

Gradient Echo versus Spin Echo T2-weighted Imaging of Deep Brain Structures of the Human Brain at 7 Tesla

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Introduction.

To date, MR imaging do not provide convincing structural biomarkers of small deep brain nuclei, such as thalamic, subthalamic or brainstem nuclei. Clinicians are in need of “biomarkers” that would help detecting specific lesions and predict the occurrence of symptoms in patients with diseases of these structures, such as Parkinsonian syndromes. In addition, the detection of these markers could be surrogate end-points to demonstrate clinical efficacy of new neuroprotective treatments and help stratify heterogeneous diseases (e.g. “benign” forms versus forms that are more prone to develop motor or non motor complications). Ultra high field imaging allows obtaining images with a very high spatial resolution and provides new contrast that can be used to study deep brain nuclei. Here, we compared spin echo and gradient echo 7T images to depict the normal anatomy of deep brain nuclei in the human brain.

Material and methods.

Six young healthy volunteers were scanned on two 7T scanner (Siemens AG, Erlangen), with a 16 channel head coil at CMRR, Minneapolis USA and with a 8 channel head coil at NeuroSpin (Gif-sur-Yvette, France). Subjects were scanned using different pulse sequences and parameters to reach high spatial resolution:

- axial T_2^* -weighted 2D Flash sequence (CMRR) (NEX=1, acquisition matrix 512x512, 20 slices, in plane resolution 0.375mmx0.375mm, slice thickness 1.9mm, TR=550ms, TE=12ms, flip angle 15°, scan time ~8min)
- coronal T_2^* -weighted 2D Flash sequence (NeuroSpin) (NEX=1, acquisition matrix 384x384, 80 slices, in plane resolution 0.5mmx0.5mm, slice thickness 0.5mm, TR=4.5s, TE=30ms, flip angle 65°, scan time 14 min)
- T_2^* -weighted 3D Flash sequence (CMRR) (TR=23s, TE=12ms, flip angle 6°, 0.675mm isotropic voxel resolution, scan time ~8min)
- axial T_2 -weighted 2D Turbo Spin Echo sequence (CMRR) (TE=4000ms to 9500ms, TE=79 to 90ms, flip angle 120°, scan time ~8min)

Results.

T_2 - and T_2^* -weighted images provided new contrasts of the thalamus showing differentiation of some thalamic subnuclei (mediodorsal, pulvinar, and lateral mass including the ventrolateral and ventral posterolateral nuclei, and the anterior nucleus). T_2^* -weighted using short TE better showed the internal medullary lamina of the globus pallidus. For the substantia nigra, the subthalamic nucleus, and the red nucleus, T_2 - and T_2^* -weighted images provided similar delineation. Fibers located between the subthalamic nucleus / substantia nigra and the lenticular nucleus (Comb system) were better showed using T_2^* -weighted images at long echo time. T_2^* -weighted images provided additional information for numerous other structures in the mesencephalon, including gray matter (periaqueducal gray matter, superior and inferior colliculi) and white matter (brachium conjunctivum, medial lemniscus, ponto-cerebellar fibers and possibly the medial longitudinal fasciculus).

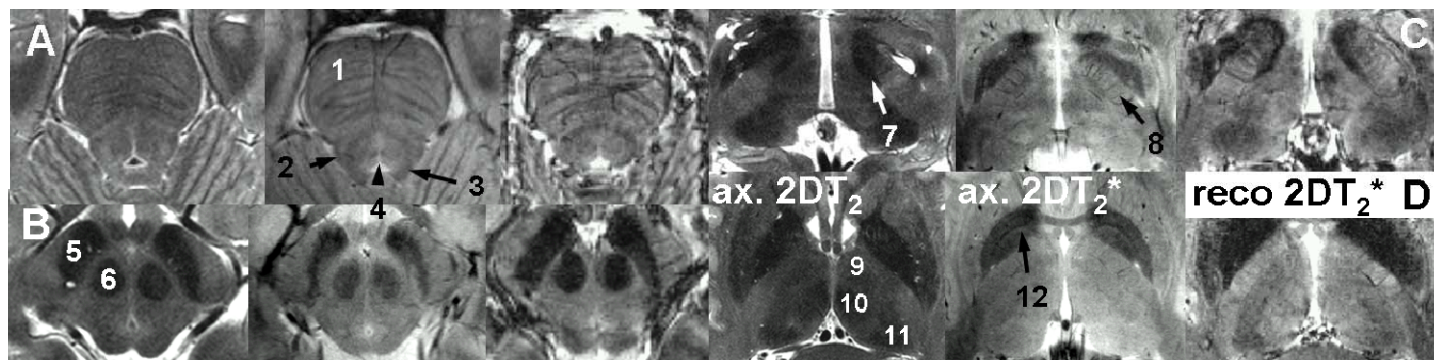


Figure 1. Axial 2D TSE T_2 - (left), 2D GE T_2^* - (middle), and reconstructions of the coronal 2D GE T_2^* -weighted images (right) passing at the level of the pons (upper left), the mesencephalon (lower left), the subthalamic nucleus (upper right), and the thalamus (lower right). 1, ponto-cerebellar fibers; 2, medial lemniscus; 3, superior cerebellar fibers; 4 periaqueducal gray matter; 5, substantia nigra area; 6, red nucleus; 7, subthalamic nucleus; 8, subthalamic nucleus / substantia nigra - lenticular nucleus fibers; 9, anterior; 10, mediodorsal; 11, pulvinar nuclei of the thalamus; 12, internal medullary lamina of the globus pallidus.

Conclusion.

At 7T, it was possible to clearly improve the detection of deep brain nuclei and fiber pathways, particularly in the mesencephalon in human healthy volunteers. New contrasts and higher spatial resolution obtained at 7T provide new markers of deep brain nuclei that can be used to study brain diseases such as Parkinsonian syndromes. Further studies will be necessary to evaluate the contribution of other sequences, such as susceptibility-weighted images.

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