Genetic Influences on Being Processed Through the Criminal Justice System: Results from a Sample of Adoptees

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Background: Behavioral genetic research has revealed that antisocial phenotypes are under genetic influence. This study examines whether genetic factors also affect the odds of being processed through the criminal justice system.

Methods: A sample of adoptees ($n = 191$–257) drawn from the National Longitudinal Study of Adolescent Health was analyzed. They self-reported on whether they had ever been arrested, sentenced to probation, incarcerated, and arrested multiple times. Assessments were also conducted of the criminal status of their biological parents.

Results: Adoptees who have a biological father or a biological mother who have been arrested previously are significantly more likely to be arrested, sentenced to probation, incarcerated, and arrested multiple times when compared with adoptees whose biological parents have not been arrested.

Conclusions: Adoptees who are genetically predisposed to antisocial phenotypes are at risk for being formally processed through the criminal justice system.

Even though crime rates have been on a downward trend during the past 15 to 20 years, criminal involvement continues to exert a significant toll on society and represents a serious public health concern. Each year in the United States, there are approximately 22 million victimization events, with nearly 5 million of these being violent incidents, such as rape, robbery, and assault (1). Beyond the physical injuries that are inflicted, crime victims are also host to a range of other maladies ranging from posttraumatic stress disorder to depression (2,3). Crime, moreover, creates a significant financial burden not only for the victim but also for government and taxpayers. One estimate, for example, revealed that the financial costs associated with crime reach a staggering burden of more than 1 trillion dollars annually (4).

The costs associated with crime are disproportionately the result of the criminal activities of the most serious violent and chronic criminals. Although these offenders make up only approximately 6% of the population, they account for more than 50% of all criminal offenses (5), and they are the ones who are the most likely to be formally processed through the criminal justice system culminating with an incarceration sentence (6,7). Understanding and identifying the etiologic origins of offenders who are processed through the criminal justice system represents a significant contribution to crime prevention efforts and to efforts designed to rehabilitate offenders. Research findings from behavioral genetic studies have been instructive in this regard by indicating that criminal involvement is a multifactorial phenotype that is likely the result of genetic predispositions and environmental liabilities (8).

In general, behavioral genetic studies do not estimate genetic influences on measures of formal contact with the criminal justice system but instead use measures of antisocial phenotypes that represent some of the strongest correlates to crime. Aggression, violence, antisocial personality disorder, self-reported crime and delinquency, and conduct disorder, for example, are frequently employed as measures of antisocial behavior. The results of the behavioral genetic studies examining these phenotypes have revealed that genetic factors explain approximately 50% of the variance in these measures, with most of the remaining variance being attributable to the effects of nonshared environmental factors plus error (9,10).

Because the antisocial measures examined in behavioral genetic studies have been shown to be highly heritable, and because these measures are strongly correlated with official criminal involvement, it stands to reason that formal processing through the criminal justice system would also be influenced by genetic factors. Antisocial phenotypes, however, represent a heterogeneous group of behaviors, and different antisocial behaviors can have different etiologies, including being influenced to different degrees by genetic and environmental factors (11) and even having different neurobiological substrates (12). Thus, extrapolating the results from studies examining crime correlates to other closely related phenotypes, such as being processed through the criminal justice system, might produce erroneous conclusions about the relative influence of genetics and the environment.

Most of the behavioral genetic research examining the genetic and environmental underpinnings to antisocial phenotypes analyzes samples of twin pairs. An alternative to this approach is the adoption-based research design. The adoption-based research design separates genetic and environmental effects by comparing the similarity of the adoptee with their biological parents and with their adoptive parents. As long as the adoptee had very limited or no exposure to their biological parents, then the only reason they should resemble their biological parents on a phenotype is because of shared genetic material. Similarly, as long as the adoptive parents are not genetically related to the adoptee, the only reason why the adoptee should resemble their adoptive parents is because of environmental effects.

In a classic adoption study examining the link between genetics and contact with the criminal justice system, Mednick *et al.* (13)

analyzed a sample of 14,427 adoptees, their biological parents, and their adoptive parents. The results of the study revealed that the odds that an adoptee would be convicted of a crime increased substantially if their biological parents had been convicted of a crime. This pattern of results indicates that there is a genetic component to criminal convictions.

Collectively, the available adoption-based research provides relatively consistent evidence indicating that variance in measures of antisocial behaviors, including contact with the criminal justice system, is partially due to genetic factors (14). The results generated from these adoption-based studies, however, are somewhat limited by the samples that have been analyzed. Specifically, most of the adoption samples were drawn from countries outside the United States or were drawn from nonrepresentative samples from just a few states (i.e., Colorado, Iowa, and Missouri). In addition, most of these samples were collected in the 1970s and 1980s, and thus whether the results would generalize to the United States in society today remains an open-empirical question. The current study is designed to address this issue by examining genetic influences on contact with the criminal justice system in a sample of adoptees drawn from a nationally representative sample of American youths.

Methods and Materials

Subjects

Subjects for this study come from the National Longitudinal Study of Adolescent Health (Add Health) (15). The Add Health is a longitudinal study consisting of a nationally representative sample of American youths who were enrolled in seventh through twelfth grade during the 1994–1995 school year. To date, four waves of data have been collected. The first round of data was collected during a regularly scheduled school day when more than 90,000 youths completed self-report surveys (i.e., Wave 1 in-school surveys). Adolescents were asked a wide range of questions about their social lives, their behaviors, and their demographic data. A subsample of youths was then selected to be reinterviewed at their home along with their primary caregiver (i.e., Wave 1 in-home surveys). During these in-home interviews, adolescents were asked more detailed questions, and they were also asked questions about sensitive topics, such as their involvement in delinquency and their sexual experiences. In total, 20,745 adolescents and 17,700 of their primary caregivers (usually the mother) participated in the Wave 1 in-home component to the Add Health study (16).

Approximately 1–2 years after the first round of data was collected, the second wave of data collection commenced. Because most of the respondents were still adolescents, the items included in the Wave 1 surveys were still relevant at Wave 2. As a result, the survey instruments were very similar between waves. For example, youths were still asked about their involvement in risky behaviors, their social and sexual relationships, and their family life. Overall, 14,738 adolescents participated in the Wave 2 component of the Add Health study. Then, between 2001 and 2002, when most of the respondents were young adults, the third round of interviews was completed. The survey instruments were thus amended to include questions that were more age-appropriate for young adults. Respondents were asked, for instance, about their employment status, their educational achievements, and their lifetime contact with the criminal justice system. More than 15,000 respondents completed the Wave 3 surveys. Finally, between 2007 and 2008 the fourth wave of data was collected. At this time, most of the respondents were between the ages of 24 and 32 years old, and so the surveys were once again revamped to include items that were

Table 1. Descriptive Statistics for Selected Add Health Study Variables

	Percentage		Frequency	
	No	Yes	No	Yes
Biological Father Arrested	72.5	27.5	166	63
Biological Mother Arrested	82.8	17.2	231	48
One Biological Parent Arrested	69.5	30.5	148	65
Both Biological Parents Arrested	93.4	6.6	199	14
Ever Arrested	63.0	37.0	293	172
Ever Sentenced to Probation	82.7	17.3	372	78
Ever Incarcerated	79.8	20.2	372	94
Arrested Multiple Times	81.4	18.6	380	87

germane to this age group. Detailed questions were asked about the respondents' current and past employment experiences, their health and economic well-being, and their involvement with the criminal justice system. Overall, 15,701 respondents were successfully interviewed at Wave 4 (16).

One unique aspect of the Add Health data is that a subsample of adoptees is embedded within the nationally representative sample. During Wave 1 interviews, youths were asked to indicate whether they were adopted. Although no follow-up questions were asked about the age at which they were adopted, one question asked the youth whether they currently lived with either of their biological parents. This question helps to delineate between those youths who were adopted (e.g., by a stepparent) but still lived with one of their biological parents versus those who were adopted into families where neither of their legal guardians was a biological parent. The final analytic sample was confined to youths who: 1) indicated that they were adopted, and 2) indicated that they were not living with either of their biological parents. The final analytic sample size ranged between $n = 191$ and $n = 257$ and varied as function of missing data for the different variables used in each of the statistical models.

Measuring Genetic Risk

The ability to tease apart genetic effects from environmental effects is facilitated by the analysis of adoptees. In samples of adoptees, the biological parents represent the genetic liability, whereas the adoptive parents represent the environmental liability. In the Add Health data, respondents were asked a number of questions about both of their biological parents. Two questions in particular were highly relevant to the current study. First, during Wave 4 interviews, respondents were asked whether their biological father had ever spent time in jail or prison. This question was coded dichotomously, where 0 = no, 1 = yes. Similarly, during Wave 4 interviews, respondents were asked whether their biological mother had ever spent time in jail or prison. Again, responses to this question were coded dichotomously, where 0 = no, 1 = yes. These two items allow for an examination of whether the criminal status of the biological father and the biological mother has independent effects on the criminal status of their adopted-away children.

Two additional genetic risk measures were also created. First, a dichotomous measure was created to indicate whether at least one of the biological parents of the respondent had been arrested (0 = no, 1 = yes). Second, another dichotomous measure was created to indicate whether both of the biological parents of the respondent had been arrested (0 = no, 1 = yes). With four different measures of genetic risk, it was possible to examine whether the effect of genetic risk was consistent across multiple measurement strategies. Table 1 contains the descriptive statistics for the genetic risk measures and the outcome measures employed in the current study.
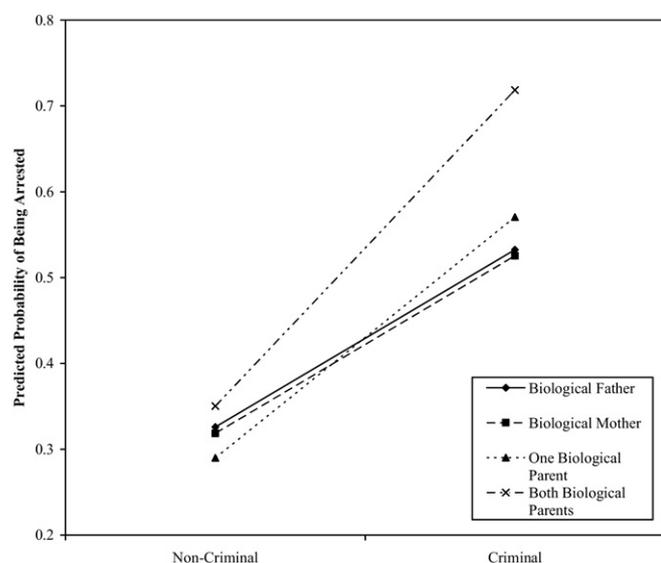
Figure 1. Predicted probability of being arrested as a function of criminality of biological parents. Biological father: b = .86, SE = .33, odds ratio (OR): 2.35, $p < .05$; biological mother: b = .86, SE = .35, OR: 2.37, $p < .05$; one biological parent: b = 1.18, SE = .34, OR: 3.25, $p < .05$; both biological parents: b = 1.56, SE = .64, OR: 4.73, $p < .05$. Models included age, gender, race, and family negativity as covariates.

Measuring Criminal Justice Processing

During Wave 4 interviews, respondents were asked a series of questions about their contact with the criminal justice system. Four of these measures had sufficient variation to examine in the present study. Specifically, respondents were asked whether they had ever been arrested (ever arrested), whether they had ever been sentenced to probation for an offense (ever probation), and whether they had ever spent time in a jail, prison, juvenile detention center, or other correctional facility (ever incarcerated). Each of these outcome measures was coded dichotomously, such that 0 = no, 1 = yes. In addition, respondents were asked the number of times they had been arrested (multiple arrests). This variable was dichotomized so that 0 = zero or one time and 1 = more than one time. Tetrachoric correlations among the four outcome measures ranged between .74 and .79, indicating they were all tapping different elements of the same construct—that is, contact with the criminal justice system.

Measuring Control Variables

To help isolate the effect of genetic risk from potential confounders, four control variables were included in all the analyses: gender, race, age, and family negativity. Gender (0 = female, 1 = male) and race (0 = Caucasian, 1 = minority) were included as dichotomous dummy variables, and age was included as a continuous variable measured in years. Family negativity was measured with the exact same scale that was employed by previous researchers analyzing the Add Health data (17). Specifically, three scales—a two-item maternal attachment scale, a five-item maternal disengagement scale, and a ten-item maternal involvement scale—all of which were measured at Wave 1, were subjected to a principal components factor analysis with varimax rotation. The results of this analysis indicated that all the scales could be accounted for by a single factor. Then, a weighted factor score was created such that higher values represented more family negativity.

Analysis

The analysis for this study proceeded in two stages. First, the effects that each of the four genetic risk measures had on each of the four outcome measures were estimated with binary logistic regression analysis. All the models controlled for the effects of gender, age, race, and family negativity. To facilitate the interpretation of the findings, the results are presented in a series of figures where the predicted probabilities are plotted across different levels of genetic risk. Second, because there are some potential shortcomings with the genetic risk measures, sensitivity analyses were conducted to examine the consistency of the results across different measurement strategies.

Results

The analysis for this study began by estimating the effects that the four genetic risk measures had on the probability of being arrested. The results of these models are presented in Figure 1, and the parameter estimates for the genetic risk measures are included at the bottom of the figure. As can be seen, the predicted probability of being arrested increased significantly across all four genetic risk measures when moving from no genetic risk (noncriminal biological parent) to genetic risk (criminal biological parent). For example, the predicted probability of being arrested among respondents without genetic risk was approximately .30. However, when genetic risk was present, this predicted probability increased markedly to between .50 and .72. Inspection of the odds ratios (ORs) revealed that the effect sizes ranged between 2.35 and 4.73. Regardless of how genetic risk was measured, having a criminal biological parent increased the odds of being arrested by at least a factor of 2.3 and sometimes by a factor of more than 4.5.

The next set of analyses examined the probability of being sentenced to probation as a function of the four genetic risk measures. As Figure 2 shows, the presence of genetic risk increased the predicted probability of being sentenced to probation. For respondents without a genetic liability, the predicted probability of being
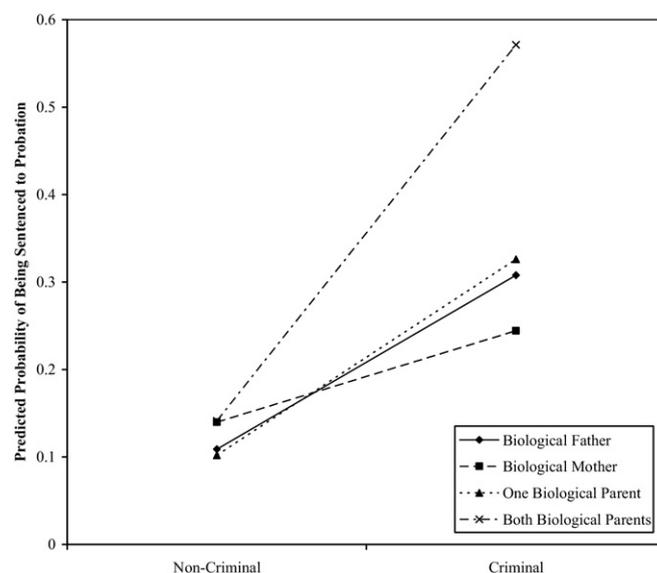

Figure 2. Predicted probability of being sentenced to probation as a function of criminality of biological parents. Biological father: b = 1.29, SE = .42, odds ratio (OR): 3.64, $p < .05$; biological mother: b = .69, SE = .42, OR: 1.99, $p > .05$; one biological parent: b = 1.45, SE = .42, OR: 4.26, $p < .05$; both biological parents: b = 2.09, SE = .73, OR: 8.10, $p < .05$. Models included age, gender, race, and family negativity as covariates.
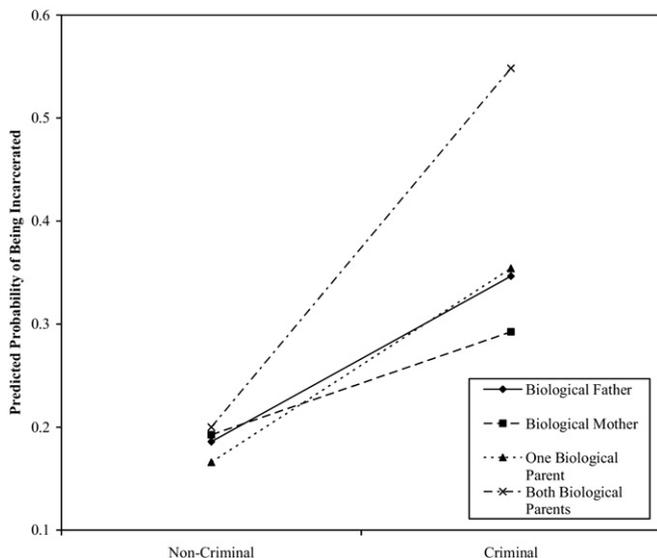
Figure 3. Predicted probability of being incarcerated as a function of criminality of biological parents. Biological father: b = .84, SE = .36, odds ratio (OR): 2.32, $p < .05$; biological mother = .55, SE = .37, OR: 1.73, $p > .05$; one biological parent: b = 1.01, SE = .36, OR: 2.76, $p < .05$; both biological parents: b = 1.58, SE = .61, OR: 4.86, $p < .05$. Models included age, gender, race, and family negativity as covariates.

Figure 4. Predicted probability of being arrested multiple times as a function of criminality of biological parents. Biological father: b = 1.13, SE = .41, odds ratio (OR): 3.13, $p < .05$; biological mother: b = 1.17, SE = .38, OR: 3.21, $p < .05$; one biological parent: b = 1.46, SE = .41, OR: 4.29, $p < .05$; both biological parents: b = 2.14, SE = .67, OR: 8.47, $p < .05$. Models included age, gender, race, and family negativity as covariates.

sentenced to probation was approximately .11, but for respondents with a genetic liability, the predicted probability increased to between .24 and .57. The results of the logistic regression equations indicate that the genetic risk measure based on whether the biological mother had ever been arrested was not related to the odds of being sentenced to probation (OR: 1.99, $p > .05$). However, all the other genetic risk measures predicted the odds of being sentenced to probation (ORs ranging between 3.64 and 8.10, $p < .05$).

Figure 3 contains the results of the models examining the probability of being incarcerated. Similar to the results presented in the previous figures, the results indicated that as genetic risk increased so too did the odds of being incarcerated. For respondents who lacked genetic risk, the predicted probabilities that they would be incarcerated were below .20 but increased quite drastically (probabilities ranged between .29 and .55) for respondents with a genetic predisposition for criminality. An examination of the logits reveals that the coefficient for the genetic risk measure based on criminality of the biological mother failed to reach statistical significance (OR: 1.73, $p > .05$), but the coefficients for the three other measures of genetic risk reached statistical significance (ORs ranged between 2.32 and 4.86, $p < .05$).

The last series of figures estimated the association between the probability of being arrested multiple times and genetic risk. The results of these models are presented in Figure 4, and the pattern of findings is consistent with those reported with the other outcome measures. As can be seen, the probability of being arrested multiple times increased dramatically for those respondents with genetic risk versus those without genetic risk. More precisely, respondents without genetic risk had a probability of being arrested multiple times that was approximately .10. For respondents who were characterized as having genetic risk, the predicted probability of being arrested multiple times ranged between .28 and .58. An inspection of the logit coefficients revealed that all four of the genetic risk measures were significantly associated with being arrested multiple times, with ORs ranging between 3.13 and 8.47 ($p < .05$).
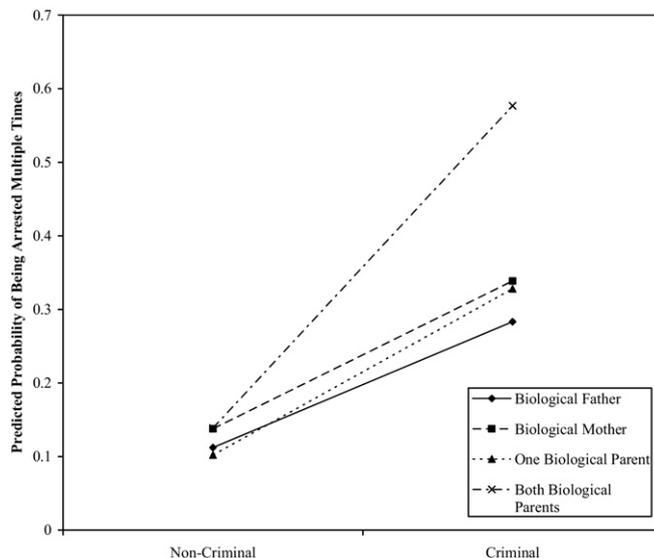
Sensitivity Analysis

Recall that respondents were only included in the final analytic sample if they indicated at Wave 1 that they were adopted and that they were not currently living with either of their biological parents. The Add Health data did not include any questions asked at Wave 1 that tapped the extent of contact that the respondent had with either of their biological parents (e.g., age at adoption or whether the adoption was an "open adoption"). Although the adoption-based research design is a powerful way to examine genetic effects, this methodology is grounded in the assumption that the adoptee had very limited or no exposure to their biological parents. If the adoptee had been exposed either to one or both of their biological parents, then the effects of the environment would be confounded with the effects of genetic factors, thus inflating the effects that the genetic risk measured had on the outcome measures. During Wave 4 interviews, however, respondents were asked a single-item measure that could be used as a proxy for the amount of contact that they had with their biological mother. Specifically, they were asked to indicate who the woman was that raised them. Responses to this item included a range of outcomes, including biological mother, adoptive mother, foster mother, aunt, sister, and grandmother. For the purposes of the current study, this item was dichotomized, such that 0 = a biologically related relative, 1 = a non-biologically related relative. The exact same question was asked about the father figure of the respondent. Again, the response was dichotomized, such that 0 = a biologically related relative, 1 = a non-biologically related relative.

All the analyses were then recalculated by comparing the results of the previous models with the results generated when only including respondents who indicated that they were reared by a non-biologically related relative. Table 2 presents the comparison of findings. The rows correspond to each of the four genetic risk measures. Model 1 (for each outcome measure) contains the OR that was estimated in the original adoption sample, and Model 2 (for each outcome measure) contains the OR that was estimated with the more restricted sample that only included cases for re-

Table 2. Sensitivity Analysis Examining Robustness of Association Between Biological Parents' Criminality and Contact With Criminal Justice System

	Ever Arrested		Ever Probation		Ever Incarcerated		Multiple Arrests	
	Model 1	Model 2	Model 1	Model 2	Model 1	Model 2	Model 1	Model 2
Biological Father	2.35[a]	4.20[a]	3.64[a]	4.04[a]	2.32[a]	2.60[b]	3.13[a]	5.16[a]
	(1.23–4.50)	(1.63–10.81)	(1.59–8.32)	(1.38–11.84)	(1.15–4.70)	(0.93–7.28)	(1.39–7.02)	(1.48–17.97)
Biological Mother	2.37[a]	2.91[a]	1.99	1.65	1.73	1.16	3.21[a]	3.33[a]
	(1.21–4.66)	(1.23–6.91)	(0.88–4.51)	(0.60–4.53)	(0.83–3.61)	(0.41–3.29)	(1.51–6.82)	(1.20–9.21)
One Biological Parent	3.25[a]	6.58[a]	4.26[a]	8.94[a]	2.76[a]	5.14[a]	4.29[a]	10.15[a]
	(1.68–6.31)	(2.23–19.40)	(1.86–9.77)	(2.52–31.69)	(1.35–5.61)	(1.64–16.12)	(1.91–9.65)	(2.37–43.56)
Both Biological Parents	4.73[a]	12.87[a]	8.10[a]	22.44[a]	4.86[a]	3.52	8.47[a]	56.08[a]
	(1.35–16.65)	(1.26–131.17)	(1.93–34.08)	(1.78–282.69)	(1.49–15.91)	(0.49–25.29)	(2.28–31.47)	(3.57–880.28)

The 95% confidence intervals for the odds ratios included in parentheses.
[a] $p < .05$, two-tailed tests.
[b] $p = .068$, two-tailed test.

spondents who were reared by a father figure who was a non-biologically related relative (equations using the biological father genetic risk measure), by a mother figure who was a non-biologically related relative (equations using the biological mother genetic risk measure), or by a mother figure and a father figure who were both non-biologically related relatives (equations using the one biological parent or both biological parents genetic risk measures). The 95% confidence intervals (CIs) for the ORs are included. Note that the CIs are quite large for the restricted sample, because of the low base rates for the outcome measures coupled with the smaller sample size ($n = 92$ to 154). The focus of these analyses, however, is on statistical significance and whether the replication models produce a pattern of results similar to those that are based on the full sample of adoptees. As Table 2 reveals, the pattern of results was virtually identical between models, with most of the ORs that were statistically significant in the full sample of adoptees also being statistically significant in the more restricted sample of adoptees. Taken together, these findings tend to suggest that the effects of the genetic risk measures are not upwardly biased due to exposure to the biological parents.

Discussion

A body of research has revealed that virtually all antisocial phenotypes are influenced to varying degrees by genetic factors (8,10). The current study extends this prior research by examining whether genetic factors affect the probability of being processed through the criminal justice system. The results of the analyses revealed that adoptees who were genetically predisposed to antisocial behavior, as measured by the criminality of their biological parents, were significantly more likely to be arrested, sentenced to probation, incarcerated, and arrested multiple times when compared with adoptees whose biological parents had not been arrested. This is the first study to document genetic influences on being processed through the criminal justice system in a sample of adoptees drawn from a nationally representative study.

Although the results of this study are consistent with evidence indicating that antisocial phenotypes are genetically influenced, caution should be exercised when interpreting the results, due to three main limitations. First, all the measures indexing contact with the criminal justice system were derived from self-reports. As a result, it is possible that subjects either intentionally or unintentionally misrepresented their contact with the criminal justice system. If the responses were systematically biased as a function of genetic risk, then the findings reported here might also be somewhat biased. Second, there

were not any questions that asked about the timing of the adoption or how much contact the subject had with their biological parents. To the extent that the adoptee had contact with either one or both of their biological parents, the genetic risk measures employed in this study would be confounded with environmental effects. Sensitivity analyses were conducted to take this possibility into account (Table 2). The results of these analyses provided evidence that the findings reported herein were not driven by environmental effects. Third, it is unclear the extent to which adoptees accurately reported the criminal status of their biological parents. If the adoptees were unaware of the criminal status of their parents, then the measures of genetic risk employed in the current study would include a significant amount of error. However, this error would result in downwardly biased effect sizes, meaning that the magnitude of the effects reported here are likely conservative estimates of the extent to which genetics affect the probability of being processed through the criminal justice system.

Current behavioral genetic research has revealed the potential importance of examining gene–environment interactions in the etiology of serious violence (18). In addition, previous studies have capitalized on the adoption-based research design to test for gene–environment interactions on antisocial phenotypes. To do so, the criminal status of the adoptive parents is used as a measure of environmental risk. The results of some of these adoption-based studies have revealed that adoptees who are at greatest risk for antisocial behaviors are those whose biological parents and whose adoptive parents have a history of criminal involvement or other forms of psychopathology (19). Although questions were asked about the criminal status of the adoptive parents (i.e., whether they had ever been arrested), only a very small percentage of adoptive parents had been arrested for a crime ($< .03\%$), making it impossible to test for gene–environment interactions. However, gene–environment interactions were explored by estimating the interaction between the measure of family negativity and the various measures of genetic risk. The results of these analyses did not provide support for gene–environment interactions in relation to being processed through the criminal justice system.

In conclusion, analysis of adoptees from the Add Health study provided evidence that a genetic predisposition to antisocial behavior was related to the probability of being processed through the criminal justice system. Replication studies, however, are needed to address the various limitations of the current study to determine the robustness of the results and whether they would be

observable in different samples, with different measures, and with different analytic techniques.

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