A Common Polymorphism in a Williams Syndrome Gene Predicts Amygdala Reactivity and Extraversion in Healthy Adults

Supplement 1

Supplementary Analyses

Proxy SNP rs6964833

We examined whether results obtained using imputed genotype data were maintained when using a proxy SNP (rs6964833) that was genotyped in a subset of the sample (n = 617). Similar to results for imputed genotype rs13227433, the proxy SNP rs6964833 predicted left threat-related amygdala reactivity, B = -.08, SE = .03, Beta = -.23, p = .013 and marginally predicted right threat-related amygdala reactivity, B = -.05, SE = .03, Beta = -.18, p = .056. This therefore increases our confidence in results based on the imputed genotype.

Genotype Grouping

Due to the small number of minor C allele homozygotes in the sample (Caucasian = 22, African American n = 2, Asian n = 3), we grouped these individuals with heterozygotes. To test whether this assumed dominant model reflected our data, we examined whether A allele homozygotes and/or C allele homozygotes differed from heterozygotes. Consistent with our genotype coding model, there was a significant difference in threat-related left amygdala reactivity between the CA and AA groups (B = -.09, SE = .04, p = .013), but not between the CA and CC groups (B = .05, SE = .09, p = .557). A similar, albeit trending pattern was observed with the right amygdala model (CA vs. AA, p = .072; CA vs. CC, p = .381).

Results Within Racial Sub-groups

To examine whether results held across racial sub-groups, we ran analyses reported in the main text within each group individually. Results were in the same direction for each group, but as expected, significance levels were reduced due to the reduction in sample size. Results for the effect of rs13227433 on left amygdala reactivity for each subgroup were as follows: Caucasian, B = -.11, SE = .04, Beta = -.27, p = .012; African American, B = -.14, SE = .08, Beta = -.44, p = .100; Asian, B = -.06, SE = .07, Beta = -.17, p = .408. Results for the right amygdala were similar: Caucasian, B = -.07, SE = .03, Beta = -.21, p = .050; African American, B = -.03, SE = .08, Beta = -.12, p = .676; Asian, B = -.05, SE = .06, Beta = -.16, p = .385. In addition, constraining parameter estimates to be equal across the three groups did not result in a significant reduction in model fit for the left amygdala, $\Delta\chi^2(2) = .53$, p = .767, or right amygdala, $\Delta\chi^2(2) = .21$, p = .900, indicating there were no significant differences in parameter estimates for the effect of genotype across the 3 racial sub-groups.

Table S1. Counts of past and current psychiatric diagnoses

Diagnosis	Count
Major depressive disorder	39
Bipolar disorder I or II	7
Bipolar disorder – Not otherwise specified	13
Hypomanic episode	5
Panic disorder	10
Agoraphobia	10
Social anxiety disorder	8
Generalized anxiety disorder	15
Obsessive compulsive disorder	10
Posttraumatic stress disorder	1
Alcohol abuse/dependence	86
Marijuana abuse/dependence	34
Eating disorder	5
Antisocial personality disorder	1
Borderline personality disorder	2

Some participants have multiple comorbid diagnoses, thus counts of individual diagnoses total higher than the number of participants with any psychiatric diagnosis (n = 157).

Table S2. Regression results

	B	SE	*p*-value
Gene to brain: rs13227433 genotype predicting left amygdala reactivity			
rs13227433	-.10	.03	.005
Age	-.01	.01	.468
Diagnosis	-.01	.03	.688
Sex	-.03	.03	.358
MDS 1	.003	.003	.382
MDS 2	.002	.002	.345
MDS 3	.001	.01	.865
MDS 4	.008	.03	.801
Brain to behavior: Left amygdala reactivity predicting extraversion			
Women			
Left amygdala reactivity	-5.59	2.73	.041
Age	-1.06	.68	.121
Diagnosis	4.34	2.29	.058
STAI Trait anxiety	-.79	.11	<.001
Men			
Left amygdala reactivity	1.66	2.44	.498
Age	-.17	.78	.831
Diagnosis	1.40	2.48	.573
STAI Trait Anxiety	-.81	.11	<.001

MDS, multidimensional scaling components; STAI, State Trait Anxiety Inventory.