-selective spin-echo sequences. In particular, imperfections in the slice profile produced by the refocusing pulse result in a loss of coherence, and when multiple echoes are collected the loss is cumulative at each refocusing step, leading to erroneous T_2 estimations. Although T_2 measurements by stepping TE values in a single spin-echo sequence can avoid that cumulative error, other mechanisms of loss of phase coherence occurs during the long TE periods due to diffusion in nonuniform B_0 and exchange of the water molecule. At higher fields these two types of effects are exacerbated by increased B_1 inhomogeneity and larger microscopic susceptibility gradients. To overcome these problems, we have been proposed the single slice multiecho adiabatic spin echo (MASE) imaging sequence. In this method, accurate T_2 maps can be obtained by a pair of adiabatic full passage (AFP) pulses having a feature of very precise slice selection. Through measuring a T_2 map of the slice across the basal ganglia region of human brain with high accuracy using this method, we have found that the transverse relaxation rate ($1/T_2$) of the tissue water in human brain at 4.7 T has a high linear correlation with the published levels of non-haemin iron content (1, 2). Shortening measurement time is a key for expanding this single slice method (2D MASE) into 3D T_2 mapping. In this work, we propose 3D MASE method of whole brain T_2 mapping by 3D Turbo-Flash imaging prepared by MASE module. This method has features of accurate T_2 mapping using adiabatic pulses and of fast imaging by 3D Turbo-Flash.

Materials and Method

Figure 1 shows our proposed 3D MASE imaging sequence for whole brain T_2 mapping. In the MASE module, magnetization decayed by T_2 without a loss of coherence can be generated by a multi-pulse spin echo sequence consisting of an adiabatic half-passage (AHP) and series of a pair of AFP pulses. This transverse magnetization is flipped back to the longitudinal magnetization by a flipback AHP pulse. After crusher gradient pulses are applied to eliminate residual transverse magnetization, signal is accumulated by 3D Turbo-Flash imaging module. For 3D T_2 mapping, multiple 3D images with different TE values by adding a pair of AHP pulses in the MASE module are collected. The case of a value of 2TE is shown in Fig. 1. To maintain constant magnetization recovered by T_1 every segment, an AHP pulse for the saturation recovery is applied before the MASE module. Signal intensity in the 3D image with nTE by this sequence can be described as $S(n\text{TE}) = (1\text{-}e^{-\text{RD}/T_1})e^{-n\text{TE}/T_2}$. After collecting multiple 3D images, T_2 maps are calculated by fitting the signal intensity of each pixel in the 3D images using that model equation of signal intensity.

All the measurements were performed on a 4.7 T whole-body MRI system (INOVA, Agilent) using a quadrature TEM head coil. For validation, T_2 measurements of a spherical phantom containing agarose gel with T_1 of 1.1 s and T_2 of 92 ms were performed by the 3D MASE method. In human brain measurements, three whole brain 3D images with TE = 26, 52, 78 ms were collected. In the turbo-Flash imaging module, TR/TE = 8.1/2.6 ms and flip angle is 15 degrees. An imaging matrix is 256 × 96 × 96 along y (read), z (slice and phase1) and x (phase2) directions with FOV of 256 × 240 × 192 mm^3, giving a spatial resolution of 1 × 2.5 × 2 mm^3. MR signals were accumulated by centric phase-encoding order with number of segments of 2 along the z direction. The relaxation delay was set to 3 s. Each 3D image was collected for 11 min, resulting 33 min for the total measurement time. T_2 values in several regions in gray and white matters (GM, WM) on the slice across the basal ganglia region were compared to T_2 values measured by the 2D MASE.

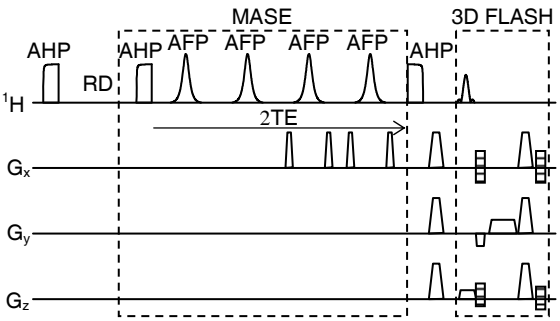

Fig. 1. 3D MASE imaging sequence for whole brain T_2 mapping. The case of echo time = 2TE is shown. RD: relaxation delay.

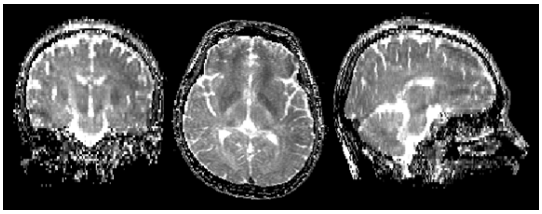

Fig. 2. A T_2 map of whole human brain measured by the proposed 3D MASE imagine sequence.

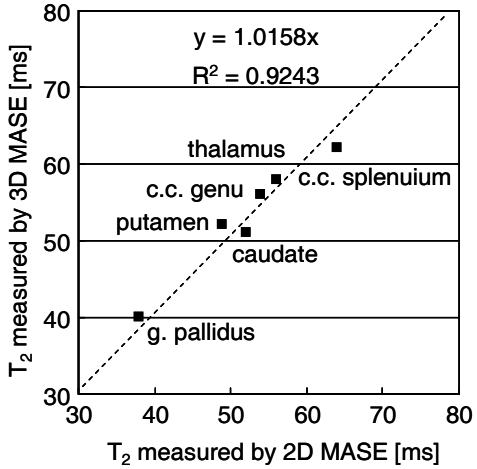

Fig. 3. Correlation of T_2 values measured by 3D MASE with those by 2D MASE.

Results & Discussion

T_2 of the gel phantom measured by 3D MASE was 90.1 ms ± 3.1 ms, which was in good agreement with T_2 of 92 ms measured by the conventional method. Figure 2 shows a whole brain T_2 map measured by 3D MASE sequence. T_2 values of the tissue in GM and WM regions measured by 3D MASE were in good agreement with those by the 2D MASE (Fig. 3).

Conclusions

We successfully implemented 3D MASE method to allow whole brain T_2 mapping with high accuracy.

References

1. F. Mitsumori, H. Watanabe, N. Takaya, M. Garwood, Magn. Reson. Med., 58, 1054-1060 (2007). 2. F. Mitsumori, H. Watanabe, N. Takaya,, Magn. Reson. Med., 62, 1326-1330 (2009).