# Optimized 3D MPRAGE: Depiction of thalamic substructures at 3T

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Introduction Deep brain stimulation of the thalamus and globus pallidus internus is becoming a more common treatment in several hyperkinetic disorders [1] and is increasingly used experimentally in the treatment of epilepsy [2]. As the substructures of the thalamus are not visible on standard T1w and T2w MR images, planning of deep brain stimulation (DBS) implantation relies on stereotactic atlas coordinates. Goal of the present work was to test, whether an optimized 3D MPRAGE protocol can depict thalamic substructures.

Methods Six healthy subjects (2 male, age 21-34 years, mean 26.5 years) were measured with an optimized 3D MPRAGE sequence on a 3T Scanner (Tim Trio, Siemens, Erlangen, Germany). Sequence parameters were as follows: 144 sagital slices, in plane resolution 1x1 mm², slice thickness 1 mm, TE 3.4 ms, TR 2300 ms, echo spacing 8.6ms, bandwidth 130Hz/px, NEX 2, flip angle 8°, time for acquisition 19:39 min. The TI = 700ms was experimentally chosen to maximize suppression of cortical gray matter, which is shorter than the usually used 900-1100ms. The resulting images were compared with a common histological atlas [3]. The lateral, anterior, posterior and medial nuclei groups, as defined by the 3D mean thalamus atlas by Krauth et al. [4], were drawn manually and the resulting volumes were compared with the 3D atlas. The nuclei of the defined groups were as followed (abbreviations taken from [5]): Anterior -: AV, AM, AD, LD Medial - CeM, CL, CM, MD, MV, Pf, sPf Lateral - VA, VL, VM, VPI, VPL, VPM Posterior - Pu, MGN, Po, LGN, Li, LP.

Results The optimized protocol had an increased contrast within the thalamus and the surrounding basal ganglia (Fig. 1). Inverted grayscale images had a contrast comparable to histological sections and identification of thalamic substructures that differ in myelin content and/or cell size was possible (Fig. 2). The average distance between AC and PC was 26.7mm (25 – 29 mm). The mean volumes of the selected nuclei groups in comparison with the 3D atlas are shown in Table 1. The mean 3D atlas was on average about 10% smaller than the in vivo data, which is most likely due to shrinkage of the reference brains from the 3D atlas during the fixation process [4,5].

Conclusion The optimized MPRAGE protocol enables an identification of thalamic substructures in a reasonable measurement time of below 20 minutes. This should increase specificity of individualized target selection in DBS.

## Literature:

[1] Welter et al. 2010, Curr Opin Neurol 23: 420-5
[2] Fisher et al. 2010, Epilepsia 51: 899-908
[3] Mai et al., Atlas of the human brain, 3rd edition, Academic Press, 2007.
[4] Krauth et al. 2010, NeuroImage 49: 2053-62.
[5] Morel et al. 1997, J Comp Neurol 387:588-630.

**Table 1:** Mean volumes of the nucleus groups in the 6 subjects in comparison with the 3D atlas by Krauth et al. [4].

| | Volume of the selected nuclei groups [mm³] | | | |
|---|---|---|---|---|
| | **Anterior** | **Medial** | **Lateral** | **Posterior** |
| **Mean/Std** | 225 ± 36 | 1503 ± 111 | 1952 ± 210 | 2113 ± 494 |
| **3D Atlas [4]** | 249 | 1380 | 1727 | 5169 |

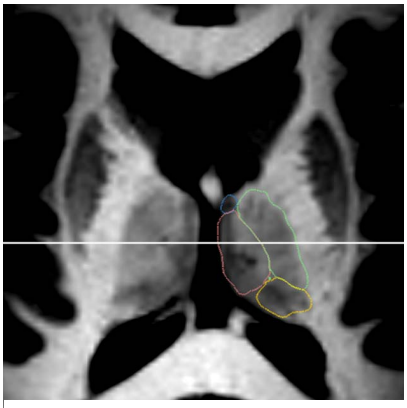

**Fig. 1:** Axial slice of the optimized MPRAGE with increased contrast in the thalamus. The white line depicts the coronal slice shown in Fig. 2. The selected nuclei groups are marked in color (blue – anterior, red – medial, green – lateral, yellow – posterior)

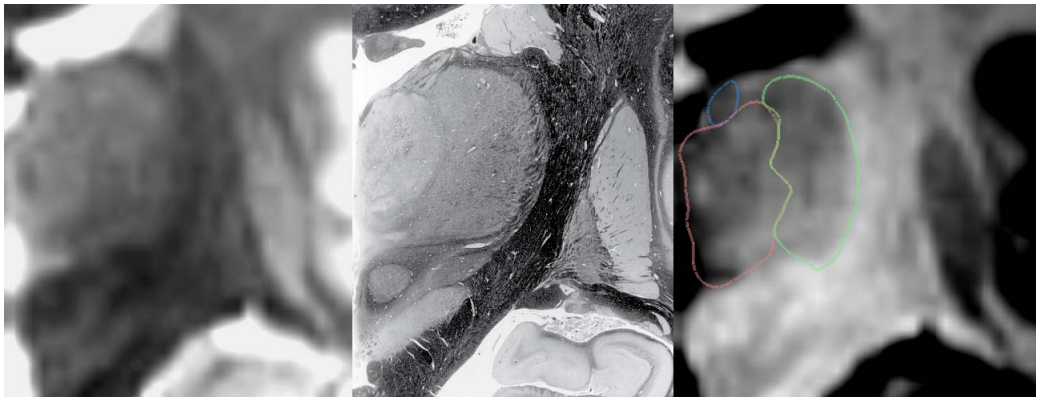

**Fig. 2:** From left to right: inverted coronal grayscale image of the thalamus, histological section from the Talairach brain and normal grayscale image with the selected nuclei groups (blue – anterior, red – medial, green – lateral). The histological sections is taken from “Atlas of the human brain" by JK Mai et al. published by Academic press [3]