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HPA Axis Multilocus Genetic Profile Score Moderates the Impact of Interpersonal Stress on Prospective Increases in Depressive Symptoms for Offspring of Depressed Mothers

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Abstract

Although offspring of depressed mothers are at an increased risk for depression themselves, not all of these children develop depression, highlighting the need to identify specific environmental and genetic moderators of risk. The goal of this study was to examine the aggregate influence of genetic polymorphisms associated with the regulation of the hypothalamic-pituitary-adrenal (HPA) axis as a potential moderator of the relation between environmental stress and prospective changes in depressive symptoms for offspring of depressed mothers. Participants were 238 mother-offspring dyads recruited from the community based on the mother’s lifetime history of major depression during the youth’s lifetime (present vs. absent). Mothers and youth completed assessments every 6 months for 2 years (5 total). Results indicated that offspring of depressed mothers showing the greatest increases in depressive symptoms during the follow up were those who had higher HPA multilocus genetic profile scores and who experienced the highest levels of interpersonal stress. These relations were significant for interpersonal stress and were not observed for non-interpersonal stress. These findings suggest that HPA multilocus genetic profile scores may be important genetic markers of stress reactivity and depression risk for offspring of depressed mothers. They also highlight interpersonal stress as a potentially modifiable risk factor for these high-risk youth.

Keywords

intergenerational transmission; depression; youth; genetics; stress

Major depressive disorder (MDD) is one of the leading causes of disability worldwide (Ferrari et al., 2013). Epidemiological data suggest that over 15% of youth will experience...
MDD by the end of adolescence (Avenevoli, Swendsen, He, Burstein, & Merikangas, 2015) and approximately 40% of these individuals will experience a recurrence of depression by the age of 24 (Lewinsohn, Rohde, Seeley, Klein, & Gotlib, 2000). One subset of youth that are at particular risk for depression are children of depressed mothers, who are 3–4 times more likely to become depressed than offspring of non-depressed mothers (see Goodman, 2007 for review). This said, the majority of these individuals do not become depressed themselves. This highlights the importance of identifying additional moderating factors, which likely include both environmental and genetic influences.

Stressful life events can greatly increase one’s risk for depression (Brown & Harris, 1978; Kessler, 1997; Mazure, 1998; Monroe, Slavich, & Georgiades, 2014) and there is evidence that children of depressed mothers experience more life stress than those of never-depressed mothers (Adrian & Hammen, 1993; Feurer, Hammen, & Gibb, 2016). One form of life stress that may be particularly important for depression risk in children and adolescents is interpersonal stress. Specifically, there is evidence that interpersonal negative life events are stronger predictors of depression risk in youth than are non-interpersonal events (Rudolph et al., 2000). This said, there are considerable individual differences in stress reactivity. Because of this, researchers have focused on understanding genetic influences that may help to identify which individuals may be most reactive to stressors in their environment. The starting point for much of this research was Caspi et al.’s (2003) seminal study showing that variation in the serotonin transporter gene (5-HTTLPR) moderated the impact of stressful life events on depression risk, though subsequent research on the role of 5-HTTLPR in depression risk has been more mixed (for reviews, see Culverhouse et al., in press; Karg, Burmeister, Shedden, & Sen, 2011; Risch et al., 2009). Since this time, a number of studies have evaluated the potential moderating role of polymorphisms in various other candidate genes considered individually (e.g., BDNF, MAOA, CRHR1; for reviews, see Cicchetti, Rogosch, & Sturge-Apple, 2007; Gatt et al., 2009; Heim & Binder, 2012; Hosang, Shiles, Tansey, McGuffin, & Uher, 2014; Melas et al., 2013).

However, several concerns have been raised about the use of single candidate genes when conducting gene × environment (G × E) research (Dick et al., 2015). Indeed, recent research has begun to show that polygenic effects within a given biological pathway are stronger than the influence of any single candidate gene examined in isolation (Nikolova, Ferrell, Manuck, & Hariri, 2011; Owens et al., 2016; Pagliaccio et al., 2014). In line with this aggregate genetic approach, a few studies have begun to examine G × E relations utilizing multilocus genetic profile scores (MGPSs). For example, a MGPS examining the aggregate influence of serotonergic genes was found to moderate the impact of interpersonal life stress on increases in depressive symptoms (Vrshek-Schallhorn, Stroud, Mineka, et al., 2015). Additionally, two separate MGPSs comprised of genes associated with the body’s stress-response system were found to interact with the experience of life stress to predict amygdala volume and function in youth and adults (Di Iorio et al., 2017; Pagliaccio et al., 2014, 2015). Importantly, in each of these studies, the MGPS exhibited greater predictive validity than any single polymorphism considered in isolation. This highlights the importance of considering the aggregate influence of multiple genes associated with a specific biological pathway.
Genes Impacting HPA Axis Functioning

Within this context, one reasonable approach is to focus on genes related to the functioning of the hypothalamic-pituitary-adrenal (HPA) axis, which coordinates the body’s response to stress (see Gunnar & Quevedo, 2007, for review). Following a stressor, corticotropin releasing hormone (CRH) is released from the hypothalamus, causing adrenocorticotropin (ACTH) to be released by the pituitary, which then causes glucocorticoids, including cortisol, to be synthesized and released by the adrenal cortex. Although moderate HPA axis activation can be adaptive as it readies individuals to face threats in their environment, HPA axis hyper-activation is associated with increased risk for depression in children and adolescents. Depressed youth also have higher levels of basal cortisol than non-depressed youth (for a review, see Lopez-Duran, Kovacs, & George, 2009), and this hypercortisolism has been found to prospectively predict depression onset in youth (Adam et al., 2010; Goodyer, Herbert, & Tamplin, 2003). Additionally, compared to never-depressed youth, depressed children and adolescents have a heightened cortisol response to psychological stressors (for reviews, see Guerry & Hastings, 2011; Lopez-Duran et al., 2009). Building from these findings and using a biological systems approach to testing a G × E model of risk for depression, our goal was to examine the combined influence of genes known to affect HPA axis functioning.

The CRHR1 gene codes for the CRH receptor and variation in CRHR1 genotype has been shown to affect the level of cortisol released in response to laboratory-based stressors in adults (Mahon, Zandi, Potash, Nestadt, & Wand, 2013) and children (Sheikh, Kryski, Smith, Hayden, & Singh, 2013). There is evidence that three single nucleotide polymorphisms (SNPs) in CRHR1 (rs7209436, rs110402, and rs242924) form a protective TAT haplotype. An individual SNP within the TAT haplotype (rs110402) has been found to predict greater cortisol reactivity for individuals exposed to childhood abuse (Heim et al., 2009; Tyrka et al., 2009). Furthermore, among individuals reporting a history of childhood abuse, those with no copies of the protective TAT haplotype, compared to those carrying one or two copies of the haplotype, reported significantly greater cortisol dysregulation (Cicchetti, Rogosch, & Oshri, 2011) and both higher current depressive symptoms and greater risk for depression (Bradley et al., 2008; Polanczyk et al., 2009; but see also Laucht et al., 2013), with risk appearing to decrease with each additional copy of the TAT haplotype present.

The FKBP5 protein plays a key role in HPA axis activity by regulating the sensitivity of the glucocorticoid receptor, with higher levels of FKBP5 expression associated with lower glucocorticoid activity (for a review, see Zannas & Binder, 2014). There is evidence that the minor T allele of the rs1360780 SNP within the FKBP5 gene is associated with increased cortisol reactivity to laboratory stressors (Ising et al., 2008; Luijk et al., 2010; Zannas & Binder, 2014). Variation in this SNP has also been shown to moderate the impact of negative life events on risk for depression in adults (Appel et al., 2011; Comasco et al., 2015; Lahti et al., 2015; Zimmermann et al., 2011), with risk higher among carriers of the minor allele.

Finally, the mineralocorticoid receptor gene (NR3C2) is also associated with HPA axis dysregulation (for a review, see DeRijk et al., 2006). For example, there is evidence that the minor G allele of the MR1180V (rs5522) SNP is associated with greater salivary and plasma
cortisol and with greater heart rate reactivity to a stressor (DeRijk et al., 2006; but see also Bouma et al., 2011). There is also evidence that MR180V forms a two-SNP haplotype with MR-2G/C (rs2070951) that predicts HPA axis functioning and risk for depression. Specifically, the CA haplotype formed by these two SNPs is associated with greater mineralocorticoid receptor protein expression (Klok, Giltay, et al., 2011; van Leeuwen et al., 2011) and decreased risk for depression in women (Klok, Giltay, et al., 2011; Vinkers et al., 2015) suggesting that, like the CRHR1 TAT haplotype, the NR3C2 CA haplotype may be protective.

The Current Study

In the current study, our goal was to test an integrated model of risk for depression in offspring of depressed mothers within the context of a multi-wave, two-year prospective study. We chose to focus on children and adolescents who would be 8 to 16 years old during the course of the study because this is a key developmental window during which rates of depression increase dramatically (Hankin et al., 1998; Rudolph & Flynn, 2014). We utilized a MGPS approach focusing on the combined influence of polymorphisms in genes known to affect HPA axis functioning (CRHR1, FKBP5, and NR3C2). We chose to focus specifically on these three genes due to their known influence on HPA axis functioning and to replicate a previously established, theoretically and biologically-driven MGPS utilized in previous research (Di Iorio et al., 2017). As noted earlier, the MGPS approach is consistent with recent research highlighting the importance of examining the aggregate influence of multiple SNPs as opposed to examining candidate genes in isolation (Nikolova et al., 2011; Owens et al., 2016; Pagliaccio et al., 2014). In focusing on environmental influences, we examined interpersonal and non-interpersonal episodic life events separately, given evidence that interpersonal, compared to non-interpersonal, events are stronger predictors of future depression (Rudolph et al., 2000) and are associated with greater HPA axis reactivity, as measured via cortisol production (Dickerson & Kemeny, 2004; Stroud, Chen, Doane, & Granger, 2016). We predicted that offspring of depressed mothers would exhibit greater prospective increases in depressive symptoms following negative life events than offspring of never depressed mothers and that these symptom increases would be highest among youth of depressed mothers who carried genotypes associated with greater HPA axis reactivity. We also predicted that these results would be stronger for interpersonal than non-interpersonal stress. Finally, exploratory analyses were conducted to examine whether youth’s age or sex moderated any of the relations.

1We did, however, differ from Di Iorio’s (2017) approach to creating the MGPS in two respects. First, for CRHR1, we focused on the established TAT haplotype, while Di Iorio et al. only included rs110402. Second, although Di Iorio and colleagues wanted to focus on NR2C2 rs2070951 (as part of a haplotype with rs5522), their panel did not include this SNP so they included a different SNP (rs4635799) that is in high LD with rs2070951 to form the NR2C2 haplotype. To be consistent with the previous literature (Klok, Giltay, et al., 2011; Klok, Vreeburg, et al., 2011; van Leeuwen et al., 2011; Vinkers et al., 2015) and with the goal of the Di Iorio paper, we focused on the rs2070951 so that we could specifically examine the NR2C2 rs2070951/rs5522 haplotype. This said, it is important to note that all significant findings in the current study were maintained when using a MGPS that precisely replicated the one used by Di Iorio et al.
**Method**

**Participants**

Participants were 238 mothers and their biological offspring recruited from the community for a study on the intergenerational transmission of depression. To qualify for the study, mothers were required to either have a history of MDD as defined by the *Diagnostic and Statistical Manual of Mental Disorders—Fourth Edition* (DSM-IV; American Psychiatric Association, 1994) during their offspring’s lifetime (n = 122) or have no lifetime diagnosis of any DSM-IV mood disorder and no current Axis I diagnosis (n = 116). Mothers were excluded if they exhibited symptoms of schizophrenia, alcohol or substance dependence in the last 6 months, or a history of bipolar disorder. Additionally, potential mothers needed to have a child between the ages of 8 and 14. If there was more than one child in this age range, one was randomly chosen for participation. For youth in our sample, the average age was 11.39 (SD = 1.93), 51.7% were female. In terms of race, 81.9% were Caucasian, 4.6% were African American, 10.5% were biracial, and 3.0% identified as another race. For mothers in our sample, the average age was 40.32 (SD = 6.72), 87.4% were Caucasian, 4.6% were African American, 4.2% were biracial, and 3.8% identified as another race. The annual family income ranged from $0–5,000 to more than $115,000 and the median annual income was $50,001–55,000. Finally, 24.8% of children were from single parent homes.

**Measures**

Mothers’ and children’s histories of MDD and other Axis I disorders were assessed using the Structured Clinical Interview for DSM-IV Axis I Disorders (SCID-I; First, Spitzer, Gibbon, & Williams, 1995) and the Schedule for Affective Disorders and Schizophrenia for School Age Children – Present and Lifetime Version (K-SADS-PL; Kaufman et al., 1997), respectively. As previously stated, 122 mothers met criteria for MDD during their offspring’s lifetime and 116 mothers reported no lifetime history of depression. In addition, 17 youth had a lifetime history of MDD at the initial assessment (15 of whom had mothers with a history of MDD). Lifetime rates of anxiety disorders in mothers were: 26 with social phobia (25 from the MDD group), 25 with post-traumatic stress disorder (PTSD; 24 from the MDD group), 21 with panic disorder (20 from the MDD group), 12 with obsessive-compulsive disorder (OCD; 10 from the MDD group), 10 with agoraphobia (8 from the MDD group), and 3 with generalized anxiety disorder (GAD; 3 from the MDD group). Lifetime rates of anxiety disorders for youth were: 12 with social phobia (10 children of mothers with MDD), 12 with separation anxiety disorder (10 children of mothers with MDD), 7 with GAD (5 children of mothers with MDD), 4 with OCD (4 children of mothers with MDD), 1 with panic disorder (whose mother had MDD), and 1 with PTSD (whose mother had MDD). A subset of 20 SCIDs and 20 K-SAD-PLs was coded by a separate interviewer to assess inter-rater reliability for diagnoses of MDD and anxiety disorders, yielding excellent kappa coefficients (all $\kappa$’s = 1.00).

Youth’s depressive symptoms were assessed using the Children’s Depression Inventory (CDI; Kovacs, 1981), which has shown excellent reliability and validity in previous research (Kovacs, 1981, 1985; Smucker, Craighead, Craighead, & Green, 1986). The CDI also
exhibited good internal consistency across all 5 time points in this study (α ranged from .85 to .89).

Youth's exposure to interpersonal and non-interpersonal episodic life stress was assessed at each time point using the UCLA Life Stress Interview for Children (LSI-C; Adrian & Hammen, 1993), which is a semi-structured interview and is modeled after contextual threat interviews (Brown & Harris, 1978). At the initial assessment, youth and their mothers were interviewed separately and were asked about any stressful life events across a variety of domains that may have occurred in the 6 months prior to the assessment. For the 6, 12, 18, and 24-month follow-up assessments, participants were asked about any stressful events since the date of their last assessment. If the dyad missed an assessment, the LSI-C focused on stress experienced during the entire time between assessments instead of just the most recent 6-month interval. In these cases, any events reported before the date of their missed appointment were summed separately from the rest of the events reported at that time period, in order to back-date the events to the appropriate time point. For any reported events, the interviewer probed further to gain objective information about the timing, duration, context, and consequences of each event. Each reported event was then presented, devoid of any subjective information, to a team of 4–7 coders who assigned a negative impact threat rating to each event. Any coding discrepancies across team members were discussed until consensus was achieved. These threat ratings ranged from “1”, which implied no stress, to “5”, for events characterized by severe stress and significant impact. Additionally, the content of each reported event was categorized as either interpersonal or non-interpersonal. An event was categorized as “interpersonal” if the stressor had significant consequences for the youth’s interpersonal relationships (e.g., a fight with a friend or the death of a family member). If the event did not have any impact on the youth’s interpersonal relationships (e.g., the youth failed an exam or sustained a physical injury), the stressor was coded as “non-interpersonal”. We calculated the total amount of interpersonal and non-interpersonal episodic stress reported at each time point by summing the stress scores separately for interpersonal and non-interpersonal events. To avoid inflation of stress scores by including reported events with a score of 1, and therefore no negative impact, we recoded the objective impact scores from 1–5 to 0–4 before summing the totals for interpersonal and non-interpersonal stress.2

Genotyping—Finally, youth’s DNA was collected and isolated from buccal cells using established methods (Freeman et al., 1997; Lench, Stanier, & Williamson, 1988). For CRHR1, 3 SNPs were genotyped – rs7209436, rs110402, and rs242924 – that form a T-A-T haplotype comprised of major alleles on each SNP (Bradley et al., 2008; Polanczyk et al., 2009). The Taqman assay IDs for rs7209436, rs110402, and rs242924 were

2The current study focused on the impact of stressful life events on increases in youth’s depressive symptoms. However, according to stress generation theory (Hammen, 1991), depressed individuals may generate additional stress in their lives, which can lead to questions of causality when examining the relation between stress and depression. Therefore, coders also assigned a dependence score to each event to signify the extent to which the occurrence of the event was due to the actions of the participant. A dependence score of “1” indicated that the event was entirely independent of the child, a score of “3” indicated mixed or indeterminate dependence, and a score of “5” indicated that the event was completely dependent on the participant. To address concerns about stress generation, all analyses were re-conducted with independent stress as a predictor variable (i.e., the sum of the impact ratings of all events coded as a “1” or “2” for dependence). Both the MDD × MGPS × stress interaction and the MGPS × stress interaction for children of depressed mothers remained significant.
The three CRHR1 polymorphisms were genotyped using fluorogenic 5’ nuclease (Taqman, Applied Biosystems, Foster City, CA) method involving reagents (VIC(tm) and FAM(tm), labeled probes, and TaqMan® Universal PCR Master Mix without AMPerase® UNG) obtained from Applied Biosystems (ABI). Genotype determination was performed using primers purchased from ABI or Integrated DNA Technologies (Coralville, IA). Genotypes were obtained using an ABI Prism 7300 Sequence Detection System using both absolute quantification and allelic discrimination modes (Livak, Flood, Marmaro, Giusti, & Deetz, 1995). All markers were found not to differ from Hardy-Weinberg equilibrium (HWE) using default parameters in Haploview (p < .001; Barrett, 2009). In order to (a) maximize the amount of information provided by the multiple markers, and (b) circumvent loss of power due to multiple testing, we utilized all of the available SNP data to identify haplotype blocks (i.e., the combinations of SNP markers that are statistically associated). Haploview was used to visualize haplotype blocks (Barrett, 2009; Barrett, Fry, Maller, & Daly, 2005). Marker to marker D’ values were as follows: rs7209436 – rs110402 = 0.95, rs7209436 – rs242924 = 0.88, rs110402 – rs242924 = 0.93. Haplotypes for both chromosomes were then confirmed and extracted using PHASE (Version 2.1, Stephens & Donnelly, 2003; Stephens, Smith, & Donnelly, 2001), requiring that the probability of a haplotype be greater than or equal to 0.80. PHASE haplotypes were used to construct diplotypes (i.e., combination of haplotypes across the pair of homologous chromosomes) that were used in the analyses. CRHR1 was coded as the number of copies of the protective TAT haplotype that were present.

FKBP5 rs1360780 was genotyped following the procedures used for CRHR1 SNPs above. The Taqman assay ID for rs1360780 was C___8852038_10. Results of an exact test for Hardy Weinberg proportions using Markov chain–Monte Carlo implementation (Engels, 2009; Guo & Thompson, 1992) yielded a p value of .0436 +/- .0002, suggesting the presence of excess homozygosity in our sample. FKBP5 was coded as the number of rs1360780 minor (T) alleles.

For NR3C2, two SNPs (rs2070951 and rs5522) were genotyped using PsychArray (Illumina) and scanned using a HiScan (Illumina) using standard manufacturer’s protocols. Quality control (QC) was performed sequentially on the PsychArray genetic data using PLINK version 1.9 (Purcell et al., 2007). First markers with a genotyping rate of less than 90% and individuals with more than 10% of their data were missing were removed. Then, markers with minor allele frequency of less than 1% and those that failed HWE (p < .001) were removed. Genotypes for rs5522 were taken directly from the PsychArray data whereas genotypes for rs2070951 were imputed using the Michigan Imputation Server (https://imputationserver.sph.umich.edu). Similar to CRHR1, Haploview was used to visualize haplotype blocks (Barrett, 2009; Barrett, Fry, Maller, & Daly, 2005). Haplotypes for both chromosomes were then confirmed and extracted using PHASE (Version 2.1, Stephens & Donnelly, 2003; Stephens, Smith, & Donnelly, 2001), requiring that the probability of a haplotype be greater than or equal to 0.80. PHASE haplotypes were used to construct diplotypes (i.e., combination of haplotypes across the pair of homologous chromosomes) that were used in the analyses. Marker to marker D’ values were as follows: rs5522 - rs2070951= 1.00. NR3C2 was coded as the number of CA haplotypes.
Multilocus genetic profile scores were then calculated by summing the number of copies of the \textit{CRHR1} TAT haplotype, rs1360780 T allele, and the \textit{NR3C2} CA haplotype present. Because the \textit{CRHR1} TAT and \textit{NR3C2} CA haplotypes are considered to be protective, they were reverse scored so that higher scores reflect greater HPA axis reactivity. Coding for each gene is described in Table 1. MGPSs ranged from 0 to 6, with larger scores reflecting more copies of genotypes associated greater HPA axis reactivity.

**Procedure**

Potential participants were recruited through a variety of means (e.g., newspaper and bus ads, flyers) and were screened over the telephone to determine their eligibility. At the initial assessment, the SCID and K-SADS-PL were administered to all mothers and youth to assess for their lifetime history of MDD and other Axis I disorders. Additionally, at the initial time point, youth were administered the CDI to assess for their current levels of depressive symptoms. DNA samples were also obtained from the youth through the collection of genetic samples at this initial assessment. Finally, at the first time point the LSI-C was conducted with both mothers and their offspring separately to assess for the amount of episodic life stress occurring in the youth’s life during the 6 months before the start of the study.

After the initial assessment, mothers and their offspring came back to the lab for 6, 12, 18, and 24-month follow-up assessments. Of the 238 participants who completed the Time 1 assessment, 202 (84.9%) completed Time 2, 187 (78.6%) completed Time 3, 161 (67.6%) completed Time 4, and 166 (69.7%) completed Time 5. Completion rates did not differ across the two mother MDD groups at any time point (lowest $p = .15$). At each time point, youth were re-administered the CDI to assess for depressive symptoms. Additionally, mothers were re-administered the depression supplement of the SCID to assess for the onset of any new episodes of MDD since their last assessment. Finally, at each follow-up appointment the LSI-C was re-administered to mothers and their offspring to assess for the amount of episodic life stress the youth experienced since the last assessment. Participants were paid $75 for their participation in the initial assessment, and an additional $50 for the completion of each follow-up assessment. All study procedures were approved by Binghamton University (SUNY)’s Institutional Review Board (protocol number 2013-09).

**Analytic Plan**

We used hierarchical linear modeling (HLM; Raudenbush & Bryk, 2002; Raudenbush, Bryk, Cheong, & Congdon, 2004) to examine the impact of maternal MDD, youth’s MGPS, episodic stress, and their interactions on changes in youth’s depressive symptoms during the study. We conducted separate analyses for interpersonal and non-interpersonal episodic stress. The Level 1 model for these HLM analyses was:

$$CDI_{ij} = \pi_{0j} + \pi_{1j} (CDI_{t-1ij}) + \pi_{2j} (\text{Episodic Stress}_{ij}) + e_{ij}$$

where $CDI_{ij}$ represents the youth’s CDI score at time $t$ for assessment $i$ and participant $j$. $CDI_{t-1ij}$ represents the youth’s CDI score at time $t-1$ for assessment $i$ and participant $j$, and $\text{Episodic Stress}_{ij}$ represents the youth’s level of stress between time $t-1$ and time $t$ for
assessment \(i\) and participant \(j\). In addition, \(\pi_{0j}\) is the CDI\(_{ij}\) intercept, \(\pi_{ij}\) is the slope of the relation between youth’s CDI score between time \(t\) and time \(t-1\) at each assessment \(i\) for participant \(j\) (i.e., the autocorrelation), \(\pi_{2j}\) is the slope of the relation between youth’s episodic stress (interpersonal or non-interpersonal) and CDI scores at time \(t\), and \(e_{ij}\) represents the error term. Importantly, including CDI at time \(t-1\) in the model while predicting CDI at time \(t\) allows us to determine whether Episodic Stress occurring between assessments predicts prospective change in youth’s depressive symptom levels between those assessments.

The Level 2 model was:

\[
\pi_{0j} = \beta_{00} + \beta_{01}(\text{MDD}) + \beta_{02}(\text{MGPS}) + \beta_{03}(\text{MDD} \times \text{MGPS}) + r_{0j}
\]

\[
\pi_{1j} = \beta_{10} + \beta_{11}(\text{MDD}) + \beta_{12}(\text{MGPS}) + \beta_{13}(\text{MDD} \times \text{MGPS}) + r_{1j}
\]

\[
\pi_{2j} = \beta_{20} + \beta_{21}(\text{MDD}) + \beta_{22}(\text{MGPS}) + \beta_{23}(\text{MDD} \times \text{MGPS}) + r_{2j}
\]

where \(\beta_{01}\) is the cross-level interaction term representing the effect of maternal MDD history (absent vs. present in youth’s life) on the CDI intercept, \(\beta_{11}\) is the cross-level interaction term representing the effect of maternal MDD history on the slope of the relation between youth’s lagged and current CDI scores, and \(\beta_{21}\) is the cross-level interaction representing the effect of maternal MDD on the slope of the relation between youth’s episodic stress (interpersonal and non-interpersonal) and CDI scores. Similarly, \(\beta_{02}\), \(\beta_{12}\), and \(\beta_{22}\) are the cross-level interaction terms representing the effect of the MGPS on the CDI intercept, the slope of the relation between youth’s current and lagged CDI scores, and the slope of the relation between episodic stress and CDI scores, respectively. \(\beta_{03}\), \(\beta_{13}\), and \(\beta_{23}\) are the cross-level interaction terms representing the effect of the mother MDD × MGPS interaction on the CDI intercept, the slope of the relation between youth’s current and lagged CDI scores, and the slope of the relation between episodic stress and CDI scores, respectively. Finally, \(\beta_{00}\), \(\beta_{10}\), and \(\beta_{20}\) are the intercept terms for each of their respective equations, and \(r_{0j}\), \(r_{1j}\), and \(r_{2j}\) are the error terms.

## Results

### Preliminary Analyses

An initial inspection of the data revealed that several variables exhibited significant skew (\(z > 3.29\); cf. Tabachnick & Fidell, 2007). These variables were transformed prior to further analysis to satisfy assumptions of normality (square root: T1-T5 Interpersonal Stress, T1-T5 Independent Stress, T1-T5 CDI; inverse: T1-T5 Non-Interpersonal Stress). Additionally,
given the presence of missing data (T2 Stress: 10.5%; T3 Stress: 18.5%; T4 Stress: 22.7%;
T5 Stress: 30.3%; CDI T1: 2.1%; CDI T2: 16.4%; CDI T3: 23.9%; CDI T4: 34.0%; CDI T5:
31.9%; NR3C2 haplotype: 2.9%), we examined whether the data were missing at random,
thereby justifying the use of data imputation methods for estimating missing values (cf.
Schafer & Graham, 2002). We found that Little’s missing completely at random (MCAR)
test, for which the null hypothesis is that the data are MCAR, was nonsignificant, $\chi^2$(966) =
1003.01, $p = .20$. Given this, maximum likelihood estimates of missing data were created
and used for all analyses. Descriptive statistics for all study variables are presented in Table
2. To facilitate comparisons with other studies, we present untransformed values for these
variables. Preliminary analyses were then conducted to determine if any of the study
variables were significantly related to youth’s MGPS. There were no significant differences
in youth’s MGPS based on mothers’ history of MDD, $t(236) = −0.59$, $p = .56$, $r$ effect size = −.04,
or youths’ sex, $t(236) = 1.26$, $p = .21$, $r$ effect size = .08. Additionally, youth’s MGPS was
not significantly associated with average levels of interpersonal, $r = .06$, $p = .39$, or non-
interpersonal, $r = .04$, $p = .58$, stress across the study.

**Vulnerability-Stress Analyses**

Next, we tested the vulnerability-stress models using HLM as described earlier. The results
of these analyses are presented in Table 3. As can be seen in the table, although none of the
main or interaction effects for mother MDD or MGPS were significant for non-interpersonal
stress, the mother MDD × MGPS × interpersonal stress interaction was significant in
predicting prospective changes in youth’s depression symptoms. To explore the form of this
interaction, we examined the MGPS × interpersonal stress interaction separately for youth of
mothers with and without a history of MDD. We found that MGPS significantly moderated
the relation between interpersonal stress and prospective changes in youth’s depressive
symptoms among offspring of mothers with a history of MDD, $t(120) = 2.55$, $p = .01$,
$r$ effect size = .23 (95% confidence interval [CI]: .05, .38), but not among offspring of never
depressed mothers, $t(114) = −0.86$, $p = .39$, $r$ effect size = −.08 (95% CI: −.26, .10). The
significant MGPS × interpersonal stress interaction for offspring of depressed mothers is
presented in Figure 1. Conducting a region of significance analysis using Preacher and
colleagues’ (2006) online computational tools, we found that the relation between
interpersonal stress and prospective increases in youth’s depressive symptoms was
significant for youth with a MGPS of 3 or greater but not among those with a lower MGPS.

Next, we conducted a series of follow-up tests to examine the robustness of these results.
Focusing on offspring of depressed mothers with a MGPS of 3 or more, we first examined
whether the relation between interpersonal stress and prospective increases in depressive
symptoms was maintained when we excluded youth with a lifetime history of MDD at the
initial assessment. Our results were maintained, $t(68) = 3.26$, $p < .01$, $r$ effect size = .37 (95%
CI: .15, .54). Next, we examined whether our results were maintained when statistically
controlling for the influence of mothers’ depressive episodes during the course of the 2-year
follow-up. Specifically, we included the number of weeks that each mother was in a major
depressive episode between each assessment as a time-varying covariate in our HLM
analyses. Again, our results were maintained, $t(71) = 2.40$, $p = .02$, $r$ effect size = .27 (95%
CI: .05, .46). Third, given potential concerns about population stratification, we examined
whether our results were maintained when focusing only on Caucasians, and they were, \( t(61) = 3.03, p < .01, r_{\text{effect size}} = .36 \) (95% CI: 0.13, 0.54). Exploratory analyses were then conducted to determine if any of these effects were moderated by youth’s age or sex. None of these analyses were significant.

Finally, we re-conducted our main analyses using individual SNPs/haplotypes instead of the MGPS to determine whether the MDD × SNP/haplotype × stress interaction was significant for any of the individual SNPs or haplotypes that make up the MGPS. None of these interactions was significant for interpersonal or non-interpersonal stress, although the MDD × \( \text{CRHR1 TAT} \) × interpersonal stress interaction approached significance, \( t(234) = 1.76, p = .08, r_{\text{effect size}} = .11 \) (95% confidence interval \[CI\]: −.01, .24). These results suggest that the MGPS results were not driven by any single haplotype/SNP acting in isolation.

**Discussion**

The primary aim of this study was to examine whether specific genetic and environmental influences could help to identify which children of depressed mothers are at greatest risk for depression themselves. In terms of genetic influences, we focused on a multilocus genetic profile score (MGPS) reflecting variants in genes known to be associated with greater HPA axis reactivity (Derijk, 2009; Ising et al., 2008; Luijik et al., 2010; Mahon et al., 2013; Pagliaccio et al., 2014; Sheikh et al., 2013; van Leeuwen et al., 2011; Zannas & Binder, 2014). In terms of environmental influences, we focused on interpersonal and non-interpersonal events separately given evidence that interpersonal events are stronger contributors to depression risk (Rudolph et al., 2000) and may be stronger predictors of HPA axis reactivity (Dickerson & Kemeny, 2004; Stroud et al., 2016) than non-interpersonal stressors. Supporting our hypotheses, we found that, among children of depressed mothers, those with a higher MGPS who also experienced higher levels of interpersonal stress experienced the greatest increases in depressive symptoms between assessments. The G × E findings were significant for interpersonal, but not non-interpersonal, stress and were not observed among children of never depressed mothers.

These results add to a growing body of research suggesting that variants in genes that help to regulate the HPA axis may moderate the impact of life stress on individuals’ risk for depression (e.g., Appel et al., 2011; Bet et al., 2009; Bradley et al., 2008). The current study extends this previous research in several important ways. It is the first study to examine whether variation in these genes moderate the impact of negative life events on prospective changes in depressive symptoms among children and adolescents. It is also the first to test this type of integrated G × E model of risk for the intergenerational transmission of depression. Although previous studies have examined whether variation in these and other genes may moderate the link between mother and child depression (e.g., Lewis, Collishaw, Harold, Rice, & Thapar, 2012), the current findings highlight the important additional role played by interpersonal stressors in understanding youths’ risk for depression. Finally, the current study is one of the first to examine an HPA axis MGPS within the context of a G × E model of depression risk. In contrast, the majority of previous research has examined variation in each gene individually and it is increasingly recognized that complex phenotypes such as depression likely result from the combined influence of multiple genes.
within specific biological pathways rather than any single gene acting in isolation. This approach is also supported by a recent study showing that although an HPA axis MGPS significantly predicted cortisol reactivity to a stressor, none of the individual SNPs were significant when examined in isolation (Pagliaccio et al., 2014).

We should also highlight that the pattern of the G × E observed in our study is consistent with differential susceptibility models of genetic influence (Belsky, 1997; Belsky, Bakermans-Kranenburg, & Van Ijzendoorn, 2007). Specifically, although a higher MGPS combined with elevated levels of interpersonal stress predicted increases in depressive symptoms for children of depressed mothers, a higher MGPS was associated with lower levels of depression in the context of low stress. Consistent with differential susceptibility models, therefore, it appears that this MGPS is associated with worse outcomes in negative environments but better outcomes in positive environments. These results add to a growing body of research suggesting that these genetic influences may be better characterized as increasing “plasticity” rather than only risk (see Bakermans-Kranenburg & van IJzendoorn, 2015; Belsky et al., 2009).

Finally, we should note that, although significant, our model only explained 12% of the variance in depressive symptom increases among the highest risk youth (offspring of depressed moms with MGPS of 3 or greater) and relatively modest increases in depressive symptoms between adjacent assessments. This said, we believe that the current results are an important first step in utilizing a MGPS approach to test G × E models of risk for the intergenerational transmission of depression. It will be important for future research to incorporate other potential influences to develop more comprehensive, unified models of risk. For example, because maternal depression is associated with both a decreased likelihood of developing a secure attachment with one’s infant (for a review, see Martins & Gaffan, 2000) and lower levels of peer support for their offspring (Lewinsohn, Olino, Klein, & others, 2005), social support and attachment styles may be important influences. Furthermore, although we focused on episodic stress, children of depressed mothers also experienced elevated levels of chronic stress compared to children of never depressed mothers (Feurer et al., 2016; Gershon et al., 2011; Hammen, Shih, & Brennan, 2004) and there is evidence that chronic and episodic stressors may be unique predictors of depression for adolescents (Vrshek-Schallhorn, Stroud, College, et al., 2015). Therefore, future studies should examine whether these different forms of stress independently interact with MGPSs to predict increases in depressive symptoms in high-risk youth. Finally, we focused on genetic variation in a select number of genes associated with HPA axis activity. There are a number of other factors that may influence the relevance of these genes to responses to interpersonal stress including epigenetic modification and other influences that modify transcription and/or translation of the gene products. However, variability in these mechanisms raises additional questions about possible tissue-specificity that are beyond the scope of these data (i.e., in contrast to epigenetic, and expression approaches, genetic variation is assumed to be largely consistent in all tissues).

The current study exhibited several strengths including the use of a theoretically-derived, biological pathway based MGPS established in previous research (Di Iorio et al., 2017), semi-structured life stress interview assessments, and a multi-wave prospective study design.
However, there were also some limitations which should be acknowledged. First, our study only examined the depressive history of mothers and its impact on offspring depressive symptoms. Because paternal history of depression also increases depression risk in offspring (Lieb, Isensee, Höfler, Pfister, & Wittchen, 2002), future studies should examine the history of MDD in both parents. Second, because we only focused on prospective changes in depressive symptoms, future research is needed to determine whether these results generalize to the prediction of depressive episodes in youth. Third, we did not assess for youth’s exposure to early life stress. There is evidence that early life stress may contribute to depression risk in adolescence through the mediating role of continued stress exposure (Hazel, Hammen, Brennan, & Najman, 2008). Although many studies have shown that early life stress interacts with HPA regulatory genes to predict depression in adults (e.g., Appel et al., 2011; Polanczyk et al., 2009), it may be that genetic influences associated with greater HPA axis reactivity do not exacerbate the impact of early life stress, per se, but rather moderate the impact of more recent life stressors that are associated with this early stress exposure. Furthermore, as early life stress may sensitize individuals to the impact of more recent stressors (Hammen, Henry, & Daley, 2000; McLaughlin, Conron, Koenen, & Gilman, 2010), it may be that individuals with high MGPS who experienced high levels of both early and recent life stress (G × early life stress × recent life stress) are at greatest risk for depression. Future studies should examine both early life and recent stressors together when considering G × E interactions and risk for depression in youth. Fourth, it is possible that the lack of support for non-interpersonal stress may have been due to the extreme skew of these variables. Therefore, although our results are consistent with prior research highlighting the importance of interpersonal stress specifically for youth depression risk (Flynn & Rudolph, 2011), future research is needed to more definitively examine the potential role of non-interpersonal stress in risk for depression among children of depressed mothers. Fifth, although our focus on a MGPS within a theory-driven biological pathway represents an advance beyond the traditional focus on a single polymorphism, the number of included variants was still rather small and it is likely that greater coverage of genes associated with HPA axis reactivity will yield stronger results. In addition, we used an additive approach in creating our MGPS, with each variant given equal weight and it is likely that future advances will allow us to provide weighted scores that better account for the individual influence of each variant. Another limitation is that our sample size is relatively small for a genetic association study. Therefore, replication with large samples are needed. Finally, because we were not able to include a replication sample as part of this study, conclusions must remain tentative pending replication.

In summary, the current study contributes to the literature on mechanisms underlying the intergenerational transmission of depression by highlighting specific genetic and environmental influences that may increase risk in children of depressed mothers. As such, it not only highlights a biological pathway underlying this risk (genes associated with HPA axis reactivity) but also a modifiable risk factor in at-risk youth (heightened levels of interpersonal stress). If replicated, these results suggest that focusing specifically on reducing levels of interpersonal stress among children of depressed mothers may help to reduce their risk for developing depression themselves.
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Figure 1.
Interpersonal Stress × MGPS Interaction for Offspring of Depressed Mothers. The shaded region is the region of the MGPS at which the slope of the relation between stress and youth’s depressive symptoms becomes significant (p < .05).
CDI = Children’s Depression Inventory. MGPS = Multilocus genetic profile score.
Table 1
Descriptive Statistics for the Polymorphisms Included in the Multilocus Genetic Profile Score

<table>
<thead>
<tr>
<th>Polymorphism</th>
<th>Coding</th>
<th>N</th>
</tr>
</thead>
<tbody>
<tr>
<td>CRHR1 TAT haplotype</td>
<td>2 copies = 0</td>
<td>25</td>
</tr>
<tr>
<td>(rs7209436, rs110402, rs242924)</td>
<td>1 copy = 1</td>
<td>122</td>
</tr>
<tr>
<td></td>
<td>0 copies = 2</td>
<td>91</td>
</tr>
<tr>
<td>FKB5</td>
<td>CC = 0</td>
<td>109</td>
</tr>
<tr>
<td>(rs1360780)</td>
<td>CT = 1</td>
<td>99</td>
</tr>
<tr>
<td></td>
<td>TT = 2</td>
<td>30</td>
</tr>
<tr>
<td>NR3C2 CA haplotype</td>
<td>2 copies = 0</td>
<td>38</td>
</tr>
<tr>
<td>(rs2070951, rs5522)</td>
<td>1 copy = 1</td>
<td>125</td>
</tr>
<tr>
<td></td>
<td>0 copies = 2</td>
<td>75</td>
</tr>
</tbody>
</table>

The HPA axis multilocus genetic profile score (MGPS) was created by summing the number of “high risk” polymorphisms across these three genes.
Table 2
Descriptive Statistics for Study Variables

<table>
<thead>
<tr>
<th></th>
<th>Depressed Mothers ((n = 122))</th>
<th>Nondepressed Mothers ((n = 116))</th>
<th>(r_{effect\ size})</th>
</tr>
</thead>
<tbody>
<tr>
<td>Youth Age</td>
<td>11.40 (2.03)</td>
<td>11.38 (1.82)</td>
<td>.01</td>
</tr>
<tr>
<td>Youth Sex (% girls)</td>
<td>50.0%</td>
<td>53.4%</td>
<td>-.03</td>
</tr>
<tr>
<td>Youth Race (% Caucasian)</td>
<td>73.8%</td>
<td>90.5%</td>
<td>-.22 **</td>
</tr>
<tr>
<td>MGPS</td>
<td>3.06 (1.14)</td>
<td>3.15 (1.24)</td>
<td>-.04</td>
</tr>
<tr>
<td>T1 CDI</td>
<td>7.26 (5.77)</td>
<td>4.74 (5.23)</td>
<td>.25 **</td>
</tr>
<tr>
<td>T2 CDI</td>
<td>6.40 (5.77)</td>
<td>3.53 (4.19)</td>
<td>.29 **</td>
</tr>
<tr>
<td>T3 CDI</td>
<td>5.76 (4.62)</td>
<td>3.64 (4.15)</td>
<td>.25 **</td>
</tr>
<tr>
<td>T4 CDI</td>
<td>5.07 (4.60)</td>
<td>2.90 (3.68)</td>
<td>.28 **</td>
</tr>
<tr>
<td>T5 CDI</td>
<td>6.02 (5.71)</td>
<td>3.65 (4.86)</td>
<td>.25 **</td>
</tr>
<tr>
<td>T1 Interpersonal Stress</td>
<td>2.63 (2.25)</td>
<td>1.54 (1.57)</td>
<td>.26 **</td>
</tr>
<tr>
<td>T2 Interpersonal Stress</td>
<td>2.39 (2.44)</td>
<td>1.00 (1.16)</td>
<td>.34 **</td>
</tr>
<tr>
<td>T3 Interpersonal Stress</td>
<td>2.40 (1.97)</td>
<td>1.38 (1.50)</td>
<td>.27 **</td>
</tr>
<tr>
<td>T4 Interpersonal Stress</td>
<td>1.99 (1.74)</td>
<td>1.13 (1.12)</td>
<td>.25 **</td>
</tr>
<tr>
<td>T5 Interpersonal Stress</td>
<td>2.07 (1.89)</td>
<td>1.36 (1.41)</td>
<td>.22 **</td>
</tr>
<tr>
<td>T1 Non-Interpersonal Stress</td>
<td>0.39 (0.59)</td>
<td>0.35 (0.50)</td>
<td>.01</td>
</tr>
<tr>
<td>T2 Non-Interpersonal Stress</td>
<td>0.48 (0.63)</td>
<td>0.49 (0.70)</td>
<td>.00</td>
</tr>
<tr>
<td>T3 Non-Interpersonal Stress</td>
<td>0.75 (1.04)</td>
<td>0.36 (0.71)</td>
<td>.25 **</td>
</tr>
<tr>
<td>T4 Non-Interpersonal Stress</td>
<td>0.50 (0.77)</td>
<td>0.43 (0.61)</td>
<td>.02</td>
</tr>
<tr>
<td>T5 Non-Interpersonal Stress</td>
<td>0.68 (0.92)</td>
<td>0.37 (0.64)</td>
<td>.23 **</td>
</tr>
</tbody>
</table>

Note. MDD = Major depressive disorder. CDI = Children’s Depression Inventory. MGPS = Multilocus genetic profile score.

* \(p < .05\);

** \(p < .01\).
Table 3
Summary of HLM analyses examining Maternal MDD × MGPS × Stress interactions predicting increases in youth’s depressive symptoms

<table>
<thead>
<tr>
<th></th>
<th>Interpersonal Stress</th>
<th>Non Interpersonal Stress</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>t</td>
<td>r_{effect size} (95% CI)</td>
</tr>
<tr>
<td>CDI, Intercept (π_{0j})</td>
<td>1.69</td>
<td>.11 (−.02, .23)</td>
</tr>
<tr>
<td>MDD (β_{01})</td>
<td>0.65</td>
<td>.04 (−.09, .17)</td>
</tr>
<tr>
<td>MGPS (β_{02})</td>
<td>−0.11</td>
<td>−.01 (−.13, .12)</td>
</tr>
<tr>
<td>MDD × MGPS (β_{03})</td>
<td>−0.67</td>
<td>−.04 (−.17, .08)</td>
</tr>
<tr>
<td>CDI <em>t-1</em> Slope (π_{1j})</td>
<td></td>
<td></td>
</tr>
<tr>
<td>MDD (β_{11})</td>
<td>1.11</td>
<td>.07 (−.06, .20)</td>
</tr>
<tr>
<td>MGPS (β_{12})</td>
<td>0.81</td>
<td>.05 (−.08, .18)</td>
</tr>
<tr>
<td>MDD × MGPS (β_{13})</td>
<td>−0.96</td>
<td>−.06 (−.19, .07)</td>
</tr>
<tr>
<td>Episodic Stress Slope (π_{2j})</td>
<td></td>
<td></td>
</tr>
<tr>
<td>MDD (β_{21})</td>
<td>−1.80</td>
<td>−.12 (−.24, .01)</td>
</tr>
<tr>
<td>MGPS (β_{22})</td>
<td>−0.84</td>
<td>−.06 (−.18, .07)</td>
</tr>
<tr>
<td>MDD × MGPS (β_{23})</td>
<td>2.15*</td>
<td>.14 (.01, .26)</td>
</tr>
</tbody>
</table>

Note. CDI = Children’s Depression Inventory. MDD = Mother history of major depressive disorder (yes, no). MGPS = Multilocus genetic profile scores.

*p < .05.