

Individualized Precision Targeting of Dorsal Attention and Default Mode Networks with Rtms in Traumatic Brain Injury-Associated Depression

Shan H. Siddiqi ([✉ shan.siddiqi@mgh.harvard.edu](mailto:shan.siddiqi@mgh.harvard.edu))

Harvard University

Sridhar Kandala

Washington University in St. Louis

Carl D. Hacker

Washington University in St. Louis

Nicholas T. Trapp

University of Iowa

Eric C. Leuthardt

Washington University in St. Louis

Alexandre R. Carter

Washington University in St. Louis

David L. Brody

Uniformed Services University of the Health Sciences

Research Article

Keywords: transcranial magnetic stimulation, traumatic brain injury, depression, individualized parcellation, resting state network, neuronavigation, fMRI

Posted Date: November 3rd, 2021

DOI: <https://doi.org/10.21203/rs.3.rs-952841/v1>

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Additional Declarations: Competing interest reported. SHS serves as a clinical consultant for Kaizen Brain Center. SHS has received research support from Neuronetics Inc. The present work was not supported by any of these entities. DLB has served as a consultant for Pfizer Inc, Intellectual Ventures, Signum Nutralogix, Kypha Inc, Sage Therapeutics, iPerian Inc, Navigant, Avid Radiopharmaceuticals (Eli Lilly & Co), the St Louis County Public Defender, the United States Attorney's Office, the St Louis County Medical Examiner, GLG, Stemmedica, and Luna Innovations. DLB holds equity in the company Inner Cosmos. DLB

receives royalties from sales of Concussion Care Manual (Oxford University Press). No conflicts of interest with the presented work. DLB is an employee of the Department of Defense; the views expressed here do not reflect those of the Uniformed Services University of the Health Sciences, the US Department of Defense, or the US Government. ECL holds equity in the companies Neurolutions and Inner Cosmos. CDH, ECL, and SHS hold intellectual property related to the use of RSNM to target TMS. The remaining authors report no conflicts of interest.

Version of Record: A version of this preprint was published at Scientific Reports on March 11th, 2023. See the published version at <https://doi.org/10.1038/s41598-022-21905-x>.

Abstract

Background

At the group level, antidepressant efficacy of rTMS targets is inversely related to their normative connectivity with subgenual anterior cingulate cortex (sgACC). Individualized connectivity may yield better targets, particularly in patients with neuropsychiatric disorders who may have aberrant connectivity. However, sgACC connectivity shows poor test-retest reliability at the individual level. Individualized resting-state network mapping (RSNM) can reliably map inter-individual variability in brain network organization.

Objective

To identify individualized RSNM-based rTMS targets that reliably target the sgACC connectivity profile.

Methods

We used RSNM to identify network-based rTMS targets in 10 healthy controls and 13 individuals with traumatic brain injury-associated depression (TBI-D). These “RSNM targets” were compared with consensus structural targets and targets based on individualized anti-correlation with a group-mean-derived sgACC region (“anti-group-mean sgACC targets”). The TBI-D cohort was randomized to receive active (n=9) or sham (n=4) rTMS to RSNM targets.

Results

The group-mean sgACC connectivity profile was reliably estimated by individualized correlation with default mode network (DMN) and anti-correlation with dorsal attention network (DAN). Individualized RSNM targets were then identified based on DAN anti-correlation and DMN correlation. Counterintuitively, anti-correlation with the group-mean sgACC connectivity profile was stronger and more reliable for RSNM-derived targets than for “anti-group-mean sgACC targets”. Improvement in depression after RSNM-targeted rTMS was predicted by target anti-correlation with the portions of sgACC. Active treatment led to increased connectivity within and between several relevant regions.

Conclusions

RSNM may enable reliable individualized rTMS targeting, although further research is needed to determine whether this personalized approach can improve clinical outcomes.

1. Introduction

The antidepressant efficacy of repetitive transcranial magnetic stimulation (rTMS) may be related to the connectivity of the stimulation target¹. Most commonly, scalp measurements or structural MRI are used to identify a target in the dorsolateral prefrontal cortex (DLPFC)². Recent studies have attempted to identify rTMS targets based on functional connectivity (FC) with “seed” regions deeper in the brain³. At the group level, antidepressant efficacy of rTMS is related to normative anti-correlation between the stimulation site and the subgenual anterior cingulate cortex (sgACC), suggesting that treatment may be suppressing activity in sgACC and the limbic system^{4–7}. Antidepressant efficacy is even more strongly related to normative connectivity between the stimulation site and a recently-derived “depression circuit” that closely overlaps with the dorsal attention network (DAN). To improve upon these group-level targets, individualized connectivity measurements have also been used to identify patient-specific stimulation sites based on connectivity to the sgACC^{8–10} or to the DAN^{11,12}. These individualized targets may be more effective than the optimal normative targets^{6,7,13,14}.

While the sgACC approach has been employed most commonly^{6,7,9,10,13–15}, this approach is limited by the fact that sgACC connectivity is unreliable at the individual level^{8,10,14,16}. Reliability assessments have shown weak test-retest correlation for sgACC connectivity to DLPFC TMS targets (spatial $r<0.5$)^{8,14} and marked variability in DLPFC targets identified based on sgACC connectivity (mean test-retest variability of 25mm)¹⁰. Targets can be identified more reliably based on connectivity to the “network” of regions most correlated with the sgACC at the group level⁸. This network may be personalized using individualized resting-state network mapping (RSNM), which can reliably map brain networks based on resting-state functional MRI (rsfMRI)^{17–21}. RSNM has been successfully used for neurosurgical pre-operative mapping²² and has recently been evaluated as a method for mapping prefrontal topography to identify rTMS targets¹².

RSNM enables precise individualized mapping of the DMN²³, which is highly correlated with sgACC and the limbic system^{24,25}. Individualized DMN mapping may thus serve as a more reliable proxy for sgACC connectivity. DMN is strongly anti-correlated with the DAN^{26–28}, so individualized DAN mapping may yield a TMS target that is reliably anti-correlated to sgACC. Indeed, RSNM studies have found that DAN usually includes a node in the DLPFC, but the precise location of this node varies greatly between individuals^{29,30}. Reliable rTMS targets have been identified at this node¹². Stimulation of this node led to changes in sgACC connectivity with the DAN stimulation sites and with the DMN¹².

Of note, much of the existing knowledge about individualized brain mapping has been based on studies of healthy individuals. It remains unclear whether this generalizes to patients with neuropsychiatric illnesses and brain injuries. Inter-individual variability may be particularly prominent in traumatic brain injury-associated depression (TBI-D), which is associated with altered FC in the DLPFC, sgACC, DAN, and DMN^{31–34}. This raises additional questions regarding the appropriateness of group-mean rTMS targets or individualized targets derived from seed-based connectivity.

As a first step to addressing these questions, we explored the differences between potential target sites generated using individualized RSNM (RSNM-based targets), standard anatomical methods (structural targets), and the point of maximal anti-correlation with the group-mean location of the sgACC (anti-group mean sgACC targets). We also explored the connectivity changes induced by stimulation of RSNM-based targets in a recent pilot clinical trial¹². We hypothesized that RSNM-based targets would approximate the sgACC connectivity profile more reliably than a group-based sgACC seed, which has previously been proposed for rsfMRI-based rTMS targeting^{6,8,10}. After stimulation of these RSNM-based targets, we hypothesized that connectivity changes would be observed in the targeted networks, that these connectivity changes would covary with antidepressant response, and that antidepressant response would be predicted by baseline sgACC connectivity to the stimulation site.

2. Methods

Full methodological details are presented in the supplement.

2.1 Standard protocol approvals and participants

Data were collected as part of a pilot randomized clinical trial of rTMS for TBI-D¹². Methods and hypotheses were pre-registered with the Open Science Foundation (osf.io/vjddq/)³⁵ and ClinicalTrials.gov (NCT02980484, posted 02 Dec 2016). The protocol was approved by the Human Research Protection Office at Washington University School of Medicine in St. Louis. All participants provided written informed consent and all procedures were carried out in accordance with relevant regulations. rTMS treatment parameters were within FDA guidelines. Participants were allocated via simple randomization to receive 20 daily sessions of active or sham rTMS with a 1:1 ratio using a random number generator, as described in our prior work. All randomization and enrollment procedures were conducted by the principal investigator (SHS). Participants and raters were blinded to the group allocation. Sham stimulation was applied using a device that produces a similar sound, but does not deliver active stimulation. Further details about the clinical trial are reported in Siddiqi et al., 2019¹².

32 potential participants were screened for the study. 15 participants (11 males, ages 19-64) were included if they scored at least 10 on the Montgomery-Asberg Depression Rating Scale (MADRS) and had a history of at least one concussive or moderate TBI. One participant in the sham group was lost to follow-up before starting treatment. The remaining 14 participants completed the intent-to-treat endpoint (MADRS after 10 treatments). Two participants (one active, one sham) missed multiple treatments due to headaches, and were thus unable to complete the full treatment course within the pre-specified 5-week timeframe; however, both completed a MADRS and MRI for intent-to-treat analysis. One participant in the sham group chose not to complete a post-treatment MRI scan. This analysis was limited to 13 subjects (10 males) who completed both the pre-treatment and post-treatment scan sessions. Of note, the clinical trial was terminated prior to the first interim analysis (planned at n=20) because the investigators left the institution for unrelated reasons.

10 healthy control subjects (3 males, ages 22-35) with no history of neuropsychiatric disease were chosen randomly from the Human Connectome Project (HCP) database³⁶. Only 10 subjects were chosen in order to approximately match the number of TBI-D patients and to confirm that utility of individualized RSN can be demonstrated with small sample sizes; clinical practicality of personalized medicine approaches may be questionable if large sample sizes are required to demonstrate their utility. We did not attempt to match these participants to the TBI-D sample because (a) HCP participants are all under age 35, and (b) no statistical comparisons were made between the two samples, since any matching attempts would be limited by the fact that the datasets were collected in different settings.

2.2 MRI acquisition and pre-processing

For TBI-D subjects, a 3T Siemens Magnetom Prisma magnetic resonance scanner was used to acquire 16.5 minutes of resting-state blood oxygen-level dependent (BOLD) data in three runs. For HCP subjects, a 3T Siemens Connectome Skyra was used to acquire 58 minutes of resting-state BOLD data in four runs. Preprocessing was conducted using in-house scripts described in Power et al., 2014³⁷. For each subject, BOLD time courses were used to construct seven individual-level RSN maps via a multilayer perceptron (MLP)-based machine learning classifier as described in Hacker et al., 2013¹⁹. To create individualized regions of interest for further analyses, a winner-take-all map was created by assigning each voxel to the network with maximum likelihood of membership. Further details are described in the supplement.

2.3 Confirmation of candidate network targets

2.3.1 Normative connectivity data

Data from the HCP 800-subject release³⁶ were used to construct normative maps of resting-state functional connectivity with the sgACC (figure 1a), as described in Weigand et al., 2018⁵. We hypothesized that the individualized map of the DAN would be most similar to the normative map of sgACC anti-correlations. We also hypothesized that the individualized map of the DMN would be most similar to the normative map of sgACC positive correlations. To initially evaluate these hypotheses, we quantified the degree of overlap between our group-based map was visually compared with individualized RSN maps for each subject (figure 1b). All subsequent analyses were conducted using subject-specific connectivity data rather than group connectome data.

2.3.2 Comparison of individualized RSN maps to sgACC seed maps

For each subject, we quantified the degree to which each of the seven individualized RSN maps overlapped with the normative sgACC seed map. The sgACC seed map was masked with each individual RSN map to identify its overlap with that network (figure 1c). This yielded a map of normative sgACC connectivity values at each voxel within each RSN. Using this map, the mean normative sgACC connectivity value of overlapping voxels was calculated for each RSN and each subject. This yielded a single metric of the degree of overlap between the continuous normative sgACC seed map and each

binary RSN map. This value was compared between DAN/DMN and the remaining RSNs by calculating Fisher's least significant difference via one-way ANOVA.

2.4 rTMS target selection and comparison

Specific analytical procedures/tools are described in the supplement.

2.4.1 Target selection

Three approaches were used to identify potential rTMS targets:

1. Individualized RSNM-based targeting – The individualized DMN map was subtracted from the individualized DAN map for each subject. The peak DLPFC cluster was identified in this map following the methods described in Siddiqi et al., 2019 (Fig. S1)¹¹.
2. Structural MRI-based targeting – Targets were chosen at DLPFC coordinates ($\pm 38, 44, 26$), which have been used for targeting at the world's current largest neuronavigated rTMS clinic³⁸.
3. Individualized anti-group mean sgACC target – this method relies on an individual subject's anti-correlation with group-mean sgACC coordinates, as described in Fox et al., 2013⁸ and implemented in Cash et al., 2020¹³ and Siddiqi et al., 2021¹⁴. The sgACC ROI was defined at the group level as a sphere centered at the coordinates (6, 16, -10)⁸.

2.4.2 Comparison of resting state functional connectivity of the potential targets

For each potential stimulation site, resting-state functional connectivity was calculated with a population-derived definition of DAN and DMN³⁹. To confirm that effects were not driven by autocorrelation between the RSNM-based DAN/DMN parcels and the consensus DAN/DMN parcels, connectivity was also calculated with the normative sgACC seed map. If effects were driven by autocorrelation, then this map would be most anti-correlated with the anti-group mean sgACC targets.

Potential target correlations with the DAN, DMN, and the sgACC seed map were compared between the different targeting methods across all subjects via within-subjects two-way ANOVA. Results from the two groups of subjects (TBI-D and healthy controls) were not compared with one another due to potential influence of methodological variability and demographic differences.

2.4.3 Comparison of spatial locations of the potential targets

For each subject, the three potential targets were also compared in terms of spatial distance between one another. The mean distances of RSNM targets and anti-group mean sgACC targets from the structural target were compared using paired t-tests. Inter-individual variances for RSNM targets and anti-group

mean sgACC targets were determined using F-tests based on the distance of each target from the mean of all coordinates generated by that method.

2.5 rTMS treatment

To explore the effects of stimulating our proposed targets, TBI-D subjects were randomized to receive 20 daily sessions of active or sham rTMS using the RSNM targets. The clinical trial protocol, results, and CONSORT checklist are described in detail in Siddiqi *et al*, 2019¹². Briefly, clinical treatment included 4000 pulses of high-frequency (10 Hz) left-sided stimulation, followed by 1000 pulses of low-frequency (1 Hz) right-sided stimulation. Using a Brainsight neuronavigation device, target coordinates were plotted on a surface reconstruction of each subject's brain. No stimulation at other targets was performed in the current study.

2.6 Treatment-induced changes

Detailed analysis parameters are described in the supplement.

2.6.1 Target stability over time

Nine TBI-D subjects were randomized to active treatment and four were randomized to sham. For each of the three targeting methods, connectivity with the normative sgACC seed map was calculated for pre-treatment and post-treatment scans. Two-way ANOVA was used to compare the three targeting methods in terms of difference in connectivity between the two time points. Again, it should be noted that only individualized RSNM-based targeting was performed.

Euclidean distances between pre-treatment and post-treatment targets were calculated for RSNM and anti-group mean sgACC targets in order to assess the stability of target location. Due to non-normal distribution of these distances, a Wilcoxon matched-pairs signed-rank test was used to compare the two targeting methods in terms of stability over time.

2.6.2 Exploratory evaluation of treatment-induced connectivity changes

To explore how the target RSNs were affected by rTMS, active and sham groups were compared in terms of treatment-induced change in connectivity. Connectivity was calculated between five *a priori* ROIs defined in the original clinical trial, including left/right stimulation sites, DAN, DMN, and sgACC. This analysis was conducted using covariance rather than correlation, since covariance is less sensitive to the potential influence of changing amplitudes of BOLD fluctuations between different time points⁴⁰.

To explore the rest of the brain was affected by rTMS, ROI-ROI connectivity was calculated with each of the 17 Yeo networks and voxel-wise connectivity was calculated with the whole brain. Active and sham groups were compared using a general linear model (GLM) with group assignment as the primary predictor, post-treatment connectivity as the outcome, and pre-treatment connectivity as a covariate.

Except where required for voxel-wise multiple comparisons correction, statistical hypothesis testing was not conducted for active-sham comparisons because the trial did not reach its original target sample size¹².

2.6.3 Prediction of antidepressant response

To examine connectivity-based predictors of response in the active treatment group, whole-brain connectivity of each stimulation site was compared with antidepressant response. For each voxel, a least squares regression model was constructed using baseline target-voxel connectivity and baseline MADRS as predictors of post-treatment MADRS. Because antidepressant response could not be assumed to be normally distributed in this small sample, all data were rank-transformed, which is consistent with prior methods described in Weigand *et al*, 2018⁵.

3. Results

3.1 Confirmation of candidate network targets

In both groups, the positive correlations in the normative sgACC seed map (figure 1a, yellow/orange regions) showed stronger overlap with the individual DMN map than with any other individualized network map (figure 2a), as quantified by the mean Fisher z-transformed voxel value of the sgACC seed map that fell within the boundaries of each network. The anti-correlations in the sgACC seed map (Fig. 1a, blue regions) showed stronger overlap with the individualized DAN map than with any other network map (figure 2a). In comparison with the other individualized networks in the TBI-D group, DAN showed significantly stronger overlap with the negative component of the sgACC seed map, while DMN showed significantly stronger overlap with the positive component of the sgACC seed map (figure 2b). The same trend was evident in the HCP group, except that the DAN-ventral attention network (VAN) difference and the DAN-frontoparietal control network (FPC) difference did not reach significance (figure 2b). Overall, DAN anti-correlation and DMN correlation provided the best individualized approximation of the sgACC seed map.

3.2 Evaluation of expected stimulation profile for each potential target

Nearly all potential targets showed positive correlation with the DAN, negative correlation with the DMN, and negative correlations with the group mean sgACC seed map (figure 3a). Within-subjects two-way ANOVA revealed a significant effect of potential targeting method on left- and right-sided target connectivity with each of these RSNs in each of the two datasets (table S1). The magnitude of these differences was similar but not identical between the two datasets (figure 3b and table S1). As expected, in comparison with each of the other two targets, the RSNM-based target showed stronger connectivity to group-mean DAN and anti-correlation to group-mean DMN in 11/13 TBI-D patients and 8/10 healthy controls ($p=0.002$, single-proportion z-test with expected proportion of 50%). Overall, RSNM-based targets

appeared to provide a better individualized approximation of the desired networks than the other two potential targeting methods.

3.3 Spatial distribution of derived targets

In both groups, RSNM-based target coordinates were spatially distinct from both comparator targets with 95% confidence intervals that were greater than zero (figure 4a-4b). The structural target was significantly closer to the RSNM target than to the anti-group mean sgACC target in both the TBI-D ($p=0.006$) and HCP ($p=4 \times 10^{-5}$) groups. The anti-group mean sgACC targets also showed wider variance between subjects than the RSNM targets for both the TBI-D ($F=0.4$, $p=0.01$) and HCP ($F=0.4$, $p=0.03$) groups (Table S2). The anatomical locations of targets generated by the different methods are depicted in figure 4b along with an example of approximate predicted stimulation volumes for each target in one representative subject. Thus, RSNM targets were less variable anatomically than anti-group mean sgACC targets.

3.4 Stability of Connectivity and Target Location before vs. after RSNM targeted rTMS Treatment in TBI-D patients

13 TBI depression patients were scanned again after a full course of active rTMS ($n=9$) or sham rTMS ($n=4$). Connectivity with the normative sgACC seed map remained relatively stable for the RSNM target and the structural target (figure 5a). Anti-group mean sgACC targets, by contrast, showed significantly different connectivity profiles between pre-treatment and post-treatment scans ($p=0.03$). These results were unchanged when repeating the analysis after controlling for active versus sham stimulation ($p=0.03$), and there was no significant effect of treatment group ($p=0.59$).

Between the two scan sessions (pre- and post-treatment), the mean absolute Euclidean distance change in target coordinates was 6.6 mm for RSNM targets and 17.7 mm for anti-group mean sgACC targets (Wilcoxon matched-pairs signed rank test $p<10^{-4}$, figure 5b). These results did not differ when repeating the analysis after controlling for active versus sham stimulation ($p<10^{-3}$), and there was no significant effect of treatment group ($p=0.14$).

Thus, after active or sham rTMS at the RSNM target, the location of the RSNM targets remained more stable than the anti-group mean sgACC targets. Consistency of connectivity was similar between RSNM targets and structural targets. Of note, we did not directly assess stability of the location of the anti-group mean sgACC targets before and after stimulation at these targets because no stimulation was performed at anti-group mean sgACC targets.

3.5 Target engagement: treatment-induced change in connectivity

In comparison with sham, active rTMS was associated with large connectivity changes in several of the *a priori* ROI pairs, including DMN to sgACC, Left to Right stimulation site, and Left stimulation site to

sgACC. There were also large changes in within-ROI connectivity in both stimulation sites and sgACC (Fig. 5c). Pre-treatment and post-treatment connectivity of each stimulation site with each of the 17 Yeo networks is depicted in Figure S2.

Results and statistical methods for exploratory analyses are detailed in the supplement. First, treatment-induced connectivity change was compared between active and sham groups. Partial Spearman correlation was computed between group and post-treatment connectivity after controlling for pre-treatment connectivity (Figure S3). For the right stimulation site, there was a decrease in FC with the cingulo-opercular network parcel ($\rho = -0.56$) and the parieto-occipital DAN parcel ($\rho = -0.55$), increase in FC with the parahippocampal/retrosplenial DMN parcel ($\rho = 0.65$) (Figure S3a), and increase in FC with a voxel cluster in the left ventral hippocampus ($r > 0.7$, corrected $p < 0.05$) (Figure S3b). For the left stimulation site, active versus sham treatment led to a trend towards decreased parieto-occipital DAN connectivity and increased prefrontal/parietal DMN connectivity (Figure S3c), as well as a decrease in FC with a voxel cluster in the dorsomedial prefrontal cortex ($r > 0.7$, corrected $p < 0.05$) (Figure S3d).

3.6 Baseline predictors of clinical efficacy

For both stimulation sites, rTMS treatment efficacy was related to baseline connectivity of the stimulation site. For the right stimulation site, antidepressant response was significantly predicted by baseline anti-correlation with bilateral sgACC, anti-correlation with motor cortex, and positive correlation with dorsal ACC (corrected $p < 0.05$) (figure 6a). For the left stimulation site, antidepressant response to rTMS was predicted by baseline correlation with right precuneus and anti-correlation with right sgACC, bilateral lateral parietal lobe, and bilateral dorsomedial prefrontal regions traditionally associated with the resting-state salience network (corrected $p < 0.05$) (Figure 6b). Permutation testing confirmed that this whole-brain map was stronger than expected by chance for the right stimulation site ($p = 0.04$), but not the left stimulation site ($p = 0.27$).

Antidepressant response was negatively correlated with the right-sided stimulation site's FC with the *a priori* subgenual ROI (Figure 6c, top panel; Spearman $\rho = 0.70$, $p = 0.03$). The left-sided stimulation site showed a trend in the same direction, but did not reach significance (figure 6d, top panel).

The voxel-wise maps of connections that predicted antidepressant response (Figures 6a and 6b) suggested that this effect was more prominent for specific subgenual regions that were only partially overlapping with the predefined sgACC ROI (Figures 6c and 6d, bottom two panels). To explore this further, the ROI-based analysis was repeated *post hoc* using recent sub-classified sgACC parcels⁴¹. Stimulation site connectivity with contralateral sgACC regions revealed strong predictive value for post-treatment MADRS (right stimulation site: $\rho = 0.90$ and 0.93 , $p = 0.001$ and 0.0003 ; left stimulation site: $\rho = 0.90$ and 0.54 , $p = 0.001$ and 0.13 , respectively). Treatment efficacy was thus predictable using baseline stimulation site connectivity.

4. Discussion

Our findings suggest that individualized RSNM may be used to reliably identify rTMS targets based on their connectivity profile. We identified subject-specific rTMS targets at the networks that are likely being approximated by sgACC connectivity maps, which have previously been shown to predict efficacy of rTMS for major depression⁵. These target coordinates were stable and spatially distinct from prior approaches. Furthermore, these individualized RSNM-based targets showed stronger functional connectivity with the intended network targets than other candidate rTMS targets, even when these networks are defined conservatively based on consensus group-mean maps. Furthermore, the RSNM-based targets approximated the sgACC connectivity map more effectively than individualized targets generated using the previously-proposed anti-group mean sgACC approach. While it appears counter-intuitive that sgACC-based targets were less connected with a map generated using sgACC as a seed, this may be because the anti-group mean sgACC approach appears to generate unreliable targets. This is consistent with our hypothesis that our RSNM-based approach would identify a target that approximates the sgACC connectivity profile more effectively than a group-based sgACC seed.

Our proposed targeting approach was based on individualized mapping of DAN and DMN. The involvement of these networks in depression treatment may be related to dysfunctional interactions between externally-oriented attention-switching, which involves the DAN, and internally-oriented emotion engagement, which involves the DMN⁴². Such interactions appear to be affected in major depression⁴³ and are modulated by deep brain stimulation of the sgACC⁴⁴. This is consistent with our finding that antidepressant response was predicted by stimulation site connectivity with a large subgenual region. Treatment was also associated with changes in subgenual connectivity to itself, to the left DAN stimulation site, and to the DMN. This further suggests that our targeting approach may indirectly identify a network that modulates subgenual connectivity.

Nevertheless, our choice of DAN and anti-DMN targeting remains speculative in the absence of a head-to-head trial of antidepressant efficacy in comparison to rTMS applied to other targets. In addition, there are several existing approaches to individualized RSN mapping^{6,16,17} and we did not assess which approach (including group-level mapping) best predicts neurophysiological and clinical response. There are also several approaches to resting-state fMRI pre-processing; for instance, our use of global signal regression may affect the identification of anti-correlated networks⁴⁵. Similarly, there are several approaches to TMS-induced electric field modeling, but we chose not to use individualized finite element modeling because this method has not yet been validated for functional connectivity analyses. Careful validation of these techniques may help to further optimize our methods.

Our interpretation of treatment-induced changes are limited by small sample size. This may increase the risk of a false negative result due to lack of power or false positive results due to chance. Furthermore, we only assessed bilateral stimulation, not unilateral, and there may be complex interactions between the two stimulation sites, the significance of which is uncertain. This does not affect our reliability assessments, but does limit our ability to confirm whether the neurophysiological and clinical effects are

consistent with our hypotheses. Importantly, prospective studies comparing unilateral stimulation vs. bilateral stimulation will be required to disentangle the neurophysiological effects of the bilateral stimulation employed in this study. It is not known whether the approach to selecting a left excitatory stimulation site should be the same as the approach used to selecting a right inhibitory stimulation site, since stimulation of the two hemispheres may have different effects⁴⁶.

Further research will be required before these findings can be considered to be generalizable. This study was conducted using cutting-edge MRI scanners and recently-optimized scan protocols, so it remains unclear whether similar results can be achieved using more readily-available equipment. The patient population was also carefully selected as patients with relatively mild TBI and clear major depressive symptoms; its applicability to primary major depression or moderate/severe TBI requires further investigation.

Despite these limitations, our results support the emerging notion that variability in effects of rTMS may be related to inter-individual variability in functional topography of the DLPFC^{1,47,48}. While the clinical implications of individualized RSN-based targeting are not yet clear, this method yields targets that are consistently connected to regions that have been implicated in antidepressant response to rTMS, including the sgACC. Stimulation of these targets also appears to modulate these key regions in a manner that is related to antidepressant response. This should help to inform an alternative and possibly more rational approach to prospective individualized target selection in future rTMS studies as well as retrospective analysis of results from existing studies.

In conclusion, the use of individualized RSN mapping for identification of distinct patient-specific rTMS targets may represent a promising method for reducing variability in targeting rTMS. This lays the foundation for development of more robust approaches for personalized medicine in neuromodulation.

Declarations

Acknowledgements: We would especially like to thank the experimental participants. We thank Dr. Abraham Snyder for logistical support with implementation of individualized RSN mapping. We thank Dr. Benjamin Srivastava for assisting with clinical assessments. We thank Linda Hood for technical support with MRI equipment. We thank Drs. Sindhu Jacob and Martin Wice for referring participants. We additionally acknowledge valuable discussions with Drs. Michael Fox, Steven Petersen, Charles Conway, Eric Wasserman, Sarah Lisanby, Bruce Luber, Andrew Drysdale, Irving Reti, Vani Rao, Maurizio Corbetta, Gordon Shulman, and Abraham Snyder which led to the conception and refinement of the study design.

Funding sources:

The study protocol was funded by the McDonnell Center for Systems Neuroscience (New Resource Proposal) and the Mallinckrodt Institute of Radiology (funding for scans). SHS received fellowship support from the Sidney R. Baer Foundation. SHS received salary support from the Center for Neuroscience and Regenerative Medicine at the Uniformed Services University for Health Sciences. DLB

was an employee of Washington University at the time the study was conducted, and is now an employee of the Uniformed Services University of the Health Science, Department of Defense.

Author Contributions: SHS, DLB, ARC, and NTT designed the clinical protocol. ARC provided rTMS expertise and equipment as well as functional connectivity expertise. CDH provided expertise and novel analytical scripts for individualized RSN mapping and functional connectivity analysis. ECL provided expertise for clinical implementation of RSN mapping techniques. SK provided expertise and developed scripts for functional connectivity processing. SHS coordinated the study, recruited subjects, administered treatments, processed MRI data, conducted functional connectivity analyses, and conducted all statistical analyses. NTT and CDH also administered study treatments. SHS, and NTT acquired MRI scans and conducted clinical assessments. SHS, DLB, and ARC wrote the manuscript with intellectual contributions from all authors.

Conflicts of interest:

SHS serves as a scientific consultant for Magnus Medical and a clinical consultant for Kaizen Brain Center. SHS has received research support from Neuronetics Inc. The present work was not supported by any of these entities.

DLB has served as a consultant for Pfizer Inc, Intellectual Ventures, Signum Nutralogix, Kypha Inc, Sage Therapeutics, iPerian Inc, Navigant, Avid Radiopharmaceuticals (Eli Lilly & Co), the St Louis County Public Defender, the United States Attorney's Office, the St Louis County Medical Examiner, GLG, Stemmedica, and Luna Innovations. DLB holds equity in the company Inner Cosmos. DLB receives royalties from sales of Concussion Care Manual (Oxford University Press). No conflicts of interest with the presented work. DLB is an employee of the Department of Defense; the views expressed here do not reflect those of the Uniformed Services University of the Health Sciences, the US Department of Defense, or the US Government.

ECL holds equity in the companies Neurolutions and Inner Cosmos.

CDH, ECL, and SHS hold intellectual property related to the use of RSNM to target TMS.

The remaining authors report no conflicts of interest.

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Figures

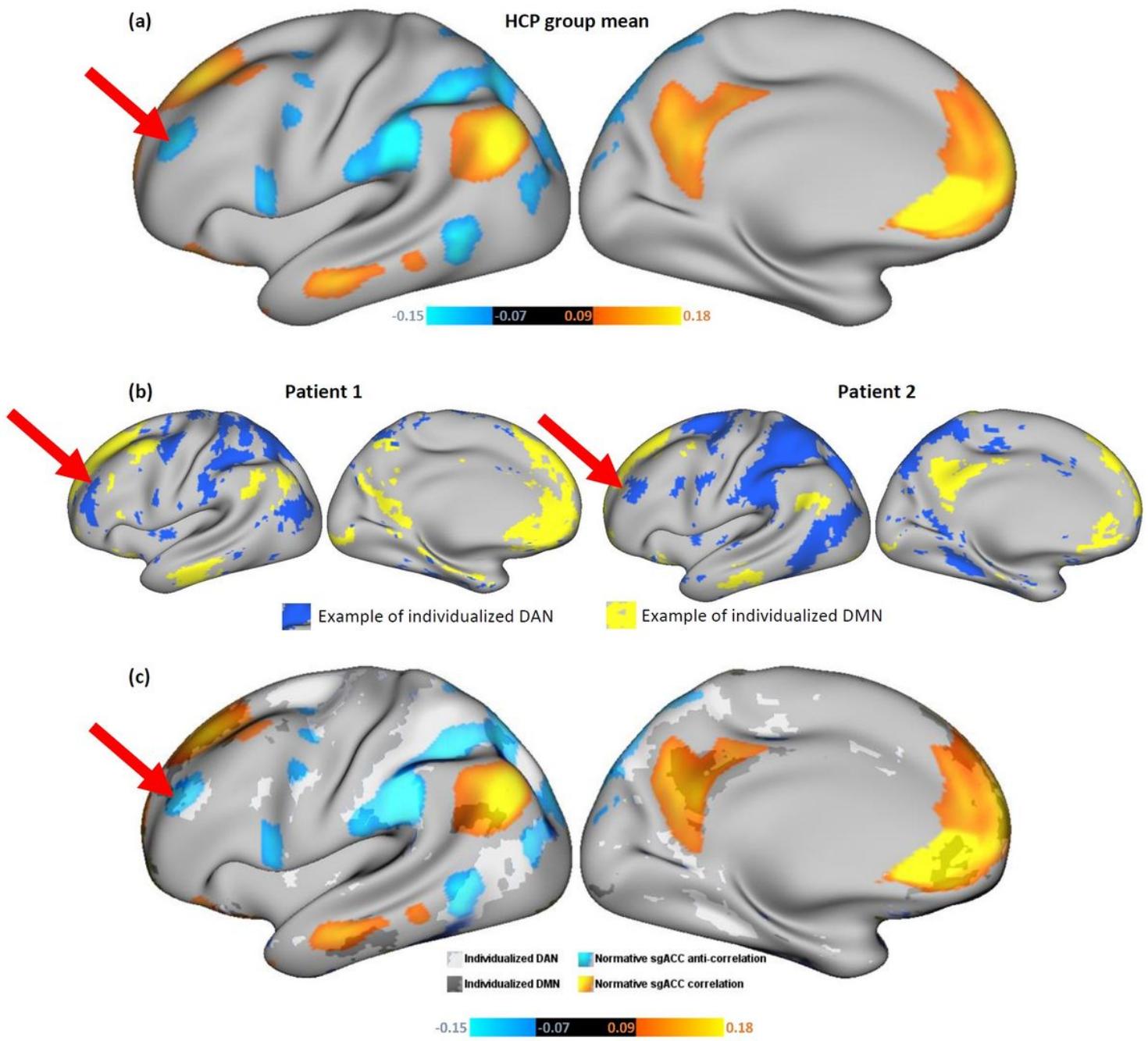


Figure 1

(a) Normative map of sgACC functional connectivity, indicating strongest areas of correlation (orange-yellow), and anti-correlation (blue). Strong normative sgACC anti-correlation is prominent at a DLPFC site (red arrow) which has previously been shown to be an effective rTMS target in major depression^{4,5}. (b) Individualized winner-take-all maps of DAN (blue) and DMN (yellow) for two representative example subjects. Red arrows depict the group-mean stimulation site, which shows differing spatial relationships with DAN in the two patients (c) Example of overlap between individualized RSNm DAN/DMN maps (from patient 2) and normative sgACC seed map.

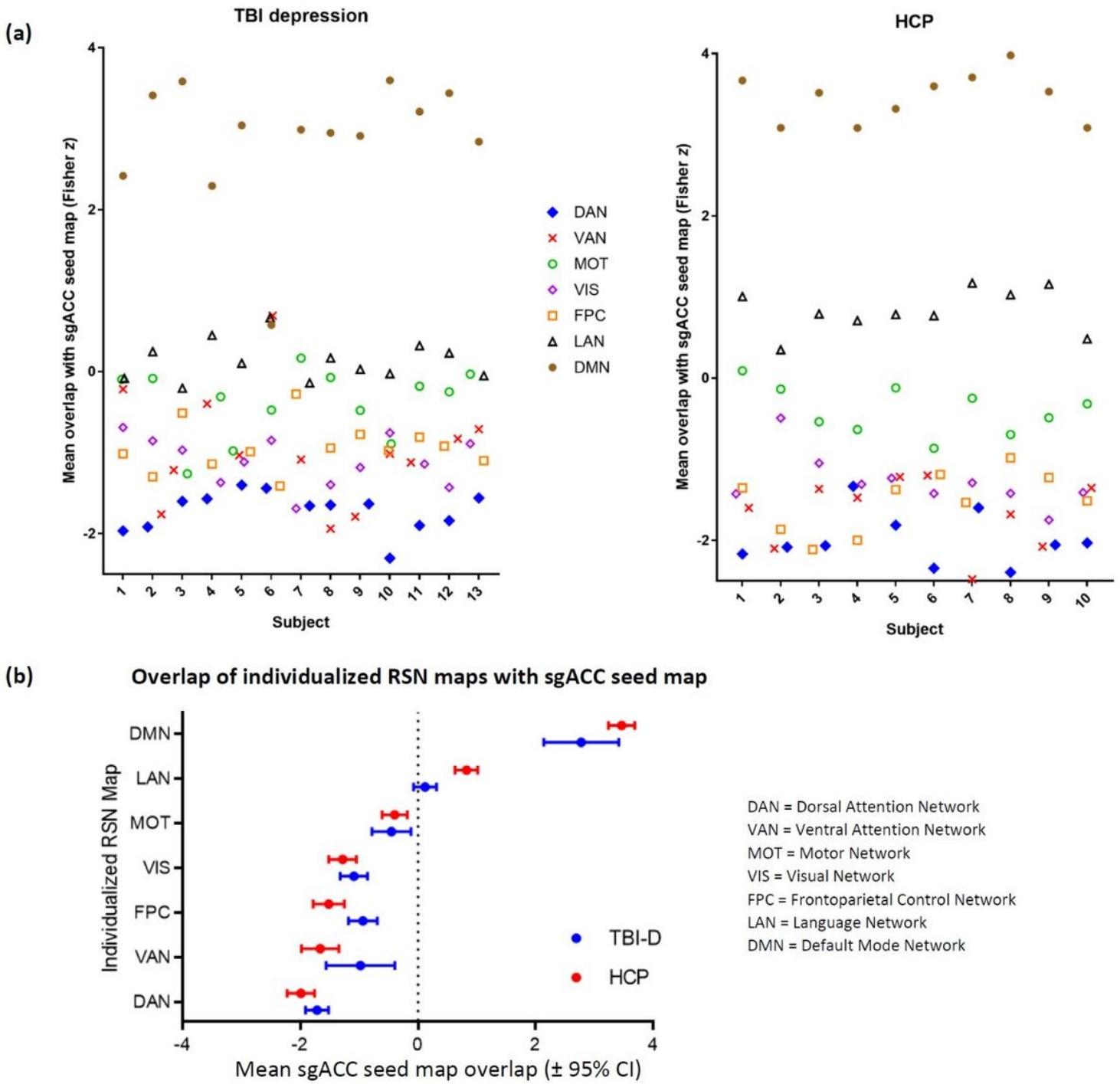


Figure 2

- (a) Individualized similarity between each RSN and the normative sgACC seed map at baseline. The group-mean sgACC seed map positive correlations overlapped more with DMN and the anti-correlations overlapped more with DAN than any other individualized RSN map for the majority of individual subjects.
- (b) Mean similarity between individualized RSNs and the normative sgACC seed map. DMN was the only network showing strong overlap with the positive correlations in the sgACC seed map. Several RSNs showed notable overlap with the anti-correlations in the sgACC seed map.

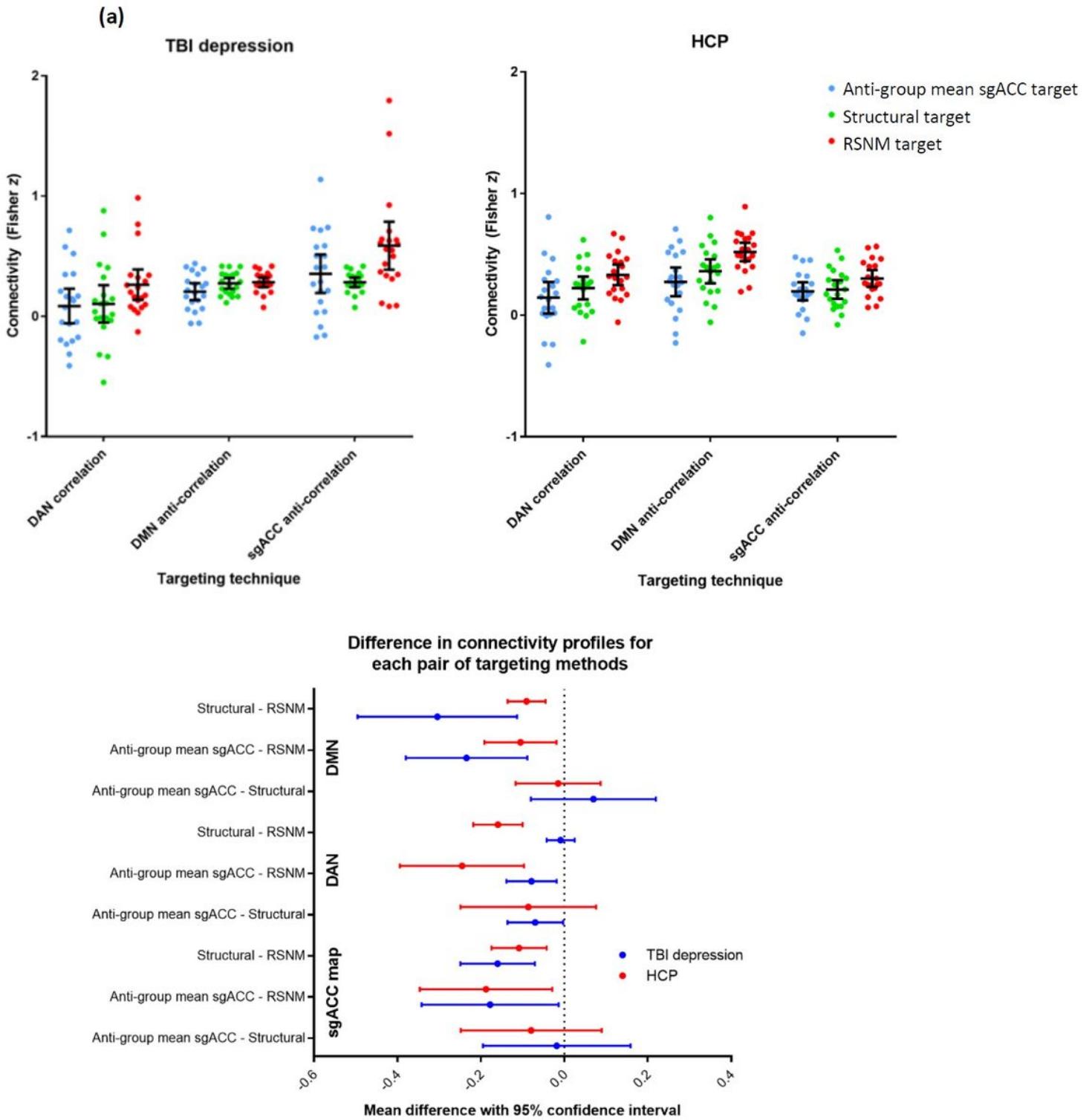


Figure 3

Functional connectivity of targets yielded by the three approaches. (a) Functional connectivity of RSNM, anti-group mean sgACC, and structural targets with DAN, DMN, and the normative sgACC connectivity map in each group. (b) Differences in connectivity profiles between the three potential targeting methods. On most metrics, RSNM targets showed significantly stronger connectivity with all three regions of interest.

(a)

Distance between targets: Mean (mm), 95% CI	TBI depression	Healthy controls
RSNM to Structural	9.4 (7.5 – 11.4)	6.6 (4.9 – 8.2)
RSNM to Anti-group mean sgACC	13.5 (10.9 – 16.2)	16.9 (15.6 – 19.2)
Anti-group mean sgACC to Structural	15.4 (12.5 – 18.2)	17.1 (14.7 – 19.5)

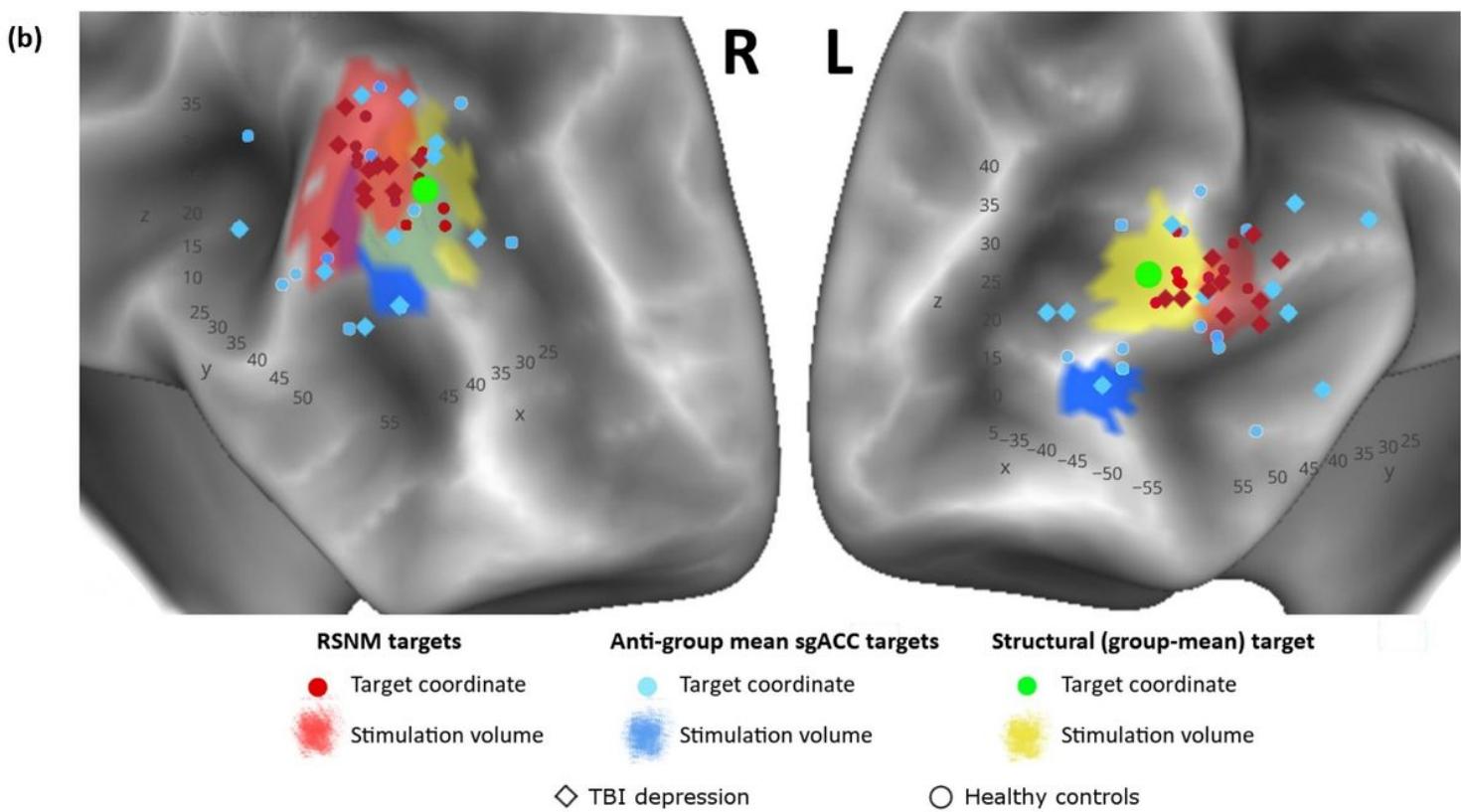


Figure 4

Anatomical distributions of targets yielded by the three approaches. Targets are displayed on a 3D surface rendering to facilitate visual comparison; the analyses were conducted in volume space. (a) Mean and 95% confidence interval for the Euclidean distance between target coordinates generated by the different methods. (b) 3D scatter plot of the target sites generated by the different methods to illustrate approximate spatial distribution of targets. Background is a representative example of a single-subject surface reconstruction with approximate predicted stimulation volumes in that subject (in the TBI depression group). These approximate stimulation volumes are cortical surface projections of the estimated 15-mm sphere centered at the stimulation site for that subject; shapes are asymmetric and irregular due to normal variation in cortical surface anatomy. Across all subjects and in this representative example, RSNM-based actual stimulation sites were different from the structural group-mean site (green dot).

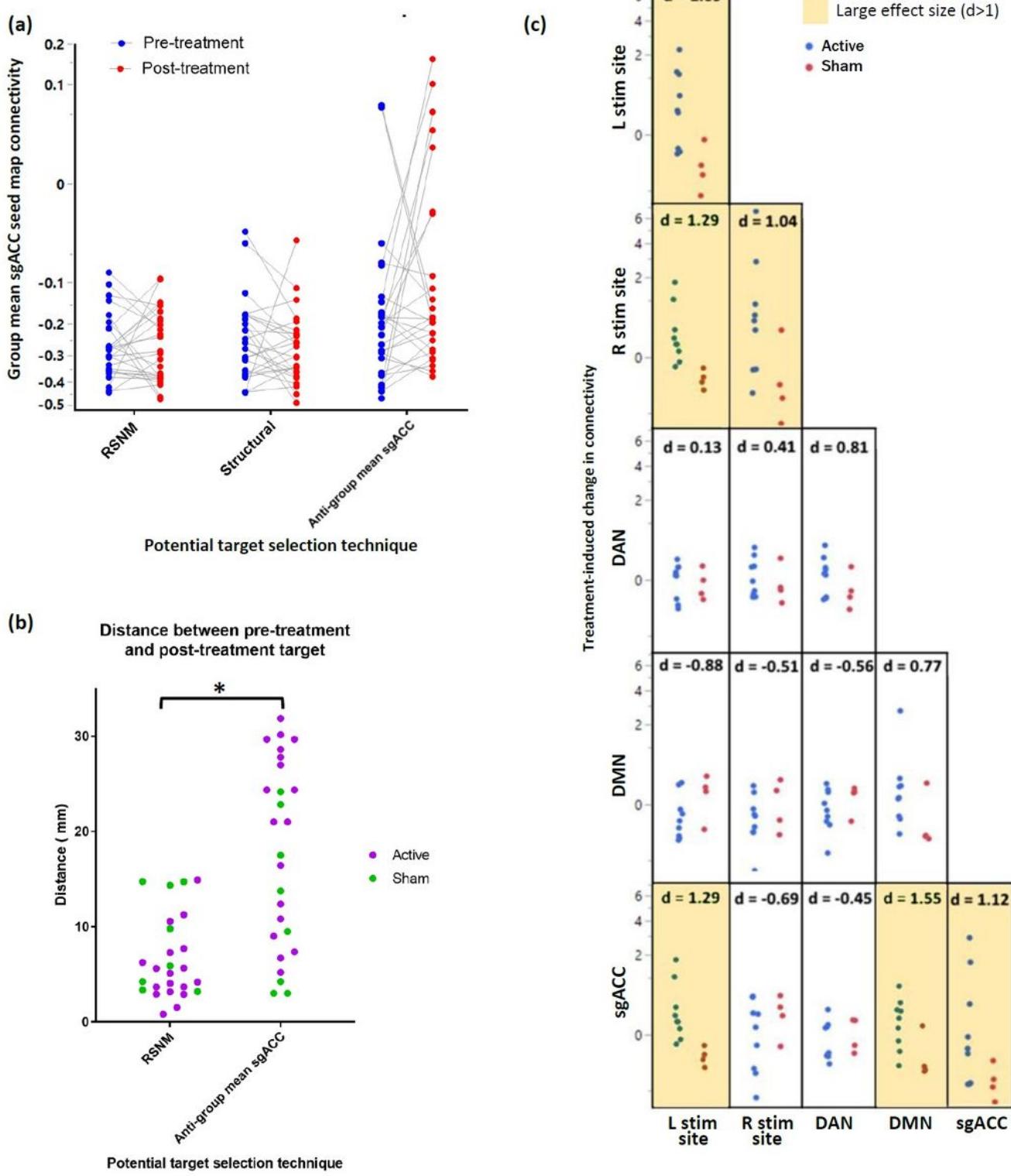


Figure 5

(a) Change in connectivity profile of left- and right-sided potential targets identified based on pre-treatment and post-treatment scans. Group mean sgACC seed map connectivity remained relatively stable for RSNM targets and structural targets but was more unstable for the potential anti-group mean sgACC targets. Each symbol represents 1 target; there were 2 targets per subject (right and left) x 13 subjects who underwent either active or sham rTMS treatment. (b) Spatial change in target coordinates

between pre-treatment and post-treatment scans. After a course of RSNM-targeted treatment, the location of the potential anti-group mean sgACC target sites changed significantly more than the location of RSNM-based target sites ($p < 0.0001$, Wilcoxon matched-pairs signed-rank test). (c) Treatment-induced change in connectivity within and between a priori ROIs. Active treatment was associated with connectivity changes within and between stimulation sites, sgACC, DAN, and DMN. Magnitude of change is quantified using Cohen's d (adapted with permission from Siddiqi et al, J Neurotrauma 2019).

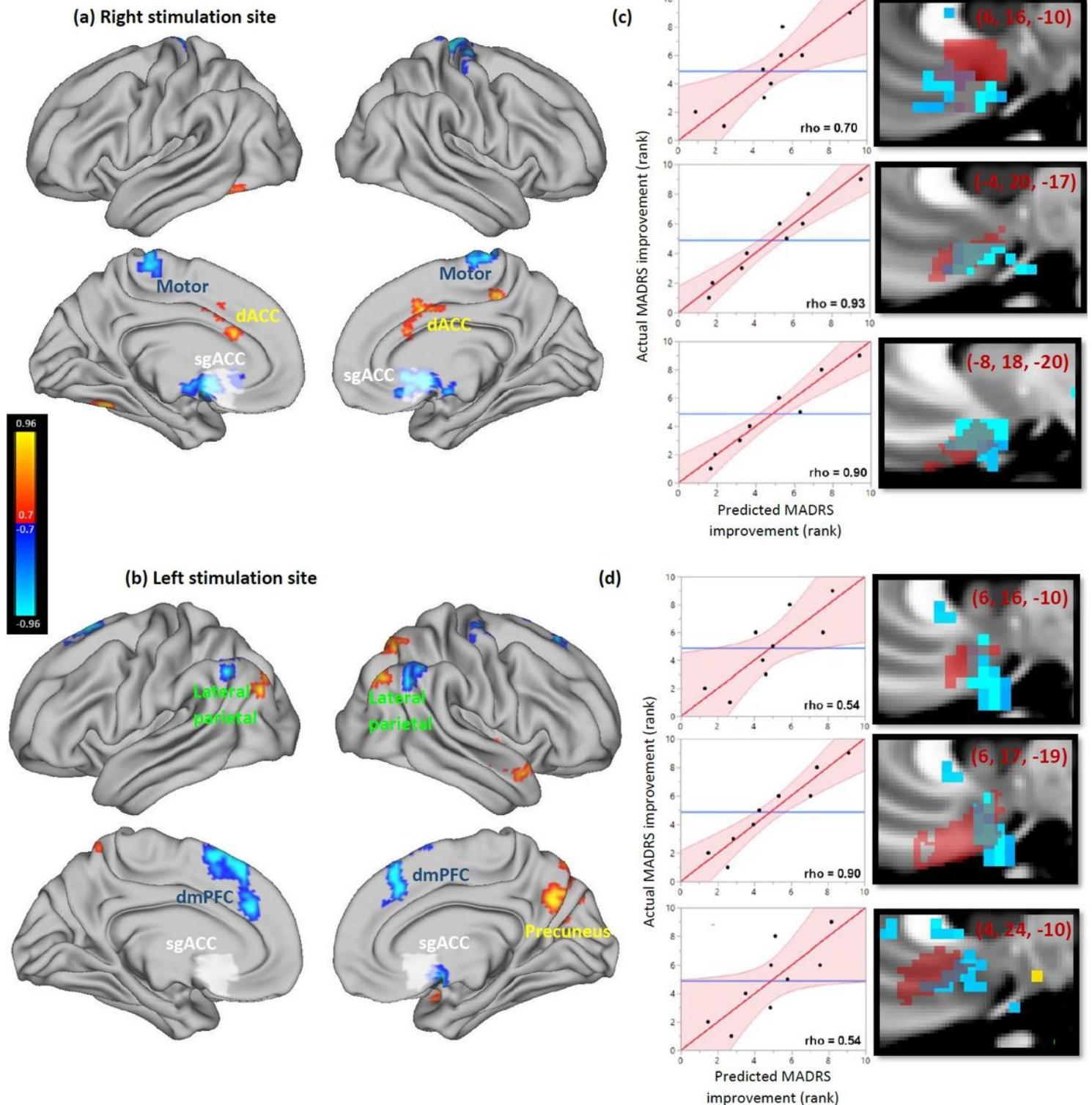


Figure 6

Connectivity profile associated with increased antidepressant efficacy of stimulation sites. White regions depict the a priori subgenual ROI. Clusters detected with threshold of $r > 0.8$ (uncorrected $p < 0.001$), minimum extent of 729 mm³, and cluster significance defined at $p < 0.05$. (a) Antidepressant response was significantly predicted by right stimulation site anti-correlation with bilateral sgACC, anti-correlation with motor cortex, and positive correlation with dorsal ACC (corrected $p < 0.05$). (b) Antidepressant response was significantly predicted by left stimulation site correlation with right precuneus and anti-correlation with right sgACC, bilateral lateral parietal lobe, and bilateral dorsomedial prefrontal cortex (corrected $p < 0.05$). (c-d) Antidepressant response was inversely related to seed-based connectivity of both stimulation sites with contralateral subgenual regions defined by a more recent cortical parcellation. Left panels depict the relationship between predicted and actual MADRS improvement, while right panels depict the overlap between the corresponding ROI (red) and the voxels whose stimulation site anti-correlation predicts MADRS improvement (blue). MNI coordinates of the center of each ROI are reported in maroon. (c) Right stimulation site connectivity with the a priori subgenual ROI (predicted MADRS change) was significantly predictive of antidepressant response ($\rho = 0.70$, $p = 0.035$). This relationship was stronger when using exploratory subgenual ROIs based on a more recent cortical parcellation ($\rho = 0.90$ and 0.93 , $p = 0.0009$ and 0.0003). (d) Left stimulation site connectivity with the a priori subgenual ROI (predicted MADRS change) appeared to predict antidepressant response, but this relationship did not reach significance ($\rho = 0.54$, $p = 0.13$). One of the two exploratory subgenual ROIs was significantly predictive of antidepressant response ($\rho = 0.90$, $p = 0.0009$).

Supplementary Files

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