

# Amygdala Function and 5-HTT Gene Variants in Adolescent Anxiety and Major Depressive Disorder

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**Background:** Associations between a functional polymorphism in the serotonin transporter gene and amygdala activation have been found in healthy, depressed, and anxious adults. This study explored these gene–brain associations in adolescents by examining predictive effects of serotonin transporter gene variants (S and L<sub>G</sub> allele carriers vs. L<sub>A</sub> allele homozygotes) and their interaction with diagnosis (healthy vs. patients) on amygdala responses to emotional faces.

**Methods:** Functional magnetic resonance data were collected from 33 healthy adolescents (mean age: 13.71, 55% female) and 31 medication-free adolescents with current anxiety or depressive disorders (or both; mean age: 13.58, 56% female) while viewing fearful, angry, happy, and neutral facial expressions under varying attention states.

**Results:** A significant three-way genotype-by-diagnosis-by-face-emotion interaction characterized right amygdala activity while subjects monitored internal fear levels. This interaction was decomposed to map differential gene–brain associations in healthy and affected adolescents. First, consistent with healthy adult data, healthy adolescents with at least one copy of the S or L<sub>G</sub> allele showed stronger amygdala responses to fearful faces than healthy adolescents without these alleles. Second, patients with two copies of the L<sub>A</sub> allele exhibited greater amygdala responses to fearful faces relative to patients with S or L<sub>G</sub> alleles. Third, although weaker, genotype differences on amygdala responses in patients extended to happy faces. All effects were restricted to the fear-monitoring attention state.

**Conclusions:** S/L<sub>G</sub> alleles in healthy adolescents, as in healthy adults, predict enhanced amygdala activation to fearful faces. Contrary findings of increased activation in patients with L<sub>A</sub>L<sub>A</sub> relative to the S or L<sub>G</sub> alleles require further exploration.

**Key Words:** Adolescence, amygdala, anxiety, depression, emotional faces, serotonin transporter gene polymorphism

Adolescent anxiety and mood disorders strongly predict adult anxiety and mood disorders (1–2), possibly through genetic influences on brain circuitry development (3). Although relationships between genetic variation and brain function characterize healthy and disordered adults (4), these have not been studied in adolescents. Assessing gene–brain relationships in youth may elucidate early risk mechanisms for these disorders.

Similar to adults, anxious and depressed adolescents exhibit signs of enhanced amygdala responsivity (5–10). These anomalies emerge when attention is focused on internal fear evaluation (7) to fearful faces (5–7), occasionally extending to angry or happy faces as well (9–10).

A variable repeat sequence polymorphism in the promoter region of the serotonin transporter (5-HTT) gene (SLC6A4) has been implicated in anxiety and depression (11). This variant involves short (S) and long (L) alleles with a recently discovered single nucleotide polymorphism (A-G substitution) within the L allele generating L<sub>A</sub> and L<sub>G</sub> alleles (12). Adult carriers of L<sub>G</sub> and

S alleles show lower levels of 5-HTT than L<sub>A</sub>-allele homozygotes (12), findings attributed to differential 5-HTT expression among allelic variants, but with mixed support (13). Nevertheless, with varying consistency, adult S-(and L<sub>G</sub>-)allele carriers report greater anxiety, depression, neuroticism, and harm avoidance (14,15). Conflicting results characterize younger samples. Although two studies found greater emotionality and shyness among S-allele carriers (16,17), others show these effects for L-allele carriers (18,19). Still others report associations only under certain environmental contexts (20–23).

Inconsistent gene–behavior associations reinforce the need to identify intermediate phenotypes, such as brain function. Among healthy and affected adults, S-(and L<sub>G</sub>-)allele carriers manifest greater amygdala activation to emotional stimuli than L-allele homozygotes (4,24–28). Here, we extend this work to adolescents by exploring effects of 5-HTT genotypes, diagnosis, and their interaction on amygdala responses to fearful faces during internal fear evaluation.

## Methods and Materials

### Participants

Thirty-one unmedicated adolescents with a current anxiety disorder, or major depressive disorder (MDD), or both and 33 psychiatrically healthy adolescents were recruited through community health practitioners and advertisements (Table 1). Data from 6 patients and 18 healthy adolescents have been presented previously (7,29). Patients with anxiety or MDD were combined based on evidence implicating 5-HTT allelic variants in risk for both (11). Excluding MDD-only patients showed no overall change in results.

Patients and healthy subjects did not differ on age [ $t(62) = .25, p = .80$ ], sex [ $\chi^2 = .08, p = .77$ ], IQ [ $t(60) = .15, p = .88$ ], or SES [ $t(55) = 1.66, p = .10$ ]. Nor were there differences in ethnic

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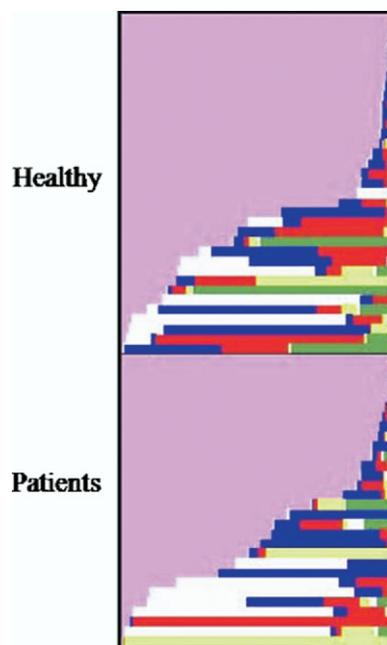
ancestry factor scores between groups [ $t_s < 1.42$ ,  $p_s = ns$ ] or between genotypes within groups [ $t_s < 1.67$ ,  $p_s = ns$ ]. These scores were produced from a seven-factor solution of 186 ancestry-informative markers that differentiate continental and certain subcontinental populations (30). Ancestry distributions of individuals in each group are presented in Figure 1.

The Kiddie Schizophrenia and Affective Disorders Schedule—Present and Lifetime Version (31) psychiatric interview was used to assign diagnoses. Of 18 anxiety-only patients, 12, 5, and 1 individuals met full criteria for one, two, and three current anxiety diagnoses, respectively; 5 patients received comorbid attention-deficit/hyperactivity disorder (ADHD) or oppositional defiant disorder diagnoses. Four patients met criteria for a past anxiety disorder, and two met criteria for prior alcohol abuse and ADHD. Other inclusion criteria comprised clinically significant symptoms for patients indexed by scores on the Pediatric Anxiety Rating Scale ( $\geq 10$ ), the Children's Depression Rating Scale ( $\geq 13$ ), and the Child Global Assessment Scale ( $< 60$ ). Exclusion criteria were current Tourette's syndrome, obsessive-compulsive

**Table 1.** Demographic, Diagnostic and Genotypic Characteristics of Healthy Subjects and Patients

	Healthy ( <i>n</i> = 33)	Patient ( <i>n</i> = 31)
<b>Demographics</b>		
Age, Mean (SD)	13.71 (2.73)	13.52 (2.32)
Males, <i>n</i> (%)	15 (46)	13 (42)
IQ, Mean (SD)	111.00 (14.62)	110.97 (17.06)
SES, Mean (SD)	52.58 (21.17)	43.42 (20.31)
<b>Ethnic Ancestry Factor Scores</b>		
Europe	.60 (.38)	.60 (.36)
Middle East	.11 (.18)	.11 (.16)
Africa	.09 (.20)	.13 (.26)
Central Asia	.10 (.16)	.07 (.18)
America	.06 (.16)	.02 (.04)
Far East Asia	.03 (.09)	.07 (.20)
Oceania	.01 (.01)	.01 (.01)
<b>Current DSM-IV Diagnoses, <i>n</i> (%)</b>		
Anxiety Disorder		25 (81)
Generalized Anxiety Disorder		15 (48)
Social Phobia		14 (45)
Separation Anxiety Disorder		5 (16)
Generalized Anxiety Disorder Only		6 (19)
Social Phobia Only		7 (23)
Separation Anxiety Disorder Only		2 (6)
Major Depressive Disorder		13 (42)
Major Depressive Disorder Only		6 (19)
<b>Genotype, <i>n</i> (Mean age, % males)</b>		
L <sub>A</sub> L <sub>A</sub>	9 (14.03, 33%)	5 (14.72, 20%)
L <sub>A</sub> L <sub>G</sub>	3 (13.25, 67%)	3 (13.97, 33%)
SL <sub>A</sub>	16 (13.51, 56%)	14 (13.44, 57%)
SS	4 (14.83, 25%)	8 (12.99, 38%)
SL <sub>G</sub>	1 (9.83, 0%)	1 (11.50, 0%)
L <sub>G</sub> L <sub>G</sub>	0	0
<b>Final Genotype Groups, <i>n</i> (%)</b>		
L <sub>A</sub> L <sub>A</sub>	9 (27)	5 (16)
L <sub>A</sub> L <sub>G</sub> /SL <sub>A</sub>	19 (58)	17 (55)
SL <sub>G</sub> /SS	5 (15)	9 (28)

L, long allele; S, short allele; SES, socioeconomic status.



**Figure 1.** Ancestry distributions across individuals in healthy and patient groups. Pink, Europe; blue, Middle East; white, Africa; red, Central Asia; green, America; yellow, Far East Asia; purple, Oceania. See journal Web site for full-color version of Figure 1.

disorder, or conduct disorder; recent exposure to trauma;<sup>1</sup> current use of any psychoactive substance;<sup>2</sup> suicidal ideation; lifetime history of mania, psychosis, or pervasive developmental disorder; and IQ  $< 70$ . The study was approved by the National Institute of Mental Health (NIMH) Institutional Review Board. All participants/parents provided written informed assent/consent. Treatment began 3 weeks after research participation.

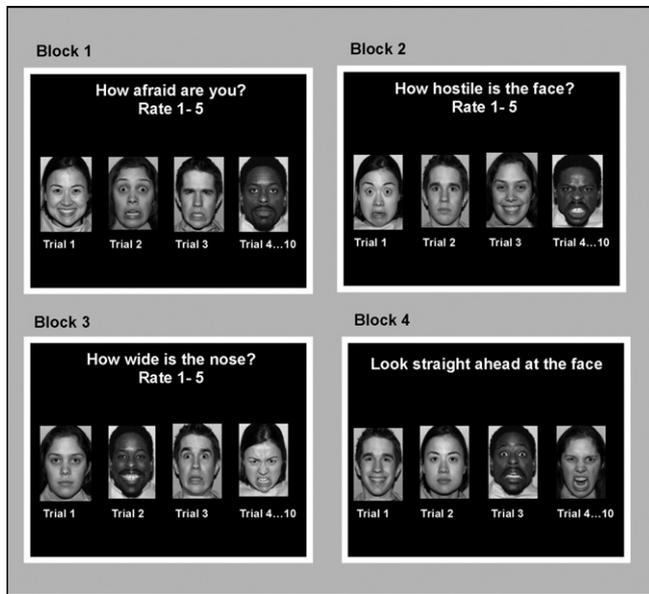
### Genotyping

DNA extraction, genotyping, and polymerase chain reaction conditions followed published protocols (12). Stage 1 genotyping distinguished short from long alleles using an allele-discriminating probe hybridized once to the 43-bp L-insertion and an internal control probe hybridized to a sequence located within the same amplicon but specific to a divergent repeat in the amplicon not involved in insertion/deletion. The L-amplicon was 182 bp, and the S-amplicon was 138 bp. Stage 2 genotyping distinguished L<sub>A</sub> from L<sub>G</sub> alleles using fluorogenic probes designed specifically for these alleles. These were labeled at the 5' end with either FAM or VIC. Genotypes were generated using ABI PRISM 7700 Sequence Detection system software (Applied Biosystems, Foster City, California). Twenty percent of the sample was genotyped twice, revealing error rates of  $< .005$  and completion rates of  $> .95$ .

Allelic frequencies for S, L<sub>A</sub>, and L<sub>G</sub> across the sample were 56 (43%), 66 (51%), and 8 (6%) respectively. Subjects belonged to one of six genotype groups (Table 1), but were assigned to three groups on the basis of functional similarity of S and L<sub>G</sub> alleles (12): L<sub>A</sub>L<sub>A</sub>, SL<sub>A</sub>/L<sub>A</sub>L<sub>G</sub>, and SS/SL<sub>G</sub>/L<sub>G</sub>L<sub>G</sub>. No differences in genotypic distribution across patients and healthy subjects emerged

<sup>1</sup>Definitions of trauma followed DSM-IV criteria for posttraumatic stress disorder, as having experienced, witnessed, or been confronted by an event or events that involved actual or threatened death or serious injury or a threat to the physical integrity of self or others.

<sup>2</sup>Medication and/or recreational drugs.



**Figure 2.** Face-processing paradigm presented during functional magnetic resonance acquisition to all subjects. The paradigm consists of four tasks (afraid, nose width and hostility ratings, and passive viewing) across 160 trials. Reprinted with permission from (37).

$\chi^2 = 2.34, p = .31$ ). Prior studies (4) and modest sample sizes warranted further grouping individuals as  $L_A L_A$  homozygotes and  $S/L_G$  carriers.

### Face-Emotion Paradigm

Procedures and stimuli have been described previously (7–9,29,32–34). Four epochs of 40 trials were presented (Figure 2): 32 trials showed different face emotions (eight fearful, eight angry, eight happy, eight neutral), and eight trials contained a fixation point. These 40 trials were divided into four blocks of 10 trials, in which eight faces and two fixation trials were presented in random order. In each block, participants completed one of four tasks that varied in attentional focus: rated subjective fear level to the face, rated the nose width on each face, rated the level of threat of each face, or passively viewed the face. Order of blocks was randomized across participants. Each block began with instructions (3000 msec) followed by 10 trials (4000 msec/trial). Intertrial intervals ranged from 750 to 1250 msec. Grayscale face stimuli were from three sources (35–37). Stimuli were displayed with Avotec Silent Vision Glasses (Stuart, Florida). Ratings and reaction times (RT) were recorded with a five-key button box (MRI Devices Corporation, Waukesha, Wisconsin).

### Magnetic Resonance Imaging Data Acquisition and Processing

Whole-brain blood oxygen level-dependent (BOLD) functional magnetic resonance imaging (fMRI) data were acquired on a General Electric (Waukesha, Wisconsin) Signa 3-T scanner. Following sagittal localization and manual shimming, functional T2\*-weighted images were acquired using an echo-planar single-shot gradient echo pulse sequence with matrix size of  $64 \times 64$ , repetition time (TR) of 2000 msec, echo time (TE) of 40 msec, field of view (FOV) of 240 mm, and voxels of  $3.75 \times 3.75 \times 5.0$  mm. Images were acquired in 23 contiguous axial slices per brain volume positioned parallel to the anterior commissure–posterior commissure line. Functional data were gathered in a single 14-min run. A high-resolution T1-weighted anatomic image was

acquired to aid spatial normalization. A standardized magnetization-prepared gradient echo sequence (180 1-mm sagittal slices, FOV = 256, number of excitations = 1, TR = 11.4 msec, TE = 4.4 msec, matrix =  $256 \times 256$ , time to inversion = 300 msec, bandwidth = 130 Hz/pixel, 33 kHz/256 pixels) was used.

Reconstructed fMRI images were examined for excessive motion ( $> 3$  mm in any plane) using MedX (Medical Numerics, Sterling, Virginia). Subsequent processing used SPM99 (University College, London, United Kingdom) and Matlab6 (Mathworks, Natick, Massachusetts). Functional data were corrected for slice timing and motion, coregistered to anatomic data, spatially normalized to a Montreal Neurologic Institute (MNI) T1-weighted template image, and resliced to 2-mm isotropic voxels. After inspecting images, event-related response amplitudes at the individual subject level for every face emotion were estimated in each attention task using the General Linear Model. Dividing each contrast image by subject-specific voxel time series means yielded percent fMRI signal change (38).

### Statistical Analyses

Ratings and RT data during “how afraid” were examined using repeated-measures analyses of variance (ANOVAs) with two between-subjects factors (Diagnosis: patients, control subjects; Genotype:  $L_A L_A$  homozygotes,  $S/L_G$  carriers) and one within-subjects factor (Face Emotion: fearful, angry, happy, neutral). Greenhouse-Geisser (G-G) adjustment was applied in cases of unequal variances.

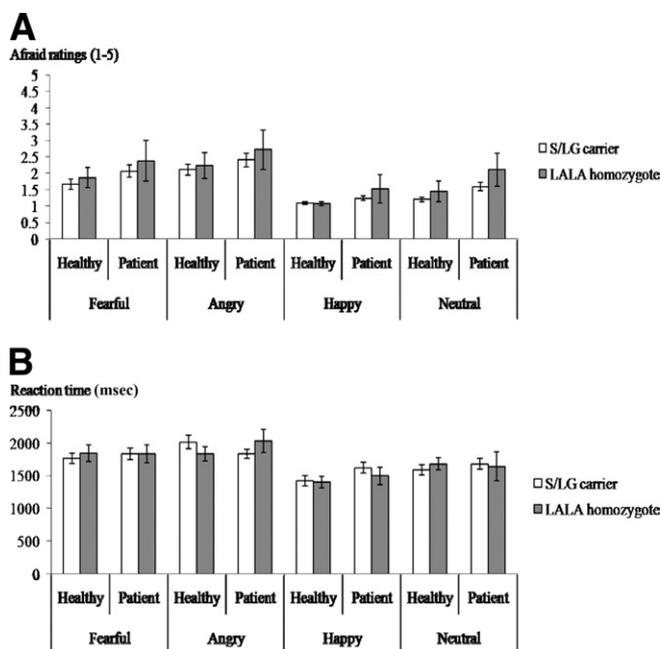
For group-level fMRI analyses, a random-effects model permitted population-level inferences (39). Analyses focused on the amygdala during “how afraid” using a region-of-interest approach (40). The boundaries of the amygdala were defined using standard anatomic criteria<sup>3</sup> on a single MNI template and applied to all normalized brains at the group level. BOLD signal changes for each event type (fearful, angry, happy, neutral faces) during afraid ratings relative to fixations were averaged across all voxels in the left and right amygdala for each subject. Left and right amygdala values were analyzed separately with repeated-measures ANOVAs in SPSS-14, examining main effects and interactions of two between-subjects factors (Diagnosis: patients, controls; Genotype:  $L_A L_A$  homozygotes,  $S/L_G$  carriers) and one within-subjects factor (Face Emotion: fearful, angry, happy, neutral). The G-G correction was applied. Because amygdala values correlated significantly with age and ethnic ancestry scores, these were covariates in subsequent analyses. Voxelwise SPM analyses using small-volume Gaussian random field correction procedures for multiple comparisons confirmed significant Genotype-by-Diagnosis interactions in the amygdala during afraid ratings.

### Results

#### Behavioral Data

Ratings and RT data during “how afraid” are presented in Figure 3. Data for three healthy participants were not recorded. Significant Face Emotion [ $F(3,171) = 33.69, p < .001$ ] and Diagnosis [ $F(1,57) = 4.99, p < .05$ ] effects emerged on ratings. Angry faces received highest ratings (2.38), followed by fearful (2.00), neutral (1.56), and happy (1.24) faces. Patients gave higher ratings to face emotions (2.02) relative to control subjects

<sup>3</sup>Consistent with a prior publication (41), the amygdala was measured from the slice at the level of the mammillary bodies to its anterior boundary, including the uncus.



**Figure 3.** (A) Afraid ratings of various face emotions (fearful, angry, happy, neutral) across healthy and anxious adolescents in each genotype group (S/L<sub>G</sub> carriers, L<sub>A</sub>L<sub>A</sub> homozygotes). (B) Mean reaction times (msec) during afraid ratings of different face emotions (fearful, angry, happy, neutral) across patient and healthy adolescents belonging to each genotype group (S/L<sub>G</sub> carriers, L<sub>A</sub>L<sub>A</sub> homozygotes). L, long; S, short allele.

(1.59). Similar Face-Emotion effects characterized RTs [ $F(3,171) = 23.29, p < .001$ ]: rating angry faces was slowest (1932.92 msec) followed by fearful (1825.83 msec), neutral (1650.47 msec), and happy faces (1492.62 msec).

**fMRI Data**

Significant effects of Diagnosis on both left and right amygdala responses indicated greater activity across Face Emotions (relative to fixations) among patients. Significant Genotype-by-Diagnosis and Genotype-by-Diagnosis-by-Face-Emotion interactions characterized right [ $F(3,159) = 2.66, p < .05$ ] but not left amygdala activity (Figure 4A). The three-way interaction was decomposed by examining Genotype and Diagnosis effects on right amygdala activity to each Face Emotion separately.

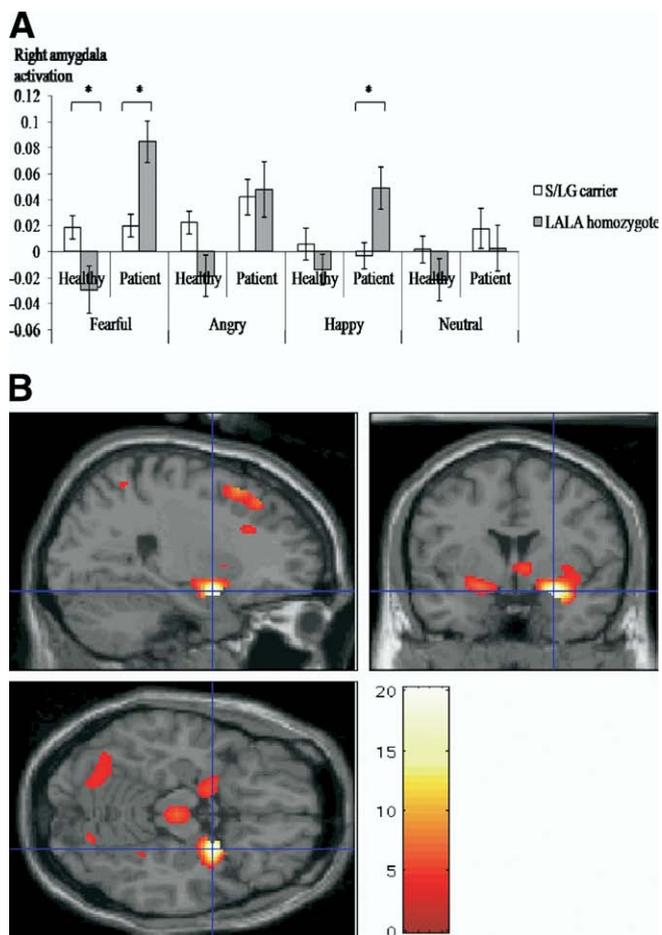
Significant Genotype-by-Diagnosis interactions characterized fearful [ $F(1,59) = 18.65, p < .001$ ] and happy [ $F(1,59) = 5.50, p < .05$ ] faces. For fearful faces, this interaction was driven by differential amygdala responses across genotype in each diagnostic group. Among healthy subjects, S/L<sub>G</sub> carriers showed greater activity than L<sub>A</sub>L<sub>A</sub> homozygotes [ $F(1,31) = 5.24, p < .05$ , Cohen's  $d = .95$ ]. In patients, greater activity occurred among L<sub>A</sub>L<sub>A</sub> individuals than S/L<sub>G</sub> carriers [ $F(1,27) = 14.17, p < .01$ , Cohen's  $d = 1.61$ ]. For happy faces, the Genotype-by-Diagnosis interaction was explained by patient data only: L<sub>A</sub>L<sub>A</sub> individuals manifested more amygdala activity than S/L<sub>G</sub> carriers [ $F(1,27) = 6.88, p < .05$ , Cohen's  $d = 1.27$ ].

Post hoc analyses contrasting amygdala responses to fearful faces across the three genotype groups (L<sub>A</sub>/L<sub>A</sub>, S/L<sub>G</sub>/L<sub>G</sub>, SS/S/L<sub>G</sub>/L<sub>G</sub>) showed that S/L<sub>G</sub>/L<sub>G</sub> and SS/S/L<sub>G</sub>/L<sub>G</sub> individuals were comparable in healthy subjects and patients, but they differed significantly from L<sub>A</sub>/L<sub>A</sub> individuals (Supplement 1). This justified pooling S- and L<sub>G</sub>-allele carriers. For happy faces, differences in amygdala responses across genotype groups were more appar-

ent in patients, but these were inconsistent. Whereas S/L<sub>A</sub>/L<sub>A</sub>L<sub>G</sub> and SS/S/L<sub>G</sub>/L<sub>G</sub>L<sub>G</sub> individuals showed similar responses, only S/L<sub>A</sub>/L<sub>A</sub>L<sub>G</sub> individuals differed significantly to L<sub>A</sub>/L<sub>A</sub> individuals (Supplement 2).

Voxelwise SPM analyses confirmed strong Genotype-by-Diagnosis interactions to afraid ratings of fearful faces in the right amygdala [ $F = 2.20, p < .001$ ] (Figure 4B; Supplement 3). All regions where significant Genotype-by-Diagnosis interactions emerged to fearful faces are shown in Table 2. Weaker interactions characterized the right amygdala during afraid ratings of happy faces [ $F = 5.44, p < .05$ ] (details on further request).

Parallel analyses employing a biallelic classification of 5-HTT genotypes (SS/SL vs. LL) on right amygdala activation yielded significant effects of Diagnosis, Face Emotion, and a two-way Diagnosis-by-Genotype interaction. Post hoc analyses showed significant Genotype-by-Diagnosis interactions for fearful [ $F(1,59) = 12.07, p < .01$ ] and happy [ $F(1,59) = 6.97, p < .05$ ] faces. For fearful faces, healthy SS/SL individuals showed greater amygdala activity than LL individuals [ $F(1,31) = 4.65, p < .05$ , Cohen's  $d = .80$ ]. Among patients, greater amygdala activity was found among



**Figure 4.** (A) Bar graphs of activation in the right amygdala for the “how afraid” condition relative to the task null-event baseline in various face emotions for patient and healthy adolescents across combined genotype groups (S/L<sub>G</sub> carriers and L<sub>A</sub>L<sub>A</sub> homozygotes). (B) The topography of peak activations in the right amygdala (Montreal Neurological Institute coordinates: 26, 2, –16) where the significant Genotype-by-Diagnosis interaction on afraid ratings of fearful faces emerged ( $p < .05$ ). L, long; S, short allele.

**Table 2.** Voxels with Significant Genotype-by-Diagnosis Interactions During Afraid Ratings of Fearful Faces ( $p < .01$ )

Brodman Area	Region	Volume (mm)	x	y	z	F	p Value
Afraid fear relative to baseline ( $p < .01$ )							
	Right amygdala	303	26	2	-16	20.20	<.001
6	Gyrus frontal superior	135	22	16	56	10.60	.002
8	Gyrus frontal superior	135	26	30	48	7.51	.008
	Left amygdala	57	-16	-4	-10	9.78	.003
	Cerebellum	48	36	-68	-22	8.91	.004
8	Gyrus frontal superior	11	-6	42	42	8.26	.006
	Brainstem	3	4	-20	-14	7.16	.01

LL than SL/SS-individuals [ $F(1,27) = 6.64, p < .05$ , Cohen's  $d = .50$ ]. For happy faces, LL individuals showed enhanced amygdala activity relative to SS/SL individuals [ $F(1,27) = 5.66, p < .05$ , Cohen's  $d = .67$ ]. Thus, results were broadly comparable to using a triallelic classification, but effect sizes for patient genotype differences were smaller. Amygdala responses to fearful and happy faces across the three genotype groups of the biallelic classification followed similar trends to the triallelic classification (Supplements 4 and 5).

To test specificity of results to the how afraid condition, analyses were repeated for data from other attention tasks, but no main or interaction effects emerged for left or right amygdala responses for triallelic or biallelic classifications. Modest sample sizes and low statistical power precluded testing a four-way Genotype-by-Diagnosis-by-Attention-by-Face-Emotion interaction.

To aid interpretation of fMRI results, we examined genotype and diagnosis effects on self-reported anxiety and depressive symptoms (42,43) among current subjects, as well as from healthy and anxious/depressed adolescents recruited for other NIMH studies ( $n > 230$ ). Neither revealed significant effects of 5-HTT genotype on symptoms.

## Discussion

Effects of 5-HTT gene variants on amygdala responses to emotional faces were studied in healthy and anxious/depressed adolescents during internal fear evaluation. A significant Genotype-by-Diagnosis-by-Face-Emotion interaction emerged on right amygdala activity, reflecting three key findings. First, in healthy adolescents, stronger amygdala responses to fearful faces characterized S/L<sub>G</sub> carriers, relative to L<sub>A</sub>L<sub>A</sub> individuals. Second, this was opposite in patients in whom L<sub>A</sub>L<sub>A</sub> individuals exhibited greater amygdala responses to fearful faces. Third, effects in patients extended to happy faces.

These data are the first to document conservation of gene-brain associations across typical development, supporting conceptualizations that S/L<sub>G</sub> alleles increase risks for psychopathology in healthy individuals (4), possibly through stress reactivity (11,44,45). However, gene-brain associations in affected adolescents differed from those in affected adults (4), with opposite gene-amygdala response patterns to fearful and happy faces. That these effects characterized happy faces as well may be because of ambiguity from discrepancies between stimulus valence and a potential threat context (9,46–48).

Although no theoretical accounts speak directly to these contrary findings in adolescent patients, three issues are relevant. First, literature on associations between 5-HTT gene variants and brain function or symptoms is mixed. A recent meta-analysis on adult gene-brain associations noted potential publication biases

when three unpublished data sets reporting no association or associations in opposite directions were excluded (4). Moreover, far fewer studies have been conducted in adult patients, calling for more independent replications generally but in especially clinical groups. Data for gene-symptom associations in adolescents are also inconsistent over whether the S or L allelic variant predicts risk for psychopathology (16–19).

Second, some anxious responses to threat show developmental differences. Relative to healthy subjects, anxious adults exhibit selective attention *toward* threat stimuli (49), whereas anxious adolescents shift attention *away* from these stimuli (50). Whether these reflect distinct compensatory responses used by affected adolescents to regulate emotional arousal is unknown, but regardless, they illustrate developmental changes in clinical behaviors. Variable expression of S/L<sub>G</sub> alleles on brain function from adolescence to adulthood among affected individuals is thus feasible.

Finally, incomplete penetrance from reduced exposure to environmental factors in patient S/L<sub>G</sub> carriers could also explain lowered amygdala activity in this group.

In summary, we present new but preliminary data on the genetics of neural function in adolescents. Although current sample sizes constrain power to interpret gene-brain associations in relation to differences across risk alleles (biallelic vs. triallelic classification; “dose-response” vs. “threshold” effect), diagnosis (anxiety vs. depression), and attentional conditions (nose ratings, hostility ratings, passive viewing), notably our effect sizes of genotype differences are comparable, if not larger, than previous studies (4) using similar-sized samples (24–28). Because imaging genetics research is still in its infancy, any data clarifying these associations is informative. Furthermore, our data lay the groundwork for considering interactions among genes, brain function, and emotional processes across development.

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*Supplementary material cited in this article is available online.*

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