On the Genetic and Genomic Basis of Aggression, Violence, and Antisocial Behavior

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Abstract and Keywords

There is a great deal of interest in examining the genetic and environmental architecture to aggression, violence, and antisocial behaviors. This interest has resulted in hundreds of studies being published that estimate genetic and environmental effects on antisocial phenotypes. The results generated from these studies have been remarkably consistent and have contributed greatly to the knowledge base on the etiology of antisocial behavior. This chapter reviews the research on the genetic basis to antisocial phenotypes by presenting the results related to the heritability of antisocial phenotypes. It also discusses some of the molecular genetic association studies as well as genome-wide association studies that focus on the development of antisocial behaviors. In doing so, it also reviews findings related to gene–environment interactions. The chapter concludes by discussing some of the ways in which these findings could be used for intervention and prevention programs.

Keywords: aggression, antisocial, biosocial, genetic, violence

INTEREST about the genetic basis to antisocial behavior has increased at a significant rate during the past two decades. Barely a week goes by without a new study reporting genetic influences on criminal, delinquent, or antisocial behavior. These reports are frequently picked up by the media and garner a substantial amount of public interest. Of all the research that is generated on the etiology of antisocial behaviors, studies examining genetic influences are most likely to produce the most controversy while at the same time resulting in the most confusion over their meaning (Beaver, 2013). Critics, for instance, argue that researchers who investigate the genetic basis to crime and delinquency are evil-minded and secretly harbor racist, fascist, or sexist beliefs. In a similar vein, there is a prevailing belief among many scholars, particularly criminologists, that should a genetic basis to crime be detected, the only policies that could emerge from such research would be oppressive and highly punitive, including the revitalization of a eugenics movement. Despite this outpouring of concern leveled by some in the academy and the public, never before has so much been written on the genetic basis of criminal behavior as there is today.

Against this backdrop, the goal of this chapter is to review the research examining the genetic and genomic foundations to aggression, violence, and antisocial behavior. Before proceeding, however, we must clarify what we mean by aggression, violence, and antisocial behavior. Unique definitions of aggression and violence as well as antisocial behaviors have been discussed in detail in previous publications (Beaver, 2009a), and we do not want to get bogged down in arguing for one definition or another. Rather, we take a relatively straightforward approach in the current chapter: When we use the (p. 266) terms *violence* and *aggression*, we are referring to behaviors for which victimization is personal and physical in nature; when we use the terms *delinquent* or *criminal involvement*, we are referring to behaviors that violate some type of legal statute; and when we use the term *antisocial behaviors*, we are referring to a wide range of behaviors that would be considered as violating conventional values or social norms in industrialized nations. This term is broad and encompasses violence, aggression, crime, delinquency, and any other behavior that violates widely accepted values and norms. For the most part, we use *antisocial behavior* when discussing broad themes and findings in the literature (because the literature employs many different outcomes [violence, crime, etc.]), but if we are speaking directly about findings that apply to just one type of behavior, then we use specific language (e.g., violent behavior or criminal involvement).

This chapter is divided into five sections. First, we present findings from the voluminous literature on the heritability of antisocial behaviors that provide us with a starting point on the extent to which genetic influences might matter for antisocial behaviors. Second, we transition into a discussion of the specific genetic polymorphisms that have been linked to various forms of antisocial behaviors. The third section focuses on contemporary cutting-edge research using genome-wide association techniques to explore the genetic basis to antisocial behaviors. Fourth, we review the literature estimating gene–environment interactions as they apply to the development of antisocial behavior. Last,

we conclude by presenting some closing remarks, including how these findings might be used for intervention and areas where future research is needed.

Heritability of Antisocial Behavior

In order to provide a starting point for the role that genes might play in the etiology of antisocial behavior, it is first important to determine the relative influence of genetic and environmental effects. Heritability estimates are useful in this regard. Heritability estimates indicate the proportion of phenotypic variance in a group or population that is accounted for by genetic variance (Plomin, DeFries, Knopik, & Neiderhiser, 2013). The variance left unexplained by heritability is accounted for by environmental influences (and error). Should genetic influences have little or no influence on antisocial behaviors, then time, energy, and other resources should not be devoted to studying the role of genes in the genesis of antisocial behaviors. If, however, genes are found to be associated with antisocial behaviors, then it would be useful to explore the genetic basis to antisocial behaviors in much greater detail. A substantial amount of research has been devoted to addressing this issue by estimating the heritability of virtually every measureable source of antisocial behavior. Heritability estimates can be generated from a number of different research designs, but the most widely used methodology is the twin-based research design.

The twin-based methodology used to estimate heritability takes advantage of the naturally occurring phenomenon of twinning. With the twinning process, there are two (p. 267) types of twins: monozygotic (MZ) twins and dizygotic (DZ) twins. MZ twins share 100% of their DNA, whereas DZ twins share 50% of their distinguishing DNA. Both types of twins, however, are assumed to share environments that are approximately the same—an assumption known as the equal environments assumption (EEA). As long as the EEA is upheld—and there is strong mathematical research showing that it is (Barnes et al., 2014)—then accurate heritability estimates can be generated. Heritability estimates are largely a function of the phenotypic similarity of MZ versus DZ twins. The logic of this approach is that the only reason why MZ twins should be more similar to each other than DZ twins (on any phenotypic measure, including antisocial phenotypes) is because MZ twins share twice as much genetic material compared to DZ twins. As the similarity of MZ twins increases relative to the similarity of DZ twins, then heritability estimates increase as well.

Not all twin-based research compares the similarity of MZ twins to DZ twins; rather, some studies exploit the relatively rare situations in which MZ twins are separated at birth and reared in separate families without even knowing that they have a long-lost twin. It is only later in life that they discover that they have an MZ twin, and thus the contact between them is limited to only later in life. These cases present a rare opportunity to estimate genetic influences by comparing the similarity of the MZ twins. Any similarity between them would be attributable to genetic influences because their environments should be orthogonal. A team of researchers at the University of Minnesota led by Thomas Bouchard has provided systematic analyses of MZ twins who were

separated at birth (Bouchard, Lykken, McGue, Segal, & Tellegen, 1990). By using this type of research design, it is possible to examine the robustness of heritability estimates across different types of twin-based analyses.

Twin-based methodologies are not the only research designs that can be used to examine the heritability of antisocial behaviors (Beaver, 2013). One alternative to twin research is the adoption-based research design (Beaver, 2011a). In adoption studies, the adopted-away child's behavior is compared to the behavior of the child's biological parents and to the behavior of the adoptive parents. If the adoptee was adopted early in life and had no contact with his or her biological parents, then the only reason the adoptee should be phenotypically similar to them is because of the genetic material the adoptee shares with his or her parents. Because the adoptee shares no genetic material with his or her adoptive parents, the only reason the adoptee should be phenotypically similar to them is because of environmental influences. Although the adoption-based research design is quite powerful, it is not used as widely as the twin-based research design largely because samples containing an adequate number of adoptees are rarer than samples of twin pairs.

Collectively, twin and adoption studies account for the vast majority of all research estimating the heritability of antisocial behaviors. Heritability estimates tend to vary, however, based on sample characteristics (e.g., age range of respondents), the precise measure of antisocial behavior being studied, and other study-specific factors. Four meta-analyses have been conducted (Ferguson, 2010; Mason & Frick, 1994; Miles & Carey, 1997; Rhee & Waldman, 2002), and a number of literature reviews have been (p. 268) completed (Beaver, 2013), in order to provide a summary of the findings across the hundreds of existing twin and adoption studies of antisocial behaviors. The results of these studies have been remarkably consistent in their conclusions, all of which indicate that approximately 50% of the variance in antisocial behaviors is accounted for by genetic factors (i.e., heritability estimates ≈ .50).

Although the meta-analytic results indicate that one-half of the variance in antisocial behavior is due to genetic influences, there is good reason to believe that when it comes to more extreme types of antisocial behaviors, heritability estimates might be significantly greater. For instance, one study estimated the heritability for different types of offenders, including those who were considered to be life-course persistent (LCP) offenders and those who were considered to be adolescence-limited (AL) offenders (Barnes, Beaver, & Boutwell, 2011). LCPs are typified as offending throughout their entire life, they engage in serious types of criminal and violent behaviors, and they account for the vast majority of all criminal offenses. ALs, in contrast, offend only during adolescence and engage in behaviors that are relatively age-appropriate (e.g., experimenting with minor forms of drug use). Heritability estimates were generated for both types of offenders, and the result revealed that as much as 70% of the variance in LCPs was accounted for by genetic influences, whereas only 35% of the variance in ALs was accounted for by genetic influences. Similar findings have been detected in other

studies whereby genetic influences tend to increase as the types of antisocial behaviors being studied increase in seriousness (DiLalla & Gottesman, 1991).

Although these findings show the consistent and relatively strong influence of genes on individual differences in antisocial behaviors, they further reveal that the environment also influences variation in antisocial behaviors. Whatever variance is not accounted for by genetic influences must be accounted for by environmental influences (or error). Following this logic, the environment appears to account for approximately 50% of the variance in antisocial behaviors, although the effect will ebb and flow in response to heritability estimates (i.e., environmental influences decrease when heritability increases and vice versa). Findings from twin and adoption studies underscore the importance of two different types of environmental influences: shared environmental influences and nonshared environmental influences (Beaver, 2008). Shared environments are environments that are the same between siblings and that work in a way that makes them more similar to each other. Examples of shared environments are family-wide parenting practices, neighborhood characteristics, and the socioeconomic status of the family. Nonshared environments are environments that are unique to each sibling and that work to make them different from each other. Examples of nonshared environments are peer groups, child-specific parenting, and unique life experiences.

What is particularly interesting about shared and nonshared environmental influences is that they have very different effects on antisocial behaviors (Plomin et al., 2013; Turkheimer, 2000). Findings from twin-based research, for example, have shown consistently that the shared environment accounts for approximately 10–15% of the variance, depending on the specific measure of antisocial behavior examined. These same studies show that approximately 40% of the variance in antisocial behaviors is accounted for by (p. 269) nonshared environmental influences (and error). These strong differential effects for the two types of environments suggest that the nongenetic etiology of antisocial behaviors is most likely to be found in nonshared environments rather than shared environments.

Estimates of genetic and environmental influences from twin- and adoption-based research designs are latent, meaning that they only provide information about the extent to which they account for phenotypic variance; they do not provide any insight into the specific genetic polymorphisms (or the particular environments) that might be accounting for the variance. Therefore, other research designs are needed to examine the precise genes that might be involved in the development of antisocial behaviors. We next turn our attention to a discussion of these research designs and the findings flowing from them.

Genetic Polymorphisms Linked to Antisocial Behaviors

Since the heritability of antisocial behaviors has been firmly established to be approximately .50, there has been a great deal of interest of trying to move past simply estimating heritability and identify the precise genes that are driving heritability estimates. These studies attempt to identify the alleles of genetic polymorphisms to determine whether they correlate with variation in measures of antisocial behavior. If a significant association is detected between certain alleles and the antisocial behavior of interest, then it can be concluded that the examined genetic polymorphism is involved, in some capacity, with the heritability of the examined behavior. The majority of research attempting to link alleles to antisocial behaviors has done so by conducting what are known as candidate gene association studies. In this work, usually only one gene (or, at most, a small handful of genes) is examined.

Scholars attempting to conduct candidate gene association studies have always been confronted with the same question: Where should they begin? The human genome is composed of tens of thousands of genes, and trying to select just one gene that is associated with antisocial behavior is akin to finding the proverbial needle in the genetic haystack. Most research has focused on genetic polymorphisms that are involved in neurotransmission because neurotransmitters and cognitive processes, in general, have been found to be linked to an assortment of antisocial behaviors. The reasoning, therefore, is that genetic polymorphisms would affect neurotransmission/cognition, and neurotransmission/cognition would, in turn, influence antisocial behaviors. When viewed in this way, genes do not code directly for antisocial phenotypes but, rather, operate through a chain of mediating variables (sometimes referred to as endophenotypes).

Candidate gene association studies have identified a number of genetic polymorphisms linked to a range of negative, maladaptive, and criminal outcomes. Although important exceptions exist, most of these studies have focused on three sets of (p. 270) genes: dopaminergic genes, serotonergic genes, and genes involved in metabolizing neurotransmitters. Dopaminergic genes, such as DAT1, DRD2/ANKK1, DRD3, DRD4, and DRD5, have been linked to drug use, gambling, alcoholism, adolescent victimization, and criminal involvement. Serotonergic genes, including 5HTTLPR, 5HTR2A, 5HTR1B, and 5HTR2C, have also been found to be associated with antisocial behaviors, such as impulsivity, gambling, conduct disorder, and criminal and delinquent involvement. The last system of genes—those that are involved in metabolizing neurotransmitters—includes polymorphisms such as monoamine oxidase A (MAOA) and catechol-*O*-methyltransferase (COMT), which have been linked to criminal and aggressive outcomes (for a review of the literature, see Beaver, 2013). MAOA, however, deserves particular attention given the substantial amount of research that has examined it.

Of all the genetic polymorphisms studied, MAOA has been most consistently associated with a wide range of antisocial behaviors. MAOA codes for the production of the MAOA enzyme, which is responsible for degrading neurotransmitters. Some of the earliest research linking MAOA to antisocial behaviors was performed by Brunner and associates (Brunner, Nelen, Breakefield, Ropers, & van Oost, 1993). Brunner’s research team was made aware of a Dutch kindred in which certain males engaged in various forms of

violent, criminal, and antisocial behavior. For example, some of the males had previously engaged in rape, arson, and also suffered from reduced neurobiological functioning. Females in the family, however, appeared to be relatively immune to this syndrome of behaviors. Brunner et al. hypothesized that these behaviors were the result of a genetic defect, and they further reasoned that the genetic defect was on the X chromosome, explaining why only males were inflicted with these behaviors. The results of genetic testing confirmed their suspicions: Males with this syndrome had inherited an MAOA gene (which is located on the X chromosome) that was defective and did not produce any MAOA. Without MAOA present, their neurotransmitter levels were unregulated and neurotransmission did not operate effectively.

Although the discovery of the mutant MAOA gene in this cohort spawned discussions about the discovery of the "crime gene," future research revealed that this mutation was not found in the general population. What this necessarily means is that this mutation could not account for crimes that were committed on an everyday basis. Research did reveal, however, that the MAOA gene was polymorphic, where two groups of alleles could be inherited: alleles that coded for the production of low-activity MAOA and alleles that coded for the production of high-activity MAOA. The low-activity alleles are considered risk alleles that confer an increased probability of engaging in antisocial behaviors. A line of research has provided relatively strong support for the link between the low-activity MAOA allele and antisocial behavior by showing a connection to delinquency, psychopathic personality traits, criminal involvement, weapon use, and gang membership (Beaver, Barnes, & Boutwell, 2014; Beaver, DeLisi, Vaughn, & Barnes, 2010; Beaver et al., 2013; Schwartz & Beaver, 2011). No other gene has been so consistently linked to antisocial behaviors as the MAOA gene.

Relatively recently, a "super" low-activity MAOA allele has been identified (known as the 2-repeat [2R] allele). This allele has been found to have an even lower level of (p. 271) activity compared with the other low-activity alleles (Guo, Ou, Roettger, & Shih, 2008). Only a few studies have examined the 2R allele of the MAOA gene, but the results have been striking: This allele has been shown to increase the risk for shooting someone, stabbing someone, being arrested, being incarcerated, engaging in crime over the life course, and engaging in a variety of serious and violent behaviors (Beaver et al., 2013, 2014; Guo et al., 2008). These findings should be interpreted with caution because only a few studies have examined the 2R allele, and all of the cited studies have analyzed the same sample.

These candidate gene association studies that focus on a single gene, although informative, are somewhat misguided. To understand why, it is first necessary to recognize how genotypic variance could ultimately produce phenotypic variance, including variance in antisocial behaviors. Regarding phenotypic variance, there are three key ways that genes could directly be responsible for producing such variance. First, one gene could be the sole cause of that phenotype. If a person possesses that gene, then he or she will develop the phenotype; if a person does not possess that gene, then he or she will not develop the phenotype. This mechanism is known as a monogenic

effect or an OGOD (one gene, one disorder) effect. Although thousands of diseases and disorders are produced by monogenic processes, complex phenotypes, including antisocial phenotypes, are not produced by such a simple genetic transmission model.

The second way that genes could directly affect antisocial behaviors is through a process known as polygenic effects. With phenotypes that are produced by polygenic effects, there are hundreds or thousands of genes that each have a small influence on the phenotype. When aggregated, however, these small effects can account for a large proportion of phenotypic variance. Under a polygenic model, single genes are neither necessary nor sufficient for the phenotype to surface; rather, genes work in a probabilistic manner whereby the possession of a single allele increases (or decreases) the probability that the phenotype will emerge. The consensus appears to be that complex phenotypes, such as antisocial phenotypes, are the result of a polygenic model pattern of transmission. This means that most genes (although not all) will likely only have a very small influence on antisocial behaviors, but when these genes are all identified collectively, they should account for approximately 50% of the variance in antisocial behaviors.

The third way that genes can produce phenotypic variance is known as a pleotropic effect. In a pleotropic model, a single gene has effects on multiple phenotypes. The effects that these genes have can be quite small (or quite large), but typically they are assumed to be part of a larger polygenic effect on each particular phenotype. Although not explored as fully as polygenic effects, there is a solid body of research indicating that pleotropic effects have direct application to criminal, violent, and antisocial behaviors.

Relatively recent research has employed a more realistic approach and instead of focusing on just one genetic polymorphism, multiple genes are studied at the same time (Beaver, 2009b; Belsky & Beaver, 2011; Schwartz & Beaver, 2014). Perhaps even more important is that these genes are not always examined in isolation but, rather, are summed together to create a polygenic risk index that includes the effects of all the genes at the same time. Findings from this line of research have been enlightening by showing (p. 272) that polygenic risk scales are more consistently predictive of antisocial behaviors compared to single-gene studies and that they typically account for a larger proportion of phenotypic variance. These findings should not be too surprising, given that antisocial phenotypes are likely developed under a polygenic model, resulting in polygenic risk indexes, as opposed to single-gene studies, predicting a greater proportion of variance in such phenotypes.

Findings from Genome-Wide Analyses

Although molecular genetic studies have provided some information about specific polymorphisms that might contribute to antisocial phenotypes, these studies have been hampered by a number of limitations, including the inability to replicate novel findings.

Fortunately, other types of research designs are available that can overcome some of these limitations. Perhaps the most cutting-edge studies conducted by behavioral scientists in recent years to identify specific genetic markers for antisocial behavior are known as genome-wide association studies (GWAS). GWAS examine whether common genetic variants across different individuals are associated with a given phenotype. GWAS research primarily focuses on assessing links between single nucleotide polymorphisms (SNPs) and certain traits. Although GWAS designs have been commonly used by medical researchers to explore associations between SNPs and disease, this sophisticated methodology has recently begun to be used by behavioral scientists to replicate previous candidate gene findings and search for additional genes involved in the development of antisocial behavior. As discussed later, GWAS offer much promise for understanding the genetic origins of antisocial behavior.

Whereas most behavioral genetic research requires the use of sibling or twin data, GWAS relies on genome-wide data, where genotyping methods are used to provide information on the genomes of several thousand unrelated individuals. In contrast to candidate gene research that focuses on examining the association between specific genes and phenotypes, GWAS genotypes individuals for millions of SNPs and examines whether the allele frequency for a commonly known SNP is different in the group with a history of antisocial behavior compared to a control group that does not have a history of antisocial behavior. If differences in allele frequency are observed through this case–control method, then this finding is interpreted as support for a link between variation in a specific gene and antisocial behavior. Due to the taxing nature of searching for specific SNPs among millions of others SNPs, very large samples are required in order to have enough statistical power for SNPs to reach genome-wide significance (which is conventionally established as $p < 5 \times 10^{-8}$). Unfortunately, this standard has been difficult to achieve for many GWAS examining antisocial behavior.

A study conducted by Dick and colleagues (2011) used genome-wide data to explore the association between specific genetic markers and conduct disorder symptomology. The results from their analysis revealed a significant genome-wide association link (p. 273) between two SNPs located in the gene C1QTNF7 and conduct disorder. Although this study was the first to provide evidence of a specific gene associated with conduct disorder symptomology, much is unknown about the gene C1QTNF7 and how it is involved in the development of conduct disorder. Another GWA study used data on a community sample of 4,816 respondents who answered self-report questions about their involvement in antisocial behavior during adulthood (Tielbeek et al., 2012). No significant genome-wide associations were found between a host of genetic polymorphisms and adult antisocial behavior. However, the strongest association between a specific genetic polymorphism and adult antisocial behavior was found when examining DYRK1A, a gene that has been associated with abnormal brain development. The authors recognize, however, that their findings may reflect a lack of statistical power to detect genome-wide significant associations, and they encourage future researchers to use larger samples.

Tiihonen et al. (2015) used genome-wide data on two independent cohorts of prisoners in Finland and found strong associations between chromosome 16q23.3 in the CDH13 gene among extremely violent offenders who were in prison for 10 or more violent crimes. Interestingly, previous research has found significant associations between the CDH13 gene and other behavioral outcomes commonly related to antisocial behavior, including autism (Sizoo et al., 2010), attention deficit hyperactivity disorder (Arias-Vásquez et al., 2011), schizophrenia (Børglum et al., 2014), and bipolar disorder (Xu et al., 2014). Findings from this recent analysis shed new light on a specific genetic polymorphism that may play an important role in the development of severe antisocial behavior, and this analysis also demonstrates how GWA research can help uncover salient genetic markers for antisocial behaviors.

Despite the growth of GWAS of antisocial behavior in the past 5 years, the majority of studies find very few significant associations between genetic polymorphisms and antisocial behavior that reach genome-wide significance; when they do, findings are often different from those of other GWA research, suggesting an inherent problem with nonreplication. However, recent GWA research has found reliable genetic associations between individual SNPs and behavioral traits when analyzing large population cohorts that are well powered for GWAS (Rietveld et al., 2014). As such, the future and promise of GWAS for antisocial behavior rely on access to large samples with genomic data and indicators of antisocial behavior. GWAS has the ability to further unpack the black box of genetic markers intimately involved in the etiological development of antisocial behavior and may help intervention/prevention science create more targeted programming efforts to reduce the social burden produced by antisocial behaviors.

Gene–Environment Interactions

It might seem as though genetic influences operate in a vacuum and are orthogonal with environmental influences. In reality, however, this simply is not the case. Unlike the outdated nature versus nurture debate, which pitted environmental influences (p. 274) against genetic influences to determine which one had the greatest impact, today there is widespread recognition that genetic and environmental influences are highly interconnected. One way that genes and the environment are intertwined is through what are known as gene–environment interactions. Gene–environment interactions refer to the process by which the effect of genes is conditional on the presence of certain environmental stimuli or where the effect of environments is conditional on the presence of certain genes. To illustrate, consider that a certain gene may increase the likelihood of aggressive behavior, but only when that gene is paired with a rearing environment that is typified by low levels of love and affection and high levels of stress, abuse, and neglect. That same gene might have no influence on aggressive behavior when it is paired with a rearing environment that has high levels of warmth, love, and attachment and the absence of abuse and neglect. In short, the environment is moderating the influence of

genetic effects on behavior. Keep in mind that the opposite process can also be at play. In this case, the environment may only have an effect on phenotypes for people who possess certain genotypes. Gene–environment interactions are quite useful in this regard because they provide an explanation for why the same environments can produce significant variation in how people respond.

A sizable amount of research has been devoted to empirically assessing the merits of gene–environment interactions as they relate to antisocial phenotypes. There are two key ways that this body of research has tested for gene–environment interactions. First, respondents can be grouped into different categories based on their exposure to environmental conditions, and then heritability estimates can be calculated for respondents in each of those categories. If heritability estimates vary between respondents who are differentially exposed to environments, then that is usually interpreted as evidence of a gene–environment interaction. For example, a sample could be divided into two groups—one group that experienced abuse in childhood and one group that did not. Heritability estimates could then be generated for both of these groups. If the heritability was greater for one group versus the other, then the most common interpretation would be that the environment is moderating the influence of genes. A number of studies have employed this approach to examine gene–environment interactions for antisocial behavior. Beaver (2011b) conducted perhaps the most exhaustive examination of gene–environment interactions on antisocial behavior using this method. He examined whether 13 different criminogenic environments, such as exposure to delinquent peers, family risk, and religiosity, moderated genetic influences on serious delinquency, violent delinquency, and victimization. The results of his analysis revealed broad support for gene–environment interactions on these antisocial phenotypes, with the effects of genes being more pronounced in the presence of criminogenic environments.

The second and more widely used approach to test for gene–environment interactions is by examining the effect of a single genetic polymorphism and a single environmental pathogen, usually within a regression-based framework. To test for a gene–environment interaction, the genetic polymorphism and the environmental pathogen are included in a regression model as a multiplicative interaction term. If that (p. 275) multiplicative interaction term is statistically significant, then that provides evidence of a gene–environment interaction. During approximately the past 10 years, there has been a proliferation of research testing for gene–environment interaction with this modeling strategy. The results of these studies have uncovered a great deal of gene–environment interactions on antisocial phenotypes. For example, dopaminergic polymorphisms have been found to interact with delinquent peers, family risk/adversity, and marital stability/status to predict variation in number of police contacts, number of criminal arrests, desistance from delinquency, and even early onset offending. Other interactions have been detected with other environments and with other systems of genes (e.g., those from the serotonergic system) to predict antisocial phenotypes.

Of all the gene–environment interactions examined, however, the gene–environment interaction between MAOA and childhood maltreatment has been the most scrutinized. The first study to show a gene–environment interaction between MAOA and child maltreatment was that of Caspi et al. (2002). In this study, they analyzed data from the Dunedin Multidisciplinary Health and Development Study. The results of their analysis revealed that MAOA did not have a statistically significant main effect on any measure of antisocial behavior. When they analyzed the effect of the MAOA gene in conjunction with childhood maltreatment, a very different pattern of results emerged. Specifically, they reported that males who carried a low-activity MAOA allele and who were maltreated during childhood accounted for only 12% of the entire sample, but they accounted for 44% of the antisocial behavior. Moreover, 85% of them were characterized as displaying some type of antisocial behavior or trait. This study provided the first evidence of a gene–environment interaction between a measured polymorphism, a measured environment, and a measured antisocial phenotype. Perhaps as a result, it has generated a considerable amount of interest and ignited a large number of replication studies.

The results of these replication studies have provided support in favor of this gene–environment interaction, but some studies have failed to confirm this interaction in independent samples (for an overview of these studies, see Byrd & Manuck, 2014). Two meta-analyses have been conducted to shed some additional light on the robustness of this gene–environment interaction. The results of both meta-analyses revealed significant support in favor of the gene–environment interaction for males (Byrd & Manuck, 2014; Kim-Cohen et al., 2006), and the most recent meta-analysis revealed a fail-safe *N* of 93 (Byrd & Manuck, 2014). This means that there has to be at least 93 unpublished studies showing no evidence of a gene–environment interaction for the results of the meta-analyses to be incorrect. Given this substantial amount of empirical support, there is good reason to believe that the gene–environment interaction between MAOA and childhood maltreatment is involved—at least in some capacity—in the production of variation in antisocial phenotypes.

Until relatively recently, the interpretation of the MAOA interaction, and all other gene–environment interactions, was quite straightforward and relied solely on the diathesis–stress model. According to the logic of the diathesis–stress model, variation in individual vulnerability to criminogenic influences was based on their genetic risk (p. 276) profiles for antisocial phenotypes. Genetic influences, in other words, set the parameters for behaviors, and environmental factors were responsible for allowing those parameters to be reached. Belsky (Belsky, 1997; Belsky & Pluess, 2009), however, has advanced a different explanation for the interpretation of gene–environment interactions, which he refers to as the differential susceptibility model. The logic of this model rests on the assumption that genetic polymorphisms should not be viewed as biological risk factors but, rather, as biomarkers of plasticity. The greater the number of plasticity alleles that an individual possesses, the more vulnerable the individual is to all environmental conditions. When viewed in this way, it is easy to understand that plasticity markers can prime an individual for antisocial phenotypes in the face of criminogenic environments and, at the same time, plasticity markers can prime an individual for prosocial

phenotypes in the face of advantageous environments. In short, genes identify how plastic an individual is, and the environment to which the individual is exposed determines how he or she will develop. The differential susceptibility model captures this process with the slogan, “for better and for worse,” which essentially means that those individuals with the greatest number of plasticity alleles will turn out the best when exposed to positive environments and the worst when exposed to negative environments (Belsky, Bakermans-Kranenburg, & Van IJzendoorn, 2007).

A good deal of research has been devoted to examining which explanation is better situated to explain gene–environment interactions for phenotypic outcomes, including antisocial outcomes. The results of these studies have not produced unequivocal results. Some studies have provided support for the diathesis–stress model, some studies have provided support for the differential susceptibility model, and some studies have provided support for both models (Belsky & Pluess, 2009). Given the importance of understanding how and why gene–environment interactions operate in the way that they do, there can be little doubt that even more research will examine the merits of these approaches in the upcoming years.

Conclusion

The past two decades have witnessed a tremendous increase in the amount of research examining the genetic foundations to virtually every measure of antisocial behavior. These findings have quickly revolutionized conventional wisdom about the etiology of antisocial phenotypes and the role that genetics plays in the development of such phenotypes. Although these findings have produced a solid knowledge base about the genetic foundation to antisocial phenotypes, this body of research remains in its infancy. As a result, there remain debates regarding the findings of many aspects of the genetic basis to antisocial behaviors (Beaver, Barnes, & Boutwell, 2015). Future research will be useful in clarifying points of disagreement and uncovering newer ways of thinking about the role that genes play in the genesis of crime, aggression, violence, and other antisocial phenotypes. As for now, and as our review has revealed, there are a number of highly (p. 277) robust findings that have been replicated so consistently that any objective, empirically guided scientist would have to believe. These include the following:

- The heritability of antisocial behavior is approximately .50. For more extreme types of antisocial behavior, the heritability is probably much greater, hovering around .70 to .80. Heritability estimates are highly robust and are built on assumptions that have been thoroughly vetted and substantiated (Barnes et al., 2014).
- Nonshared environmental influences—as opposed to shared environmental influences—account for the overwhelming majority of all environmental variance in antisocial behaviors.

- Although a significant amount of research has been devoted to examining the molecular genetic basis to antisocial behaviors, only a handful of polymorphisms have been consistently linked to antisocial behavior. Nonreplication of novel molecular genetic findings remains a problem.
- Genetic polymorphisms involved in neurotransmission have most frequently been connected to antisocial phenotypes.
- Genome-wide association studies suggest that genes involved in cognitive ability and the development of psychiatric disorders are commonly associated with various forms of antisocial behavior.
- Genetic and environmental influences frequently interact to predict variation in antisocial outcomes.
- Of all the gene–environment interactions detected, that between MAOA and childhood maltreatment has been the most consistent and the most widely replicated.

There can be little doubt that the amount of research devoted to the genetic basis to criminal behavior has only just begun and that there will continue to be an exponential growth in this line of research in the near future. As increasingly more research is accumulated, there will be questions regarding the manner in which findings flowing from this body of literature can be used by the criminal justice system. Although genetic research has not made any significant contributions to policies focused on the reduction of antisocial behavior in the past few decades, we offer two possibilities. First, criminological research examining the effectiveness of rehabilitation programs has shown that not all offenders are equally amenable to change (Smith, Gendreau, & Swartz, 2009). Rather, high-risk offenders are much more likely to reap the benefits of rehabilitation programs compared to low-risk offenders. Currently, a number of actuarial risk assessment tools are used to determine risk level. Findings from genetic research could easily be integrated into these tools, whereby offenders are genotyped for certain polymorphisms that might increase their risk level. Of course, the extent to which genetic research could help delineate offender risk will depend largely on future research being able to identify replicable results that link certain polymorphisms to criminal and antisocial behaviors.

The second way in which genetic findings might be able to guide policy is by providing more individualized treatment and rehabilitation services. There is now a solid pool (p. 278) of research showing variation in response to rehabilitation programs among individual offenders (Smith et al., 2009). Specifically, certain individual-level characteristics, such as age and gender, moderate program effectiveness. This pattern of findings has resulted in an attempt to match treatment to specific offender characteristics in order to increase program effectiveness. To date, there has not been any systematic approach to examine whether genotype might moderate success rates of rehabilitation programs. Even so, given that genes have been shown to moderate responses to environments in general (in the form of gene–environment interactions discussed previously), it would make logical and intuitive sense to believe that genes

could also moderate rehabilitation program effectiveness. Only time will tell, but given the potential payoffs, including the payoff of increased public safety, research and resources should be devoted to the possibility that genes moderate the effectiveness of rehabilitation programs.

This is an exciting time to be examining the various ways in which genetic influences may contribute to the development of antisocial behaviors. Although much has been learned about the genetic etiology of antisocial phenotypes, numerous mysteries still remain. There can be little doubt, however, that as the amount of genetic research continues to accrue, many of these mysteries will be solved and the solutions used in a progressive way to promote a better, safer society.

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