Links between atypical local and long-distance connectivity in autism

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PARTICIPANTS

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39 typically developing (TD) and 39 participants with ASD Matched on age, nonverbal IQ, and average head motion (RMSD)

Group		Sex	Handedness	Age M(SD) Range	Nonverbal IQ M(SD) Range	RMSD M(SD) Range
ASD	39	6 female	7 left	14.1 (2.5) 9.2-17.9	107.1 (13.6) 80-136	.065 (.034) .018148
TD	39	7 female	5 left	14.0 (2.2) 9.6-17.8	107 (13.7) 62-129	.065 (.038) .017168
				p = .821	p = .990	p = .980

DATA ACQUISITION

A 6:10 minutes resting-state scan was acquired on a GE 3T MR750 scanner (TR: 2000ms; TE: 30ms; 3.4mm isotropic voxels).

- DATA PREPROCESSING
 Motion, slice-time, and field-map correction
 Co-registration of functional to anatomical images
- Standardization to MNI space

- Statial smoothing to Gmm FWHM Bandpass filtering (.008 < f < .08 Hz) Removal of nuisance regressors (6 rigid-body motion, signal from white matter, ventricular matter, and derivatives) Analysis conducted with global signal regression (GSR) Time points with motion >.5mm (and following 2 time points) were censored Participants with \geq 150 time points remaining were selected

METHODS

to 1

1. DATA ANALYSIS: Local Connectivity (ReHo)

- **Regional homogeneity (ReHo)** uses Kendall's coefficient of concordance (KCC) to assess homogeneity of a given center voxel and its neighboring voxels. Within a given cluster of voxels, KCC is equal to the parameter *W* (ranging from 0
 - $W = \sum_{i}^{\infty} (R_i)^2 n(\overline{R})^2$

$$\frac{1}{12}K^2(n^3-n)$$

- Individual voxel-wise ReHo maps were obtained and were standardized to KCC-ReHo z-values.
- Group differences examined with a two-sample t-test
- Monte-Carlo simulation applied to correct for multiple comparisons

2. DATA ANALYSIS: Long-Distance Connectivity

- Significant clusters from between-group t-test (comparing ReHo KCC) were used to create seeds for whole brain (long-distance) fcMRI analyses.
- A large significant ReHo overconnectivity cluster in posterior regions was split into 3 equal parts (dorsal, middle (pericalcarine), and ventral), based on z-
- coordinates, and whole brain analyses were run separately for each seed. Mean time series were extracted from each seed and were correlated with voxel time courses across the brain in each participant . Fisher's r-to-z' transformation was conducted to transform these correlation
- coefficients to normally distributed values for subsequent t-tests. Statistical maps were cluster-corrected at p < .05.

REFERENCES

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