

Heritability of functional connectivity in the Mexican population

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Objective

The aim of this study is to estimate the heritability of brain functional connectivity in a sample of Mexican twins.

Methods

We acquired 300 EPI volumes (the first 5 previous volumes were discarded) of T2*w BOLD contrast images (TR:2000 ms, TE:15 ms, 3.2 x 3.2 x 3.2 mm³) during an eyes-open resting state in 204 twins (72 MZ and 31 DZ; 167 women; 31.8±9.5 years of age). These were preprocessed with fMRIPrep (slice timing correction, distortion correction, motion correction, bias field correction, and registered to the MNI152NLin6Asym space) and xcp_d (bandpass filter 0.01-0.1 Hz, despiking, scrubbing volumes with a frame-wise displacement higher than .25 mm, regression of 6 motion parameters and their derivatives, 5 principal components of white matter and cerebrospinal fluid, scanner drift, the mean global signal, and an intercept for a total of 25 parameters). Then, the mean signal from 333 regions of the Gordon atlas was extracted, correlated, fisher transformed, and the average functional connectivity within regions of 10 previously described networks (Left and Right Fronto-parietal, Default, Salience, Ventral Attention, Dorsal Attention, Cingulo-opercular, Retrosplenial-Temporal, Somato-motor, and Auditory).

An ACE and AE model were used to estimate the heritability (h^2), and the effect of shared environment (C) on the functional connectivity of these networks. The AE model was chosen when its AIC was lower than the AIC of the ACE model. 95% confidence intervals were calculated to test the significance of these estimates.

Results

The following networks showed significant heritability: Salience ($h^2=.32$, 95%CI=.09-.5), Left Fronto-Parietal ($h^2=.28$, 95%CI=.05-.48), Auditory ($h^2=.40$, 95%CI=.19-.52), and Somato-Motor ($h^2=.48$, 95%CI=.30-.62). Additionally, the Default mode network showed a significant effect of shared environment (C=.45, 95%CI=.28-.59).

Conclusions

The variance in the functional connectivity of some brain networks is explained by additive genetic factors.