bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

On the heritability of criminal justice processing

Brian B. Boutwell*
Saint Louis University
boutwellb@slu.edu (email)

Eric Connolly
Pennsylvania State University, Abington

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Abstract

An impressive number of researchers have devoted a great amount of effort toward examining various predictors of criminal justice processing outcomes. Indeed, a vast amount of research has examined various individual- and aggregate-level predictors of arrests, incarceration, and sentencing decisions. To this point, much less attention has been devoted toward uncovering the relative contribution of genetic effects on variation in criminal justice processing. As a result, the current study employs a behavioral genetic design in order to help fill this void in the existing literature. Using twin data from a nationally representative sample of youth, the current study produced evidence suggesting that genetic factors accounted for at least a portion of variance in risk for incarceration among female twins and probation among male twins. Shared and nonshared environmental influences accounted for the variance in risk for arrest among both female and male twins, probation among female twins, and incarceration among male twins. Ultimately, then, it appears that risk for contact with the criminal justice system and criminal justice processing is structured by a combination of factors beyond shared cultural and neighborhood environments, and appear to also include genetic factors as well. Moving forward, continuing to not use genetically sensitive research designs capable of estimating the role of genetic and nonshared environmental influences on criminal justice outcomes may result in misleading results.

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

One of the overarching questions in criminological and criminal justice research concerns uncovering variables that predict contact with the criminal justice (CJ) system (Sampson and Lauritsen, 1997). To be sure, a wealth of research has examined factors thought to increase the likelihood of arrest and formal processing and little debate exists concerning at least one fact: contact with the CJ system is not a random occurrence (Sampson and Lauritsen, 1997). Indeed demographic factors, including race (Sampson and Lauritsen, 1997; Walsh, 2004), age (Moffitt, 1993), and gender (Ferguson and Horwood, 2002), as well as personality traits and developmental processes (Gottfredson and Hirschi, 1990; Moffitt, 1993) all correlate with varying levels of risk for arrest, incarceration, and formal sentencing. What is noticeably lacking, however, is an effort to examine the role of genetic factors in predicting contact with the CJ system (Beaver, 2011).

The evidence implicating genetic factors as source of variance for antisocial and criminal behavior in general is overwhelming (Ferguson, 2010; Mason and Frick, 1994; Miles and Carey, 1997; Plomin et al., 2013; Rhee and Waldman, 2002). The vast majority of researchers in criminology, however, have labored under the assumption that genetic factors play only a minimal part in predicting whom in the population will be arrested, incarcerated, and formally sentenced (Cullen, 2011). This approach may ultimately prove short sighted given the wide array of human outcomes influenced by genetic factors (Turkheimer, 2000). The current study, thus, is intended to be a step toward uncovering sources of variation—both environmental and genetic—for criminal justice processing. First, however, it is important to discuss prior research pertaining to the heritability of antisocial, aggressive, and criminal behaviors.

THE HERITABILITY OF ANTISOCIAL BEHAVIOR

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Evidence concerning the heritability of human behavior can be traced largely to work in the field of behavior genetics (Plomin et al., 2013). The science of behavior genetics is devoted to examining the origin of individual differences (Turkheimer, 2000). Put differently, behavioral genetic research utilizes sibling pairs of varying degrees of genetic relatedness (i.e., monozygotic (MZ) twins, dizygotic (DZ) twins, full-siblings, and half-siblings) in order to uncover sources of variation for physiological, pathological, psychopathological, and behavioral outcomes (Turkheimer, 2000). Because MZ twins share, on average, twice as much genetic material as DZ twins, it is assumed that if MZ twins resemble one another more closely than DZ twins for a certain trait then genetic factors may be contributing to variation in that particular outcome (Plomin et al., 2013). If the similarity of DZ twins and full-siblings, which share on average 50% of their genetic material, is greater than that of half-siblings, which share 25% of their genetic material, moreover, the conclusion regarding genetic influences is further underscored (Plomin et al., 2013).

Put more directly, behavioral genetic research divides trait variance into that which is the result of heritability (h^2), that which is the result of the shared environment (c^2), and that which is due to the non-shared environment (e^2) (Plomin et al., 2013). Prior researchers have discussed these concepts in great detail so they will not be belabored here (Beaver et al., 2008). For definitional purposes, however, heritability refers the proportion of variance in a given trait due to variation at the genetic level. The shared environment represents environmental influences that serve to increase the resemblance of twins or siblings on the outcome measure under investigation. Non-shared environments represent the unique experiences of twins or siblings that function to create differences on the outcome measure under investigation between children

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

in the same family. Taken together, h^2, c^2, e^2 will always sum to yield 100 percent of the variance in a given outcome measure (Beaver et al., 2008; Plomin et al., 2013).

The application of behavior genetic techniques is common in a range of disciplines outside of criminology (Rhee and Waldman, 2002). Behavior genetic methodologies, however, have recently gained some traction in the study of crime and delinquency (Beaver et al., 2009; DeLisi et al., 2008). This growing line of research has produced evidence that abstention from delinquency (Boutwell and Beaver, 2008), onset of delinquency (DeLisi et al., 2008), chronic criminality (Barnes et al., 2011; Barnes and Boutwell, 2012), changes in delinquency (Barnes and Boutwell, 2012; Connolly, Schwartz, Nedelec, Beaver, and Barnes, 2015) delinquent peer affiliation (Beaver et al., 2009), and victimization (Barnes et al., 2011; Beaver et al., 2009) are all, to some degree, heritable.

Importantly, personality traits corresponding to risk of criminal and delinquent behavior have also shown evidence of being under genetic influence (Krueger et al., 2008). Studies, for example, examining low self-control (Beaver, Ratchford, and Ferguson, 2009; Beaver et al., 2008; Boisvert et al., 2011; Connolly and Beaver, 2014; Wright and Beaver, 2005; Wright et al., 2008), negative emotionality (Krueger et al., 2008), and psychopathy (Beaver et al., 2011) have produced consistent evidence that personality constructs positively correlated with crime and criminality are influenced by genetic factors. Taken as a whole, what this body of evidence suggests is that the behaviors which are likely to increase the risk of arrest (i.e., delinquency), as well as the personality constructs that are associated with those behaviors (i.e., self-control), are influenced to varying degrees by genetic factors. What is less clear, however, is whether actual instances of contact with the criminal justice system—including arrests and convictions—are

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

heritable. Despite limited research in this regard, there is reason to suspect that formal processing through the justice system may be influenced by genetic factors.

GENETIC CONTRIBUTORS OF CRIMINAL JUSTICE PROCESSING

Early evidence concerning the role of genes in predicting criminal justice processing outcomes was produced by Mednick and his colleagues (1984) using a sample of adoptees. Mednick et al. (1984) examined both property and violent criminal convictions in adopted away children and their biological parents. While the results indicated that genetic factors may influence convictions for property crime (adopted children correlated significantly with their biological parents for this variable), there was no significant correlation between adopted children and biological parents for violent criminal convictions.

A more recent analysis of adoptees was conducted by Beaver (2011) using data on individuals participating in the National Longitudinal Study of Adolescent to Adult Health (Add Health). In order to indirectly tap genetic risk factors for antisocial behavior, subjects who reported having a biological parent previously incarcerated were considered to be genetically vulnerable for criminal involvement. The results were indeed stark. Subjects, for example, who reported two biological parents with a criminal history were over four times more likely to be arrested, over four times more likely to be incarcerated, over eight times more likely to be sentenced to probation, and approximately eight times more likely to be arrested multiple times.

Beaver and Chaviano (2011) adopted a slightly different approach and tested whether measured genes had an impact on the likelihood of contact with the criminal justice system in a sample of Hispanic respondents. Using data from the Add Health study, Beaver and Chaviano (2011) examined whether certain dopaminergic genes influenced whether individuals were ever

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

arrested, sentenced to probation, incarcerated, or arrested multiple times. For each outcome, genetic risk factors increased the likelihood of criminal justice processing. As scores on an index of genetic risk increased, so too did the odds of being arrested, incarcerated, sentenced to probation, and arrested multiple times.

Schwartz and Beaver (2011) also employed a molecular genetics approach and tested whether certain environmental factors conditioned the influence of genetic factors in the prediction of criminal justice outcomes. Drawing on prior literature linking variants of the monoamine oxidase A (MAOA) gene to violent forms of criminal behavior (Beaver et al., 2009; Brunner et al., 1993), these researchers tested whether exposure to perceived prejudice moderated the influence of MAOA on self-reported arrest. The findings from their study suggested that the impact of MAOA on being arrested was conditioned by the respondent's perceived level of prejudice. These results dovetail with prior work indicating that stressful, negative, and even abusive environments condition the influence of MAOA in the prediction aggressive and violent behavior (Caspi et al., 2002; Kim-Cohen et al., 2006).

THE CURRENT STUDY

The studies just described provide an indication that criminal justice processing may be influenced by genetic factors, however, there is little evidence directly pertaining to the heritability of contact with the CJ system. Thus, the current study is intended to directly test this proposition. It is important to note that the current study utilizes the same criminal justice processing variables as prior research (Beaver, 2011; Beaver and Chaviano, 2011; Schwartz and Beaver, 2011). This analysis, however, differs from earlier work in at least four important respects. First, Beaver (2011) utilized adopted siblings in the Add Health and the current study

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

uses the subsample of biologically related siblings. The current analysis excludes any siblings who were unrelated, yet residing in the same home. Essentially, the sample of participants analyzed here represents a different sample from that of Beaver (2011).

Second, Beaver's (2011) analysis employed an indirect measure of genetic risk to estimate the broad effects of the genome on risk for criminal justice processing. The current study analyzes sibling pairs in order to calculate pair similarity for a range of important criminal justice processing variables. Third, using behavioral genetic techniques, the current study is intended to estimate the proportion of variance in criminal justice processing that is accounted for by latent genetic and environmental influences. This was not the intent of prior research (Beaver, 2011). Fourth, and finally, prior researchers examining the role of genetic factors in criminal justice processing have examined the impact of measured genes (Beaver & Chaviano, 2011; Schwartz & Beaver, 2011). As prior researchers have noted, however, candidate gene studies have some inherent limitations (Chabris et al., 2015; Dick et al., 2015) and thus it is important to examine these outcomes using multiple different quantitative research strategies.

METHODS

Data

The data included in this study were taken from the fourth wave of the National Longitudinal Study of Adolescent to Adult Health (Add Health) (Harris et al., 2006). The Add Health is a multi-wave sample spanning decades of development beginning in early adolescence and traversing into adulthood. Data collection began in 1994 while respondents were enrolled in middle and high school. Three waves of subsequent data collection were undertaken with respondents at each wave reporting on topics ranging from their personality traits, sexual

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

involvement, criminal involvement, victimization experiences, as well as their family structures and existing medical conditions.

A useful feature of the Add Health sample is that siblings pairs, of varying degrees of genetic relatedness (i.e., monozygotic (MZ) twins, dizygotic (DZ) twins, full siblings, half-siblings, and non-related siblings (i.e., step-siblings living together in the same home), were actively recruited for participation in data collection (Harris et al., 2006). Subjects indicating that they had a sibling were (along with their co-twin) selected with 100 percent certainty (Harris et al., 2006). The resulting sampling procedure netted 307 MZ twin pairs and 452 DZ twin pairs. The current study analyses twin pairs who provided a response to each criminal justice outcome. As such, the final analytic sample included 214 MZ twin pairs and 326 DZ twin pairs.

Measures

CJ Contact. During the fourth, and most recent, wave of data collection respondents in the Add Health sample were asked to indicate whether they had ever been arrested, incarcerated, or placed on probation (Beaver, 2011; Beaver & Chiavano, 2011; Schwartz & Beaver, 2011). Responses to the arrest and incarceration items were coded dichotomously so that 1 = yes and 0 = no. Responses to the item assessing probation, however, was originally coded so that 0 = zero times, 1 = once, and 2 = more than once. For ease of interpretation, the item assessing probation during the fourth wave was dichotomized so that 1 = ever convicted/placed on probation and 0 = no convictions/probation sentences.

PLAN OF ANALYSIS

The plan of analysis for the current study involves a series of steps intended to systematically examine the genetic and environmental contributions to contact with the criminal

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

justice system and criminal justice processing. The first step involved calculating between-sibling correlations for MZ twins and DZ twins to estimate concordance rates for arrest, incarceration, and probation. This step was carried out to examine whether genetic influences may explain a degree of variation in liability for each outcome. If concordance on an outcome for MZ twins (who share close to 100% of their genetic material) is stronger than concordance for DZ twins (who share, on average, 50% of their genetic material), then this can be interpreted as preliminary evidence suggesting that genetic factors account for a degree of variation in the outcome measure.

The second step was to calculate intraclass odds ratios for each of the outcomes described above (Cho et al., 2006). The logistic regression equation estimated in this phase of the analytical process assumes the following form:

$$\log_e [P(K1)/1- P(K1)] = b_0 + \exp(b_1(K2))$$

The interpretation of coefficient b_1 remains straightforward, although it departs slightly from other forms of logistic regression analysis. In this case, the coefficient is transformed (i.e., exponentiated) so that the parameter estimate captures the odds that sibling 1 has a 1 on the outcome variable based on their sibling's (i.e., sibling 2) score on the same measure—in this case one of the criminal justice processing items (Barnes et al., 2011). Importantly, genetic influences from this portion of the analysis are inferred if the similarity of sibling pairs increases along with their genetic relatedness (i.e., if MZ twins are more similar than DZ twins) (Barnes et al., 2011).

The third step in study was to directly estimate the proportion of variance in each criminal justice measure as well as the composite criminal justice measure that was the result of genetic and environmental influences. In order to estimate these effects, a series of univariate ACE models were fitted to the data. Biometric ACE models are capable of partitioning variance

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

of a measurable outcome into three latent variance components: an additive genetic component (symbolized as A), a shared environmental component (symbolized as C), and a nonshared environmental component, which also includes measurement error (symbolized as E). Variation in an outcome explained by additive genetic effects suggests that genetic differences between-sibling pairs explain individual differences in the outcome under investigation.

Variation in an outcome explained by shared environmental effects suggests that shared environmental experiences between siblings explain similarities in a given outcome under investigation. In contrast, variation in an outcome accounted for by nonshared environmental effects suggests that unique environmental experiences between siblings explain differences in an outcome under investigation. The nonshared environmental component also includes the effects of measurement error. The assumptions of the twin-based research design have been tested several different times and in many different ways with results indicating that the twin-based research method produces reliable and stable estimates of genetic and environmental effects on phenotypic variance, even when underlying assumptions are violated (Barnes et al., 2014). Given the dichotomous nature of the data, liability-threshold ACE models were estimated to assess the magnitude of additive genetic, shared environmental, and nonshared environmental effects on risk for arrest, incarceration, and probation (Prescott, 2004). ACE models were estimated using the statistical software program M*plus* 7.1 (Muthén & Muthén, 1998-2011) with a weighted least squares estimator (i.e., WLSMV). Model fit was evaluated based on an adjusted χ^2 difference test statistic, the comparative fit index (CFI), and the root mean square error of approximation (RMSEA). Based on prior literature, the following model fit cutoff points were used to assess satisfactory model fit: CFI $\geq$ .90, TLI $\geq$ .95, and RMSEA $\leq$ .05 (Hu & Bentler, 1999).

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

RESULTS

Table 1 presents the descriptive statistics for each outcome measure. As can be seen, close to 28% of the twin sample reported having been arrested in their lifetime. Males were significantly more likely to report having been arrested compared to females ([1], $\chi^2 = 44.96$, $p < .01$). Table 1 also shows that 15% of the twin sample reported having been incarcerated in their lifetime and close to 12% of the sample reported having been on probation in their lifetime. Males were significantly more likely to report having been incarceration ([1], $\chi^2 = 36.20$, $p < .01$) and on probation ([1], $\chi^2 = 54.67$, $p < .01$) compared to females.

Insert Table 1 about Here

Table 2 contains the between-sibling tetrachoric correlation estimates for arrest, incarceration, and probation. Estimates from the full twin sample including same-sex female and male twins revealed that MZ twins reported stronger concordance for arrest, incarceration, and probation, compared to DZ twins. However, the pattern of correlations was slightly altered when examining female and male twins separately. Specifically, concordance rates for arrest were slightly stronger for female MZ twins compared to same-sex female DZ twins and considerably stronger for incarceration. However, same-sex female DZ twins reported slightly stronger rates of concordance for probation compared to female MZ twins, but the correlations were non-significant. With respect to male twins, male MZ twins demonstrated slightly stronger concordance for arrest compared to same-sex male DZ twins and moderately stronger rates of concordance for probation. The strength of with-pair concordance for incarceration between male MZ and same-sex DZ twins was almost identical and non-significant.

Insert Table 2 about Here

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Table 3 contains the results of the intraclass logistic regression analysis described in the plan of analysis. As can be seen in Table 3, the odds of arrest were significantly higher if MZ twins reported having a co-twin who was also arrested (*OR* = 7.02, $p < .01$, 95% CI: 3.48-14.18). This estimate was higher compared to DZ twins who reported having a co-twin who was also arrested (*OR* = 3.98, $p < .01$. 95% CI: 2.41-6.59). This pattern of results was consistent across all other outcomes when examining the full twin sample where the odds of incarceration and probation diminished as the degree of genetic relatedness decreased. When female and male twins were examined separately, however, the odds of arrest were significantly higher for female and male MZ twins compared to same-sex DZ twins, but the odds of probation for female MZ twins were non-significant and smaller compared to same-sex female DZ twins, while the odds of incarceration for male MZ and same-sex DZ twins were non-significant.

Insert Table 3 about Here

The final step in the analytic plan was to directly estimate the proportion of variance in criminal justice processing measures that was attributable to genetic and environmental effects. We fitted a series of univariate ACE models to the data on arrest, incarceration, and probation. Based on the evidence from previous steps in the analysis on sex differences in the magnitude of genetic and environmental effects on variation in risk for criminal justice processing, model fit statistics were used to evaluate whether model parameters could be equated across sex without significant loss of fit to the model. Results indicated that model parameters could be equated across sex without significant loss of fit for arrest ([3] $\Delta\chi^2 = 3.51$, $p = .26$), but not for incarceration ([3] $\Delta\chi^2 = 1.03$, $p = .001$) and probation ([3] $\Delta\chi^2 = .09$, $p = .001$). As such, a univariate ACE model was estimated to assess the magnitude of genetic and environmental effects on risk for arrest using the full twin sample, while ACE models for incarceration and

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

probation were estimated separately for female and male twins. Table 4 presents the parameter estimates from a series of models examining the proportion of variance in risk for arrest accounted for by additive genetic, shared environmental, and nonshared environmental effects. As can be seen, constraining the additive genetic component to 0, which resulted in a CE model, improved overall model fit and provided the best fit to the data ($\Delta\chi^2 = 5.77$, $\Delta df = 1$, $p = .02$, CFI = .97, RMSEA = .05). Standardized parameter estimates from the best-fitting CE model suggested that 54% of the variation in liability for arrest was accounted for by shared environmental effects, while 46% of the variation in liability was accounted for by nonshared environmental effects.

Insert Table 4 about Here

Table 5 presents the standardized parameter estimates from the estimated ACE models examining the magnitude of genetic and environmental effects on risk for incarceration and probation among female twins. Model fit indices indicated that an AE model for incarceration fit the data best ($\Delta\chi^2 = .03$, $\Delta df = 1$, $p = .85$, CFI = .93, RMSEA = .04) where additive genetic influences accounted for 60% of the variation in liability for incarceration and nonshared environmental influences accounted for 40% of the variation in liability. The best-fitting univariate model for probation included only shared and nonshared environmental parameters ($\Delta\chi^2 = .00$, $\Delta df = 1$, $p = 1.00$, CFI = .80, RMSEA = .06). As a result, the parameter estimates from the best-fitting model suggested that 49% of the variation in liability for probation was accounted for by shared environmental influences, while 51% of the variance in liability was accounted for by nonshared environmental influences.

Insert Table 5 about Here

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Table 6 presents the standardized parameter estimates from the univariate ACE models for incarceration and probation among male twins. Model fit indices indicated that a CE model fit the data adequately ($\Delta\chi^2$ = .02, Δdf = 1, p = .88, CFI = .87, RMSEA = .09). Results from the CE model suggested that 26% of the variance in liability for incarceration among male twins was accounted for by shared environmental influences, while 74% of the variance in liability for incarceration was accounted for by nonshared environmental influences. With respect to probation, model fit statistics suggested that an AE model provided the best fit to the data ($\Delta\chi^2$ = .1.44, Δdf = 1, p = .22, CFI = .90, RMSEA = .05). Parameter estimates from the best-fitting AE model indicated that 57% of the variance in liability for probation was accounted for by additive genetic influences, while the remaining 43% of variance in liability for probation was accounted for by nonshared environmental influences.

Insert Table 6 about Here

DISCUSSION

Criminology has devoted a great deal of effort to understanding why some individuals in the population are more likely to come into contact the criminal justice system. Further understanding the underlying influences on the predictors of arrest, incarceration, and formal sentencing remain central to the research agendas for both criminologists and criminal justice practitioners. The current study was intended to press forward in this area of research by examining the genetic and specific environmental underpinnings of various measures of criminal justice processing (arrest, incarceration, and probation). While prior research suggests that criminal justice processing is not beyond the reach of genetic influence (Beaver, 2011; Beaver and Chaviano, 2011), less research has used behavioral genetic methods to assess the extent to which genetic and environmental influences account for variation in risk for criminal justice

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

processing. The present study extended this line of work by examining a sample of male and female twins from a nationally representative survey of youth. The results yielded two key findings that deserve further attention.

First, our results revealed that shared and nonshared environmental influences accounted for the variance in liability for arrest among female and male twins. Interestingly, shared environmental influences explained the majority of the variance in risk for arrest suggesting that common environmental experiences play an important role in explaining why some come into contact with the criminal justice system. Although speculative, some possible mechanisms involved in the shared environmental influence on arrest might include shared subcultural values, socioeconomic factors, or even neighborhood factors (see also, Burt, 2009). Given the significant role of the non-shared environment as well, techniques such as those utilized by Beaver (2008) will be useful in further exploring whether differences in exposure to key crime correlates, like delinquent peer groups, might also be important.

Second, results from the univariate biometric models examining female and male twins separately revealed that additive genetic and nonshared environmental influences explain variation in liability for incarceration among females and probation among males. Alternatively, the shared and nonshared environment appeared to explain variation in liability for probation among females and incarceration among males. While it is tempting to speculate about why genetic influences were different for different traits in males and females, we should resist making strong inferences until our findings can be replicating using larger, more powerful samples. Nonetheless, what is clear is that the non-shared environment consistently emerged as significant for every CJ processing variable. What this means is that future research on this topic

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

will by necessity need to make use of twin and sibling designs in order to more thoroughly document the possible causes and correlates of criminal justice processing (Beaver, 2008).

The current study was not without limitation and it is important to discuss potential shortcomings prior to concluding. The first limitation concerns the measurement utilized to assess formal contact with the criminal justice system. Respondents were asked to self-report their contact with the justice system, and as a result, issues with misreporting due to concerns over social desirability could potentially impact the findings reported here. Even so, there is evidence suggesting that self-reported items are both reliable and valid instruments for assessing criminal involvement (Piquero, Farrington, and Blumstein, 2003; Thornberry and Krohn, 2000). The use of self-reported items, then, may help to side step many of the potential problems surrounding the use of official statistics (i.e., the justice system can only process crimes that are known to the police).

Ultimately, the findings presented here offer further evidence that criminal justice outcomes are influenced by a combination of genetic, shared environmental, and nonshared environmental factors (Beaver, 2008; 2011; Beaver and Chaviano, 2011; Schwartz and Beaver, 2011). When considered alongside the mass of evidence pertaining to the origins of virtually every other human outcome these results are to be expected (Turkheimer, 2000). Indeed, the sources of human variation for criminal behavior involve, to varying degrees, *both* genes and environments. Unfortunately, most criminological research examining criminal justice processing outcomes do not focus on assessing or controlling for latent genetic effects, which ultimately make it impossible to distinguish between shared and non-shared environmental effects (Beaver, 2008). In light of the current results, future studies now have even more reason to employ genetically sensitive designs (Barnes et al., 2014). The question of whether genes

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

influence criminality has always been an empirical one and the tools necessary for addressing it are becoming readily accessible to criminologists. For criminology to remain a relevant voice in the study of human behavior there needs to be a shift towards directly examining both genetic and environmental factors in studies pertaining to crime and criminal justice outcomes (Barnes et al., 2014; Cullen, 2011).

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

REFERENCES

Barnes, J.C., Beaver, K.M., and Boutwell, B.B. (2011). Examining the genetic underpinnings to Moffitt's developmental taxonomy: A behavioral genetic analysis. *Criminology, 49*, 923-54.

Barnes, J.C. and Boutwell, B.B. (2012). On the relationship of past to future involvement in crime and delinquency: a behavioral genetic analysis. *Journal of Criminal Justice*, *40*, 94-102.

Barnes, J.C., Boutwell, B.B., and Fox, K.A. (2011). The effect of gang membership on victimization: a behavioral genetic explanation. *Youth Violence and Juvenile Justice*, In press.

Barnes, J. C., Wright, J. P., Boutwell, B. B., Schwartz, J. A., Connolly, E. J., Nedelec, J. L., & Beaver, K. M. (2014). Demonstrating the validity of twin research in criminology. *Criminology*, *52*(4), 588-626.

Beaver, K.M. (2008). Nonshared environmental influences on adolescent delinquent involvement and adult criminal behavior. *Criminology*, *46*, 341-369.

Beaver, K.M. (2011). Genetic influences on being processed through the criminal justice system: Results from a sample of adoptees. *Biological Psychiatry*, *69*, 282-287.

Beaver, K.M., Barnes, J.C., May, J.S., Schwartz, J.A. (2011). Psychopathic personality traits, genetic risk, and gene-environment correlations. *Criminal Justice and Behavior*, *38*, 896-912.

Beaver, K.M., Boutwell, B.B., Barnes, J.C., and Cooper, J.A. (2009). The biosocial underpinnings to adolescent victimization: results from a longitudinal sample of twins. *Youth Violence and Juvenile Justice*, *7*, 223-238.

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Beaver, K.M. and Chaviano, N. (2011). The association between genetic risk and contact with the criminal justice system in a sample of hispanics. *Journal of Contemporary Criminal Justice*, *27*, 81-94.

Beaver, K.M., DeLisi, M., Vaughn, M.G., and Barnes, J.C. (2009). Monoamine oxidase a genotype is associated with gang membership and weapon use. *Comprehensive Psychiatry*, *51*, 130-134.

Beaver, K.M., DeLisi, M., Vaughn, M.G., and Wright, J.P. (2010). The intersection of genes and neuropsychological deficits in the prediction of adolescent delinquency and low self-control. *International Journal of Offender Therapy and Comparative Criminology, 54,* 22-42.

Beaver, K.M., DeLisi, M., Vaughn, M.G., Wright, J.P., Boutwell, B.B. (2008). The relationship between self-control and language: Evidence of a shared etiological pathway. *Criminology, 46,* 939-969.

Beaver, K.M., Ratchford, M., & Ferguson, C.J. (2009). Evidence of genetic and environmental effects on the development of low self-control. *Criminal Justice and Behavior, 36,* 1158-1172.

Beaver, K.M., Shutt, J.E., Boutwell, B.B., Ratchford, M., Roberts, K., & Barnes, J.C. (2009). Genetic and environmental influences on levels of self-control and delinquent peer affiliation: Results from a longitudinal sample of adolescent twins. *Criminal Justice and Behavior, 36,* 41-60.

Boisvert, D., Wright, J.P., Knopik, V., & Vaske, J. (2011). Genetic and environmental overlap between self-control and delinquency. *Journal of Quantitative Criminology,*DOI: 10.1007/s10940-011-9150x

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Boutwell, B.B and Beaver, K.M. (2008). A biosocial explanation to delinquency abstention. *Criminal Behavior and Mental Health*

Brunner H.G., Nelen, M., Breakefield, X.O., Ropers, H.H., and van Oost, B.A. (1993). Abnormal behavior associated with a point mutation in the structural gene for monoamine oxidase a. *Science*, *262*, 578-80.

Burt, S.A. (2009). Rethinking environmental contributions to child and adolescent psychopathology: A meta-analysis of shared environmental influences. *Psychological bulletin*, *135*(4), 608.

Caspi, A., McClay, J., Moffitt, T. E., Mill, J., Martin, J., Craig, I. W., Taylor, A., and Poulton, R. (2002). Role of genotype in the cycle of violence in maltreated children. *Science*, *297*, 851-854.

Chabris, C. F., Lee, J. J., Cesarini, D., Benjamin, D. J., & Laibson, D. I. (2015). The fourth law of behavior genetics. *Current directions in psychological science*, *24*(4), 304-312.

Cho, H., Guo, G., Iritani, B.J., and Hallfors, D.D. (2006). Genetic contribution to suicidal behaviors and associated risk factors among adolescents in the U.S. *Prevention Science*, *7*, 303-11.

Connolly, E. J., & Beaver, K. M. (2014). Examining the genetic and environmental influences on self-control and delinquency: Results from a genetically informative analysis of sibling pairs. *Journal of Interpersonal Violence*, *29*, 707-735.

Connolly, E. J., Schwartz, J. A., Nedelec, J. L., Beaver, K. M., & Barnes, J. C. (2015). Different slopes for different folks: Genetic influences on growth in delinquent peer association and delinquency during adolescence. *Journal of Youth and Adolescence*, *44*, 1413-1427.

Cullen, F.T. (2011). Beyond adolescence-limited criminology: choosing our future-the 2010

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

american society of criminology sutherland address. *Criminology*, *49*, 287-330.

DeFries, J.C., and Fulker, D.W. (1985). Multiple regression analysis of twin data. *Behavior Genetics*, *15*, 467–73.

DeLisi, M., Beaver, K.M., Wright, J.P., and Vaughn, M.G. (2008). The etiology of criminal onset: the enduring salience of nature and nurture. *Journal of Criminal Justice*, *36*, 217-223.

Dick, D. M., Agrawal, A., Keller, M. C., Adkins, A., Aliev, F., Monroe, S., Hewitt, J. K., Kendler, K. S., & Sher, K. J. (2015). Candidate gene–environment interaction research: Reflections and recommendations. *Perspectives on Psychological Science*, *10*, 37-59.

Ferguson, Christopher J. 2010. Genetic contributions to antisocial personality and behavior: A meta-analytic review from an evolutionary perspective. *Journal of Social Psychology*, *150*, 1-21.

Ferguson, D.M. and Horwood, L.J. (2002). Male and female offending trajectories. *Developmental and Psychopathology*, *14*, 159-177.

Gottfredson, M. and Hirschi, T. (1990). *A general theory of crime.* Stanford, CA: Stanford University Press.

Harris, K. M., Halpern, C. T., Smolen, A., and Haberstick, B. C. (2006). The national longitudinal study of adolescent health (Add Health) twin data. *Twin Research and Human Genetics*, *9*, 988-997.

Kim-Cohen, J., Caspi, A., Taylor, A., Williams, B., Newcombe, R., Craig, I. W., and Moffitt, T.E. (2006). MAOA, maltreatment, and gene-environment interaction predicting children's mental health: New evidence and a meta-analysis. *Molecular Psychiatry*, *11*, 903-913.

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Krueger, R.F., South, S., Johnson, W., and Iacono, W. (2008). The heritability of personality is not always 50%: gene-environment interactions and correlations between personality and parenting. *Journal of Personality*, *76*, 1485-1522.

Mason, D.A. and Frick, P.J. (1994). The heritability of antisocial behavior: A meta-analysis of twin and adoption studies. *Journal of Psychopathology and Behavioral Assessment*, *16*, 301-323.

Mednick, S. A., Gabrielli, W. F., and Hutchings, B. (1984). Genetic influences in criminal convictions: Evidence from an adoption cohort. *Science*, *224*, 891-894.

Miles, D.R. and Carey, G. (1997). Genetic and environmental architecture on human aggression. *Journal of Personality and Social Psychology*, *72*, 207-217.

Moffitt, T.E. (1993). Adolescence-limited and life-course persistent antisocial behavior: A developmental taxonomy. *Psychological Review*, *100*, 674-701.

Muthén, L. K., & Muthén, B. O. (1998-2012). *Mplus User's Guide*. Los Angeles, CA: Muthén and Muthén.

Pike, A., Reiss, D., Hetherington, E. M., and Plomin, R. (1996). Using MZ differences in the search for nonshared environmental effects. *Journal of Child and Adolescent Psychiatry*, *37*, 695-704.

Piquero, A. R., Farrington, D.P., and Blumstein, A. (2003). The criminal career paradigm. *Crime and Justice*, *30*, 359-506.

Plomin, R., J.C. DeFries, V.S. Knopik, and J.M. Neiderhiser. (2013). *Behavioral Genetics*, 6th ed. New York: Worth.

Prescott, C.A. (2004). Using the Mplus computer program to estimate models for continuous and categorical data from twins. *Behavior Genetics*, *34*, 17-38.

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Rhee, S.H. and Waldman, I.D. (2002). Genetic and environmental influences on antisocial behavior: A meta-analysis of twin and adoption studies. *Psychological Bulletin*, *128*, 490-529.

Rodgers, J.L., and Kohler, H.P. (2005). Reformulating and simplifying the DF analysis model. *Behavior Genetics*, 35, 211–17.

Sampson, R.J. and Lauritsen, J.T. (1997). Racial and ethnic disparities in crime and criminal justice in the united states. *Crime and Justice*, *21*, 311-374.

Schwartz, J.A. and Beaver, K.M. (2011). Evidence of a gene × environment interaction between perceived prejudice and maoa genotype in the prediction of criminal arrests. *Journal of Criminal Justice*, *39*, 378-384.

Thornberry, T. P., and Krohn, M.D. (2000). The self-report method for measuring delinquency and crime. In measurement and analysis of crime and justice, Vol. 4 of Criminal Justice 2000. Washington, D.C.: National Institute of Justice, Office of Justice Programs, U.S. Department of Justice.

Turkheimer, E. (2000). Three laws of behavior genetics and what they mean. *Current Directions in Psychological Science*, *9*, 160-164.

Walby, Kevin., and Nicolas Carrier. 2010. The rise of biosocial criminology: Capturing observable bodily economies of 'criminal man.'. *Criminology and Criminal Justice*, *10*, 261-285.

Walsh, T. (2004). *Race and crime: A biosocial analysis*. New York: Nova Science.

Wright, J.P., & Beaver, K.M. (2005). Do parents matter in creating self-control in their children? A genetically informed test of Gottfredson and Hirschi's theory of low self-control. *Criminology*, *43*, 1169-1201.

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Wright, J.P., Beaver, K.M., DeLisi, M., and Vaughn, M.G. (2008). Evidence of negligible parenting influences on self-control, delinquent peers, and delinquency in a sample of twins. *Justice Quarterly*, *25*, 544-569.

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Table 1. Descriptive Statistics

	Percent	Min	Max	*N*	(*df*) χ^2
Arrest					
Total Sample	27.88%	0	1	1,090	
Female	18.99%	0	1	558	(1) 44.96**
Male	37.21%	0	1	532	
Incarceration					
Total Sample	15.59%	0	1	1,090	
Female	9.13%	0	1	558	(1) 36.20**
Male	22.36%	0	1	532	
Probation					
Total Sample	11.92%	0	1	1,090	
Female	4.83%	0	1	558	(1) 54.67**
Male	19.36%	0	1	532	

Notes: ** $p < .01$

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Table 2. Sibling Correlations for Arrest, Incarceration, and Probation

	Tetrachoric Correlations		
	Arrest	Incarceration	Probation
Total Sample			
MZ	.62**	.44**	.53**
DZ	.48**	.28*	.38**
Female			
MZ	.59**	.59**	.45
DZ	.45**	.31*	.50
Male			
MZ	.63**	.26	.50*
DZ	.51**	.25	.35*

Notes: ** $p < .01$; * $p < .05$

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Table 3. Intraclass Odds Ratios for Arrest, Incarceration, and Probation

	Intraclass Odds Ratio		
	Arrest	Incarceration	Probation
Total Sample			
MZ	7.02**	4.31**	7.28**
	[3.48-14.18]	[1.76-10.56]	[2.32-22.78]
DZ	3.98**	2.39*	3.47**
	[2.41-6.59]	[1.22-4.69]	[1.67-7.19]
Female			
MZ	6.58**	7.88**	7.06
	[2.41-17.97]	[2.21-28.10]	[.61-42.71]
DZ	4.08**	3.12*	8.12*
	[1.62-10.25]	[1.63-13.25]	[1.06-57.51]
Male			
MZ	7.26**	2.40	5.42*
	[2.69-19.58]	[.64-8.90]	[1.44-16.38]
DZ	4.33**	2.12	2.92*
	[2.22-8.47]	[.95-4.75]	[1.26-6.76]

Notes: ** $p < .01$; * $p < .05$

Table 4. Univariate ACE Estimates for Arrest for Female and Male Twins (*N* = 540 pairs)

		A	C	E	$\Delta\chi^2$	Δ df	*p*	CFI	RMSEA
	Models								
Arrest									
	ACE	.28	.34	.37**	-	-	-	.97	.05
		[-.10-.66]	[.04-.63]	[.23-.52]					
	AE	.70**	.00	.30**	14.65**	1	<.001	.93	.07
		[.57-.83]	[.00-.00]	[.17-.42]					
	CE	**.00**	**.54****	**.46****	**5.77***	**1**	**.02**	**.97**	**.05**
		[.00-.00]	**[.44-.64]**	**[.36-.55]**					
	E	.00	.00	1.00***	355.74**	2	<.001	.00	.26
		[.00-.00]	[.00-.00]	[1.00-1.00]					

Notes: Best-fitting ACE model is bolded. Results are standardized parameter estimates with 95% confidence intervals in parentheses.
** $p < .01$; * $p < .05$

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Table 5. ACE Parameter Estimates for Same-Sex Female Twins (*N* = 260 pairs)

	A	C	E	$\Delta\chi^2$	Δ df	*p*	CFI	RMSEA
Models								
Incarceration								
ACE	.55	.04	.40*	-	-	-	.85	.07
	[-.30-1.41]	[-.69-.77]	[.14-.66]					
AE	**.60****	**.00**	**.40****	**.03**	**1**	**.85**	**.93**	**.04**
	[.35-.84]	**[.00-.00]**	**[.15-.64]**					
CE	.00	.49**	.51**	16.48*	1	.03	.85	.06
	[.00-.00]	[.28-.70]	[.30-.71]					
E	.00	.00	1.00**	65.91**	2	<.001	.00	.16
	[.00-.00]	[.00-.00]	[1.00-1.00]					
Probation								
ACE	.00	.49**	.51**	-	-	-	.61	.10
	[.00-.00]	[.18-.79]	[.20-.81]					
AE	.62*	.00	.37	28.11**	1	<.001	.72	.08
	[.20-1.04]	[.00-.00]	[-.04-.79]					
CE	**.00**	**.49****	**.51****	**.00**	**1**	**1.00**	**.80**	**.06**
	[.00-.00]	**[.18-.79]**	**[.20-.81]**					
E	.00	.00	1.00**	28.11**	2	<.001	.00	.13
	[.00-.00]	[.00-.00]	[1.00-1.00]					

Notes: Best-fitting ACE model is bolded. Results are standardized parameter estimates with 95% confidence intervals in parentheses.
** $p < .01$; * $p < .05$

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Table 6. ACE Parameter Estimates for Same-Sex Male Twins (*N* = 280 pairs)

	A	C	E	$\Delta\chi^2$	Δ df	*p*	CFI	RMSEA
Models								
Incarceration								
ACE	.03	.24	.73	-	-	-	.69	.13
	[-.78-.86]	[-.33-.80]	[.37-1.07]					
AE	.36*	.00	.64**	1.88	1	.17	.74	.11
	[.08-.63]	[.00-.00]	[.36-.91]					
CE	**.00**	**.26***	**.74****	**.02**	**1**	**.88**	**.87**	**.09**
	[.00-.00]	**[.07-.45]**	**[.55-.92]**					
E	.00	.00	1.00***	20.76**	2	<.001	.00	.15
	[.00-.00]	[.00-.00]	[1.00-1.00]					
Probation								
ACE	.31	.20	.49**	-	-	-	.85	.07
	[-.44-1.06]	[-.34-.73]	[.19-.79]					
AE	**.57****	**.00**	**.43****	**1.44**	**1**	**.22**	**.90**	**.05**
	[.31-.81]	**[.00-.00]**	**[.18-.68]**					
CE	.00	.40**	.60**	1.84	1	.17	.88	.06
	[.00-.00]	[.22-.58]	[.41-.77]					
E	.00	.00	1.00***	57.49**	2	<.001	.00	.14
	[.00-.00]	[.00-.00]	[1.00-1.00]					

Notes: Best-fitting ACE model is bolded. Results are standardized parameter estimates with 95% confidence intervals in parentheses.
** $p < .01$; * $p < .05$

bioRxiv preprint doi: https://doi.org/10.1101/107748; this version posted February 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.