

# The Dopamine D<sub>3</sub> Receptor Gene and Posttraumatic Stress Disorder

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The dopamine D<sub>3</sub> receptor (*DRD3*) gene has been implicated in schizophrenia, autism, and substance use-disorders and is related to emotion reactivity, executive functioning, and stress-responding, processes impaired in posttraumatic stress disorder (PTSD). The aim of this candidate gene study was to evaluate *DRD3* polymorphisms for association with PTSD. The discovery sample was trauma-exposed White, non-Hispanic U.S. veterans and their trauma-exposed intimate partners ( $N = 491$ ); 60.3% met criteria for lifetime PTSD. The replication sample was 601 trauma-exposed African American participants living in Detroit, Michigan; 23.6% met criteria for lifetime PTSD. Genotyping was based on high-density bead chips. In the discovery sample, 4 single nucleotide polymorphisms (SNPs), rs2134655, rs201252087, rs4646996, and rs9868039, showed evidence of association with PTSD and withstood correction for multiple testing. The minor alleles were associated with reduced risk for PTSD ( $OR$  range = 0.59 to 0.69). In the replication sample, rs2251177, located 149 base pairs away from the most significant SNP in the discovery sample, was nominally associated with PTSD in men ( $OR = 0.32$ ). Although the precise role of the D<sub>3</sub> receptor in PTSD is not yet known, its role in executive functioning and emotional reactivity, and the sensitivity of the dopamine system to environmental stressors could potentially explain this association.

The dopamine system is involved in incentive/reward motivation (Beninger, 1983; Berridge & Robinson, 1998), motor control, and impulsivity (Dalley et al., 2007) and has been linked to the pathophysiology of substance-related disorders (Heidbreder et al., 2005; Pierce & Kumaresan, 2006), depression (Weiss et al., 1981), schizophrenia, and response to antipsychotic drugs (Schwartz, Diaz, Pilon, & Sokoloff, 2000).

The functioning of the dopamine system is thought to be affected by environmental stressors, and this sensitivity may help explain the link between life stress and onset of psychotic symptoms (Furuyashiki, 2012). There are two main types of dopamine receptors: D<sub>1</sub>-like (D<sub>1</sub> and D<sub>5</sub>) and D<sub>2</sub>-like (D<sub>2</sub>, D<sub>3</sub>, and D<sub>4</sub>); the former have stimulatory effects and the latter are inhibitory. The D<sub>3</sub> receptor has particular relevance to psychiatric phenotypes (e.g., psychiatric disorders and related endophenotypes) because it is expressed in brain regions thought to govern emotion and emotional responses to stress, reward motivation, and executive function (Sokoloff, Giros, Martres, Bouthenet, & Schwartz, 1990), such as the nucleus accumbens, and to a lesser extent, the anterior cingulate gyrus, amygdala, and hippocampus (Gurevich & Joyce, 1999; Pennartz, Groenewegen, & Da Silva, 1994). The D<sub>3</sub> receptor has been associated with startle reactivity (Halberstadt & Geyer, 2009), sensorimotor gating (Bristow et al., 1996; Giakoumaki, Roussos, Frangou, & Bitsios, 2007; Swerdlow et al., 2009), stress-related behaviors (Xi et al., 2004), memory, social recognition and responding (Loiseau & Millan, 2009; Watson et al., 2012), and cognitive impairment (Millan et al., 2010).

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Prior research suggests that the dopamine D<sub>3</sub> receptor gene (*DRD3*) may play a role in the etiology of a wide range of psychopathology including schizophrenia (Crocq et al., 1992; Dominguez et al., 2007; Ishiguro, Okuyama, Toru, & Arinami, 2000; Kennedy et al., 1995; Talkowski et al., 2006; Williams et al., 1998; Zhang et al., 2011), autism spectrum disorders (de Krom et al., 2009; Staal & de Krom, 2012), alcohol craving (Agrawal et al., 2013), nicotine dependence (Wei et al., 2012), depression (Dikeos et al., 1999), impulsivity among violent offenders (Retz et al., 2003), and obsessive-compulsive personality disorder (Light et al., 2006). The association between *DRD3* and multiple psychiatric disorders is consistent with the finding that genes exert shared effects across mental disorders (Smoller et al., 2013); this suggests the importance of evaluating genes shown to have association with one psychiatric phenotype in other psychiatric populations.

The D<sub>3</sub> receptor's relationship to psychiatric impairment may be mediated by the receptor's role in stimulus and stressor-related behavior, social learning, memory, executive functioning, and emotional reactivity. These processes are particularly relevant to posttraumatic stress disorder (PTSD) as the *Diagnostic and Statistical Manual (DSM-IV*; 4<sup>th</sup> ed., American Psychiatric Association [APA], 1994) lists heightened fear responsiveness to stressors (e.g., hyperarousal symptoms, emotional reactivity to trauma cues) and executive function deficits (e.g., concentration problems, difficulty regulating anger and other emotions) as symptoms of the disorder. Given this, we sought to conduct the first candidate gene study of which we are aware of the association between *DRD3* and PTSD using data from two distinct samples. We expected variants in the *DRD3* gene to be associated with lifetime PTSD diagnosis in both samples. Given prior evidence for sex differences in the prevalence of PTSD (Kessler, Sonnega, Bromet, Hughes, & Nelson, 1995), and genetic work suggesting that *DRD3* may be related to alcohol dependence in men, but not women (Wodarz et al., 2003), we also evaluated if sex moderated the association between polymorphisms in *DRD3* and PTSD. We hypothesized that the association between SNPs in *DRD3* and PTSD would be larger in men compared to women.

## Method

### Participants

The discovery sample included 852 participants (590 veterans and 262 intimate partners) who participated in one of two research studies. Genetic variation differs across ancestral groups such that a given variant may be more common in one racial group than another (referred to as population stratification) and this can yield spurious genetic association results if the phenotype of interest also varies by racial group. Given this, we focused our analyses on the largest homogenous subpopulation in our sample and identified this group on the basis of their genetic variation. Specifically, ancestry was determined with the program STRUCTURE, which performs a Bayesian clustering

analysis to assign subjects to ancestry groups, using 10,000 randomly chosen markers with minor allele frequency (MAF) > .05 (Falush, Stephens, & Pritchard, 2003; Pritchard, Stephens, & Donnelly, 2000). This process identified three groups, the largest of which was 540 participants who self-identified as White non-Hispanic. From this group, we eliminated 49 participants who did not report exposure to a *DSM-IV*-defined traumatic event, yielding a final sample of 491 (364 veterans and 127 nonveteran partners). Trauma-exposure histories as a function of sex are detailed in Wolf et al. (2013): Men and women did not differ in total trauma exposure, but men were more likely to report combat exposure and women more likely to report sexual trauma. We also evaluated the possibility of population substructure, wherein genetic variation differs by subpopulations within a given racial group (e.g., White participants with northern vs. southern European ancestry), as allele frequency differences across these subpopulations may also lead to spurious genetic association results. There was no evidence of PTSD-associated population substructure in this sample (Logue et al., 2013). The majority of participants were male (65.0%), and the mean age was 51.95 years ( $SD = 11.06$ , range: 21–75). In this sample, 60.3% ( $n = 296$ , comprising 251 veterans and 45 non-veteran partners) met *DSM-IV* diagnostic criteria for lifetime PTSD.

The replication sample comprised 601 trauma-exposed African American (per self-report and confirmed by multidimensional scaling analysis of genome-wide SNP data in PLINK; Purcell et al., 2007) men and women living in Detroit, Michigan, who participated in one of three waves of data collection in the Detroit Neighborhood Health Study (DNHS; additional details provided in Goldmann et al., 2011; Logue et al., 2013; Uddin et al., 2010). The sample we evaluated in the current study was predominately female (57.2%), and the mean age was 52.59 years ( $SD = 16.16$ , range: 18–95 years). Participants had been exposed to one or more traumas (see Breslau et al., 1998); 23.6% ( $n = 142$ ) met criteria for presumed lifetime PTSD as determined by structured interview administered over the telephone (see below).

### Measures

The Clinician Administered PTSD Scale (CAPS; Blake et al., 1995) was administered in the discovery sample. It assesses the 17 *DSM-IV* PTSD symptoms on frequency and intensity scales (each ranging from 0–4). PTSD diagnosis was calculated using a commonly used and validated scoring rule (Weathers, Ruscio, & Keane, 1999), which required endorsement of at least one reexperiencing, three avoidance and numbing, and two hyperarousal symptoms, each at a frequency of 1 or greater and an intensity of 2 or greater. Interrater reliability for lifetime diagnosis, as determined by a second rater making independent ratings from videotaped recordings of approximately 25% of the total participant interviews was excellent ( $\kappa = .87$ ).

The Traumatic Life Events Questionnaire (TLEQ; Kubany et al., 2000) was administered in the discovery sample. It is a

self-report instrument that assesses history of exposure to 22 different types of traumatic experiences that meet the *DSM-IV* PTSD Criterion A1. The measure also assesses whether the experience met Criterion A2 and asks the respondent to indicate the number of times each event occurred on a 7-point scale ranging from 0 = *never* to 6 = *more than five times*. The TLEQ has shown good test-retest reliability and predictive validity with respect to PTSD diagnoses (Kubany et al., 2000).

In the replication sample, the PTSD Checklist (Weathers, Litz, Herman, Huska, & Keane, 1993) was administered as an interview over the telephone. It assessed the extent to which participants had been bothered by each of the 17 *DSM-IV* PTSD symptoms on a 1 = *not at all* to 5 = *extremely* scale in relation to a specific stressful event. To meet presumptive criteria for the diagnosis, participants had to endorse *DSM-IV* PTSD Criteria A1 and A2, at least one reexperiencing, three avoidance and numbing, and two hyperarousal symptoms, each at a symptom rating of 3 (*moderately*) or higher, and endorse clinically significant impairment in functioning. In addition, the diagnosis required that the symptoms were present for at least a month (Goldmann et al., 2011).

## Procedure

In the discovery sample, participants completed one of two research protocols with identical interview assessment procedures and the data from the two studies were combined for these analyses. One study recruited trauma-exposed military veterans and their cohabitating intimate partners; the other recruited trauma-exposed military veterans who screened positive for PTSD over the telephone. Both studies included comprehensive structured diagnostic interviews of all participants that were digitally videotaped for purposes of quality control and evaluating interrater reliability. The studies were approved and reviewed annually by the VA Boston Healthcare System institutional review board.

DNA was isolated from peripheral blood samples on a Qiagen AutoPure instrument with Qiagen reagents and samples normalized using PicoGreen assays (Invitrogen). Samples were run on an Illumina OMNI 2.5–8 array and scanned using an Illumina HiScan System according to the manufacturer's protocol. DNA was available from 810 participants and from this group, we eliminated seven samples that had overall call rates less than 95%; the call rate in the remaining sample was 99.3%. Additional details of the quality control procedures are described in detail elsewhere (Logue et al., 2013). We restricted our attention to the 26 *DRD3* single nucleotide polymorphisms (SNPs) with minor allele frequency (MAF) greater than 5%. None of these SNPs failed a test of Hardy-Weinberg Equilibrium (i.e., all  $p > .01$ ).

In the replication sample, participants were recruited from a probability sample of Detroit-area households. Each wave of data collection included a 40-minute phone interview, for which participants received \$25. They also completed an in-person sample collection, including blood for genotyping, for which

they also received \$25. DNA was extracted from whole blood or saliva and evaluated on an Illumina HumanOmniExpress BeadChip. We evaluated all *DRD3* SNPs available on this chip; 11 of these overlapped the SNPs evaluated in the discovery sample.

## Data Analysis

*DRD3* is located on chromosome 3 and spans 70,756 bases between 113,847,499 and 113,918,254 base pair (bp); SNP locations were derived from the hg19 human-genome assembly (February 2009). SNPs in *DRD3* were examined for association with lifetime PTSD diagnosis using the standard  $\chi^2$  case/control test of association in PLINK in both samples (separately); this is an allelic test which compares the frequency of the minor allele in cases and controls under the assumption of an additive model (Purcell et al., 2007). We corrected for multiple-testing across the gene using the MAX(T) permutation procedure with 5,000 replications. In follow-up analyses in both samples, we entered total trauma exposure and the SNPs into a logistic regression in PLINK to evaluate if doing so changed the results of the SNP main effects. Because the discovery sample included 116 couples, we also modeled the nonindependence of these couples using a sandwich estimator to adjust the standard errors in Mplus 7.11 (Muthén & Muthén, 2012) and determined if doing so changed our main SNP effects in the discovery sample only. In both samples, we also stratified the sample by sex and evaluated the SNP main effects in each group separately to determine potential sex-specific effects and used the PLINK logistic regression test to evaluate if any of the SNPs interacted with (i.e., were moderated by) sex. Given that in the discovery sample, men were more often exposed to combat and women more often exposed to sexual assault (see Wolf et al., 2013), we also evaluated if combat exposure or sexual assault history interacted with the SNPs using PLINK logistic regression tests. Linkage disequilibrium (LD) was evaluated using the program Haploview (Barrett, Fry, Maller, & Daly, 2005). Among the 491 participants evaluated in the discovery sample, there was no missing phenotype data; the genotyping rate for the *DRD3* SNPs under investigation was greater than 99.9%. There was no missing data in the replication sample.

## Results

We first evaluated the SNP main effects in the discovery sample. Six of the 26 SNPs in *DRD3* showed nominal evidence of association ( $p < .05$ ) with lifetime PTSD (see Table 1 and Figure 1). Four of these withstood correction for multiple testing: rs2134655, rs201252087, rs4646996, and rs9868039, with corrected  $p$  values ranging from .005 to .049 (see Table 1). For each of these SNPs, the minor allele was less common among individuals with PTSD, suggesting a protective effect against risk for PTSD (odds ratios [ORs] ranged from 0.59 to 0.69; see Table 1). These four SNPs were in high LD with each other (see Table 2). The prevalence of lifetime PTSD among

Table 1

SNPs in *DRD3* (Chromosome 3) With at Least Nominal Evidence of Association With Lifetime PTSD in the Discovery and/or Replication Samples

Sample	SNP	bp	Minor allele	Freq aff	Freq unaff	OR	<i>p</i> (uncorrected)	<i>p</i> (corrected)
D	<b>rs9868039</b>	113846542	A	.41	.50	0.6883	.004	.049
D	rs9817063	113847108	G	.53	.44	1.427	.007	.069
D	<b>rs4646996</b>	113849565	A	.44	.54	0.6724	.002	.029
D	<b>rs2134655</b>	113858201	A	.28	.32	0.5907	.0003	.005
R	rs2251177	113858350	G	.11	.15	0.6733	.063	.597
D	<b>rs201252087</b>	113861589	G	.38	.48	0.6447	.0009	.013
D	rs963468	113862887	A	.45	.36	1.457	.005	.051

Note. *N* = 491 for discovery sample; *N* = 601 for replication sample. SNPs that were significant after permutation testing are in bold font. *DRD3* = dopamine receptor D<sub>3</sub>; PTSD = posttraumatic stress disorder; SNP = single nucleotide polymorphism; D = discovery sample; R = replication sample; bp = base pair; freq = frequency; aff = affected; unaff = unaffected; OR = odds ratio.

participants with one copy of the protective allele on rs2134655 (the most significant SNP) was 33.3%; it was 62.0% for those with no copies of the minor allele (there were no participants with two copies of the minor allele). The pattern of results for these four SNPs was unchanged when total trauma exposure was included in the analysis; results were also unchanged when we modeled the nonindependence of the 116 couples included in the analyses.

We next evaluated these associations in men and women separately. In men (*n* = 339), the same six SNPs that were nominally significant in the full sample again showed nominally significant associations with PTSD. One of these (rs201252087) withstood correction for multiple testing (*OR* = 0.60, uncorrected *p* = .003, corrected *p* = .039). In women (*n* = 215), that same SNP (rs201252087) was not significantly associated with

PTSD (*OR* = 0.69, uncorrected *p* = .100, corrected *p* = .568). Only one SNP (rs2134655) showed a nominally significant association with PTSD in women, but it did not withstand multiple testing correction (*OR* = 0.59, uncorrected *p* = .031, corrected *p* = .234); that SNP also evidenced a nominally significant association in the male subsample that did not withstand permutation testing (*OR* = 0.61, uncorrected *p* = .010, corrected *p* = .104). There was no evidence that sex moderated the SNP main effect for rs201252087 (interaction term *p* = .675, smallest *p* for any of the other SNP × Sex interaction terms = .207). We found no evidence of SNP interactions with sexual assault history or combat exposure.

The four SNPs showing evidence of association with PTSD in the discovery sample (rs2134655, rs201252087, rs4646996, and rs9868039) were not on the SNP array used in the

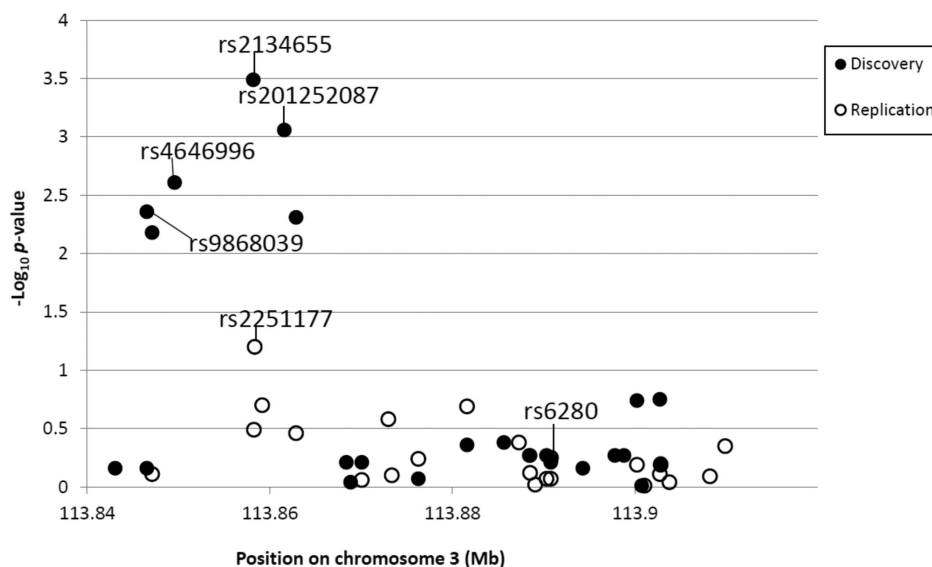


Figure 1. The figure shows the nominal (uncorrected) *p* values (in  $-\log_{10}$ ) at each base pair location for all single nucleotide polymorphisms (SNPs) evaluated for association with posttraumatic stress disorder in the discovery (filled circles) and replication (open circles) samples. The four SNPs that were significant after permutation testing in the discovery sample (*N* = 491) and the most significant SNP in the replication sample (*N* = 601) are identified, as is rs6280, a commonly studied *DRD3* polymorphism.

Table 2  
Linkage Disequilibrium Among the Four *DRD3* SNPs Showing the Strongest Association With PTSD in the Discovery Sample

SNP	1.		2.		3.	
	<i>D'</i>	<i>R</i> <sup>2</sup>	<i>D'</i>	<i>R</i> <sup>2</sup>	<i>D'</i>	<i>R</i> <sup>2</sup>
1. rs9868039						
2. rs4646996	.89	.68				
3. rs2134655	.99	.42	.99	.36		
4. rs201252087	.99	.86	.99	.75	.99	.75

Note. *N* = 491. *D'* is an index of linkage disequilibrium. *DRD3* = dopamine receptor D<sub>3</sub>; PTSD = posttraumatic stress disorder; SNP = single nucleotide polymorphism.

replication sample. Of the 23 SNPs available for analysis in the replication sample, only rs9828046 and rs2251177 were located in close physical proximity (< 150 bp) to rs2134655, the most strongly associated SNP in the discovery sample. None of the SNPs in the replication sample evidenced a significant association with PTSD in the full sample; however, one SNP, rs2251177 located at 113,858,350 bp, just failed to meet the threshold for a nominal association (*OR* = 0.67, uncorrected *p* = .063, corrected *p* = .597; see Table 1). The prevalence of PTSD among those with two copies of the minor allele at this location was 21.4%; it was 17.3% for those with one copy and 25.7% for those with no copies. This SNP is 149 bp away from the most significant SNP identified in the discovery sample (rs2134655) and 3,239 bp away from the second most significant SNP identified in the discovery sample (rs201252087). When trauma exposure was included in the model the association became nonsignificant in the full sample (*OR* = 0.69, *p* = .106). We also stratified this sample by sex and evaluated the SNPs separately for men (*n* = 257) and women (*n* = 344). In the men, the G allele of rs2251177 showed evidence of a nominally significant association with PTSD (*OR* = 0.32, uncorrected *p* = .011) although the corrected *p* value after permutation testing was .172. This SNP remained nominally significant with trauma included in the model (*OR* = 0.35, uncorrected *p* = .031). None of the SNPs were significant in the female subsample (association result for rs2251177: *OR* = 0.86, uncorrected *p* = .544, corrected *p* = 1.0). The test of the SNP × Sex interaction for rs2251177 failed to reach statistical significance (*p* = .093); none of the other SNPs evidenced a significant SNP × Sex interaction. We were unable to test for SNP interactions with trauma type in this sample as we did not have data on specific trauma types.

## Discussion

*DRD3* has previously been associated with a broad range of psychiatric disorders and the receptor encoded by the gene is important for executive functioning, emotional reactivity, and responding to environmental stressors. Given this, we exam-

ined the gene in relationship to PTSD. In our discovery sample of White, non-Hispanic trauma-exposed veterans and their spouses, four SNPs (rs2134655, rs201252087, rs4646996, and rs9868039) were associated with lifetime PTSD after adjustment for multiple testing. In an independent sample of trauma-exposed African Americans, one SNP (rs2251177), in close physical proximity to the most significant SNP identified in the discovery sample (rs2134655), evidenced a nominally significant association with PTSD in the male subsample; this same SNP just failed to meet the threshold for a nominal association with PTSD in the full replication sample. The minor alleles of these SNPs were protective against risk for PTSD, given trauma exposure. We would not expect rs2134655 (the most significant SNP identified in the discovery sample) to be significant in the replication sample because of differences in the MAF across Caucasian and African American populations (27.4% vs. 6.1%, respectively, per the International HapMap Project). Similarly, we would not expect rs2251177 (the most significant SNP identified in the replication sample) to be significant in the discovery sample because that SNP is monomorphic (i.e., invariant) among the Caucasian population. Nevertheless, the physical proximity of these two SNPs may suggest that a single risk locus in this region of *DRD3* is implicated in risk for PTSD (i.e., these SNPs may be markers for the same functional variant).

The SNP that showed the strongest association with PTSD in the discovery sample (rs2134655) has also been implicated in prior work with other psychiatric disorders. In a study of White individuals living in the United States, it was nominally associated with schizophrenia (Talkowski et al., 2006), and in samples of European ancestry, this SNP was part of a haplotype block associated with risk for schizophrenia with the T allele protective (Costas et al., 2009). That effect was consistent with the direction of effect in this study.

Other SNPs associated with PTSD in this study have been shown to be related to other psychiatric phenotypes. For example, rs9817063, which was nominally associated with PTSD in the discovery sample, was nominally associated with activity in the ventral striatum (as assessed via functional magnetic resonance imaging) and with treatment response to electroconvulsive therapy for depression (Dannowski et al., 2011). In addition, rs963468, which just failed to meet the corrected *p*-value threshold for statistical significance in the discovery sample, was implicated as part of a haplotype block in risk for schizophrenia (Nunokawa et al., 2010) and also showed a nominal association with nicotine dependence (Huang, Payne, Ma, & Li, 2008).

The precise role of the D<sub>3</sub> receptors in PTSD and associated disorders has not yet been elucidated, but the available evidence suggests it plays a role in at least two processes of relevance to PTSD: amygdala-mediated fear and anxiety processes and executive functioning. The receptor has been shown to be upregulated in basal, central, and lateral amygdaloid nuclei in individuals with depression (Klimek, Schenck, Han, Stockmeier, & Ordway, 2002) and also appears to mediate anxiety

following a social stressor (Hood et al., 2010). Imaging studies suggested that increased D<sub>2</sub> and D<sub>3</sub> receptor availability in prefrontal regions was associated with greater amygdala response to unpleasant images (Kobiella et al., 2009). Similarly, in animal models, the D<sub>3</sub> receptor plays a role in behavioral responding to stressors (Xi et al., 2004). These studies have relevance to PTSD as imaging research implicates enhanced amygdala activation and fear responding in PTSD (Patel, Spreng, Shin, & Girard, 2012). Moreover, heightened negative emotional reactivity to trauma cues, anger, and hypervigilance are symptoms of PTSD that may be related to the functioning of the D<sub>3</sub> receptors in the limbic brain regions governing emotional arousal and reactivity.

The prefrontal cortex and D<sub>3</sub> receptor also play a role in working memory and executive function (Black et al., 2002). Evidence for this comes from research suggesting that D<sub>3</sub> antagonists are potential therapeutic agents for the treatment of the cognitive dysfunction and confusion common to psychosis (Joyce & Millan, 2005) and from work showing the role of D<sub>3</sub> receptors in working memory (Ersche et al., 2011). Moreover, the Ser9Gly *DRD3* polymorphism has been shown to be associated with perseverative errors (Lane et al., 2008) as well as with other indices of executive functioning (Bombin et al., 2008). PTSD also is associated with executive function deficits (Polak, Witteveen, Reitsma, & Olf, 2012), decreased activation of prefrontal brain regions (Patel et al., 2012), and impaired concentration. Together, this raises the possibility that dysfunction at the site of D<sub>3</sub> receptors at least partially accounts for the cognitive deficits seen in PTSD. More research is needed to directly test this possibility.

Finally, prior research suggests that the D<sub>3</sub> receptors function differently in men compared to women. In one study, men expressed greater amounts of dopamine in striatal brain regions following exposure to amphetamine (Munro et al., 2006). D<sub>2</sub>/D<sub>3</sub> receptor availability was also shown to confer risk for nicotine dependence in men, but not women (Brown et al., 2012) and may be more strongly associated with the positive symptoms of schizophrenia in men compared to women (Glenhoj et al., 2006). Sex-specific effects of the gene have also been reported previously: The BA11 *DRD3* polymorphism was associated with alcohol dependence among men, but not women, with a history of delirium tremens (Wodarz et al., 2003). In this study, we did not find evidence of statistically significant genotype by sex interactions; this issue would benefit from further investigation in larger samples that are adequately powered to detect if sex moderates the main effects of these SNPs.

Limitations of the study include the relatively small sample size for genetic association analysis and the inability to compare the exact same polymorphisms across the discovery and replication samples. It is difficult to conduct comparisons across different racial and ethnic groups due to differences in genetic variation (i.e., MAF) across these groups, thus our replication sample was not ideal for confirming results observed in the discovery sample. We were also unable to disentangle the potential effects of sex from those of trauma exposure history;

moreover, we were underpowered to detect sex-specific effects. Thus, our findings with respect to potential sex differences should be interpreted with caution and considered preliminary. In the replication sample, PTSD was assessed using an interview version of a self-report measure, which is not the gold standard for diagnostic assessments. In addition, we have previously reported results of a genome-wide genetic association study (i.e., an atheoretical, empirical test) with PTSD (Logue et al., 2013) in this sample and that study did not find an effect for *DRD3* when genome-wide association standards (i.e.,  $p < 5 \times 10^{-8}$ ) were applied; however, we think it is important to conduct a hypothesis-driven candidate gene study as this may identify weaker effects attributable only to a subset of the population that would otherwise be missed in genome-wide scans. This is the first study of which we are aware to report an association between *DRD3* and PTSD, and, as such, additional replication is needed.

In conclusion, the results of this study provide initial evidence that polymorphisms in *DRD3*, perhaps reflecting a single risk locus, may be associated with lifetime PTSD diagnosis. The findings are consistent with the results of prior genetic research on other psychiatric phenotypes and with studies of the role of the D<sub>3</sub> receptor in emotional reactivity and executive functioning. The relationship between *DRD3* and PTSD may also be a reflection of the sensitivity of the dopamine system to stress.

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