

Tract-based spectroscopy of the cingulum at 7 Tesla

R. Mandl¹, M. van den Heuvel¹, D. Klomp², V. Boer², J. Siero³, P. Luijten², and H. Hulshoff Pol¹

¹Psychiatry, Rudolf Magnus Institute of neuroscience, UMC Utrecht, Utrecht, Netherlands, ²Radiology, UMC Utrecht, Utrecht, Netherlands, ³Neurosurgery, Rudolf Magnus Institute of neuroscience, UMC Utrecht, Utrecht, Netherlands

The cingulum tract is an elongated and curved white matter fiber bundle that connects the cingulate gyrus with the hippocampal gyri in each of the two hemispheres of the brain (fig. 1A). To detect possible subtle disease-related differences in metabolite concentrations (e.g. glutamate/glutamine, creatine) in the cingulum spectroscopic information is needed. Here we propose to use reconstructed cingulum tracts during acquisition to position a high spatial resolution chemical shift imaging (CSI) 2D-slice [1] and to use these fiber tracts in post-processing to select those voxels from the CSI slice that are part the cingulum (fig 1B). The spectra of the selected voxels are processed per voxel and then combined yielding one average spectrum for each cingulum. In this way large parts of the cinguli are included while partial voluming with grey matter or other white matter tracts is kept to a minimum. The aim of this study is to show the feasibility of the method.

Three healthy volunteers were scanned after they signed written informed consent. Data was acquired using a Philips 7 Tesla whole body scanner (Philips, Best) equipped with a quadrature transmit coil and a 16 channel parallel receive coil. Two SS-EPI DTI sets were acquired (60 slices; no gap; 104×104 acquisition matrix; FOV=231×231 mm; slice thickness 2 mm; TR/TE = 7184 ms/ 75 ms; 30 different diffusion-weighted gradient directions; b = 1000 s/mm²; 5 diffusion-unweighted scans; scan time per DTI set 4.5 minutes). On-the-fly fiber tracking was performed with the FiberTrack package (part of the Philips acquisition software) and results were used to plan the CSI acquisition (32×32 matrix; TR/TE = 1 s / 1.4 ms; slice thickness 7.5 mm; voxel size = 5×5×7.5 mm³; total acquisition time 12.5 minutes). During post-processing the left and right cingulum tracts were reconstructed [2]. The individual spectra of CSI voxels that are part of the left or right cingulum were automatically corrected for zero and first order phase shifts and water signal was automatically filtered out. For each of the processed CSI voxels the overlap between the cingulum tract was computed and used to weigh their contribution to a mean spectrum. Finally, the individual CSI voxel spectra were fitted to this average spectrum to correct for small displacements and differences in scale and then the final weighted-average spectrum was computed to which a polynomial baseline correction was applied.

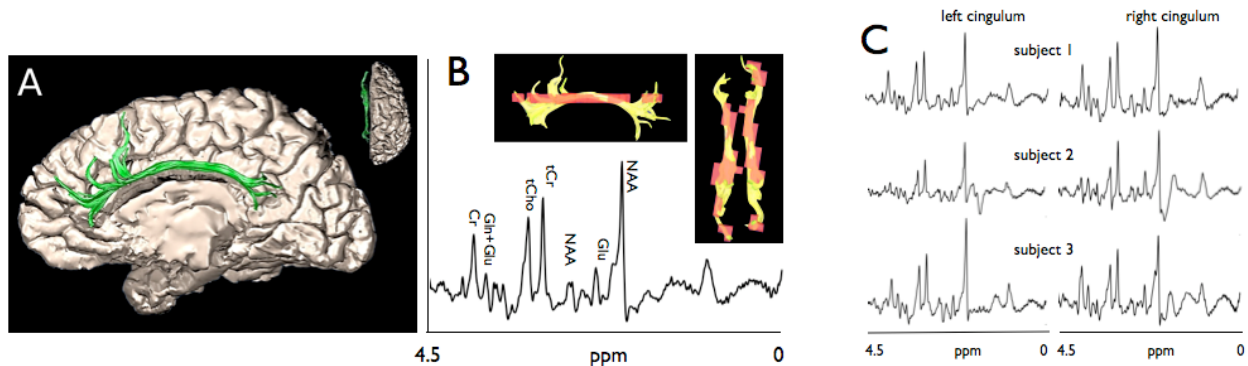


Figure 1: A) reconstructed left cingulum B) average spectrum for the left cingulum of subject 1 (selected CSI voxels for the left and right cingulum shown in red) C) average spectra of the left and right cinguli for all three subjects

The results (fig 1C) show very similar spectra for all subjects suggesting that the reliable acquisition of spectral information of the cingulum is feasible. This method can be applied to diseases implicating abnormalities in the white matter such as schizophrenia. When studying the cinguli one CSI slice can be used to obtain information on metabolic concentrations for both left and right cingulum allowing us to search for possible disease-related lateralization effects. We note however that this method is not limited to the cingulum but can be applied to virtually every fiber bundle in the brain.

The authors wish to thank Fredy Visser for technical support and Anouk Marsman for assistance with the data acquisition.

[1] Boer V, van Gorp J, Luijten P, Klomp D. (2009): High field MR spectroscopy of the human brain at short TE and TR. *proc. 17th ISMRM*:4313

[2] van den Heuvel M, Mandl R, Luigjes J, Hulshoff Pol H. (2008): Microstructural organization of the cingulum tract and the level of default mode functional connectivity. *J Neurosci* 28(43):10844-51