Diffusion tensor MRI can anatomically segment human amygdaloid subnuclei *in vivo*

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Introduction

The histology of the amygdala in animal and human cadaver brain has been much studied, due to its importance in several disease and emotional states. Using standard MRI methods, the amygdala appears as a poorly differentiated grey matter area, impossible to segment into its known subnuclei. The existence of differential projections and inputs of specific amygdaloid nuclei strongly suggests, however, that distinct fiber orientation clusters might exist within the amygdala. In this study we show for the first time evidence for the segmentation of amygdaloid nuclei using DTI data obtained in-vivo. This finding has important implications for functional studies seeking to discriminate distinct roles of these nuclei in the processing of emotions, cognitive function, and psychiatric disorders.

Materials and methods

Fifteen healthy subjects (7 females and 8 males between the ages of 22-35) data underwent DTI scanning in a 3 Tesla Magnetom Trio scanner equipped with an 8-channel head array coil. High-resolution T1-weighted images were acquired using a twice-refocused spin-echo echo-planar imaging sequence (TE = 100 ms, TR = 12 s, 128 x 128 image matrix, FOV = 220 x 220 mm²) with an isotropic voxel resolution of 1 mm providing 60 diffusion-encoding gradient directions with a b-value of 1000 s/mm². The measurement of 72 slices with 1.7 mm thickness covered the entire brain. Random noise in the data was reduced by averaging 3 acquisitions. Additionally, fat saturation was employed, together with 6/8 partial Fourier imaging, Hanning window filtering, and parallel GRAPPA acquisition. The brain images were then co-registered into Talairach space and posteriorly, a non-linear registration to a standard MNI template was performed using LIPSIA software. Motion correction for the 180 diffusion-weighted images was combined with a global registration to the T1 anatomy computed with the same method. The gradient direction for each volume was corrected using the rotation parameters.

Amygdala delineation was done either by means of an automatic Freesurfer tool (2) operating with T1-weighted images of each volunteer or by applying to each brain after spatial normalization, an amygdala mask based on a histological study (1) of ten human cadaver brains, selecting the 70% probability contour. An automatic k-means algorithm clustering the angular distance between the major eigenvectors in each voxel within the amygdala mask was then applied to the amygdala DTI data, thus defined, with k= 3. Data from 15 subjects, normalized to the same template brain, were analyzed in this way, and probability maps for each cluster were constructed as a form of average.

Results and discussion

At least three clusters were found consistently across all subjects regarding localization and fiber orientation, independent of the amygdala mask used. These were reasonably consistent with histological data for the major amygdaloid nuclei. This constitutes the first evidence for identification of the human amygdaloid nuclei in-vivo by automatic clustering using diffusion data. It is striking that although the fractional anisotropy of the diffusion data is quite low in this region, there is still enough information to provide this reliable structural detail.

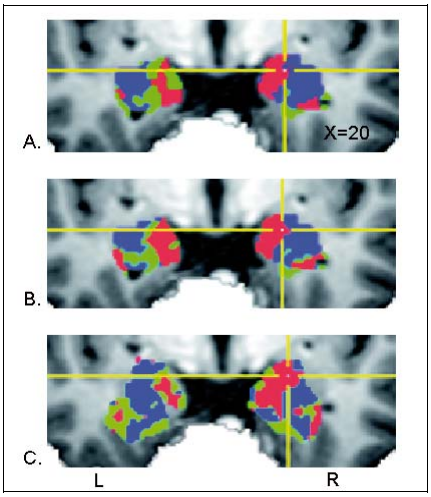

Fig.1. a) manual clustering; b) k-means automatic clustering (T1-based amygdala mask); c) k-means automatic clustering (histology-based mask).

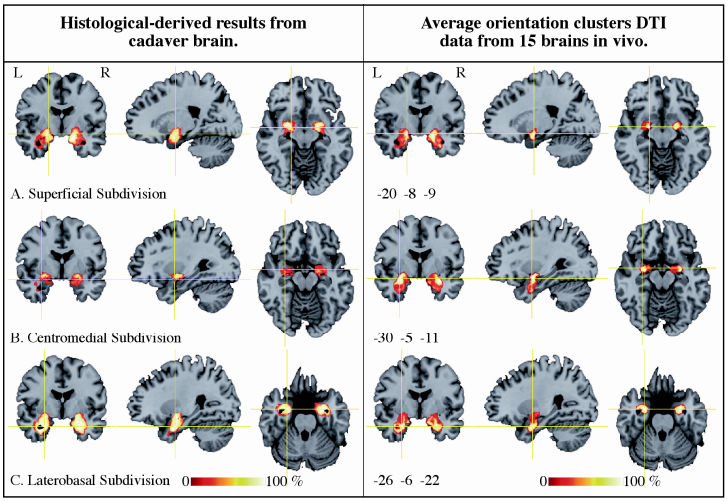

Fig.2. Comparison of the clusters found in a probabilistic map across all 15 subjects using diffusion data with the results from histological studies showing the different nuclei.

References

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