Does Marriage Moderate Genetic Effects on Delinquency and Violence?

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ABSTRACT

Using data from the National Longitudinal Study of Adolescent Health (Add Health), we investigate whether marriage moderates genetic effects on delinquency and violence. In contrast to existing gene-environment research that typically focuses on one or a few genetic polymorphisms, our approach considers the effects of 881 single nucleotide polymorphisms (SNPs) in 103 genes for the gene-by-marriage interaction. The 103 genes are predominantly related to aggression and risky behavior. We extend a recently developed mixed linear model using the SNP data to estimate a heritability parameter—the proportion of variance in the phenotype that is explained by the SNPs' cumulative additive effects. We compare the proportion of variance in delinquency and violence explained by 881 SNPs among married and unmarried individuals. The results show that the collective influence of the SNPs is considerably smaller for those who are married. Because issues such as selection, confounding and heterogeneity may bias the estimate of the gene-by-marriage interaction, we conduct a series of analyses to address these issues. The findings are supportive of the inference that the gene-by-marriage interaction results are not seriously affected by these issues.

INTRODUCTION

The impact of marriage on individuals' well-being has long been studied. Married individuals exhibit higher levels of healthy behaviors, survival probability, wages and so forth than unmarried individuals (Waite 1995). Of particular interest has been the inhibiting effect of marriage on antisocial behavior such as delinquency and crime. Studies have found that the transition to marriage is linked to a decline in antisocial behavior. This association is reported in quantitative and qualitative research (Farrington and West 1995; Sampson and Laub 1990; Shover 1996), and it is noted in multiple cohorts (King, Massoglia and Macmillan 2007; Sampson and Laub 1993), and in different countries (Blokland and Nieuwbeerta 2005; Laub and Sampson 2003; Theobald and Farrington 2009).

In recent years, researchers have increasingly incorporated genetic variables to examine the effects of social institutions and environments on antisocial behavior (Caspi et al. 2002; Foley et al. 2004; Guo, Roettger and Cai 2008; Simons et al. 2011). The findings that social factors interact with genes to influence antisocial behavior underline the importance of gene-environment interaction (G×E) (G×E interaction refers to processes wherein genetic influences depend on environmental factors, or vice versa). However, existing G×E research almost exclusively focuses on one or a few genetic variants. Unlike rare Mendelian traits that are determined by a single gene or allele (Glazier, Nadeau and Aitman 2002), overall genetic influence on antisocial behavior comprises a large number of genetic effects (Anholt and Mackay 2012). Furthermore, multiple genes potentially work with the environment to determine the probability of the manifestation of antisocial behavior. Therefore, it is essential to examine more than a few genetic variants in G×E research on antisocial behavior.

We extend previous G×E research by considering a large number of genetic variants. Drawing on data from the National Longitudinal Study of Adolescent Health (Add Health), we examine whether marriage moderates the effects of 881 single nucleotide polymorphisms (SNPs) in 103 genes on delinquency and violence. To do so, we employ a recently developed mixed linear model implemented in the genome-wide complex traits analysis (GCTA) software (Yang et al. 2010; Yang et al. 2011). This new method uses the SNP data to estimate a heritability parameter—the proportion of variance in the phenotype that is jointly explained by the SNPs. We examine the gene-by-marriage interaction by comparing the proportion of variance in antisocial behavior explained by 881 SNPs among married and unmarried individuals. Our results show that the collective influence of the SNPs is considerably smaller among married individuals.

Issues such as selection, confounding and heterogeneity can bias the estimate of the gene-by-marriage interaction. In this article, we conduct a series of analyses to address these issues. The results suggest that these issues do not pose serious threats to the validity of the gene-by-marriage findings.

BACKGROUND

Marriage and Antisocial Behavior

Social scientists have long noticed that marriage is an important life-course transition with seemingly far reaching impact. In general, married individuals consider marriage a long-term contract (Waite 1995). To maintain the contract, married individuals tend to do things that pay off in the long run, and refrain from behaviors that bring instant gratifications or the possibility of harmful consequences. This is supported by the findings that marriage may deter criminal activity and deviant behavior (e.g., Blokland and Nieuwbeerta 2005; Farrington and West 1995; Horney, Osgood and Marshall 1995; King et al. 2007; Sampson and Laub 1993; Warr 1998). The effect of marriage on antisocial behavior may be thought of as the result of three processes.

First, marriage may strengthen connections within the family. Married couples are connected to each other in relationships for which there are strong social norms. Married people tend to fulfill normative expectations implied by the institution of marriage. Derived from social control theory (Hirschi 1969), Sampson, Laub and colleagues focus on bonds and ties created within marriage (Laub, Nagin and Sampson 1998; Laub and Sampson 2003; Sampson and Laub 1993; Sampson, Laub and Wimer 2006). In this line of research, it is proposed that marriage establishes strong bonds and ties that prevent individuals from committing crime over the life course. Interpersonal attachment to a partner serves as a control mechanism within marriage. Over time married individuals invest more and more socially and even financially in a marriage. Engaging in criminal activity is not a rational choice because it threatens that investment. Summarizing the position, Sampson and Laub (1993: 141) state that marriage creates "interdependent systems of obligation and constraints that impose significant costs for translating criminal propensities into action."

Second, marriage may weaken connections outside of the family that might lead to antisocial behavior. Peer influence can be a major source of variation in antisocial behavior (Osgood et al. 1996). The transition to marriage usually means that routine activities are primarily devoted to the spouse and family. Warr (1998) shows that marriage may weaken or disrupt connections with peers including delinquent ones. Following the transition to marriage, time spent with peers decreases dramatically. As a result, opportunities and motivations to engage in crime and delinquency are significantly limited. Warr finds that these changes largely account for the association between marriage and antisocial behavior. In addition, obligations that come with marriage tend to leave less time for leisure activities outside of the family (Osgood and Lee 1993). As such, unstructured socializing with delinquent peers may also be limited.

Third, marriage may lead to changes at the psychological level and, by extension, alter one's perception of antisocial behavior. Because marriage implies meaningful commitment, married persons may develop a sense of obligation to their partners that reduces the appeal of behaviors that might threaten the relationship. Giordano and colleagues (2002) show that cognitive and identity transformations are at work when individuals desist from antisocial behavior. After getting married, individuals may be open to make cognitive changes and treat the relationship seriously. For example, stealing, drug use and other deviant behavior are no longer viewed proper and viable. Consequently, deviant behavior is less likely to occur. In a similar vein, Giordano et al. (2007) demonstrate that emotional regulation is important to the success of desistance. The authors find that negative emotions associated with crime and the ability to manage emotions may lead to a decline in criminal activity. An implication of these findings is that marriage might involve changes in emotional regulation that help individuals desist.

Gene-Environment Interaction Research on Antisocial Behavior

In the past few years, social scientists have broadened the scope of their investigation into complex traits and behaviors by incorporating genetic information (e.g., Boardman, Benjamin W. Domingue and Fletcher 2012; Caspi et al. 2002; Mitchell et al. 2011). This research underscores the role of G×E interaction. G×E studies on antisocial behavior have focused on the effects of one to five genes—the monoamine oxidase A (*MAOA*) gene, the dopamine D2 receptor (*DRD2*) gene, the serotonin transporter gene (*5-HTT*), the dopamine receptor gene (*DRD4*), and the dopamine transporter gene (*DAT1*). Researchers have found that genetic variants in these genes interact with the social environments and social contexts to influence antisocial behavior.

Using a sample of individuals followed from birth to adulthood, Caspi and colleagues (2002) report that the effect of childhood maltreatment on antisocial behavior is weaker among individuals with high *MAOA* activity than those who have low *MAOA* activity. Similarly, Foley et al. (2004) show that childhood adversity increases conduct disorder for persons with low *MAOA* activity. Using data from Add Health, Guo and colleagues (2008) incorporate individual difference at the molecular genetic level into a social-control, life-course model on serious and violent delinquency. The authors find that genetic variants in the *DRD2* and *MAOA* genes interact with family, school and social network. For example, for youths with the *DRD2**178/304 genotype, having daily meals with parents is associated with a reduction in the genetic effect on delinquency compared with those who have the *DRD2**178/178 or *DRD2**304/304 genotype. Recently, Simons and colleagues (2011) use a sample of individuals followed from 5th grade into early 20s to investigate G×E interactions on aggression. The authors report that the presence of both s-allele (i.e., short allele) in the *5-HTT* gene and l-allele (i.e., long allele) in the *DRD4* gene interacts with social environment (measured by scales of harsh parenting, racial discrimination, neighborhood victimization, and violent peers) to affect aggression, aggression-related cognitive schemas, and chronic anger.

Marriage is an important social institution that may also moderate genetic effects on antisocial behavior. To date, there is only one study that examines whether marriage interacts with genetic variables to foster desistance from delinquency (Beaver et al. 2008). The authors examine the interactions between marriage and five genetic polymorphisms in the *DAT1*, *DRD2*, *DRD4*, *5-HHT*, and *MAOA* genes using data from Add Health. The authors report significant interactions (at the 0.10 level) among males, but not among females, or the male-female-combined sample; and the temporal order between marriage and delinquency is not considered in the analysis.

Genetic Effects on Antisocial Behavior

In the aforementioned G×E studies, genetic effects are almost exclusively represented by only a few genetic variants. Antisocial behavior, however, is influenced by a large number of small genetic effects (Craig and Halton 2009). Hence it is important to take into account multiple genes to better understand antisocial behavior. The effects of 881 SNPs in 103 genes are considered for the gene-by-marriage interaction in the current analysis.

Researchers have identified numerous genes and biological mechanisms related to antisocial behavior in the human population. Using twin and adoption data, genetic contributions to antisocial behavior are found to be considerable (Rhee and Waldman 2002). With molecular genetic data, researchers start to uncover the influences of specific genes and biological factors. Genetic analyses have implicated the *MAOA* (Manucka et al. 2000), *SLC6A4* (Murphy et al. 2008), *TPH1* (Hennig et al. 2005), 5-HT1B hetero-receptors (Soyka et al. 2004), Dopamine-β-hydroxylase (DβH) (Hess et al. 2009) and GABA neurotransmitters (Miczek et al. 2002) among many others in predisposition towards aggression, delinquency and violent behavior in human populations (for a review see Craig and Halton 2009). Biological mechanisms, for example, likely pathways implicated in aggression, have been also reported. The likely pathways include cortisol levels that monitor the hypothalamus, pituitary and adrenal (HPA) axis (Shirtcliff et al. 2005), levels of the serotonin metabolite 5-hydroxy-indole acetic acid (5-HIAA) in cerebrospinal fluid (CSF) (Coccaro et al. 1997), and, potentially serotonin mechanisms, insulin levels and glucose metabolism (Linnoila and Virkkunen 1992).

Studying model organisms can help identify genes for antisocial behavior in humans. Humans share biological similarities with non-human animals to some extent. In humans and non-humans there are common neurochemical and anatomical systems that are activated when aggressive behavior occurs (Nelson and Trainor 2007). Rodents are among the ideal animals that can be studied to provide new knowledge for genetics of aggression in humans. About 90% of genes in rats are orthologous to genes in humans (Consortium 2004). In other words, most of the genes in rats and humans are copies of the same genes of the last common ancestor of rats and humans. In addition, the phenotype of model organisms can be measured more precisely, and the genetic background and environmental conditions can be controlled more easily. Anholt and Mackay (2012) report that researchers successfully identify genes and pathways that influence aggression by employing quantitative trait locus (QTL) mapping and analysis of single-gene mutations in mice. In the genotype data used in our analysis, of the 103 genes taken into consideration, 39 genes are known to be related to aggression in mice.

Selection, Confounding, and Population Heterogeneity

A challenging issue for G×E studies is to identify a causal environment (Conley 2009). In our case, the environment—marriage—is not a random event. Experiments cannot be performed to assess the marriage effect. It is likely that issues such as selection, confounding and population heterogeneity pose threats to the marriage-antisocial-behavior association, thereby undermining the validity of the gene-by-marriage interaction results.

Differential selection is one of the biggest threats to claim a causal effect of marriage (e.g., King et al. 2007; Sampson et al. 2006). Suppose, for example, that delinquent persons selfselect out of marriage—either by remaining single or being more likely to divorce. Then it is not marriage that makes individuals less antisocial, but rather that only people who do not engage in deviant behavior get married. If that is the case—most married individuals are less antisocial than unmarried individuals because of selection, the observation that genetic effects on delinquency depend on marital status possibly just reflects the difference in genetic effects between delinquent and non-delinquent persons.

Age may have a confounding effect on the inhibiting effect of marriage. Delinquency usually peaks during adolescence and young adulthood, and declines dramatically thereafter (Hirschi and Gottfredson 1983). In other words, along with a decline in antisocial behavior most people experience major changes in life circumstances such as marriage. Thus, it can simply be that older individuals are more likely to get married and less likely to act antisocially. In this scenario, the interaction effect of marriage, at least to some extent, represents the effect of age or maturity on antisocial behavior.

A third issue involved in the desistance process is that the effect of marriage may not be universal for every individual due to population heterogeneity, which refers to the situation in which individuals differ in propensity to commit deviant behavior (DeLisi 2005; Nagin and Paternoster 2000). Moffitt (1993, 1994) argues that that there are two groups of individuals. One group repeatedly engages in deviant behavior over the life course, and the other group acts delinquently primarily during adolescence. Persistent offenders do not practice much pro-social behavior during early childhood. As a result, it might be expected that marriage does not have as much impact on persistent offenders as it does on others. The gene-by-marriage interaction, therefore, may vary in magnitude for persistent and non-persistent offenders. In this article, we conduct analyses to examine whether the effect of marriage is affected by the three issues.

DATA AND MEASURES

Data

Our analysis uses the sibling sample of Add Health. Add Health is a nationally representative sample of U.S. adolescents in grades 7-12 in 1994-95. The first wave of data collection took place in the 1994-95 school year. A sample of about 20,000 adolescents was drawn. Respondents were surveyed through in-school questionnaires and in-home interviews. Three subsequent waves of data were collected at respondents' homes in 1996 (Wave II), 2001-02 (Wave III) and 2007-08 (Wave IV) (Harris 2011). A wide range of information including social background, behavior, health and psychological traits was collected at each wave. In addition, the data has rich information on participants' parents, friends and romantic partners.

The sibling sample consists of 2,612 respondents, and was comprised of full biological siblings, monozygotic twins, dizygotic twins and singletons. At Wave III, saliva of the sibling sample was collected and genotyped. Our genotyping of this sibling sample is funded by a major National Science Foundation grant. DNA was isolated from buccal cells at the Institute of Behavior Genetics at the University of Colorado, Boulder. The average yield of DNA was 58 ± 1 µg. The genotype data used in this analysis were based on an Illumina GoldenGate assay. The GoldenGate array targeted 1,536 SNPs including 186 ancestral informative markers (Enoch et al. 2006). A total of 1,140 SNPs in 130 genes were successfully genotyped and survived cleaning. The number of respondents whose DNA was successfully genotyped was 2,281. After excluding the ancestral informative markers and SNPs in the sex chromosomes, we selected 881 SNPs in 103 genes for the current analysis. The vast majority of the 103 genes were chosen because of their implications in aggression and risky behaviors including alcohol use, smoking and substance abuse. Particularly, of the 103 genes 39 genes reviewed and summarized by Maxson (2009) are associated with aggression in transgenic or knock-out studies of mice. There were 403 SNPs in the 39 genes in the data.

Measures

Delinquency and Violence

Delinquency and violence at Waves III and IV are the dependent variables. A 12-item scale and an 8-item scale are used to measure delinquency and violence respectively. The scales are constructed based on 12 questions asked at Waves I through IV in Add Health. The questions are a variation of a scale that is widely used in research on delinquency and crime (Thornberry and Krohn 2000). The 12 questions are grouped into nonviolent and violent categories. Nonviolent delinquency includes stealing amounts larger or smaller than $50, breaking and entering, and selling drugs within the past 12 months. Violent delinquency includes serious physical fighting that resulted in injuries needing medical treatment, use of weapons to get something from someone, physical fighting between groups, shooting or stabbing someone, deliberately damaging property, carrying a weapon (unavailable at Wave IV), and pulling a knife or gun on someone within the past 12 months. The scale of violence is a sum of items in the violent category, while the scale of delinquency is a sum of items in both the nonviolent and violent categories. The two scales are closely related to the ones used in other analyses of Add Health data (Hagan and Foster 2003; Haynie 2001).

To protect privacy and increase reporting accuracy, respondents are instructed to answer these sensitive questions with use of audio computer-assisted self-interview (audio-CASI). The computers give instructions on how to complete the answers, and respondents hear the questions via headphones. With self-administered and computer-assisted techniques, the rate of response to sensitive questions can be increased (Tourangeau and Smith 1996; Wright, Aquilino and Supple 1998).

Desistance

Desistance can be defined either as a process or an end state (Laub and Sampson 2001). Mulvey and colleagues (2004) point out that treating desistance as a process requires more frequent assessments of the behavior, and treating desistance as an end state requires a longer time frame. In this study, we focus on comparing the prevalence of delinquency and violence between the married and unmarried. Following the majority of research (e.g., Horney et al. 1995; Laub et al. 1998; Piquero et al. 2002; Theobald and Farrington 2009; Warr 1998), we assume that only individuals who are delinquent in the first place can desist from delinquency and violence. Respondents who score at least 1 on either the delinquency or violence scale at Waves I and II are included in our sample. Those who score zero on both scales, which means they do not report any delinquent acts at Waves I and II, are excluded. The final sample consists of 1,254 individuals.

Marriage and Its Temporal Relation with Delinquency and Violence

To isolate the effect of marriage on antisocial behavior, it is crucial to sort out the temporal order between marriage and the occurrence of delinquency and violence. At Waves III and IV, respondents are asked to report the number of times they have been married and the start and end dates of each marriage, if any. However, we only know of delinquent and violent behavior that occurs in the 12 months before the interview. No exact timing of the behavior within this 12-month window is available. As the data allow, we define marital status in a prudent way. Figure 1 is an illustration of how marital status is defined. We divide marriages into two groups based on whether the marriage ends before the 12-month window. The first group of marriages (types A to D represented by the white lines in Figure 1) overlaps the 12-month window. We assume that these marriages could influence delinquency and violence that occur during this timeframe. Individuals in this group are coded as married. The other group of marriages (type E represented by the black line in Figure 1) are those that end at least 12 months prior to the interview. We assume that these marriages could not influence delinquency and violence during this timeframe. Individuals in this group are coded as unmarried. The number of marriages for each type is in the parentheses. There are two marriages that have missing values for the start date of marriage, but the couples are still married when interviewed. We assume these two marriages belong to the first group and code the individuals as married.

Figure 1 about here

Marriage and Cohabitation

Cohabitors differ from married persons on a range of characteristics (Smock 2000). With respect to crime, using data from a sample of serious offenders, Horney et al. (1995) show that cohabitation is positively associated with felonies and drug dealing, but not associated with assault and property crime. Using National Longitudinal Survey of Youth data, Duncan et al. (2006) find that frequency of binge drinking and marijuana use decrease after marriage. But the inhibiting effect of cohabitation on the two outcomes is observed only among women, not among men. These findings imply that mechanisms for antisocial behavior may be different between cohabitors and married persons. Therefore, we first compare the levels of delinquent and violent behavior in married, cohabitating and single individuals. The results (not shown) suggest that cohabitors and single persons tend to report higher levels of antisocial behavior than married persons after controlling for the control variables (control variables will be described later). Thus marital status is coded as dichotomous—married vs. unmarried individuals, namely, cohabitating and single persons.

Most of the studies that report the inhibiting effect of marriage use data in which respondents married in the 1950s, 1960s or 1980s (e.g., Farrington and West 1995; King et al. 2007; Laub and Sampson 2003). An advantage of the Add Health data is that martial relationships are measured in more recent years—2001-02 and 2007-08. We can test whether the marriage effect extends to a more recent cohort in recent years.

Control Variables

Control variables include age, gender, race, education, employment, whether going to church weekly, household size, verbal IQ score (PVT score), parental education, closeness to parents, and bio-ancestry scores. Missing values in the control variables are imputed by the multiple imputation technique (Rubin 1987). We do not impute missing values in delinquency, violence, and marriage. The estimation of bio-ancestry scores relies on 121 of the 186 targeted ancestral informative markers successfully genotyped. The 121 markers are used to distinguish three major continental populations—African, East Asian, and European. The bio-ancestry scores are obtained using the method proposed by Pritchard and colleagues (2000). Each respondent is assigned three scores—African, East Asian, and European. The sum of the three scores for an individual is 1. Table 1 presents means, percentages, and standard deviations as well as brief descriptions for variables used in the analysis.

Table 1 about here

ANALYTICAL STRATEGY

Assessing the Effect of Marriage on Delinquency and Violence

Prior to the investigation of whether marriage interacts with genetic variants to influence antisocial behavior, we first examine the effect of marriage on antisocial behavior. The effect of marriage is assessed in Generalized Estimating Equation (GEE) (Liang and Zeger 1986). Equation (1) below describes the structure of the model.

$$Y_{ib} = \beta_0 + \beta_1 X_{ib} + \beta_2 Z_{ib} + \beta_3 Z'_{ia} \tag{1}$$

where Y_{ib} is the delinquent or violent behavior for individual i at Wave b, that is, Wave III or IV; X_{ib} is the marital status for individual i at Wave b; Z_{ib} represents the control variables for individual i measured at Wave b including age, age squared, gender, race, education, employment status, whether going to church weekly, household size; Z'_{ia} represents the control variables for individual i measured at Wave a, that is, Wave I, including PVT score, parental education, and closeness to parents. The within-person correlations are addressed in the GEE models. The within-family correlations are also addressed as the data contain twins or siblings from the same family. Table 2 reports the results.

Modeling the G×E Interaction

To model the interaction between 881 SNPs and marital status, we extend the mixed linear model implemented in the GCTA software (Yang et al. 2010; Yang et al. 2011). This model uses SNP data to estimate a heritability parameter—the collective influence of SNPs, that is, the proportion of phenotypic variance that is accounted for by the linear, additive effects of SNPs. There is a major difference between this mixed linear model and twin studies that also estimate heritability. In the mixed linear model, estimates are based on alleles at the molecular level, whereas in twin studies, without direct measures of genes, estimates primarily rely on the comparison of phenotypic correlations between monozygotic and dizygotic twins. This mixed linear model has been used to examine the effect of genes on complex traits such as human height (Yang et al. 2010), economic and political preferences (Benjamin et al. 2012), self-employment (Loos et al. 2013) and several common diseases (Lee et al. 2011).

Equation (2) below describes the basic structure of the mixed linear model.

$$Y = X\beta + W\mu + \varepsilon \tag{2}$$

where Y is the delinquency or violence; β is a vector of fixed effects for controls including age, age squared, gender, bio-ancestry scores, education, employment status, whether going to church weekly, household size, PVT score, parental education, and closeness to parents; μ is a vector of SNP effects with $\mu_i \sim N(0, \boldsymbol{\sigma}^2_{\mu})$ where i=1,…, N with N being the number of SNPs; ε is a vector of residual effects with $\varepsilon_j \sim N(0, \boldsymbol{\sigma}^2_{\varepsilon})$ where j=1,…,n, with n being the number of individuals in the sample; W is a standardized genotype matrix with the ijth element $w_{ij} = (s_{ij} - 2p_i)/\sqrt{[2p_i(1 - p_i)]}$ where s_{ij} is the number of copies of the reference allele for the ith SNP of the jth individual and p_i is the frequency of the reference allele.

Next, by defining $g = W\mu$, $\mathbf{A} = WW'/N$ and $\sigma_g^2 = N\sigma_\mu^2$, Equation (2) is mathematically equivalent to Equation (3), which can be estimated by the restricted maximum likelihood (REML) approach.

$$Y = X\beta + g + \varepsilon, \text{ with Variance} = \mathbf{A}\,\sigma_g^2 + I_\varepsilon\sigma^2_\varepsilon \tag{3}$$

where g is an n*1 vector of the total genetic effects of the individuals with $g \sim N(0, \mathbf{A}\,\sigma_g^2)$, **A** is the genetic relationship matrix (GRM) between individuals and $\boldsymbol{\sigma}^2_g = N^*\boldsymbol{\sigma}^2_\mu$ is the total genetic variance explained by the SNPs. Hence σ_g^2 can be estimated by the restricted maximum likelihood approach, depending on the GRM estimated from the SNPs.

The gene-by-marriage interaction is assessed by comparing the proportion of variance explained—$(\sigma^2_g / (\sigma^2_g + \sigma^2_\varepsilon)$ in Equation (3)—between married and unmarried individuals. This form of G×E interaction is different from the traditional form of G×E interaction in which a multiplicative interaction term is added in a regression. Conceptually, both the two forms of G×E interaction examine the processes by which the effects of genes are conditioned by environmental factors or vice versa. In the traditional form of G×E interaction, when modeling the interaction between marriage and 881 SNPs, it is most likely that one needs to either put 881 two-way interactions in a regression, or run 881 regressions with each regression containing one two-way interaction. In our approach, 881 SNPs are simultaneously considered as random effects.

The proportion of variance explained is estimated for antisocial behavior at Waves III and IV separately. Specifically, we take the following steps to obtain the proportion of variance explained. First, the sample is divided into two groups—the married and the unmarried. Second, we perform subsample selection. The mixed linear model requires individuals in the analysis to be genetically unrelated because if related persons are included, the estimate of genetic effects would be biased by phenotypic correlations of, for example, siblings who share common environments. Given that the sample consists of siblings and twins, to get an analytical subsample in which individuals are unrelated we randomly select an individual from every family. We do this separately for the married group and the unmarried group. Next, we repeat the subsample selection process 1,000 times to avoid the arbitrariness of which person in the family is selected. Final results are averaged over results obtained from 1,000 analytical subsamples in the GCTA software. The Kolmogorov-Smirnov (KS) tests are conducted to compare the distribution of 1,000 proportions of variance explained between the married and the unmarried. Table 3 reports the results.

The Gene-Environment Correlation

Gene-environment correlations (rGEs) refer to situations in which genotypes are non-randomly associated with environments. rGEs may bias estimates of G×E interactions (Jaffee and Price 2007; Wagner et al. 2013). We test whether the 881 SNPs are associated with marital status controlling for the control variables using the mixed linear model. The association is not significantly different from 0 (p=0.82). The evidence suggests that the rGE does not confound the G×E interaction results in this study.

RESULTS

Marriage and Antisocial Behavior

Table 2 presents the effect of marriage on delinquency and violence at Waves III and IV estimated in the GEE models. Married individuals show a significant decrease on delinquency and violence scales of 0.34 and 0.17 respectively. This suggests that getting married may decrease the likelihood of behaving antisocially. Control variables such as female, Asian and Other races, college degree or more, and being employed are negatively associated with the delinquency or violence scale. For example, being employed is associated with a decline of 0.26 in delinquency, and 0.20 in violence.

Table 2 about here

The Gene-by-Marriage Interaction

We now turn to Table 3 to see whether marriage moderates the genetic effects on delinquency and violence. The results are obtained from the mixed linear models implemented in the GCTA software. The left panel of Table 3 reports models in which Wave III antisocial behavior is the dependent variable; and the right panel reports models in which Wave IV antisocial behavior is the dependent variable. The results are averaged results over analysis of 1,000 subsamples.

In Table 3 we first present the proportion of variance in delinquency and violence explained by the 881 SNPs. Overall, the proportion of variance explained is significantly smaller in married individuals than in unmarried individuals, suggesting that marriage may suppress the collective influence of the genes. At Wave III, the SNPs jointly account for about 1% (0.01) and 3% (0.03) of the variance in delinquency and violence respectively in unmarried individuals, while the SNPs explain virtually no variance in the married. Similarly, at Wave IV the SNPs account for 1% (0.01) of the variance in violence among the unmarried and virtually none among the married. However, variance in delinquency at Wave IV is not explained by the SNPs for either the married or the unmarried.

Effects of the control variables are also reported in Table 3. Note that in each mixed linear model, the control variables and the dependent variable are from the same wave—Wave III or IV. The exceptions are PVT score, parental education and closeness to parents as these controls are measured at Wave I only. The results indicate that older persons, women, persons with a college degree or more, and with employment are less likely to behave antisocially. Because in genetic analysis using bio-ancestry scores to adjust for population stratification is a recommended method (McCarthy et al. 2008), we control for bio-ancestry scores in the mixed linear models. Replacing bio-ancestry scores with self-reported race yields similar results because bio-ancestry scores are highly correlated with self-reported race.

Table 3 about here

Addressing Selection, the Confounding Effect of Age, and Population Heterogeneity

The results above suggest that marriage plays an important role in the desistance process. As mentioned previously, issues of selection, age, and population heterogeneity may hinder the conclusion that marriage causes desistance from delinquency and violence, and threaten the validity of the gene-by-marriage interaction findings. We address the three issues and present the results in Tables 4 and 5.

As for selection, we test whether delinquent persons are less likely to get married. If earlier delinquency and violence at Waves I and II (1994-95 and 1996) are not a significant predictor for marital status at Waves III and IV (2001-02 and 2007-08), it suggests that selection based on antisocial behavior might not pose a serious threat to the deterrent capacity of marriage. Logistic GEE models are used to assess the effects of variables. The dependent variable, marital status, is a dichotomous variable with 1 indicating that a person is married and 0 otherwise. Control variables are age, gender, race, whether going to church weekly, household size, PVT score, parental education, and closeness to parents. The within-family correlations are addressed in the GEE models.

Table 4 reports the results. In the left panel, the four models predict marital status at Wave III using measures of delinquency and violence at Waves I and II. In the right panel the four models predict marital status at Wave IV by the same antisocial behavior. The results show that none of the coefficients for delinquency and violence are statistically significant. In other words, the probability of getting married is not associated with the level of delinquency or violence earlier on.

Table 4 about here

To address the potential confounding effect of age, we first randomly exclude a subset of young unmarried individuals to generate a new sample so that the mean ages for married and unmarried individuals are the same. In our sample, the mean age for married and unmarried individuals is 26 and 24 respectively. In the new sample, the mean ages for the two groups are both 26. We call this new sample the age-comparable sample. A similar method has been used to equalize age in two groups in previous studies (e.g., Uggen 2000). Next, using this age-comparable sample analyses are carried out to examine whether marriage may suppress antisocial behavior in Equation (1), and whether marriage interacts with the genes in the mixed linear models.

In the left panel of Table 5, the results are obtained from the GEE models using the age-comparable sample. The marriage effect remains. Married individuals score 0.43 less on delinquency and 0.20 less on violence than unmarried individuals. We also re-estimate the eight mixed linear models in Table 3 using the age-comparable sample. The re-estimation yields similar results (results not shown) to those presented in Table 3. Therefore, we are more confident in saying that age does not confound the marriage-antisocial-behavior association.

Recall that population heterogeneity refers to the way that individuals differ in propensity to engage in antisocial behavior: a small group of individuals in the population are repeatedly involved in offending activity over the life-course, whereas the majority is antisocial primarily during adolescence. There are 55 respondents who score 1 or more on the violent behavior scale for all four waves. These 55 respondents are considered a small group of persistent offenders, and coded as persistent offenders. The remaining individuals are coded as non-persistent offenders.

In the right panel of Table 5, we explore the possibility that the deterrent capacity of marriage differs between persistent and non-persistent offenders. We add a dummy variable for the 55 persistent offenders and an interaction between marriage and the dummy variable. The main effects of “marriage” and “persistent offender” are both highly significant. Married persons experience a decrease in the delinquency and violence scales of 0.28 and 0.13 respectively. As expected, persistent offenders exhibit higher levels of delinquency and violence—2.39 and 1.72

respectively. However, the interaction between “marriage” and “persistent offender” is not statistically significant. Therefore, there is no evidence supporting the idea that marriage acts differently on the behaviors of persistent and non-persistent offenders.

Table 5 about here

CONCLUSION

This study investigates whether marriage moderates the effects of 881 SNPs on delinquency and violence using longitudinal data from Add Health. Our main findings show that 881 SNPs predominantly related to risky behaviors and aggression explain much less of the variance in delinquency and violence among married individuals than unmarried individuals, implying that marriage may suppress the collective genetic influence. We also demonstrate an innovative approach to modeling the G×E interaction. Social scientists are mostly interested in complex traits and behaviors such as cognitive ability, longevity, drug use, educational attainment and so on. Complex traits and behaviors are affected by many genes. This highlights the importance of incorporating a large number of genetic variables into the analysis. Yet it is challenging to model interaction effects between an environment and such a large number of genetic variants. By extending the mixed linear model (Yang et al. 2010; Yang et al. 2011), our approach considers the overall influence of more than 800 SNPs for the G×E interaction.

Our results suggest that marriage is associated with lower levels of antisocial behavior, and the inhibiting effect appears to be pronounced among married people, but not among cohabiting couples. Prior studies show that cohabitors tend to report lower levels of interpersonal commitment to partners than married individuals, and cohabitation is viewed as an alternative to singlehood, rather than an alternative to marriage (Manning and Smock 2005; Stanley, Whitton and Markman 2004). These characteristics would translate into weak connections to partners and an incomplete sense of obligations. Hence the inhibiting effect of marriage may not extend to cohabitation.

Moreover, evidence supports the inference that marriage causes declines in antisocial behavior, and therefore supports the validity of the gene-by-marriage interaction results. Selection, age, and population heterogeneity do not seem to pose serious threats. Our results are consistent with those of previous work that addresses causality in the marriage-crime nexus. This body of work shows that marriage may causally inhibit crime and deviant behavior using policy changes as natural experiments (Cáceres-Delpiano and Giolito 2008; Edlund et al. forthcoming), and using techniques such as propensity score matching and inverse probability of treatment weighting (King et al. 2007; Sampson et al. 2006; Theobald and Farrington 2009). With respect to population heterogeneity, we find that marriage does not influence differently for persistent and non-persistent offenders. This pattern emerging from the sample of the general U.S. population is consistent with Blokland and Nieuwbeerta's (2005) finding based on a sample of the general Dutch population that the effect of marriage is the same for sporadic and low-rate offenders. Interestingly, in the same article using data from a sample of Dutch criminal offenders Blokland and Nieuwbeerta find that the inhibiting effect of marriage only exists among low- and moderate-rate offenders, but not among high-rate offenders. Future work might examine how and why the marriage effect varies in different populations.

Several limitations should be acknowledged. The current analysis uses 881 SNPs. We are unable to estimate the effects of genetic variants that are not covered by the SNP arrays. In addition, the 881 SNPs and causal alleles for delinquency and violence may not be in complete linkage disequilibrium. Therefore, the collective influence of the SNPs is likely to be underestimated. Also, this particular mixed linear model framework does not allow for analysis of genetically related individuals, resulting in reduction in sample size. Due to this, our ability to investigate the roles of other factors in the desistance process is limited. For example, prior research suggests that gender contingencies are relevant to the marriage effect, and males tend to benefit more from the inhibiting influence of marriage (Duncan et al. 2006; Giordano et al. 2002; King et al. 2007; Sampson et al. 2006). Ideally, with a larger sample we could examine gender differences by comparing married men and married women. In addition, attachment to marriage and the quality of the relationship are potentially important predictors (Capaldi, Kim and Owen 2008; Sampson and Laub 1990). Unfortunately, such information is not available in Add Health. Future G×E research might consider using a larger sample to examine the role of gender and marital quality.

Growing evidence has implied that to better understand environmental influences on complex traits and behaviors one might need to consider G×E interaction (Freese 2008). There are at least two challenging tasks for social scientists interested in G×E interaction. The first task is to identify “truly exogenous, causal environmental effects… [and this] is the same task facing all social scientists who seek to rule out genetic (or other unobserved) factors when assessing causal, environmental effects” (Conley 2009: 244). The second task is to creatively use a variety of methods to detect G×E interactions (Shanahan and Boardman 2009). This article is just one example of how researchers may undertake these two tasks. Although we can never prove that marriage is truly exogenous, we conduct a series of analyses and the results suggest that marriage may lead to the desistance process. Furthermore, our method is one of the first attempts to innovatively model G×E interaction. Now in many large-scale social survey data, SNP data is increasingly available. For example, the Health and Retirement Study (Crimmins et al. 2009) recently releases genotype data that contains millions of SNPs. Rich datasets offer opportunities for future G×E research employing different study designs and methods to gain a more comprehensive understanding of complex traits and behaviors.

Table 1. Descriptive statistics for variables used in the analysis

		Wave I	Wave II	Wave III	Wave IV
		1994-95	1996	2001-02	2007-08
Dependent variable					
Delinquency (mean and S.D.)		----	----	0.99	0.69
				(2.10)	(1.56)
Violence (mean and S.D.)		----	----	0.55	0.47
				(1.31)	(1.08)
Key independent variable					
Marital status (percent)	Married	----	----	16	43
	Unmarried	----	----	84	57
Delinquency (mean and S.D.)		2.96	2.00	----	----
		(3.90)	(3.16)		
Violence (mean and S.D.)		1.91	1.20	----	----
		(2.65)	(2.05)		
Control variable					
Age (mean and S.D.)		15.46	16.39	21.80	28.26
		(1.60)	(1.62)	(1.64)	(1.68)
Gender[a] (percent)	Female	42	----	----	----
	Male	58	----	----	----
Race[a] (percent)	Asian	6	----	----	----
	American Indian	3	----	----	----
	Black	17	----	----	----
	Multiracial	5	----	----	----
	Other	1	----	----	----
	White	67	----	----	----
Bio-ancestry score[a]	African ancestry	0.19	----	----	----
(mean and S.D.)		(0.35)			
	East Asian ancestry	0.12	----	----	----
		(0.25)			
	European ancestry	0.70	----	----	----
		(0.39)			
Education (percent)	No college	----	----	51	34
	College	----	----	48	55
	Missing	----	----	1	10
Employment (percent)	Unemployed	----	----	30	17
	Employed	----	----	70	72
	Missing	----	----	0	11
Going to church (percent)	Less than weekly	61	61	83	76
	Weekly or more	38	33	16	13
	Missing	2	6	1	10

Household size (percent)	<3	1	8	29	30
	3-6	67	66	58	51
	>6	33	26	13	8
	Missing	0	0	0	11
PVT score (percent)	<90	23	----	----	----
	90-110	48	----	----	----
	>110	26	----	----	----
	Missing	3	----	----	----
Parental education (percent)	Below high school	12	----	----	----
	High school	29	----	----	----
	More than high school	55	----	----	----
	Missing	4	----	----	----
Closeness to parents (percent)	Not Close: “somewhat”, “very little” and “not at all” close	39	----	----	----
	Close: “very much” and “quite a bit” close	60	----	----	----
	Missing	2	----	----	----
Number of individuals[b]		1,253-1,254	1,196-1,254	1,252-1,254	1,118-1,254

Note: [a]: The distributions of gender across four waves are almost identical. So are race and bio-ancestry score. Information at Wave I is presented for the three variables.

[b]: We impute control variables to the maximum sample size—1,254. We do not impute the dependent variables and key independent variables. The sample sizes for the dependent variables and key independent variables are smaller than or equal to 1,254.

Standard deviation in parentheses

Table 2. The effect of marriage on delinquency/violence, generalized estimating equations

	Delinquency in 2001-02 and 2007-08 Waves III and IV	Violence in 2001-02 and 2007-08 Waves III and IV
Married (ref: unmarried)	-0.34***	-0.17***
Age	-0.27	-0.09
Age^2	0.00	0.00
Female (ref: male)	-0.64***	-0.43***
Race (ref: White)		
Asian	-0.24*	-0.11
Black	0.00	0.08
Multiracial	-0.02	0.03
American Indian	0.16	-0.04
Other	-0.57**	-0.32*
Education (ref: no college)		
College or more	-0.15	-0.15**
Employment (ref: unemployed)		
Employed	-0.26**	-0.20**
Going to church (ref: less than weekly)		
Weekly or more	-0.17	-0.10
Household size (ref: 3-6)		
<3	0.07	0.04
>6	-0.07	0.02
PVT score (ref: 90-110)		
<90	-0.03	0.02
>110	0.03	-0.03
Parental education (ref: high school)		
Below high school	-0.01	-0.06
More than high school	0.11	0.05
Closeness to parents (ref: close)		
Not close	0.14	0.04
Number of individuals	1,254	1,254
Number of observations	2,367	2,369

*$p<0.05$; **$p<0.01$; ***$p<0.001$ (two-tailed tests)

Table 3. Proportions of variance in delinquency/violence explained by 881 SNPs, and effects of control variables, mixed linear models estimated in GCTA

	Delinquency in 2001-02 Wave III		Violence in 2001-02 Wave III		Delinquency in 2007-08 Wave IV		Violence in 2007-08 Wave IV	
	Married	Unmarried	Married	Unmarried	Married	Unmarried	Married	Unmarried
Proportion of variance explained by 881 SNPs	0.00[a]	0.01***[a]	0.00[a]	0.03***[a]	0.00[a]	0.00[a]	0.00[a]	0.01***[a]
Effects of control variables								
Age	0.98	-0.55	0.70	-0.03	0.01	-3.94*	0.16	-1.88*
Age^2	-0.02	0.01	-0.02	0.00	0.00	0.07**	0.00	0.03*
Female (ref: male)	-0.44*	-0.87***	-0.29*	-0.59***	-0.07	-0.61***	-0.08	-0.38**
European ancestry	-0.08	0.28	-0.04	0.23	0.22	0.11	0.12	0.00
African ancestry	-0.16	0.2	-0.16	0.23	0.24	0.07	0.11	0.14
Education (ref: no college)								
College or more	-0.14	-0.23	-0.02	-0.24*	-0.30*	-0.21	-0.31**	-0.11
Employment (ref: unemployed)								
Employed	-0.19	-0.14	-0.13	-0.10	-0.20	-0.61*	-0.11	-0.44*
Going to church (ref: less than weekly)								
Weekly or more	-0.25	-0.27	-0.28	-0.13	0.02	-0.11	0.06	-0.04
Household size (ref: 3-6)								
<3	0.06	0.11	0.02	0.05	0.14	0.08	0.12	0.05
>6	-0.05	-0.18	-0.17	0.01	0.06	0.17	0.12	0.06
PVT score (ref: 90-110)								
<90	-0.29	0.13	-0.15	0.14	0.00	-0.14	0.03	-0.10
>110	0.00	0.09	-0.04	0.02	-0.07	0.24	-0.03	0.13
Parental education (ref: high school)								
Below high school	-0.32	0.14	-0.22	0.02	-0.29	0.15	-0.16	-0.01
More than high school	-0.01	0.22	0.01	0.10	0.16	-0.10	0.18	-0.15
Closeness to parents (ref: close)								
Not close	0.27	0.06	0.13	0.01	0.06	0.20	0.00	0.04
Number of individuals	191	837	193	837	428	546	428	546

Note: [a]: Kolmogrov-Smirnov test of whether the distribution of proportions of variance estimated in married individuals is smaller than in unmarried individuals.
*p<0.05; **p<0.01; ***p<0.001

Table 4. Addressing selection: Testing whether more antisocial individuals are less likely to get married by using delinquency/violence at Waves I/II to predict marital status at Waves III/IV, generalized estimating equations

	Married in 2001-02, Wave III				Married in 2007-08, Wave IV			
Delinquency in 1994-1995, Wave I	0.03	----	----	----	-0.02	----	----	----
Violence in 1994-1995, Wave I	----	0.05	----	----	----	-0.02	----	----
Delinquency in 1996, Wave II	----	----	0.02	----	----	----	-0.02	----
Violence in 1996, Wave II	----	----	----	0.02	----	----	----	-0.03
Age	0.36***	0.36***	0.36***	0.36***	0.23***	0.23***	0.22***	0.22***
Female (ref: male)	0.72***	0.74***	0.71***	0.71***	0.35**	0.36**	0.41**	0.41**
Race (ref: White)								
Asian	0.01	0.01	0.10	0.10	-0.69*	-0.70*	-0.73*	-0.74*
Black	-1.08***	-1.10***	-1.07***	-1.07***	-1.04***	-1.03***	-1.05***	-1.05***
Multiracial	-0.07	-0.08	-0.29	-0.28	0.18	0.17	0.12	0.11
American Indian	0.20	0.20	0.44	0.44	-0.03	-0.05	0.07	0.06
Other	0.10	0.09	-0.03	-0.03	-0.55	-0.55	-0.53	-0.53
Going to church (ref: less than weekly)								
Weekly or more	0.01	0.01	-0.23	-0.24	0.25	0.25	0.24	0.25
Household size (ref: 3-6)								
<3	-0.63	-0.62	0.18	0.19	0.59	0.59	-0.27	-0.27
>6	0.15	0.15	0.18	0.18	0.00	0.00	0.07	0.07
PVT score (ref: 90-110)								
<90	0.31	0.30	0.28	0.28	0.00	0.01	-0.06	-0.05
>110	-0.15	-0.14	-0.17	-0.17	-0.12	-0.12	-0.11	-0.11
Parental education (ref: high school)								
Below high school	-0.14	-0.15	-0.27	-0.27	0.04	0.04	0.05	0.05
More than high school	-0.26	-0.25	-0.25	-0.25	0.13	0.12	0.11	0.11
Closeness to parents (ref: close)								
Not close	-0.02	-0.02	-0.10	-0.09	0.00	-0.01	0.04	0.04
Number of individuals	1,252	1,252	1,195	1,195	1,120	1,120	1,066	1,066

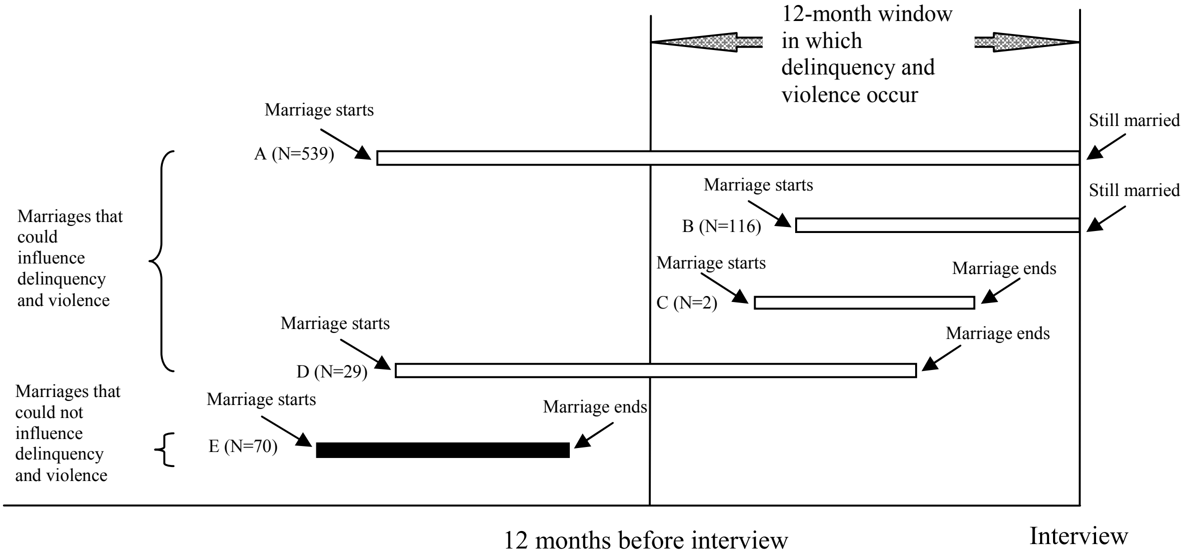
**p*<0.05; ***p*<0.01; ****p*<0.001

Table 5 Addressing the confounding effect of age and population heterogeneity: Testing the marriage effect using the age-comparable sample, and testing whether the marriage effect differs for persistent offenders, generalized estimating equations

	Age-comparable sample[a]		Original sample	
	Delinquency in 2001-02 and 2007-08 Waves III and IV	Violence in 2001-02 and 2007-08 Waves III and IV	Delinquency in 2001-02 and 2007-08 Waves III and IV	Violence in 2001-02 and 2007-08 Waves III and IV
Married (ref: unmarried)	-0.43***	-0.20***	-0.28***	-0.13**
Persistent offender (ref: non-persistent offender)	----	----	2.39***	1.72***
Persistent offender × married	----	----	0.18	0.37
Age	0.09	0.09	-0.27	-0.08
Age^2	0.00	0.00	0.00	0.00
Female (ref: male)	-0.42***	-0.28***	-0.51***	-0.33***
Race (ref: White)				
Asian	-0.15	-0.01	-0.15	-0.04
Black	0.01	0.10	-0.08	0.03
Multiracial	0.08	0.09	-0.14	-0.06
American Indian	0.10	-0.07	0.21	0.00
Other	-0.44*	-0.26	-0.47**	-0.25*
Education (ref: no college)				
College or more	-0.13	-0.08	-0.12	-0.13*
Employment (ref: unemployed)				
Employed	-0.30*	-0.22*	-0.24*	-0.18**
Going to church (ref: less than weekly)				
Weekly or more	-0.05	-0.02	-0.14	-0.08
Household size (ref: 3-6)				
<3	0.08	0.08	0.06	0.03
>6	0.02	0.05	-0.05	0.04
PVT score (ref: 90-110)				
<90	-0.06	-0.03	-0.03	0.02
>110	0.01	-0.05	0.01	-0.03
Parental education (ref: high school)				
Below high school	-0.15	-0.10	-0.04	0.03
More than high school	0.00	0.00	0.14	0.04
Closeness to parents (ref: close)				
Not close	0.15	0.03	0.14	0.04
Number of individuals	1,168	1,168	1,254	1,254
Number of observations	1,544	1,546	2,367	2,369

Note: [a]: In the age-comparable sample, the mean ages are 26 for both married and unmarried individuals after randomly excluding a subset of young unmarried individuals. In the original sample, the mean age is 26 for married individuals and 24 for unmarried individuals.
*$p<0.05$; **$p<0.01$; ***$p<0.001$

Figure 1. Temporal order between marriage and delinquency/violence: Distinguishing marriages that could influence delinquency/violence, and marriages that could not



▭ represents marriages that overlap the 12-month window, and could influence delinquency and violence that occur in the 12-month window (types A through D).

▬ represents marriages that end 12 months before the interview, and could not influence delinquency and violence that occur in the 12-month window (type E).

Note: N in parentheses indicates the number of marriages for each type.
Two marriages are intact when interviewed but their start dates are missing. We consider these two marriages could influence delinquency and violence.

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