

# The Biological Effects of Trauma

Shareefa Dalvie<sup>a, b</sup> Nikolaos P. Daskalakis<sup>c, d</sup>

<sup>a</sup>Department of Psychiatry and Neuroscience Institute, University of Cape Town, Cape Town, South Africa;

<sup>b</sup>Department of Paediatrics and Child Health, University of Cape Town, Cape Town, South Africa; <sup>c</sup>Stanley Center for Psychiatric Research, Broad Institute of MIT and Harvard, Cambridge, MA, USA; <sup>d</sup>Department of Psychiatry, McLean Hospital, Harvard Medical School, Belmont, CA, USA

The experience of psychosocial trauma or adversity is ever-pervasive in our society. A global population survey showed that 70% of respondents were exposed to traumas such as collective violence, interpersonal or intimate partner violence, and accidents/injuries [1]. This is alarming given that trauma or stress experienced during childhood and adulthood increases the risk for the development of psychopathology such as posttraumatic stress disorder and depression [2, 3], and physical ill health such as cardiovascular disease and diabetes [4–6]. Exposure to certain traumas appears to be sex-specific. For example, males are more likely to experience non-sexual assault and combat-related trauma, and females are more likely to be exposed to sexual assault and childhood sexual abuse. Overall, females report lower rates of trauma exposure but are twice as likely to be diagnosed with posttraumatic stress disorder than males [7], potentially indicating that trauma type, frequency, and timing may increase the risk for this disorder [8].

Exactly how an environmental exposure (such as trauma) “gets under our skin,” that is, affects our biology in a long-lasting manner, remains unclear. One potential mechanism is via epigenetic modifications during critical periods in development which may lead to developmen-

tal programming of long-lasting adaptive and/or maladaptive responses to changes in the early life environment [9]. Epigenetics is the study of heritable changes in gene function that are not due to changes in the DNA sequence [10]. The most studied epigenetic changes in clinical settings, using peripheral (e.g., whole blood and saliva) and brain samples, are alterations in methylation at CpG dinucleotides. Early adversity has shown to increase or decrease the DNA methylation (DNAm) status of several CpG sites, mostly located in the regulatory regions (e.g., gene promoters) and in the genes *SLC6A4* (serotonin transporter), *NR3C1* (glucocorticoid receptor), *FKBP5* (regulates glucocorticoid receptor activity), and *IL6* (pro-inflammatory cytokine) [11, 12]. Many studies conducted in populations at risk for psychopathology show that the observed DNAm changes are in association with risk alleles; thus, suggesting that DNAm may mediate the observed gene-by-trauma interactions [13]. However, these candidate gene-by-environment interactions are not always replicated in the general population [14]. A more recent study showed that genetics and gene-by-childhood trauma interactions account for the majority of variance in DNAm compared to childhood trauma alone [15]. It is worth noting that genetic variation has

also shown to influence risk for exposure to early adversity [16]. This is referred to as gene-environment correlation, defined as the genetic differences in exposure to certain environments [17, 18].

The pattern of epigenetic modifications generally correlates with the corresponding gene expression profile, where an overall negative correlation between promoter DNAm and gene expression has been canonically observed [19, 20]. As with DNAm, significant differences in gene expression levels have been observed in individuals who have experienced trauma compared to those who have not [21]. Furthermore, a distinct immune-related gene expression profile, known as common conserved transcriptional response to adversity, characterized by upregulation of the expression of genes involved in inflammation and downregulation of genes involved in type I interferon responses and antibody synthesis, has been observed in individuals exposed to chronic threat [22]. This type of immune transcriptional response has been seen in childhood trauma survivors, without any psychiatric diagnoses, after an acute psychosocial stressor [23]. The downstream effects of these immune-related gene expression changes in the peripheral and brain tissues, as a result of trauma, still need to be fully understood.

Interestingly, accumulating evidence suggests that the effects of trauma can be inherited intergenerationally. One of the first studies to observe this phenomenon was in the offspring of holocaust survivors who had a higher rate of psychopathology [24]. However, this offspring population also reported higher levels of childhood trauma [25] and resilience [26]. The intergenerational effects of trauma have also been studied in mothers who were pregnant during the Apartheid era in South Africa – the offspring of young mothers who had experienced greater stress had increased psychiatric morbidity than those whose mothers had experienced less traumatic stress during this time period [27]. Trauma is thought to be “transmitted” across generations through epigenetic mechanisms. For example, the offspring of Holocaust survivors had lower blood DNAm in *FKBP5*, especially in those whose mothers were exposed during childhood [28, 29], while their parents showed opposite effects (i.e., increased DNAm) at this gene [28]. Further, blood transcriptome analyses revealed glucocorticoid and immune-related gene alterations in association with parental Holocaust exposure [30]. Whole genome-wide DNAm analysis showed that individuals exposed to famine in utero had differential DNAm in regions related to development [31]. Another study showed that maternal expo-

sure to childhood abuse was associated with sex-specific DNAm and expression alterations of the *BDNF* gene (encodes a neurotrophic factor) in the offspring [32]. Another multigenerational analysis of DNAm found limited evidence for intergenerational transmission [33]. These findings provide some evidence of the role that epigenetic influences may have in the intergenerational “transmission” of trauma; however, further research is needed to delineate and understand the exact mechanisms involved.

Studies on trauma, particularly trauma experienced during early life, are limited by methodological challenges. For example, many studies use retrospective self-report measures when assessing trauma, and this can be influenced by recall bias and an individual’s subjective interpretation of an adverse event. Indeed, a systematic review found low concordance between prospective and retrospective measures of childhood maltreatment [34]. Furthermore, the method of data collection may also have an influence: face-to-face interviews may result in different trauma prevalence being recorded compared to telephone, self-administered, or computer-assisted surveys [35]. Finally, many of the published studies use peripheral measures of DNAm, which need to be expanded to large-scale molecular investigations of postmortem brains [36], and cell type-specific alterations [37].

It is clear that there is still much that we do not know about the effects of trauma on our biology, and much more investigation into this area is needed. Findings from research on the effects of trauma may inform the development of targeted intervention programs, with the ultimate goal of significantly decreasing the prevalence of trauma and its psychosocial and biological impact.

### **Conflict of Interest Statement**

In the past 3 years, N.P.D. has held a part-time paid position at Cohen Veterans Bioscience, has been a consultant for Sunovion Pharmaceuticals, and is on the scientific advisory board for Sentio Solutions for unrelated work.

### **Funding Sources**

N.P.D. was supported by NIMH P50-MH115874.

### **Author Contributions**

S.D. and N.P.D. researched the topic, co-wrote the manuscript, and approved the final version of the manuscript.

## References

- 1 Benjet C, Bromet E, Karam EG, Kessler RC, McLaughlin KA, Ruscio AM, et al. The epidemiology of traumatic event exposure worldwide: results from the World Mental Health survey consortium. *Psychol Med.* 2016;46(2): 327–43.
- 2 Myers HF, Wyatt GE, Ullman JB, Loeb TB, Chin D, Prause N, et al. Cumulative burden of lifetime adversities: trauma and mental health in low-SES African Americans and Latino/as. *Psychol Trauma.* 2015;7(3):243.
- 3 Mersky JP, Janczewski CE, Nitkowski JC. Poor mental health among low-income women in the US: the roles of adverse childhood and adult experiences. *Soc Sci Med.* 2018;206: 14–21.
- 4 Le Carolyn MH, Neylan TC, Na B, Regan M, Zhang Q, Cohen BE. Lifetime trauma exposure and prospective cardiovascular events and all-cause mortality: findings from the Heart and Soul Study. *Psychosom Med.* 2013; 75(9):849.
- 5 Basu A, McLaughlin KA, Misra S, Koenen KC. Childhood maltreatment and health impact: the examples of cardiovascular disease and type 2 diabetes mellitus in adults. *Clin Psychol.* 2017;24(2):125–39.
- 6 Suglia SF, Koenen KC, Boynton-Jarrett R, Chan PS, Clark CJ, Danese A, et al. Childhood and adolescent adversity and cardiometabolic outcomes: a scientific statement from the American Heart Association. *Circulation.* 2018;137(5):e15–28.
- 7 Tolin DF, Foa EB. Sex differences in trauma and posttraumatic stress disorder: a quantitative review of 25 years of research. 2008.
- 8 Kimerling R, Allen MC, Duncan LE. Chromosomes to social contexts: sex and gender differences in PTSD. *Curr Psychiatry Rep.* 2018;20(12):1–9.
- 9 Chen M, Zhang L. Epigenetic mechanisms in developmental programming of adult disease. *Drug Discov Today.* 2011;16(23–24):1007–18.
- 10 Dupont C, Armant DR, Brenner CA, editors. *Epigenetics: definition, mechanisms and clinical perspective. Seminars in reproductive medicine.* NIH Public Access; 2009.
- 11 Daskalakis NP, Yehuda R. Site-specific methylation changes in the glucocorticoid receptor exon 1F promoter in relation to life adversity: systematic review of contributing factors. *Front Neurosci.* 2014;8:369.
- 12 Neves I, Dinis-Oliveira RJ, Magalhães T. Epigenomic mediation after adverse childhood experiences: a systematic review and meta-analysis. *Forensic Sci Res.* 2019:1–12.
- 13 Klengel T, Mehta D, Anacker C, Rex-Haffner M, Pruessner JC, Pariante CM, et al. Allele-specific FKBP5 DNA demethylation mediates gene-childhood trauma interactions. *Nat Neurosci.* 2013;16(1):33–41.
- 14 Border R, Johnson EC, Evans LM, Smolen A, Berley N, Sullivan PF, et al. No support for historical candidate gene or candidate gene-by-interaction hypotheses for major depression across multiple large samples. *Am J Psychiatry.* 2019;176(5):376–87.
- 15 Czamara D, Tisink E, Tuhkanen J, Martins J, Awaloff Y, Drake AJ, et al. Combined effects of genotype and childhood adversity shape variability of DNA methylation across age. *Transl Psychiatry.* 2021;11(1):88–11.
- 16 Dalvie S, Maihofer AX, Coleman JRI, Bradley B, Breen G, Brick LA, et al. Genomic influences on self-reported childhood maltreatment. *Transl Psychiatry.* 2020;10(1):38–12.
- 17 Jaffee SR, Price TS. Genotype-environment correlations: implications for determining the relationship between environmental exposures and psychiatric illness. *Psychiatry.* 2008; 7(12):496–9.
- 18 Schulz-Heik RJ, Rhee SH, Silvern L, Lessem JM, Haberstick BC, Hopfer C, et al. Investigation of genetically mediated child effects on maltreatment. *Behav Genet.* 2009;39(3):265–76.
- 19 van Eijk KR, de Jong S, Boks MP, Langeveld T, Colas F, Veldink JH, et al. Genetic analysis of DNA methylation and gene expression levels in whole blood of healthy human subjects. *BMC Genomics.* 2012;13(1):636.
- 20 Bell JT, Pai AA, Pickrell JK, Gaffney DJ, Pique-Regi R, Degner JF, et al. DNA methylation patterns associate with genetic and gene expression variation in HapMap cell lines. *Genome Biol.* 2011;12(1):R10.
- 21 Minelli A, Magri C, Giacomuzzi E, Gennarelli M. The effect of childhood trauma on blood transcriptome expression in major depressive disorder. *J Psychiatr Res.* 2018;104:50–4.
- 22 Cole SW. The conserved transcriptional response to adversity. *Curr Opin Behav Sci.* 2019;28:31–7.
- 23 Schwaiger M, Grinberg M, Moser D, Zang JC, Heinrichs M, Hengstler JG, et al. Altered stress-induced regulation of genes in monocytes in adults with a history of childhood adversity. *Neuropsychopharmacology.* 2016; 41(10):2530–40.
- 24 Yehuda R, Schmeidler J, Wainberg M, Binder-Brynes K, Duvdevani T. Vulnerability to posttraumatic stress disorder in adult offspring of Holocaust survivors. *Am J Psychiatry.* 1998;155(9):1163–71.
- 25 Yehuda R, Halligan SL, Grossman R. Childhood trauma and risk for PTSD: relationship to intergenerational effects of trauma, parental PTSD, and cortisol excretion. *Dev Psychopathol.* 2001;13(3):733–53.
- 26 Braga LL, Mello MF, Fiks JP. Transgenerational transmission of trauma and resilience: a qualitative study with Brazilian offspring of Holocaust survivors. *BMC Psychiatry.* 2012; 12(1):134–11.
- 27 Kim AW, Mohamed RS, Norris S, Richter L, Kuzawa C. Psychological legacies of intergenerational trauma under South African Apartheid: prenatal stress predicts increased psychiatric morbidity during late adolescence in Soweto, South Africa. *medRxiv.* 2021.
- 28 Yehuda R, Daskalakis NP, Bierer LM, Bader HN, Klengel T, Holsboer F, et al. Holocaust exposure induced intergenerational effects on FKBP5 methylation. *Biol Psychiatry.* 2016; 80(5):372–80.
- 29 Bierer LM, Bader HN, Daskalakis NP, Lehrner A, Provençal N, Wiechmann T, et al. Intergenerational effects of maternal holocaust exposure on FKBP5 methylation. *Am J Psychiatry.* 2020;177(8):744–53.
- 30 Daskalakis NP, Xu C, Bader HN, Chatzinakos C, Weber P, Makotkine I, et al. Intergenerational trauma is associated with expression alterations in glucocorticoid- and immune-related genes. *Neuropsychopharmacol.* 2021; 46(4):763–73.
- 31 Tobi EW, Goeman JJ, Monajemi R, Gu H, Putter H, Zhang Y, et al. DNA methylation signatures link prenatal famine exposure to growth and metabolism. *Nat Commun.* 2014; 5(1):5592–14.
- 32 Pilkay SR, Combs-Orme T, Tylavsky F, Bush N, Smith AK. Maternal trauma and fear history predict BDNF methylation and gene expression in newborns. *PeerJ.* 2020;8:e8858.
- 33 Peter CJ, Fischer LK, Kundakovic M, Garg P, Jakovcevski M, Dincer A, et al. DNA methylation signatures of early childhood malnutrition associated with impairments in attention and cognition. *Biol Psychiatry.* 2016; 80(10):765–74.
- 34 Baldwin JR, Reuben A, Newbury JB, Danese A. Agreement between prospective and retrospective measures of childhood maltreatment: a systematic review and meta-analysis. *JAMA Psychiatry.* 2019;76:584–93.
- 35 Koenen KC, Roberts AL, Stone DM, Dunn EC. The epidemiology of early childhood trauma. In: Lanius RA, Vermetten E, Pain C, editors. *The impact of early life trauma on health and disease: the hidden epidemic. 1.* UK: Cambridge University Press; 2010.
- 36 Girgenti MJ, Wang J, Ji D, Cruz DA, Stein MB, Gelernter J, et al. Transcriptomic organization of the human brain in post-traumatic stress disorder. *Nat Neurosci.* 2020:1–10.
- 37 Nagy C, Maitra M, Tanti A, Suderman M, Thérout JF, Davoli MA, et al. Single-nucleus transcriptomics of the prefrontal cortex in major depressive disorder implicates oligodendrocyte precursor cells and excitatory neurons. *Nat Neurosci.* 2020;23(6):771–81.