The intrinsic network organization differs in individuals with alcohol use disorders (AUD) as a function of relapse status

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Introduction

Coordinated activity within intrinsic connectivity networks (ICN) and differentiated activity between the ICNs is a crucial feature of the brain's functional organization. Neurotransmitters like glutamate and GABA are involved in orchestrating the exhibitory/inhibitory balance of the activity that shapes the intrinsic network-architecture of the brain at rest. Chronic alcohol exposure and abstinence during treatment have been shown to result in region-specific neuroadaptions in glutamatergic and GABAergic synaptic transmission.

Aim & Hypothesis

We aimed to model the sub-network brain organization in AUD individuals at 1 month (TP1) and 4 months (TP2) of treatment in order to better understand how the ICN organization of the brain relates to the outcome of their treatment.
Hypotheses:
1. Abstainers and relapsers (those who resumed alcohol consumption between TP1 and TP2) show altered sub-network quality when compared with the light-drinking controls at both TP.
2. Relapsers and abstainers show differences in sub-network quality when compared with each other at both TP.

Methods

All participants underwent a 3T resting-state fMRI scan (8min) at an interval of three months. 115 datasets) with 5min of clean data were left for further analysis after rigorous control for motion artefacts.
The AICHA atlas was used to partition the brain into 384 ROIs. The Louvain algorithm adapted for undirected connection matrices with positive and negative weights (BCT toolbox, Version 2015) was run for each participant 10,000x and the Q* values computed. The Louvain algorithm partitions the brain network into non-overlapping sub-networks and Q* quantifies the number of within-sub-network connections in relation to change-expected within-sub-network connections (Rubinov & Sporns, 2011). A $Q^* < 0.3$ (Meunier et al., 2009) indicates a low degree of clearly identifiable networks and can be interpreted as an indicator for a low brain organization. Two-sided Wilcoxon-Rank-Sum-Tests were used to test the two hypotheses that the distribution of the Q* values of the controls, abstainers, and relapsers were significantly different at each TP.

Results

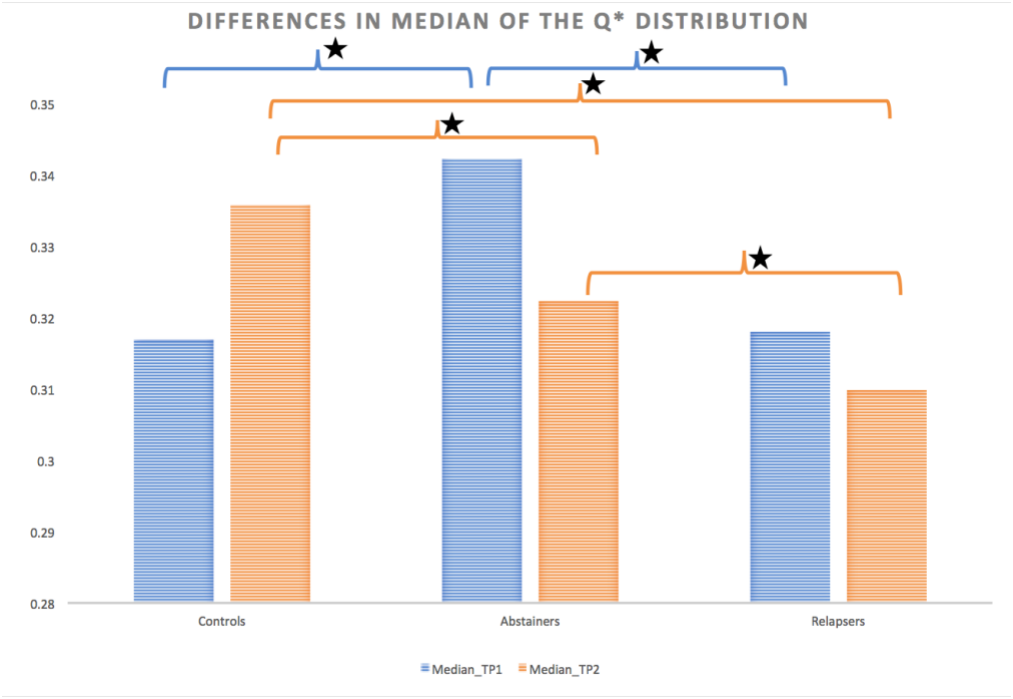
	N	Median Q* at TP1	Comparisons at TP1	p Value
LD Controls	33	0.3170	LD Controls vs Abstainers	$p < 0.05$
Abstainers	12	0.3424	LD Controls vs Relapsers	$p = 0.16$
Relapsers	23	0.3180	Abstainers vs Relapsers	$p < 0.05$
		Q* Median at TP2	**Comparisons at TP2**	
LD Controls	23	0.3358	LD Controls vs Abstainers	$p < 0.05$
Abstainers	10	0.3222	LD Controls vs Relapsers	$p < 0.05$
Relapsers	14	0.3099	LD Controls vs Relapsers	$p < 0.05$

The two patient groups showed a decrease in Q* from TP1 to TP2 while the controls showed an increase. Latter may suggest that only controls were returning for follow-up who were more comfortable with the testing situation and that was affecting the data quality. However, none of these changes were not significant.

Conclusions

We found differences in the brain's sub-network organization in controls, abstainers and relapsers at both TP. The group differences in brain-network organization may reflect greater neuroplasticity in abstainers than relapsers at TP1 and normalization at follow-up. The network organization does not change as much in the relapsers during treatment.

Figure



Highlights

- We modeled the resting-state functional intrinsic organization of the brain's sub-networks in controls and individuals who were able to abstain from alcohol or relapsed to drinking during alcoholism treatment.
- Group differences in the identifiability of sub-networks (Q*) across the groups may reflect neuroplasticity during treatment.
- Q* may be used as a new connectivity biomarker of alcohol relapse.