The Reconstruction of Hippocampus Network by QBI Tractography

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INTRODUCTION

The hippocampus (HC) is one of the core regions in the limbic system. The function of HC is involved in the formation of episodic memory and is also responsible for spatial navigation and spatial memory. Therefore, the function of HC was found to be related to some deficits in psychological disorders, such as schizophrenia [1] and Alzheimer's diseases [2]. A current issue on HC is, however, the lack of the evidence to map appropriately between valid structure connectivity and the functional connectivity. The interrupted knowledge conceals that how HC functions as an important role in the process of cognitive function. In this study, Q-Ball Imaging (QBI) tractography technique was employed to provide advanced information in structural connectivity, especially in the regions with intravoxel heterogeneity [3]. On the other hand, resting-state functional Magnetic Resonance Imaging (rfMRI) brought the information of functional connectivity of HC. The combined information facilitates to provide more detail to understand the mechanism of HC.

METHODS

There were 32 healthy participants recruited in this study, including 17 females and 15 males (mean age: 25.2±3.6yrs). The data acquisition of QBI was on a 3T Siemens Trio MRI scanner, a whole-body Tim system. QBI with 162 diffusion encoding directions was performed by using echo planar imaging (EPI) sequence with TR=9500 ms, TE=123 ms, FOV=192*192mm^2, matrix size=96*96, b value=3000s/mm^2, and voxel size=2*2*2mm^3. The rfMRI was obtained with parameters of TR=2000ms, TE=30ms, FOV=220*220mm^2, matrix size=64*64, and voxel size=3.4*3.4*4mm^3. For QBI tractography, the following steps were employed sequentially: distortion correction of eddy current by Brainvisa diffusion toolbox (http://brainvisa.info/), Rician noise correction of diffusion weighted images by non-local means filter (http://www.irisa.fr/visages/benchmarks/), motion correction by registration function of SPM2, and QBI reconstruction based on spherical harmonic with series order=8. Bilateral hippocampus defined by Automated Anatomical Labeling (AAL) template was used in whole brain fiber tracking by MFACT algorithm with a length threshold of ODF (ODF_{td}) 0.9 and a tract-turning angle threshold (TTA) of 60 degree [3]. Other regions, such as Insula (29&30), amygdala (41&42), putamen (73&74), thalamus (77&78) and anterior (31&32), middle (33&34), and posterior cingulum (35&36) were also selected to extract the fiber bundles between themselves and hippocampus. Only fornix was delineated by hand. The cut-off threshold to reproduce HC network was set at the 1/3 of total amount of passing fibers with each connection. Besides, the rfMRI was analyzed through software SPM and REST (http://restfmri.net/forum/). The seed point was put at right-side Hippocampus (30, -16, -14) and left-side Hippocampus (-30, -16, -14). The second–level analysis of rfMRI was under statistical criteria of family-wise error rate (FWE), p-value < 0.0001, T-value > 8.61 with extent threshold voxel=0.

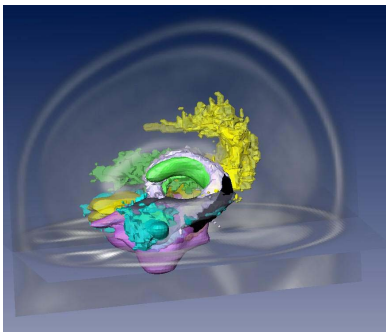

Figure 1 QBI Tractography of HC

RESULTS

Population-based probabilistic pathways are demonstrated by collecting the QBI tractography in 32 subjects. Anatomical connectivity with higher probabilities from HC to those selected regions is shown in Figure 1. Neural bundles with different color coding display the different trajectories linked to HC (black). Cingulum, fornix, HC-thalamus, HC-insula, HC-putamen, and HC-amygdala tracts are drawn by yellow, light purple, green, cyan, light gray and dark purple respectively. Moreover, Table 1 presents the results of rfMRI. The associated regions are sorted and listed by the level of significance. The QBI data falls on the areas exactly on the list.

Table 1 Cluster result of rfMRI

Seed point at Right Hippocampus			Seed point at Left Hippocampus		
Coordinates	Areas	Voxel-level T value	Coordinates	Areas	Voxel-level T value
(30, -16, -14)	Right Hippocampus	67.24	(-30, -16, -14)	Left Hippocampus	44.63
(-15, 14, -12)	Left Superior Orbital Gyrus	22.82	(15, 14, -8)	Right Rectal Gyrus	24.74
(-12, 14, -10)	Left Rectal Gyrus	22.57	(-22, 0, -18)	Left Parahippocampal Gyrus	23.76
(15, 18, -10)	Right Rectal Gyrus	22.50	(30, -18, -8)	Right Hippocampus	23.62
(-10, 8, -4)	Left Caudate Nucleus	22.37	(32, -10, -14)	Right Amygdala	23.43
(8, 10, -8)	Right Olfactory Cortex	22.33	(-30, -4, -12)	Left Amygdala	22.90
(-12, 18, -5)	Left Caudate Nucleus	22.30	(-12, 0, 4)	Left Pallidum	22.41
(-18, 10, -15)	Left Inferior Frontal Gyrus	22.20	(12, -15, 0)	Right Thalamus	22.28
(22, 15, -14)	Right Inferior Frontal Gyrus	21.81	(22, 2, -20)	Right Parahippocampal Gyrus	21.76
(20, 20, -10)	Right Superior Orbital Gyrus	21.58	(22, 2, 12)	Right Putamen	21.08
(-15, 5, -18)	Left Olfactory Cortex	21.06	(15, 2, 5)	Right Pallidum	20.82
(-22, 10, 0)	Left Putamen	21.05	(24, 12, -12)	Right Inferior Frontal Gyrus	20.40
(28, 10, -14)	Right Insula Lobe	20.00	(-20, 14, -5)	Left Putamen	20.14
(20, 20, 2)	Right Caudate Nucleus	19.68	(-22, -24, 12)	Left Thalamus	19.92
(20, 0, -15)	Right Parahippocampal Gyrus	19.34	(12, 4, 0)	Lateral Globus Pallidus	19.36
(-4, -54, 58)	Left Precuneus	18.90			
(-30, -4, -12)	Left Amygdala	18.89			
(5, 38, 24)	Right Anterior Cingulate Cortex	18.84			
(-4, 35, 12)	Left Anterior Cingulate Cortex	18.83			
		18.71			
(-22, -5, 4)	Left Pallidum	18.66			
(34, -22, 2)	Right Putamen	18.60			
(4, -80, -28)	Cerebellar Vermis	18.48			
(12, -8, -14)	Right Hippocampus	18.46			

DISCUSSION

QBI tractography sketches the network of HC and the population-based probability of each connection. The loss or break-down on these neural pathways might be involved in the malfunction of some psychological disorders. That is, this evidence from the HC network might be able to contribute to future investigation of the psychological disorders with dysfunction of memory and spatial navigation. Although the preprocessing procedure for QBI reconstruction has been done properly, some confounding factors still exist in the data acquisition, tracking algorithm and selection of seed region, such as image resolution, noise effect, and complicated structures with various nucleuses in the limbic system. Therefore, using the population-based probabilistic pathways to estimate the possible connection of HC might be more suitable to overcome the errors and provides the rich information for further application. The follow-up of current study should be to use the higher-significant areas from rfMRI as seed point to make the reconstruction of HC network more completely.

REFERENCE

[1] Fitzsimons, J., et al., Schizophrenia Research, p39-46, 2009. [2] Zarei, M., et al., NeuroImage, p1-8, 2010. [3] Chao, Y-P, et al., Human Brain Mapping, p.3172-3187, 2009. [4] O'Keefe, J. and Nadel, L., Oxford University Press, 1978.

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