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## Intrinsic functional organization underlying intrinsic response inhibition network

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Background: Previous studies suggest that widespread brain areas are engaged in successful response inhibition<sup>1</sup> and interconnected into an integrative network<sup>2</sup>. However little is known about the functionally specific subsystems underlying the response inhibition network and the key regions integrating information within and across different functional systems. To address these questions, we explored the intrinsic functional architecture of the response inhibition network from the perspective of modules and hubs using graph-theory. Methods

Network construction 56 subjects with resting-state fMRI and T1-weighted images from the Connectivity-based Brain Imaging Research Database at Beijing Normal University were used<sup>3</sup>. 91 Nodes were generated from the clusters activated in response inhibition revealed by our meta-analyses results<sup>4</sup> (Fig. 1). Each node had a radius of 6 mm. Edges were defined as the strength of the interregional resting-state functional connectivity. To denoise spurious interregional correlations, a significance level-based method



Fig. 1Response inhibition activation map

was applied to individual correlation matrices (q<0.01, FDR corrected). Then, the mean functional connectivity matrices averaged across participants were obtained for the following analysis.

Module We detected the modular structure using a spectral optimization algorithm. To test whether the network modularity Q was significantly higher than those of random networks, a Z test was performed with the Q values generated from 1000 random graphs preserving the same degree distribution.

Hub detection Degree and participation coefficient (PC) were calculated to profile different aspects of node importance. Two types of hubs were defined. Connector hubs were nodes holding both high degree and PC Z scores (> 0.85) of the detected modules; provincial hubs were nodes with high within-module degree Z scores (>

0.85) but without meeting the criteria of connector hubs.

**Results**: Modularity Q was significantly higher than those of random networks (Z=29.28, p<0.001), indicating a strong modular structure. Three modules, were obtained (Fig. 2), the frontoparietal network (FPN, Red nodes), the dorsal attention network (DAN, blue nodes), and the ventral attention network (VAN, green nodes).

For connector hubs (Fig. 3a), all three modules are interconnected through the bilateral anterior cingulated gyrus. In addition, hubs connecting the FPN and the





Fig. 2 Module structure of response inhibition network. (a) Eurotional connectivity map; (b) Module structure. FPN, frontoparietal network (Red nodes); DAN, dorsal attention network (Blue nodes); VAN, ventral attention network (Green nodes)

DAN were found in the right parietal operculum cortex, the FPN and the VAN in the right inferior frontal gyrus and the right superior frontal gyrus, and the DAN and the VAN in the right precentral gyrus. For provincial hubs (Fig. 3b), besides different peripheral parts of the bilateral anterior cingulated gyrus, the right angular gyrus and the precentral gyrus serve as the provincial hubs for the FPN, the right pallidum and the right thalamus were hubs for the DAN, and the left anterior cingulated gyrus and the right operculum central cortex were hubs for the VAN.

**Conclusions**: Our findings show that the response inhibition network was intrinsically organized into three interconnected modules, corresponding to three functionally specific subsystems identified by previous studies<sup>2.4</sup>. A set of hub regions, corresponding nicely with previous literature, were found to capture different and important aspects of the functional network topological properties.

## References

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