Improved Structural MRI of Mouse Brain In Vivo by Combined T1 and T2 Mapping at 9.4 T

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Introduction

Apart from high spatial resolution, a sufficient contrast-to-noise ratio is essential for distinguishing neuronal structures. Here, we used high-resolution 3D MRI at 9.4 T to improve the structural delineation of anatomical details in the cerebellum and hippocampus of healthy adult mice in vivo. The approach was based on the determination of T1 and T2 relaxation time maps and a combination of the information in a suitably synthesized T1+T2 map.

Methods

Healthy adult NMRI mice underwent 3D MRI at an isotropic resolution of 117 µm (9.4 T, Bruker Biospin GmbH, Germany). T1 mapping used a segmented 3D inversion-recovery FLASH sequence (flip angle 4°, TR = 6 s, matrix 192 × 192 × 96, 12 segments) yielding 30 images with different inversion times (minimal TI = 5 ms, spacing 155 ms). T2 mapping relied on a modified 3D CPMG sequence (TR = 2 s, matrix 128 × 128 × 40) resulting in 16 images with different echo times (minimal TE = 8 ms, spacing 8 ms). Both image sets were resized and smoothed (interpolation factor = 2, Gaussian kernel with $\sigma = 1$) prior to a pixelwise fit to the assumed signal evolution

T1 analysis: $S(TI) = | B - A \exp(-TI / T1) |$

T2 analysis: $S(TE) = A \exp(-TE / T2) + B$

via a nonlinear Levenberg-Marquardt algorithm. A combined "T1+T2" map was obtained by scaling the T2 relaxation time values by a factor of 30 and adding them to the T1 relaxation time values.

Results and Discussion

High-resolution T2 maps appeared with a sufficient SNR and a convincing gray vs. white matter contrast. However, fine structures such as the cerebellar white matter (WM) and the densely packed inner granular cell layer (GL) resulted in very similar T2 values (Fig.1, left, yellow arrow). Nevertheless, both structures separated well from the surrounding and less dense outer molecular layer (ML; for comparison see histology in Fig. 2, left). On the other hand, high-resolution T1 maps revealed a strong delineation of the cerebellar white matter, whereas the contrast between granular cell layer and molecular layer is less prominent (Fig. 1, middle). The combination of T1 and T2 information in the form of a "T1+T2" map (Fig. 1, right), however, added the advantages of both: white matter, granular cell layer, and molecular layer could be better distinguished as separate structures (best seen in the zoomed view and when using false color coding in Fig. 2). Also other neuronal structures such as the dentate gyrus and the CA1 to CA3 regions of the hippocampus as well as the surrounding external capsule (Fig.1, white arrow) were nicely visible on the combined T1+T2 map.

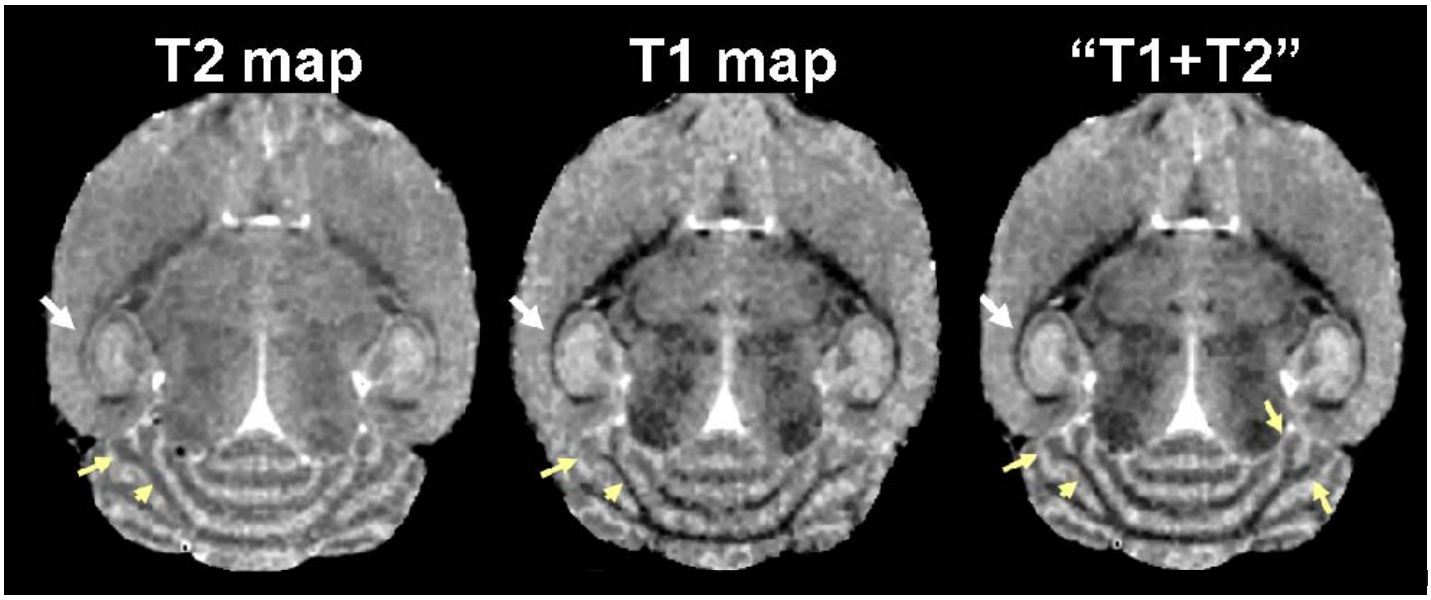

Fig. 1: T2, T1, and T1+T2 maps of the same animal in vivo: hippocampus (white arrow) and cerebellar structures (yellow arrows).

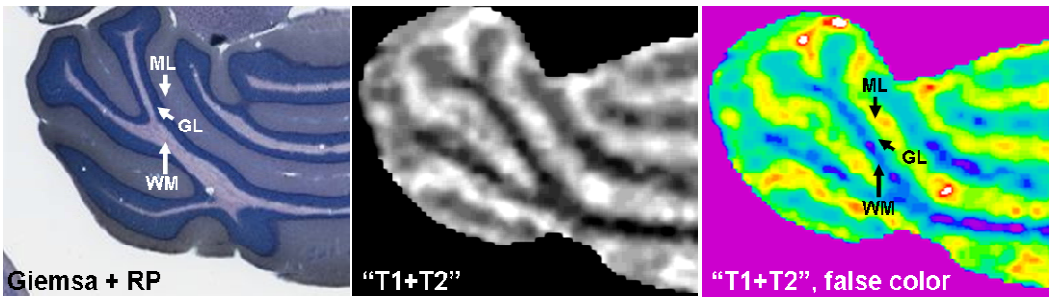

Fig. 2. Mouse cerebellum: histology (http://brainmaps.org/), T1+T2 map, color-coded T1+T2 map.

Conclusion

A combination of high-resolution T1 and T2 maps at high field can be exploited for an improved structural delineation of the mouse brain in vivo.

An application of these techniques to genetically modified mice with alterations in the molecular layer is in preparation.