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Associations between the SS Variant of 5-HTTLPR and PTSD Among Adults with Histories of Childhood Emotional Abuse: Results from Two African American Independent Samples

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Abstract

Background—Prior studies have found that the *5-HTTLPR* polymorphism in the promoter region of the serotonin transporter gene (*SLC6A4*) interacts with stressful life events to increase general risk for PTSD, but this association has not extended to African American samples. Further, little is known about the effects of this interaction on specific PTSD symptom clusters, despite indications that clusters may have different biological substrates. The current study examined the interaction between exposure to childhood emotional abuse and *5-HTTLPR* genotype on risk for PTSD symptom severity and severity of specific PTSD symptom clusters in two African American samples.

Methods—Participants were 136 African American household residents from Detroit, MI and 546 African American patients recruited from waiting rooms in primary care clinics in Atlanta, GA. Participants reported emotional abuse exposure and PTSD symptom severity, and provided DNA for triallelic *5-HTTLPR* genotyping. Analysis of covariance (ANCOVA) was used to examine main effects and interactions.

Results—In both African American samples, *5-HTTLPR* genotype modified the effect of emotional abuse on PTSD symptom severity. Participants with the low-expression SS genotype

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who were exposed to emotional abuse had significantly lower reexperiencing and arousal symptom severity scores.

Limitations—The DNHS genetic sample size was small, and abuse data were assessed retrospectively.

Conclusions—The SS variant of *5-HTTLPR* appears to buffer against developing the reexperiencing and arousal symptoms of PTSD in two independent African American samples exposed to childhood emotional abuse. Findings also highlight the importance of considering emotional abuse experiences in patients with suspected PTSD.

Keywords

PTSD; child abuse; gene-environment interaction

Introduction

Posttraumatic stress disorder (PTSD), which includes intrusive recollections, avoidance, and arousal symptoms (Association, 2000), is a debilitating and costly mental health condition reported by ~8% of the U.S. adult population (Kessler et al., 1995). The *5-HTTLPR* polymorphism in the promoter region of the serotonin transporter gene (*SLC6A4*) has been implicated in risk for PTSD, however results have been inconsistent as to whether the less transcriptionally efficient ‘S’ allele is a risk or protective factor for the disorder. Of the twelve studies examining *5-HTTLPR* and PTSD symptoms, two have suggested that the L’/L’ genotype interacts with trauma exposure to predict increased risk for PTSD (Grabe et al., 2009, Thakur et al., 2009), thereby suggesting that the ‘S’ allele may serve a protective function. However, nine have found that the ‘S’ allele is a risk factor for PTSD in the presence of various types of trauma exposure (Kolassa et al., 2010, Lee et al., 2005, Mercer et al., 2011, Wang et al., 2011, Holman et al., 2011, Xie et al., 2009, Xie et al., 2012), particularly for individuals living in more stressful environments (Kilpatrick et al., 2007, Koenen et al., 2009). A recent multisite study found that the interaction between the ‘S’ allele and exposure to trauma on PTSD only held for European Americans, but not African Americans (Xie et al., 2012), and at least one study of African Americans found no association between *5-HTTLPR* and lifetime PTSD (Mellman et al., 2009). Although Whites in the US are more likely to report exposure to a traumatic event, Blacks have a slightly higher risk of PTSD (Roberts et al., 2011), therefore, better understanding whether genetic variants such as *HTTLPR* interact with trauma exposure to predict PTSD is of critical importance.

Emotional abuse refers to a variety of negative experiences within a family including isolating (e.g., preventing child from interacting with friends/family), spurning (e.g., calling a child derogatory names), terrorizing (e.g., threatening a child with injuries), and denying emotional responsiveness (e.g., giving a child the “silent treatment”) (Brassard and Donovan, 2006). In a national study, parents nearly universally admitted to using psychological aggression as a disciplinary tactic, although the prevalence of more severe emotional abuse ranged from 20–50% depending on the age of the child (Straus and Field, 2003). Emotional or verbal abuse has been associated with brain abnormalities (Choi et al.,

2009, Tomoda et al., 2011, Teicher et al., 2006) and a host of negative psychosocial sequelae in adulthood including heightened PTSD severity (Spertus et al., 2003, Yehuda et al., 2001). Emotional abuse also has been shown to interact with low expression alleles of *5-HTTLPR* to predict depression and risk factors for depression (Antypa and Van der Does, 2010, Grabe et al., 2012, Stein et al., 2007); however, there have been no published GxE studies examining whether *5-HTTLPR* moderates the effects of childhood emotional abuse specifically on lifetime PTSD symptoms in adulthood.

Prior studies have typically examined the interactive effects of the *5-HTTLPR* genotype and trauma exposure on the overall PTSD diagnosis; however, PTSD is a syndrome comprised of heterogeneous symptom clusters that typically do not load on a single higher-order factor (e.g., (King et al., 1998)), thus, genes could influence certain dimensions of this syndrome, but not others. In the only studies to examine GxE interactions on specific symptom clusters of PTSD, findings regarding *5-HTTLPR* have been mixed. For example, among college students exposed to a mass shooting, those with the low expression 'S' alleles of *5-HTTLPR* had higher PTSD symptoms relative to those with 'L' alleles, and this effect related only to the arousal and avoidance symptoms of PTSD (Mercer et al., 2011). Among adults in a community with high exposure to a hurricane, findings differed slightly such that the low expression 'S' alleles of *5-HTTLPR* were significantly associated with reexperiencing and anxious arousal symptoms of PTSD but not the avoidance symptoms (Pietrzak et al., 2012). Neuroimaging studies suggest that *5-HTTLPR* 'S' allele is associated with attentional biases towards negative stimuli (Beevers et al., 2009) and heightened amygdala activation when presented with aversive stimuli (Heinz et al., 2007), suggesting differential genetic influences on specific biological processes and brain structures implicated in the development of particular PTSD symptom clusters. Thus, understanding of the precise influence of *5-HTTLPR* on PTSD symptoms may be limited by prior research focusing on the overall diagnosis rather than on specific symptom clusters.

To better understand how African American heritage affects associations between *5-HTTLPR* and overall PTSD as well as specific symptom clusters of PTSD, the current study used two independent samples of African American participants from different geographic regions in the US to examine whether those with one or two 'S' alleles reported more severe PTSD symptoms when exposed to childhood emotional abuse. A secondary aim of the study was to examine whether this GxE interaction was specific to certain symptom clusters (e.g., reexperiencing and arousal; (Pietrzak et al., 2012)), but not others (i.e., avoidance).

Methods

Participants

Participants for the current study were drawn from two sources: the Detroit Neighborhood Health Study (DNHS) and the Grady Trauma Project (GTP). The DNHS is a longitudinal representative telephone survey of household residents in Detroit, MI; 136 African American participants with complete genotype, trauma exposure, and PTSD data were included. The GTP is a large study of highly traumatized, low-income urban-dwelling individuals recruited from medical clinics in Atlanta, GA; 546 participants with complete genotype, trauma exposure, and PTSD data were included.

Measures

Demographic Information. In the DNHS and GTP, race/ethnicity, age, gender, income level, highest education completed, and marital status were collected. Age and gender were included in models as covariates.

Posttraumatic Stress Disorder—In the DNHS, lifetime exposure to 19 different traumatic events was assessed. Participants identified a worst event, and were cued to think of the period following the event during which symptoms were most frequent and intense, and were then asked whether they had ever been bothered by each of the 17 symptoms using a modified version of the PTSD Checklist-Specific version (Weathers et al., 1993). Each symptom was rated on a Likert-style scale from 1 to 5 indicating how much they had been bothered from “not at all” to “extremely”. Items were summed to yield a total severity score as well as severity scores for the PTSD symptom clusters. The PCL-S has excellent internal consistency (Cronbach’s $\alpha=0.93$), reliability, and validity as well as good psychometric properties when evaluated against a subsample of in-person clinical interviews (Uddin et al., 2010). To capture lifetime “worst” PTSD, the worst PTSD severity score reported at any DNHS wave was used to create the “worst” severity score; the same approach was used for the worst symptom cluster scores. Based on factor analytic studies suggesting that four symptom clusters best fit the data (Pergadia et al., 2011), we constructed and used the reexperiencing, avoidance, numbing, and arousal symptom clusters in analyses. At each wave, coefficient alpha for the total and subscale scores ranged from .76 to .93. In the GTP, trauma exposure was assessed with the Traumatic Experiences Inventory (TEI) (Schwartz et al., 2005), a 14-item screen for history of traumatic events. Past two-week PTSD was assessed with the Modified PTSD Symptom Scale (MPSS) (Falsetti et al., 1993), a psychometrically reliable 17-item self-report scale assessing PTSD symptomatology over the prior two weeks with a range from 0 to 51 (Coffey et al., 1998, Foa et al., 1993, Foa and Tolin, 2000). Symptoms were rated on a 4-point scale (ranging from 0 “not at all” to 3 “5 or more times per week”) and, consistent with prior literature, were combined to reflect overall symptom severity (Binder et al., 2008, Schwartz et al., 2005). Severity scores for the reexperiencing, avoidance, numbing, and arousal symptom clusters were also used in analyses. Coefficient alpha for the total, reexperiencing, avoidance, numbing, and arousal symptom scores was .92, .83, .74, .79, and .82, respectively.

Emotional Abuse

In the DNHS, two items from the Childhood Trauma Questionnaire (CTQ) (Bernstein and Fink, 1998) were used to assess emotionally abusive experiences during childhood (until age 11): 1) People in my family yelled or screamed at me; 2) People in my family said hurtful or insulting things to me. Respondents answered on a scale from 1 ‘never true’ to 5 ‘very often true.’ The items were summed and individuals who scored a 6 or higher on the total were considered to have experienced moderate to severe abuse. The internal consistency reliability for these two items was .72. In the GTP, the five-item emotional abuse subscale of the CTQ was administered. The three additional items were: 3) People in my family called me things like “stupid”, “lazy”, or “ugly”; 4) I thought that my parents wished I had never been born; 5) I believe that I was emotionally abused. Coefficient alpha for the 5 items in this sample was .85. Consistent with the scoring manual (Freedman et al., 1998), individuals

who scored a 13 or higher were considered to have experienced moderate to severe emotional abuse.

Procedures

Institutional Review Board approval was obtained from the University of Michigan and Emory University Medical Center for the DNHS and GTP, respectively. Following informed consent, DNHS participants were screened for lifetime trauma exposure, including emotional abuse, using telephone interview procedures described elsewhere (Uddin et al., 2010). Although two-hundred thirty-five participants were genotyped for triallelic *5HTTLPR* polymorphisms, only 136 African American participants had complete emotional abuse and PTSD data and were included in this analysis. DNA was isolated from whole blood. Whole-blood derived genomic DNA was isolated from 400µl of whole blood using either the DNA Mini Kit (Qiagen, Valencia, CA) following the manufacturer's recommended protocol.

Genotyping for DNHS

Samples from 54 African American DNHS participants were genotyped as previously described in (Koenen et al., 2011). For an additional 82 participants for whom limited amounts of DNA were available, DNA samples were subjected to whole genome amplification (WGA) using the Qiagen© Repli-G Mini kit following the manufacturer's recommended protocol. WGA DNA was then cleaned using the QiaAmp DNA Blood Mini kit following the manufacturer's recommended protocol. Resulting samples were then PCR amplified with identical primers used in (Koenen et al., 2011) using the Takara Taq PCR kit, along with the cycling parameters of 94°C initial for 1 minute followed by 35 cycles of: 94°C denature for 30 seconds, 66°C annealing temperature for 30 seconds and 72°C extension for 2 minutes; and a final extension at 72°C for 5 minutes. All PCR products (i.e. derived from WGA and non-WGA samples) were identified as short (S) or long (L) alleles through visualization on a 2% agarose gel stained with ethidium bromide. To further discern the functionally distinct L_A and L_G alleles [32], individuals with nonhomozygote SS genotypes ($n=82$) were subjected to restriction enzyme digestion with *MspI* [33]. Digested products were then size fractionated and visualized using a 2% agarose gel. Genotypes were grouped according to functional classification: 1) S/S were classified as S'/S' (low); 2) L_A /S and L_A / L_G were classified as L'/S' (intermediate); 3) L_A / L_A were classified as L'/L' (high). A minimum of five percent of samples were retested to ensure consistency in results.

Participants for the GTP were approached in the waiting rooms of primary care or obstetric/gynecologic clinics of Grady Memorial Hospital in Atlanta, GA. Because not all participants were literate, self-report instruments were administered verbally by a trained bachelor's level interviewer following informed consent. All participants were paid \$15 for these interviews. A subset of participants provided saliva samples at times of this assessment.

Genotyping for GTP. Saliva was collected into Oragene saliva kits (DNA Genotek, Inc.). Genotyping of *5-HTTLPR* utilized the following primers (forward: 50-Hex-TGAATGCCAGCACCTAACC-30; reverse: 50-ATACTGCGAGGGGTGCAG-30). PCR was carried out in 384-well plates in a 10 ml volume with 10 ng DNA. Each PCR reaction contained 0.5 mM of each primer, 0.08 mM of dATP, dCTP, and dTTP, and 0.04 mM of

dGTP, 0.2 mM of 7-deaza GTP (Amersham Biosciences/GE Healthcare, Piscataway, NJ), 5% DMSO, and 1.25U of AmpliTaq Gold (Applied Biosystems). The cycling parameters were as follows: 95°C for 5 min, then 94°C for 30 sec, 63°C for 30 sec, and 72°C for 1 min for 1 cycle, then the annealing temperature reduced to 62°C for one more cycles and then to 59.5°C for 38 cycles. Five microliters of the resulting PCR products was then digested with 5U MspI (New England Biolabs) in a total volume of 10 ml for 90 min at 37 C to detect the A/G SNP rs25531 shown to influence the functional effects of the long and short alleles (Hu et al., 2006). The digested PCR products were then separated using an Applied Biosystems 3100 genetic analyzer and analyzed with Applied Biosystems Genemapper 4.0 software. Fragment lengths for the L_A allele are 291 bp, 148 for the L_G, and 247 bp for the S allele. The VL fragment was 335 bp and the XL fragment was 375 bp. The call rate was 94.6%. Genotypes were grouped according to functional classification: 1) S/S were classified as S'/S' (low); 2) L_A/S and L_A/L_G were classified as L'/S' (intermediate); 3) L_A/L_A were classified as L'/L' (high).

Statistical Analyses

First, demographic information for each sample is presented and significant differences between the samples are noted. Second, descriptive information for the study variables of interest for each sample is presented; Hardy-Weinberg equilibrium also was tested in each sample. The prevalence of PTSD diagnosis is presented for descriptive purposes only as the severity scores were the outcomes of interest in models. Third, to rule out gene-environment associations, chi-square analyses were used to examine associations between *5-HTTLPR* and emotional abuse. Fourth, analysis of covariance (ANCOVA) was used to predict PTSD total severity as well as each cluster severity score while controlling for age and gender; F values and significance levels are presented in Table 3. The first two models separately examined the main effects of *5-HTTLPR* alleles and emotional abuse (present versus absent); the third model examined the interaction between *5-HTTLPR* alleles and emotional abuse on PTSD symptom severity. Functionally classified *5-HTTLPR* was entered as a 3-level variable in primary analyses (0 = SS, 1 = SL, 2 = LL for 0, 1, and 2 high activity alleles, respectively); however, secondary analyses examined any 'S' allele versus other genotypes.

Results

Demographic characteristics and chi-square/ANOVA comparisons are presented for the DNHS and GTP samples in Table 1. Although both samples had statistically equivalent proportions of women and employment, the GTP sample was younger on average. DNHS participants reported a greater household annual income and were more likely to have attended some college relative to GTP; GTP participants were significantly less likely to have ever been married relative to DNHS participants.

Genotype frequencies, emotional abuse frequencies, and PTSD total and symptom cluster severity scores are presented in Table 2. Genotypes were in Hardy-Weinberg equilibrium in the DNHS ($\chi^2=1.79$, $p>.05$) and GTP ($\chi^2=2.01$, $p>.05$) (Rodriguez et al., 2009), and the SL variant of *5-HTTLPR* was most common. Approximately one-third of the DNHS participants reported experiences that met the threshold for moderate/severe emotional

abuse, whereas one-sixth of the GTP participants met criteria for moderate/severe emotional abuse. A greater proportion of GTP participants met criteria for PTSD; however, the PTSD severity scores are not directly comparable between samples due to the use of different assessment measures.

Prior to examining the main effects and interaction of *5-HTTLPR* and emotional abuse on PTSD symptom severity, associations between emotional abuse and triallelic *5-HTTLPR* were examined in each sample to exclude the possibility of a gene-environment correlation. *5-HTTLPR* was not associated with emotional abuse in the DNHS, $\chi^2(2,147) = 3.92$, $p = 0.14$, or GTP, $\chi^2(2,589) = 0.94$, $p = 0.63$.

F values and significance levels from ANCOVA models testing the main effects and interactions between *5-HTTLPR* and emotional abuse on PTSD symptom severity are presented in Table 3. Among DNHS participants, *5-HTTLPR* did not have a main effect on PTSD symptom total or on any of the PTSD symptom clusters; however, emotional abuse was significantly associated with the PTSD total score as well as the reexperiencing, avoidance, and numbing symptoms of PTSD. A significant interaction was observed between *5-HTTLPR* genotype and emotional abuse on worst reexperiencing and arousal symptom severity after controlling for age and sex. Specifically, among those with the low expression SS alleles, those with childhood emotional abuse reported lower reexperiencing and arousal severity relative to non-emotional abuse victims. Among those with moderate/severe emotional abuse, those with higher expression LL alleles had significantly greater PTSD symptom severity than those with the lower expression SS alleles. The interaction between *5-HTTLPR* and emotional abuse did not reach statistical significance for total PTSD symptom severity, nor was the interaction significant for the avoidance and numbing symptom severity.

Among GTP participants, *5-HTTLPR* genotype exerted a significant main effect on total PTSD symptom severity such that those with the low expression/SS alleles had lower total PTSD symptom severity relative to those with the higher expression/SL or LL alleles. Emotional abuse exerted a significant main effect on total PTSD symptom severity as well as each of the PTSD symptom clusters. A significant interaction between *5-HTTLPR* genotype and emotional abuse emerged for the reexperiencing, numbing, and arousal symptom clusters such that symptoms were lowest among those with the SS genotype and increased to be highest among those with the LL genotype. Symptoms were particularly elevated among those with emotional abuse and the LL genotype. Those with the SS genotype had similar low levels of PTSD when emotional abuse was both present and absent. However, this interaction did not meet statistical significance for the PTSD total symptom score, and there was no significant interaction for avoidance symptoms.

Secondary Analyses

Any 'S' allele interacted with emotional abuse to predict lifetime worst arousal in DNHS, $F(1,129) = 4.80$, $p = .03$, and GTP, $F(1,538) = 5.70$, $p = .017$. In GTP, any 'S' allele also interacted with emotional abuse to predict re-experiencing symptoms, $F(1,538) = 3.76$, $p = .053$.

Discussion

This study is the first to document a potentially protective effect of the SS variant of 5-*HTTLPR* on the relationship between childhood emotional abuse and lifetime PTSD symptoms in two independent African American samples from different geographic regions within the US. In both samples, the low expression variant of 5-*HTTLPR* buffered against more severe PTSD symptoms among African Americans exposed to emotional abuse, and the high expression alleles conferred the greatest risk for PTSD symptoms. This interaction effect was found for the reexperiencing and arousal symptoms in both samples, and for the GTP sample, this interaction also extended to the numbing symptoms.

Findings add to a growing literature documenting associations between activity in the promoter region of the serotonin transporter gene and the trauma exposure-PTSD relationship. However, consistent with (Xie et al., 2012), results suggest that prior findings that low expression alleles at this locus increase risk for PTSD when exposed to trauma (Kilpatrick et al., 2007, Koenen et al., 2009, Kolassa et al., 2010) may not hold for African American individuals. Rather, the low expression variant of 5-*HTTLPR* may protect against the development of more severe PTSD among trauma-exposed African Americans. With few exceptions (Mellman et al., 2009, Xie et al., 2012), prior research examining the interaction between 5-*HTTLPR* and trauma exposure has not specifically focused explicitly on African American samples. In contrast to the current study, which found a protective effect of the SS genotype relative to other variants, Mellman (Mellman et al., 2009) and Xie (Xie et al., 2012) both failed to find an effect between 5-*HTTLPR* and PTSD symptoms in African Americans. This finding may be attributable to the increased frequency of the low expression/SS genotype in the DNHS (SS = 24.5%) and GTP (SS = 20.5%) relative to the 6.8% found in (10) and the 11% found in (13). The findings from the current study also may contrast with previous reports by examining the PTSD symptom clusters instead of focusing exclusively on PTSD total scores or diagnosis. Had the current study only focused on PTSD total scores, our interactions would not have reached statistical significance. Additionally, it is possible that the short allele may confer benefit for individuals living in higher risk environments like Detroit or Atlanta,; in contrast, for individuals living in relatively less risky environments where potentially traumatic events are perhaps more isolated and time constrained, this genotype may be less adaptive. Indeed, prior studies have often focused on populations with exposure to discrete traumatic events (e.g., hurricane exposure) (Kilpatrick et al., 2007) rather than exposure to ongoing threat or stress. However, at least one study with Israeli soldiers suggests that among soldiers who developed vigilance to combat threat cues, those with S alleles were less likely to develop PTSD relative to those with L alleles (Wald et al., 2013). Thus, in environments characterized by more chronic stress or threat, the S alleles may have a protective effect relative to the L alleles, perhaps by increasing the ability to attend and respond to risk cues adaptively. The 5-*HTTLPR* SS genotype also has been differentially linked to central nervous system (CNS) serotonin activity in European and African Americans such that African Americans with the SS genotype had higher levels of CNS serotonin turnover, whereas European Americans with the SS genotype had lower levels of CNS serotonin turnover (Williams et al., 2003). Thus, this study contributes to accumulating evidence that the SS genotype may operate differently in African American

and European American individuals, although it is unclear whether the observed effects are specific to race or to divergent environmental context (e.g., sustained vs. discrete traumatic event exposure).

In addition to finding a buffering effect of the SS genotype on the childhood trauma-adult PTSD relationship, the present study also extends the GxE literature on PTSD in two important ways. First, the current study supported prior findings detailing associations between childhood emotional abuse and PTSD (Spertus et al., 2003, Yehuda et al., 2001) and suggested that the interaction between emotional abuse and 5-HTTLPR is not specific to depression, but extends to PTSD as well. Second, consistent with emerging research (e.g., (Pietrzak et al., 2012)), but in contrast to a prior study (Mercer et al., 2011), the gene $\times$ environment effect was specific to the reexperiencing and arousal symptom clusters in both samples. It is possible that the low expression 5-HTTLPR alleles may exert a protective effect on the development of intrusive and arousal symptoms in the presence of emotional abuse by reducing attentional biases towards negative stimuli and decreasing arousal in the amygdala circuitry (Beevers et al., 2009, Heinz et al., 2007). However, it is important to note that in the GTP, 5-HTTLPR interacted with emotional abuse to also predict numbing symptoms. Failure to find a significant interaction for numbing symptoms in the DNHS could be due to limited power or it could reflect true differences in samples. Thus, these findings warrant further investigation.

Findings should be interpreted within the context of study limitations. First, the sample size for the DNHS was not especially large ($n = 136$) and findings may not generalize to larger samples. However, relatively consistent findings between the DNHS and the much larger replication sample from the GTP ($n = 546$) somewhat mitigate concerns about generalizability to other African American samples. Second, data on childhood abuse experiences were collected retrospectively, which could increase the possibility of recall biases. However, the CTQ is a well-validated and reliable measure of childhood abuse that has been used in numerous studies of this kind (Roy et al., 2010, Roy et al., 2007). Third, procedures, while similar for both studies, were not identical. However, it is notable that results were relatively consistent across studies despite different sample recruitment methods, different type of DNA samples (blood vs saliva), different allele frequencies within each sample, and the use of different PTSD instruments and different assessment time-frames.

These limitations notwithstanding, the current study adds important information to the growing GxE literature on the role of 5-HTTLPR and childhood abuse in PTSD symptom severity and suggests that associations among these variables may operate differently in African American samples relative to European American samples.

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Table 1

Sample Demographics for the Detroit Neighborhood Health Study (DNHS) and Grady Trauma Project (GTP)

	DNHS (<i>n</i> = 136)	GTP (<i>n</i> = 546)	χ^2/F (p)
% female	93 (68.4%)	335 (61.4%)	2.30 (0.13)
Mean (SD) Age	54.57 (16.25)	40.91 (13.86)	98.36 (<0.001)
Employed (yes)	39 (28.9%)	177 (32.5%)	0.64 (0.42)
Income			34.75 (<0.001)
<\$15K	52 (41.3%)	329 (61.8%)	
\$15k–\$25K	34 (27.0%)	142 (26.7%)	
>\$25K	40 (31.7%)	61 (11.5%)	
Highest education			15.23 (<0.001)
Less than HS	26 (19.1%)	124 (22.8%)	
HS or GED	39 (28.7%)	233 (42.8%)	
Some college or more	71 (52.2%)	187 (34.4%)	
Marital Status			32.03 (<0.001)
Married	32 (23.5%)	79 (14.5%)	
Divorced/separated	64 (47.1%)	157 (28.9%)	
Never married	40 (29.4%)	307 (56.5%)	

Table 2

Prevalence of genotype frequency, emotional abuse, and PTSD Diagnosis in the DNHS and GTP; Means and Standard Deviations for PTSD Total and Subscale Scores by Sample

	DNHS (n = 136)	GTP (n = 546)
5-HTTLPR Genotype		
SS (%)	34 (25.0%)	109 (20.0%)
SL (%)	60 (44.1%)	288 (52.7%)
LL (%)	42 (30.9%)	149 (27.3%)
Emotional Abuse (%)	43 (31.6%)	89 (16.3%)
PTSD diagnosis (%)	33 (22.4%)	172 (31.5%)
PTSD Total [M (SD)]	40.70 (14.68)	10.98 (11.37)
Reexperiencing [M (SD)]	12.71 (4.95)	2.66 (3.45)
Avoidance [M (SD)]	4.17 (2.45)	1.96 (2.18)
Numbing [M(SD)]	8.51 (4.58)	2.60 (3.54)
Arousal [M (SD)]	11.50 (5.09)	3.82 (4.09)

Note: PTSD was assessed with the PTSD Checklist (PCL) in the DNHS and with the PTSD Symptom Scale (PSS) in the GTP. The PCL total score ranged from 17-85, and the PSS total score ranged from 0-48.

F-values and Significance Levels for Analysis of Covariance Models Testing Gene by Environment Interactions on PTSD Total and Cluster Symptom Severity in the DNHS and GTP

Table 3

	DNHS				GTP					
	Total Severit y	Re- exp	Avoi d	Num b	Arous al	Total Severit y	Re-exp	Avoid	Numb	Arousal
Main Effects										
5-HTTLPR	0.62	0.03	0.27	2.32	1.29	2.60*	2.18	0.57	2.91 ⁺	2.18
Emotional Abuse	8.86**	3.99*	4.41*	11.11***	2.64	50.67***	29.89***	25.12***	48.94***	40.11***
Interaction										
5-HTTLPR × Emotional Abuse	2.67 ⁺	4.08*	0.46	0.44	5.80**	2.97 ⁺	3.56*	0.30	3.57*	3.18*

Note: Main effects and interaction models control for age, and % female;

*** p <0.001,
** p<0.01,
* p<0.05,
+ p <0.1