

A Systematic Analysis of Association Fiber Tracts in Chronic Alcoholics Found Significant Deficit of White Matter Integrity in Superior Longitudinal Fasciculus using Diffusion Spectrum Imaging Tractography

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Introduction

Excessive chronic alcohol use was found association with significant shrinkage of the cortical tissue and degradation of fibers that carry information between neurons. Previous studies showed the degradation of white matter systems associated with alcoholism, especially in corpus callosum and cingulum [1-2]. However, a systematic analysis of association fiber tracts is still lacking. Therefore, in this study, we used diffusion spectrum imaging (DSI) tractography to identify the trajectories of all major association fiber tracts, and performed the tract-specific analysis with generalized fractional anisotropy (GFA), a metric of structural homogeneity, along the target tracts to investigate the effect of alcohol on white matter microstructure alteration.

Materials and Methods

Subjects Ten alcoholics (age range: 37–52 years; mean±SD: 43.9±4.6 years) and 10 healthy controls (age range: 38–52 years; mean±SD: 44.3±4.6 years) were recruited in the study. All subjects were right-handed male. **DSI acquisition and analysis** MR experiments were performed on a 3T MRI scanner (Trio, Siemens, Erlangen, Germany). Both T2-weighted images and DSI were acquired with the same slice orientation and coverage. The T2-weighted images were acquired using a turbo spin echo sequence, TR/TE = 5920/102 ms, matrix size = 256×256, spatial resolution = 0.98×0.98 mm², and slice thickness = 3.9 mm. DSI was performed using a twice-refocused balanced echo diffusion echo planar imaging sequence [3], TR/TE = 9100/142 ms, image matrix size = 128×128, spatial resolution = 2.9×2.9 mm², and slice thickness = 2.9 mm. A total of 203 diffusion encoding gradients with the maximum diffusion sensitivity (b_{max}) of 6000 s/mm² were applied on the grid points in the 3D q-space with |q| ≤ 3.6 units. DSI analysis was performed based on the relationship that the echo signal S(q) and the diffusion probability density function P(r) were a Fourier pair [4]. The orientation distribution function (ODF) was determined by computing the second moment of P(r) along each radial direction [5]. The intravoxel fiber orientations were determined by decomposing the original ODF into several constituent ODFs [6]. The vectors of those primary orientations were used for further tractography reconstruction. The value of GFA at each voxel was quantified based on the shape of the original ODF [7]. **Tractography reconstruction and GFA analysis** Tractography was reconstructed using a streamline-based algorithm adapted for DSI data using in-house software (DSI studio, <http://dsi-studio.labsolver.org/>). One of the decomposed fiber vectors in the white matter pixels was used as a seed vector to produce one fiber tract. A step of 0.4 pixel was tracked forward from the seed vector, and all vectors in the nearest voxels were evaluated to determine the proceeding orientation for the next step. A vector with closest orientation to the starting vector was chosen if it was within 45° deviation. Tracking stopped if no such vectors were found in the nearest voxels. The procedure of the fiber tracking was iterated by randomly selecting the seed vectors in the pixels covering each association fiber tract. Seven association fiber tracts were reconstructed, including arcuate fasciculus (AF), cingulum bundle (CB), inferior fronto-occipital fasciculus, stria terminalis, uncinate fasciculus, fornix and superior longitudinal fasciculus (SLF). The tract-specific analysis was performed based on the mean path of individual fiber tract [8]. Comparison of averaged GFA values was performed between control and alcoholic groups using two-tailed t test and the difference was considered statistically significant if $p < 0.05$.

Results

The tractography results are shown in Figure 1. By tract-specific analysis, no significant differences were found in all the association fiber tracts except SLF. As shown in Figure 2, our results showed that GFA in the SLF was reduced in the alcoholic group compared to the control group bilaterally. On left side, the averaged GFA values were 0.1845 ± 0.0172 and 0.2186 ± 0.045 for alcoholic and control groups, respectively ($p = 0.0408$). On right side, the GFA values were 0.1853 ± 0.0174 for alcoholic group and 0.2013 ± 0.0198 for control group ($p = 0.0246$).

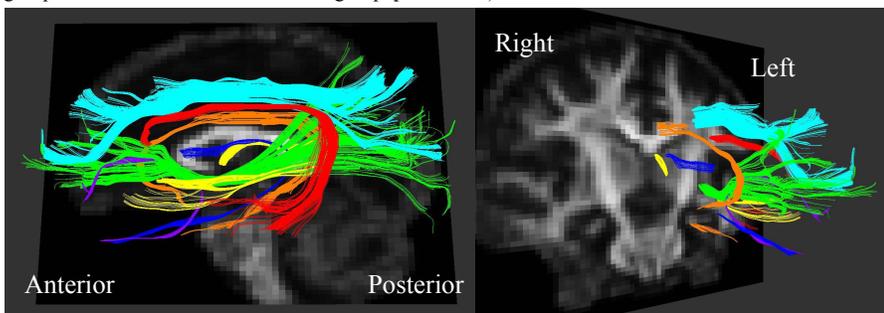


Figure 1. The tractography results in sagittal view (left) and coronal view (right) of seven association fiber tracts illustrated in different colors, arcuate fasciculus (red), cingulum bundle (orange), fornix (yellow), inferior fronto-occipital fasciculus (green), superior longitudinal fasciculus (cyan), stria terminalis (blue)

Discussions

In this study, a systematic approach combining fiber tracking and tract-specific analysis has been applied to investigate the relationship between the effect of alcoholic use and microstructural alteration of association fiber tracts. Other than voxel-based analysis, the tract-specific approach provides a better way to illustrate the change along a specific tract, not just a specific region. Among all the association fiber tracts, a significant GFA deficit was found in bilateral SLF in chronic alcoholics, suggesting that SLF is most vulnerable to alcohol exposure among association fibers. Although no significant difference was found in other association fibers, there might be some subtle differences that were smeared out by the averaged GFA value along the whole fiber tract. Furthermore, marginally significant difference was found in right CB and left AF. Therefore, a future study with a larger subject number is needed to analyze the GFA profile of the tract and to further explore the effects of alcohol on the microstructure of association fibers.

References

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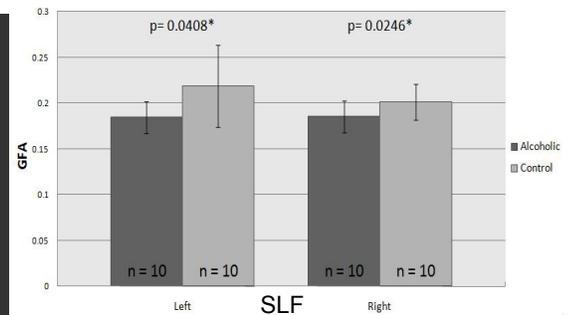


Figure 2. The comparison of averaged generalized fractional anisotropy (GFA) values of bilateral superior longitudinal fasciculus (SLF) between alcoholic and control groups using tract-specific analysis.