

Available online at www.sciencedirect.com



PSYCHIATRY COMPREHENSIVE

Comprehensive Psychiatry 55 (2014) 93-103

www.elsevier.com/locate/comppsych

# Exploring whether genetic differences between siblings explain sibling differences in criminal justice outcomes

Joseph A. Schwartz<sup>a,\*</sup>, Kevin M. Beaver<sup>a,b</sup>

<sup>a</sup>College of Criminology and Criminal Justice, Florida State University, Tallahassee, FL 32306-1127, USA <sup>b</sup>Center for Social and Humanities Research, King Abdulaziz University, Jeddah, Saudi Arabia

# Abstract

Research has revealed that despite many similarities, siblings raised within the same household have also been found to be markedly different from one another. Behavioral differences between siblings have been primarily attributed to differential exposure to a wide variety of environmental influences. The potential role that between-sibling genetic differences play in the development of behavioral differences has been overlooked in the extant literature. The current study examines the association between differences in three dopaminergic polymorphisms (*DAT1*, *DRD2*, and *DRD4*) and differences in arrest, incarceration, and multiple arrests between siblings. Between-sibling difference scores were estimated for each examined polymorphism and each criminal justice outcome measure (along with all controls). Ordinary least squares (OLS) regression models were estimated to examine the potential association between genetic differences between siblings and differences in experiences within the criminal justice system. Models were estimated for the full sample and then for the same-sex male and female subsamples separately. The results provide preliminary evidence that between-sibling differences in some of the examined dopaminergic polymorphisms are associated with differences in contact with the criminal justice system. Findings are discussed in more detail and suggestions for future research are also provided.

© 2014 Elsevier Inc. All rights reserved.

## 1. Introduction

Despite many similarities, biological siblings have also been found to be measurably different from each other across a wide range of attributes including personality traits [1,2], intelligence [3], and even antisocial conduct [4]. Findings from both classic [5] and more recent [4,6,7] studies collectively suggest that siblings who are reared within the same household tend to display behavior patterns that are quite different from one another. While the extant literature seems to provide evidence suggesting that siblings raised within the same household can be demonstrably different from one another, two distinct limitations remain present. First, studies that have attempted to identify factors that contribute to behavioral differences have typically focused solely on the potential association between environmental and behavioral differences [4,8,9]. While environmental differences represent one possible explanation of discordant sibling behavioral outcomes, a complementary line of research indicates that genetic differences may also play a role [10-17]. Despite evidence that genetic factors play a role in the development of antisocial behaviors, to our knowledge no studies have examined whether differences in measured genetic polymorphisms significantly explain differences in criminal behavior between siblings.

The second oversight within the extant literature involves the behavioral outcomes examined. More specifically, previous studies tend to focus on behaviors that are related to or associated with criminal behavior, such as antisocial personality traits [1,2,18,19] and externalizing behaviors [20–

This research uses data from Add Health, a program project directed by Kathleen Mullan Harris and designed by J. Richard Udry, Peter S. Bearman, and Kathleen Mullan Harris at the University of North Carolina at Chapel Hill, and funded by Grant P01-HD31921 from the Eunice Kennedy Shriver National Institute of Child Health and Human Development, with cooperative funding from 23 other federal agencies and foundations. Special acknowledgment is due to Ronald R. Rindfuss and Barbara Entwisle for assistance in the original design. Information on how to obtain the Add Health data files is available on the Add Health Web site (http://www.cpc.unc.edu/addhealth). No direct support was received from Grant P01-HD31921 for this analysis.

<sup>\*</sup> Corresponding author. College of Criminology and Criminal Justice, Florida State University, 634 W. Call Street, Tallahassee, FL 32306-1122, USA. Tel.: +1 850 644 9180; fax: 850 644 9614.

E-mail address: jas10t@my.fsu.edu (J.A. Schwartz).

<sup>0010-440</sup>X/\$ - see front matter © 2014 Elsevier Inc. All rights reserved. http://dx.doi.org/10.1016/j.comppsych.2013.06.002

22], but have not yet explored which factors contribute to between-sibling differences in contact with the criminal justice system. Since the results of these studies are limited to large, overarching behavioral and personality characteristics related to or associated with criminal behavior, they cannot directly identify specific factors that contribute to between-sibling differences in experiences in the criminal justice system.

The current study aims to address these gaps in the extant literature by examining whether genetic differences between siblings contribute to differences in experiencing specific criminal justice outcomes. More specifically, the associations between sibling differences in three dopaminergic polymorphisms (i.e., *DAT1*, *DRD2*, and *DRD4*) and sibling differences in three specific experiences in the criminal justice system (i.e., arrest, multiple arrest, and incarceration) are examined.

#### 2. Behavior genetic research

The majority of studies that have examined the role that genetic factors play in the etiology of antisocial behavior fall within the discipline of behavior genetics [15,23]. Behavior genetic studies effectively generate estimates of the amount of phenotypic variance that may be explained by three latent factors: the shared environment, the nonshared environment, and genetics. Methodologies that allow for this type of variance decomposition require the use of genetically related siblings or adoptees in which each sibling pair's genetic relatedness is known. Most often, such methodologies use samples consisting of monozygotic (MZ) and dizygotic (DZ) twin pairs, but studies also frequently include other types of sibling pairs.

An impressive number of behavior genetic studies have examined a wide range of criminal and antisocial phenotypes [10,13,14,16]. In general, heritability estimates vary from sample to sample, but studies that have decomposed the variance of antisocial behavioral phenotypes reveal relatively consistent estimates. A number of literature reviews and metaanalyses have found that genetic factors account for approximately 50% of the variance in antisocial behaviors, while nonshared environmental factors account for approximately 40%-50% and shared environmental factors account for the remaining 0%-10% of the variance [10–17]. According to Moffitt [15], over 100 studies have examined genetic influences on antisocial behavior providing overwhelming evidence that genetic factors account for a significant portion of the overall variance in antisocial behaviors.

Behavior genetic research provides important information regarding genetic influences on antisocial behavior, however, such studies provide latent measures of genetic influences that take into account variability throughout the entire genome [24]. In this way, behavior genetic studies provide estimates of the amount of variance explained by genetic factors, but such studies are unable to identify specific genetic variants that influence the examined phenotype. While the findings from previous studies have revealed that antisocial behaviors are heritable [25,26], the underlying etiology of antisocial behaviors remains largely unknown. Performing an examination of the association between specific polymorphisms and antisocial outcomes can provide a much more thorough understanding of how such polymorphisms influence antisocial behaviors.

# 3. Dopaminergic genes and antisocial behaviors

In order to more clearly identify the role that genetic influences play in the etiology of antisocial behaviors, some studies have focused on examining the association between measured genetic polymorphisms and phenotypic outcomes, including antisocial behavior. The results of some of these studies indicate a significant association between certain polymorphisms and antisocial outcomes [27,28]. Genes involved with the regulation of the neurotransmitter dopamine have been the focus of a number of studies examining the association between polymorphisms and antisocial behavior [29-32]. Such studies have found a significant association between a number of different dopaminergic polymorphisms and antisocial outcomes that include alcohol dependence and abuse [33], attention-deficit hyperactivity disorder [34], internalizing disorders [35] and aggression [32]. Overall, the association between three specific dopaminergic polymorphisms and antisocial behaviors has been consistently studied.

First, the 40-base-pair (bp) variable number of tandem repeats (VNTR) of the dopamine transporter gene (*DAT1*) has been consistently linked to antisocial outcomes [36]. The two most common alleles for this polymorphism are the 9-repeat (9R) and 10-repeat (10R) alleles, with most human research comparing the differential effects associated with carrying these alleles. Findings from these studies have indicated that the 10R allele, compared to the 9R allele, is related to a number of antisocial outcomes in humans including alcohol consumption [37], ADHD [38], internalizing disorders [35], and selection into delinquent peer groups [39]. In addition, a study conducted by Guo and colleagues [31] found that subjects who possessed one or two 10R alleles were nearly twice as likely to engage in both serious and violent delinquency than subjects with two 9R alleles.

Second, the dopamine D2 receptor gene (*DRD2*) has been mapped to location 11q23 [40] and has a single nucleotide polymorphism (SNP) in the 3'UTR resulting in two possible alleles: the A-1 allele and the A-2 allele. The A-1 allele has been found to be associated with antisocial behaviors including conduct disorder [41], drug addiction [42], alcoholism [43,44], novelty seeking [45], and antisocial personality disorder [46].

Third, the dopamine D4 receptor gene (*DRD4*) is another dopamine receptor gene that has been linked to antisocial and maladaptive outcomes. *DRD4* has been mapped to location 11p15.5, and has a polymorphism that is the result of a 48 bp

Download English Version:

# https://daneshyari.com/en/article/317580

Download Persian Version:

https://daneshyari.com/article/317580

Daneshyari.com