



Letter to the Editor

Brain derived neurotrophic factor (BDNF) polymorphism Moderates the interactive effect of 5-HTTLPR polymorphism and childhood abuse on diagnoses of major depression in women


To the Editors:

There is growing interest in identifying specific genetic influences that may moderate the impact of environmental stressors (E) on depression risk. The majority of studies have focused on 5-HTTLPR, though findings have been mixed (Karg et al., 2011), suggesting the presence of unmeasured moderating influences. There is evidence that 5-HTTLPR \times E effects on depression may be stronger among individuals carrying the BDNF Met allele than among those homozygous for the Val allele (e.g. Kaufman et al., 2006).

This study aimed to replicate and extend previous research by testing a 5-HTTLPR \times BDNF Val66Met \times E model of risk, oversampling for women with histories of MDD and focusing on histories of childhood abuse as environmental stressors. We predicted that the 5-HTTLPR \times childhood abuse interaction would be stronger for women carrying at least one copy of the BDNF Met allele than for women homozygous for the Val allele, with the greatest risk for depression observed among women with a history of childhood abuse with at least one copy of the 5-HTTLPR S (or L_G) allele and the BDNF Met allele.

A total of 181 women with a history of MDD and 174 who had no lifetime history of any DSM-IV mood disorder and no current Axis I diagnosis were investigated (*M* age=40.11, *S.D.*=6.79, 87.9% Caucasian). Participants' histories of DSM-IV Axis I disorders were assessed using the Structured Clinical Interview for DSM-IV Axis I Disorders (SCID-I; First et al., (1995)). A subset of 20 SCID interviews was coded by a second interviewer and inter-rater reliability for diagnoses of MDD was excellent (κ =1.00). The Childhood Trauma Questionnaire (CTQ; Bernstein et al., 2003) was used to assess participants' histories of childhood emotional, physical, and sexual abuse. In this population sample, CTQ exhibited good internal consistency (emotional abuse α =0.86, physical abuse α =0.85, sexual abuse α =0.96). Women were coded as having no history of abuse (*n*=232), or having a history of any moderate abuse (*n*=123). The 5-HTTLPR S alleles, rs25531 SNP and BDNF Val66Met were assayed using previously reported methods (Pooley et al., 2003; Wendland et al., 2006). Observed genotype frequencies did not differ from Hardy Weinberg equilibrium (p =0.85; χ^2 =0.28, p =0.60). Less than 5% of the data were missing and Little's missing completely at random (MCAR) test was non-significant, χ^2 =27.13 (25), p =0.35, suggesting that the data were missing at random. Therefore, multiple imputation was used to generate 20 datasets and the results presented reflect pooled estimates across these datasets, yielding more reliable parameter estimates than other methods of dealing with missing data (see Schafer and Graham, 2002). We should note, however, that the results were maintained using the original unimputed dataset.

Preliminary analyses indicated that women's history of childhood abuse was not significantly related to their 5-HTTLPR (χ^2 =0.33, p =0.60, ϕ =0.03) or Val66Met (χ^2 =2.54, p =0.13, ϕ =-0.11) genotype, suggesting the lack of any significant gene-environment correlations with these two polymorphisms.

Using a hierarchical logistic regression analysis with women's history of MDD (yes, no) serving as the criterion variable, we entered each of the main effects in step 1. We found a significant main effect of childhood abuse (Wald=42.51, p <0.001, OR=5.21, CI=3.22–8.89), but not 5-HTTLPR (Wald=1.10, p =0.31, OR=1.31, CI=0.78–2.25) or BDNF Val66Met (Wald=0.72, p =0.42, OR=1.21, CI=0.78–2.04). In the second step, we entered each of the two-way interactions. None of these was significant: 5-HTTLPR \times childhood abuse (Wald=0.10, p =0.83, OR=0.86, CI=0.57–5.84), Val66Met \times childhood abuse (Wald=1.73, p =0.23, OR=0.27, CI=0.53–5.12), and 5-HTTLPR \times Val66Met (Wald=3.16, p =0.09, OR=0.33, CI=0.23–2.14). In the third step, we entered the three-way Val66Met \times 5-HTTLPR \times childhood abuse interaction, which was significant (Wald=4.47, p =0.04, OR=14.39, CI=1.15–172.10).

To examine the form of this interaction, we tested the 5-HTTLPR \times childhood abuse interaction separately among carriers of the BDNF Met allele (*n*=133) versus those homozygous for the Val allele (*n*=222). Among carriers of the BDNF Met allele, the 5-HTTLPR \times childhood abuse interaction significantly predicted women's history of MDD (Wald=5.63, p =0.02, OR=12.38, CI=1.60–106.98). In contrast, among women homozygous for the Val allele, the 5-HTTLPR \times childhood abuse interaction was not significant (Wald=0.10, p =0.83, OR=0.86, CI=0.22–3.37). Focusing next on the impact of childhood abuse among carriers of the BDNF Met allele as a function of 5-HTTLPR genotype, we found that the link between women's histories of childhood abuse and MDD was significant among Met carriers with at least one copy of the 5-HTTLPR S' allele (*n*=99; Wald=19.25, p <0.001, OR=16.28, CI=4.70–57.93) but not among Met carriers homozygous for the L_A allele (*n*=34; Wald=0.22, p =0.86, OR=0.93, CI=0.26–7.24). We should also note that all of these results were maintained when we limited our sample to Caucasians (*n*=306) Fig. 1.

These findings suggest that the previous mixed findings observed in studies testing 5-HTTLPR \times E models of risk for depression may have been partially due to the failure to account for epistatic influences. In this study, the predicted 5-HTTLPR \times childhood abuse interaction was only significant among women carrying at least one copy of the BDNF Met allele, but not among those homozygous for the Val allele. Future research is needed to determine whether these findings generalize to predicting prospective onsets of MDD and to

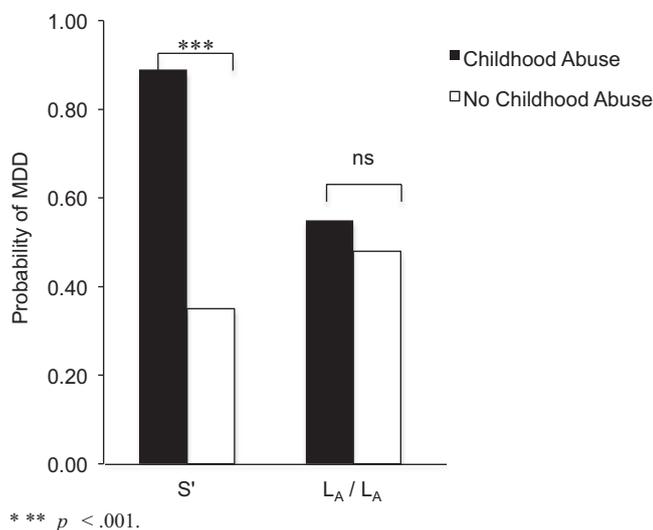


Fig. 1. Supporting a $G \times G \times E$ model of risk, history of childhood abuse increased the probability of MDD, but only among carriers of both the *BDNF* Met and 5-HTTLPR S' alleles.

examine specific mechanisms by which early adversity contributes to depression risk among genetically more reactive individuals as these mechanisms might provide useful targets of intervention.

Acknowledgments

This project was supported by National Institute of Child Health and Human Development Grant HD057066, National Institute of Mental Health Grants MH098060, and 1S10RR023457-01A1 and Shared equipment grants (ShEEP) from the Medical Research Service of the Department of Veteran Affairs. The views expressed in this article are those of the authors and do not necessarily reflect the position or policy of the Department of Veterans Affairs or the National Institutes of Health. We would like to thank Ashley Johnson, Lindsey Stone, Andrea Hanley, Katie Burkhouse, Mary Woody, Sydney Meadows, and Michael Van Wie for their help in conducting assessments for this project.

References

- Bernstein, D.P., Stein, J.A., Newcomb, M.D., Walker, E., Pogge, D., Ahluvalia, T., Stokes, J., Handelsman, L., Medrano, M., Desmond, D., Zule, E., 2003. Development and validation of a brief screening version of the Childhood Trauma Questionnaire. *Child Abuse and Neglect* 27, 169–190.
- First, M.B., Spitzer, R.L., Gibbon, M., Williams, J.B., 1995. Structured Clinical Interview for the DSM-IV Axis I Disorders. Biometrics Research Department, NY State Psychiatric Institute, New York.
- Karg, K., Burmeister, M., Shedden, K., Sen, S., 2011. The serotonin transporter promoter variant (5-HTTLPR), stress, and depression meta-analysis revisited: evidence of genetic moderation. *Archives of General Psychiatry* 68, 444–454. <http://dx.doi.org/10.1001/archgenpsychiatry.2010.189>.
- Kaufman, J., Yang, B.-Z., Douglas-Palumberi, H., Grasso, D., Lipschitz, D., Houshyar, S., Gelernter, J., 2006. Brain-derived neurotrophic factor-5-HTTLPR gene interactions and environmental modifiers of depression in children. *Biological Psychiatry*, 59; pp. 673–680. <http://dx.doi.org/10.1016/j.biopsych.2005.10.026>.
- Pooley, E.C., Houston, K., Hawton, K., Harrison, P.J., 2003. Deliberate self-harm is associated with allelic variation in the tryptophan hydroxylase gene (TPH A779C), but not with polymorphisms in five other serotonergic genes. *Psychological Medicine* 33, 775–783.
- Schafer, J.L., Graham, J.W., 2002. missing data: our view of the state of the art. *Psychological Methods* 7, 147–177.
- Wendland, J.R., Martin, B.J., Kruse, M.R., Lesch, K.P., Murphy, D.L., 2006. Simultaneous genotyping of four functional loci of human SLC6A4, with a reappraisal of 5-HTTLPR and rs 25531. *Molecular Psychiatry* 11, 224–226.

Anastacia Y. Kudinova, Brandon E. Gibb
Binghamton University (SUNY), United States
E-mail address: akudino1@binghamton.edu (A.Y. Kudinova)

John E. McGeary
Providence Veterans Affairs Medical Center, Department of Psychiatry and Human Behavior, Alpert Medical School, Brown University, United States

Valerie S. Knopik
Department of Psychiatry and Human Behavior, Alpert Medical School, Brown University Division of Behavioral Genetics, Rhode Island Hospital, Providence, RI, United States

Received 25 June 2014
29 September 2014
21 October 2014

Available online 13 November 2014