HHS Public Access

Author manuscript

Curr Opin Psychol. Author manuscript; available in PMC 2020 June 01.

Published in final edited form as:

Curr Opin Psychol. 2019 June ; 27: 82–87. doi:10.1016/j.copsyc.2018.09.008.

Every Contact Leaves a Trace: Contact with the Criminal Justice System, Life Outcomes, and the Intersection with Genetics

Ryan T. Motz[1], **Peter Tanksley**[1], **Hexuan Liu**[1,2], **Tesfaye B. Mersha**[3,4], and **J.C. Barnes**[1]

[1]School of Criminal Justice, University of Cincinnati, Cincinnati, OH, 45221, USA

[2]Institute for Analytics Innovation, University of Cincinnati, Cincinnati, OH, 45221, USA

[3]Department of Pediatrics, University of Cincinnati, Cincinnati, OH, 45229, USA

[4]Cincinnati Children's Hospital, Cincinnati, OH, 45229, USA

Abstract

Contact with the criminal justice (CJ) system is a relatively common occurrence in the United States. Criminologists and sociologists have long considered the impact of contact with the CJ system on later-in-life outcomes. This body of work has revealed a great deal of heterogeneity in life outcomes, suggesting individual differences are important to consider. At the same time, recent advances in the genomic sciences have allowed researchers to gather information from across the entire genome and to summarize that information into polygenic scores. In the present review, we consider how polygenic scores might be used to advance research into the impact of CJ system contact on life outcomes. In particular, we emphasize the importance of gene-environment interaction (G×E). We suggest that contact with the CJ system might represent a substantively important environmental moderator of polygenic risks. But we caution that studying the moderating role of contact with the CJ system will have its own complications— points that scholars must begin to consider and discuss now that the genomic era has reached the social sciences.

Keywords

contact with the criminal justice system; genome-wide; polygenic scores; gene-environment interaction

Locard's exchange principle[1], named for the French pioneer of the forensic sciences, states that every contact leaves a trace. Although this is traditionally understood to mean that individuals leave marks on their environment, there is one type of contact that likely leaves an indelible mark on the person: contact with the criminal justice (CJ) system. Criminologists have long studied the individual-level predictors of CJ contact [2,3]; however, isolating the effects of CJ contact on the individual has proven difficult due to

various concerns over confounding [4]. These difficulties arise from the limitations of traditional sociological approaches that largely ignore biological factors. Individual outcomes result from a complex interplay between one's genetic make-up and the environmental agents to which he/she is exposed. This review integrates criminological theories and recent findings from genomic studies to improve our understanding of how socio-environmental stressors (like contact with the CJ system) and genomic information synergistically influence life outcomes—the type of approach that has been labeled socio-genomics [5,6]. To illustrate this approach, we will draw on several examples from the literature and we will also consider possibilities for new research agendas surrounding the respiratory condition of asthma. Integrating the socio-genomic perspective with research on contact with the CJ system can provide a new perspective to address the long-standing question: what trace does CJ contact leave behind?

Contact with the Criminal Justice System

The American CJ system is a convoluted organization that, at its core, seeks to punish wrongdoing and prevent future criminal acts. To enact such punishment, offenders must come into contact with the CJ system in one way or another. Contact with the system can vary by type and degree of severity, ranging from brief interactions with police officers to long-term prison sentences.

Contact with the CJ system—in any form—is a relatively common event in the United States, at least compared to other nations. State and local law enforcement agencies make around 13 million arrests in a given year [7]. While many arrests end in relatively minor forms of punishment—such as citations or community service—others will require the offender to be placed under supervision. As a result, on any given day in the United States, approximately 5 million people are under the community supervision of a probation or parole department [8] with another 2.2 million behind the bars of a jail or a prison [9]. When these numbers are observed at the individual-level, roughly 30% of Americans will, at some point in their lifetime, be arrested [10-12] and an estimated 6-10% of the American population will spend time in a state or federal prison [13,14].

In this review, we primarily focus on one type of contact with the CJ system: incarceration within a prison. Receiving a prison sentence is one of the most severe punishments one can receive in the American CJ system. Additionally, there is now a large body of research that seeks to understand the impact of incarceration on later-in-life socioeconomic outcomes such as educational attainment [15], employment and income [16], as well as health outcomes including rates of infectious diseases (e.g., HIV, Hepatitis) [17], stress related symptoms (e.g., PTSD) [18], early mortality [19], and perhaps its impact on respiratory problems related to asthma [20]. But while incarceration seems to have net negative effects on the relationships, health, and future opportunities of most offenders, for some offenders, incarceration seems to serve as a positive turning point, helping them to reform and become contributing members of society upon release [21]. At the same time, incarceration has even been shown to have little-to-no effect on the life outcomes of other inmates [22].

Recognizing these points raises an important empirical question: why do individuals respond differently to incarceration experiences? Criminologists have explored this question and research has shown heterogeneous responses to prison can be tied to a range of characteristics that define the prison experience as well as to individual differences that inmates bring into the prison environment. For instance, some argue that manifestations of negative outcomes are the result of the deprivations, strains, and frustrations that are inflicted by the institutional environment and the experience of incarceration (i.e., the “pains of imprisonment”) [23]. Yet others hold that negative health, social, economic, and behavioral outcomes are not the direct result of incarceration but rather they reflect the characteristics, traits, skills, and predispositions that an individual brings with them into their incarceration experience [24].

We will build on this prior work that suggests part of the reason inmates vary in their response to the prison environment may be due to their individual differences. In so doing, we blend socio-environmental arguments with individual differences arguments (e.g., intrinsic and extrinsic factors) by integrating them with modern advances in another area of research: behavioral genetics. Doing so may allow for the development of an integrated framework that meets at the intersection of criminology with biological variation including genetics, leading to a more holistic and accurate account of the variation that is so often observed in offender responses to prison experiences.

Gene-Environment (G×E) Interaction: Incarceration as a Moderator of Genetic Risk

Behavioral genetics is a field of study that aims to understand how genetic variation, in combination with socio-environmental factors, affects human behavior. Early work in behavioral genetics sought to decompose variation in observed outcomes to estimate the unique role of genetic and environmental influences on behavioral outcomes [25,26]. But more recent advances have demonstrated it is difficult to consider genetic and environmental aspects of human behavior in isolation because an individual’s actions are usually affected by a complex interplay between the two. This means offender responses to prison experiences may vary depending on an individual’s genetic make-up. Thus, gene-environment interaction (G×E)—which recognizes this interplay of genetic influences and environmental factors—appears to be the rule and not the exception [27].

In humans, several experimental designs (including natural experiments), including family, twin, and adoption studies, as well as analytic genetic approaches, such as linkage analysis, candidate gene and genome-wide association testing, have been used to study the genetics of human phenotypes [28,29]. At the same time, conceptual development of the G×E perspective has reached the point where there are now several typologies to be considered (e.g., differential susceptibility [30], social push [31], and biological sensitivity to context [32]). One of the more predominantly discussed frameworks is the diathesis-stress model. This model emphasizes the likelihood of an outcome is expected to multiplicatively increase when a genetic risk (i.e., the diathesis) is combined with a detrimental context (i.e., the stress) [33]. While the diathesis-stress model has been used to explore the complex

relationship between genotype and a wide variety of socio-environments, one specific environmental context yet to be considered in depth is contact with the CJ system and, specifically, incarceration.

Historically, the common line of research used to explore G×E has been the candidate gene approach, which explores associations between a limited number of genetic variants identified *a priori* (i.e., due to a known association with a biological function). It should be noted, however, that a number of shortcomings related to this approach have now been identified [34-36]. Because candidate gene approaches examine genes with known functionality *a priori*, the approach is limited in terms of discovery in the functional pathways of interest. This is a serious issue because most human phenotypes are complex traits that do not follow a one-gene, one-disorder mechanistic pathway. Instead, most human phenotypes are polygenic [37], meaning the candidate gene approach is unable to account for the entire variance and the rich complexity of most traits.

Recent advances in genomic technology now allow researchers to assess millions of markers across the human genome at relatively low cost. These advancements have made it possible to identify genome-wide markers that are associated with complex traits of interest to social scientists. By conducting what are known as genome-wide association studies (GWAS), researchers have successfully identified associations between genetic variants and complex traits such as educational attainment [38], subjective well-being [39], depression [40], antisocial behavior [41], and intelligence [42]. Moreover, modern genomics research offers a way to model polygenic effects on these outcomes [43] by compiling the genetic variants identified by GWAS into polygenic scores (PGS). These developments have allowed social scientists to begin integrating genomic findings into research on human behavior, leading to the development of a new area of inquiry known as socio-genomics [5].

With the emergence of socio-genomics and the ability to produce genome-wide scores of genetic risk has come further development of the G×E paradigm. Through this G×E paradigm researchers can glean a more accurate depiction of the negative (or positive) life outcomes that occur upon release from prison. In particular, recall the diathesis-stress model predicts that an outcome is most likely to occur when genetic risk for the outcome is combined with a high-risk socio-environmental context. In this way, the pains of imprisonment associated with the experience of incarceration lead to a high stress environment, which in and of itself heightens a particular inmate's risk for certain life outcomes. Yet the outcome is even more likely to manifest for those individuals who also carry a heightened polygenic risk for that outcome. In other words, it may be the combination of what an inmate brings into prison (i.e., a diathesis, operationalized as a PGS) and the deprivations of the environment (i.e., the stress of the prison environment) that lead to a heightened risk for deleterious health and social outcomes for some prisoners.

Methodological Considerations

While we believe the G×E framework will be useful in the quest to better understand the influence of CJ contact on later-in-life outcomes, there are several important methodological concerns that must be considered. First, polygenic score (PGS) analyses rely on the findings

of genome-wide association studies (GWAS). Most GWAS, however, rely on samples of primarily individuals of European descent [44]. This may lead to inaccurate results for individuals from other ancestral backgrounds like those of African or Latino ancestry [45]. As of 2016, only 3% of all GWAS had been conducted among individuals of African ancestry [46]. In fact, GWAS conducted in European ancestry do not replicate, or have opposite, attenuated, or enhanced effects among individuals of other ancestries, including African ancestry [47,48]. As a result, PGSs generated from European ancestry based GWAS may not generalize to other ancestral populations due to variation in linkage disequilibrium, allele frequency, and population structure. Thus, it is essential that ancestry be considered in genome-wide analysis and interpretations.

There are various ways through which ancestry can be controlled in a genomic analysis. The conventional method is to restrict all analyses to individuals who identify as non-Hispanic White. But this sort of stratification could negatively impact inferences for a socio-genomic analysis of contact with the CJ system on later-in-life outcomes. For instance, not only are minorities overrepresented in the American CJ system [49], but research has also demonstrated minorities tend to experience worse outcomes after contact compared to White offenders [4]. Thus, if socio-genomic analysts are forced to restrict their samples to non-Hispanic Whites, then the potential benefits of such research (e.g., if a discovery is made that can help alleviate the negative consequences of CJ contact) may represent yet another source of inequality for minorities [50]. Thus, we encourage future work to consider the ways in which socio-genomics research can be expanded to address important social concerns that stem from the well know racial inequality in CJ system contact [51,52].

Second, in many instances, the focus on genetic individual differences potentially opens the door for genetic confounding in the form of gene-environment correlations (*r*GE), and in particular, active *r*GE [53]. Unless steps are taken to specifically address this sort of selection bias, any G×E analysis assessing incarceration experience as a moderator of genetic risk might produce results that are confounded (see Panel A of Figure 1) [54]. In order to avoid genetic confounding of this sort, researchers must rely on methodological designs that are capable of ruling it out or they must study specific genetic risks that are unlikely to affect incarceration risk. To illustrate, we will consider what we believe to be a good candidate for G×E research that also avoids *r*GE with CJ contact: the respiratory condition of asthma.

The etiology of asthma has a significant genetic component [55] and studies have shown that the polygenic risk of asthma is predictive of respiratory symptomologies across the life-course [56]. Furthermore, studies have demonstrated that previously incarcerated populations show a higher prevalence of asthma than the general population [20]. Despite its prevalence among ex-offenders, it is unlikely (except through complicated pathways that are unlikely to have large effects) that a genetic risk for asthma influences selection into incarceration (i.e., little-to-no *r*GE). In this way, asthma represents a genetic risk that is not likely to be confounded with incarceration but that might still affected by it (see Panel B of Figure 1).

Conclusion

If every contact leaves a trace, Locard's principle would predict that contact with the CJ system, such as through incarceration, would leave a large mark indeed. In this article, we proposed that the G×E framework allows researchers to understand the long under-explained heterogeneity in inmate outcomes. And, when paired with non-confounded genetic risks identified by recent socio-genomic research (e.g., asthma), G×E approaches can move the field closer to identifying mechanisms that are potentially amenable to policy changes. Yet, many questions remain—questions that we do not have the space to explore in this article. For instance, can we use the results from socio-genomics research as predictors of treatment success or long-term prognosis? Can we use these findings to identify targets for safe and effective interventions? *Should* we use such findings to inform these questions? These are important questions that scholars and philosophers must begin to consider because the socio-genomic era is upon us.

Acknowledgements

This work was supported by National Institutes of Health grant R01HL132344 (T.B.M). The authors declare no conflicts of interest.

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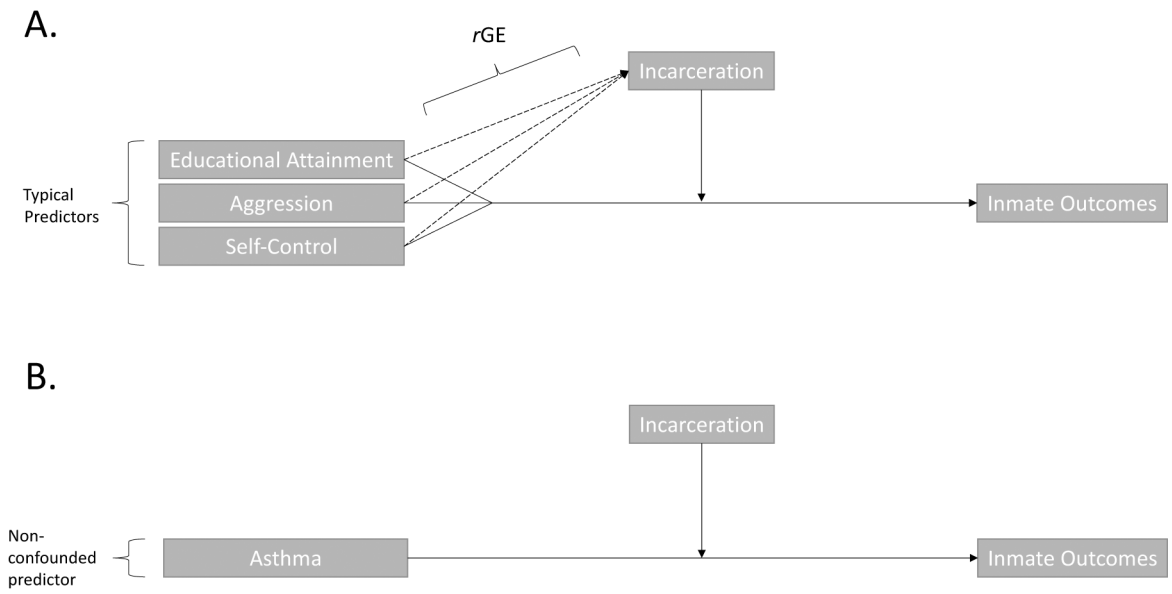

Figure 1. Conceptual Models Using Incarceration as a Moderator of Genetic "Risk"

Notes: *Panel A :* The causal pathways between the kinds of predictors favored by criminologists (e.g., educational attainment, aggression, self-control) and inmate outcomes later in life are long and most likely confounded with incarceration risk. The use of polygenic scores for these traits will introduce the gene-environment correlation (*r*GE) into the analysis, biasing the result gene-environment interaction (G×E). *Panel B*: The respiratory condition of asthma represents a predictor of later-in-life outcomes for inmates that is not likely confounded with incarceration risk (i.e., a genetic risk for asthma likely avoids *r*GE effects because its effect on incarceration is reasonably assumed to be negligible).