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Gene by Social Context Interactions for Number of Sexual Partners among White Male Youths: Genetics-Informed Sociology¹

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This study sets out to investigate whether introducing molecular genetic measures into an analysis of sexual partner variety will yield novel sociological insights. The data source is the white male DNA sample in the National Longitudinal Study of Adolescent Health. The authors' empirical gene-environment interaction analysis produces a robust protective effect of the 9R/9R genotype relative to the Any10R genotype in the dopamine transporter gene (*DAT1*). This protective effect tends to be lost in schools in which higher proportions of students start having sex early, as well as in individuals with relatively low cognitive ability. The genetics-informed sociological analysis here suggests that explaining a human trait or behavior may require a theory that accommodates the complex interplay between social contextual and individual influences and genetic predispositions.

INTRODUCTION

Advances in Molecular Genetics and Our Objectives

Risky sexual behavior often plays a critical role in the spread of sexually transmitted diseases (STDs), including HIV among adolescents and young

¹ This research uses data from Add Health, a program project designed by J. Richard Udry, Peter S. Bearman, and Kathleen Mullan Harris and funded by a grant from the National Institute of Child Health and Human Development (P01-HD31921), with cooperative funding from 17 other agencies. Special acknowledgment is due to Andrew

adults (IOM 1997). Sociological work on risky sexual behavior has demonstrated the importance of social contexts at the levels of the individual, family, neighborhood, and school (Furstenberg et al. 1987; Brewster 1994; Browning, Leventhal, and Brooks-Gunn 2005). In this study, we set out to investigate whether introducing molecular genetic measures into analysis of sexual partner variety will lead to novel sociological insights.

The notion that individuals may differ with respect to genetic predispositions is not new. Twins and siblings have long been used to estimate the proportion of variance in an outcome due to innate influences, but the findings have frequently been questioned because the two fundamental assumptions of equal environment and assortative mating remain controversial.

Earlier efforts linking genetic variants and human outcomes often suffer from small sample sizes, population admixture, multiple testing, inappropriate controls, and nonreplication (Ioannidis et al. 2001; Cardon and Palmer 2003; Ioannidis et al. 2003). Convincing evidence arrived recently. The year 2007 saw an unprecedented succession of discoveries in the genomics of complex traits (e.g., Frayling et al. 2007; Pennisi 2007; Scott et al. 2007; Sladek et al. 2007; Steinthorsdottir et al. 2007; Zeggini et al. 2007). These discoveries identified genetic variants associated with acute lymphoblastic leukemia, obesity, type 2 diabetes mellitus, prostate cancer, breast cancer, and coronary heart disease. All of the evidence has been replicated multiple times in large independent samples. These discoveries in human genetic variation were chosen by the American Association for the Advancement of Science as the journal *Science*'s breakthrough of the year (Pennisi 2007).

If individuals do differ in genetic susceptibilities for diseases, it will be a small stretch to suggest that individuals may also differ in genetic propensities for other traits and behaviors that are of interest to sociologists. The important question, however, is whether bringing in genetics will advance sociology. In this study, we develop the theoretical concept of genetics-informed sociology, outlining specific ways sociological analysis may benefit from genetic information. Our empirical investigation, carried out in an analysis of multilevel social contexts, has two objectives: establishing the main effect of genotype on number of sexual partners and exploring how the influences of social contexts may be exacerbated or mitigated by genotype.

Smolen and John K. Hewitt of the Institute for Behavior Genetics at the University of Colorado for DNA isolation and genotyping. We gratefully acknowledge support from the NIH (grants R03 HD042490-02 and R03 HD053385-01 to Guang Guo) and from the NSF (grant no. SES-0210389 to Guang Guo). Direct correspondence to Guang Guo, Department of Sociology, University of North Carolina, Chapel Hill, North Carolina 27599-3210. E-mail: guang_guo@unc.edu

Consequences of Pattern of Sexual Partnering

A large number of sexual partners is an important indicator of an elevated risk of contracting an STD, including HIV (Cates and Stone 1992; Kost and Forrest 1992). With a pair of sexual partners potentially “exposing” themselves to every person with whom each of them has ever had sex and every person with whom each of those previous partners has ever had sex, and so on, the risk of STD tends to increase exponentially (Moody 2002).

In the United States, STDs disproportionately affect young people. Of the estimated 18.9 million new STD infections that occurred in 2000, 9.1 million (48%) occurred among people ages 15–24 (Weinstock, Berman, and Cates 2004). A recent Centers for Disease Control and Prevention (CDC) study reveals that around 26% of American women ages 14–19 are infected with a sexually transmitted infection (CDC 2008). Chlamydia, gonorrhea, vaginitis, and pelvic inflammatory disease all have the highest prevalence rates among adolescents, and these diseases become dramatically less prevalent with increasing age (Hatcher and Hagan 1998). Adolescents are more susceptible to STDs than adults because they have a higher probability of having multiple sexual partners (IOM 1997).

Multilevel Social Contexts and Pattern of Sexual Partnering

Sociologists have had a long-standing interest in the influences of multilevel social contexts on youth sexual behavior. Structural deficits in families, neighborhoods, and schools are generally considered to have negative impacts on adolescents’ sexual activity. It is also essential to include demographic and other individual factors as controls. In this section, we identify, describe, and justify social contextual factors that are used to build a sociological model of number of sexual partners. The model serves as groundwork for testing the effects of genetic variants.

Family structure and household socioeconomic status (SES) are two main family characteristics that are routinely used to predict adolescent behaviors. There are many theoretical reasons to expect weaker parental control over adolescents in nonintact and lower SES families (Hetherington 1979; Thornton 1991). Single parents are naturally less available for monitoring and supervising children than two parents would be, and the financial difficulties often experienced by single-headed households frequently lead single parents (who are more often than not the mothers) to enter the labor force or to increase their hours of employment. This can further reduce single parents’ capacity to interact with their children.

Families with high SES have more resources to support and promote their children’s healthy development. These families typically provide

their children with better neighborhoods, schools, and peer groups. All of these advantages may help reduce risks for early sexual activity.

Recent years have witnessed markedly increased efforts to investigate the influences of neighborhoods and schools on sexual activity during adolescence and young adulthood (Billy, Brewster, and Grady 1994; Brewster 1994; South and Baumer 2000; Browning and Olinger-Wilbon 2003; Browning et al. 2005). Neighborhoods of residence and schools are particularly important social contexts for young people, because their social space is limited to certain geographic areas. Concentrated poverty in a neighborhood lowers the effectiveness of local institutions including schools, voluntary organizations, and informal neighbor networks. These contextual deficits, in turn, tend to impact negatively on adolescent outcomes (Sampson, Raudenbush, and Earls 1997; Leventhal and Brooks-Gunn 2000).

Religiosity at the contextual level is emphasized in the “moral community” thesis (Stark, Kent, and Doyle 1982; Stark 1996; Stark and Bainbridge 1996). The thesis argues that religion should be understood as not only an individual trait, but also a group property. Regardless of an individual’s own religiosity, living in a religious community protects teens from “deviant” behaviors.

Furstenberg et al. (1987) highlighted the importance of the prevalence of sexual activity in a community. These authors noted that African-American youths attending predominantly black schools were nearly four times more likely to report having had sexual intercourse than their counterparts in predominantly white schools. They concluded that divergent sexual norms influenced the tendency toward early sexual initiation among African-Americans.

Several authors, including Furstenberg et al. (1987), noted that evaluating the normative explanation is not a straightforward matter (Moore, Simms, and Betsey 1986; Brewster 1994; Lauritsen 1994). School racial composition and neighborhood racial segregation generally reflect structural conditions and opportunity factors. The structural socioeconomic conditions could still be the underlying causes of the normative differences even if evidence is available for the normative explanation.

Social control theory has often been invoked to explain young people’s sexual behavior, but it is also recognized that social control is not the only mechanism through which social contexts influence sexual behavior (Udry 1988; Thornton 1991; Lauritsen 1994). Social control theory assumes a universal human tendency to pursue pleasure and postulates that the pursuit tends to become excessive unless checked by painful consequences. The theory is prominent in the study of criminal behavior (Hirschi 1969; Gottfredson and Hirschi 1990).

Sexual activity, however, differs from most criminal activity in a number

of ways (Udry 1988). It is by and large pleasurable. Many criminal acts are for economic gain rather than pleasure. In addition, it is age graded. Sexual activity is discouraged or prohibited in adolescence, but after adolescence it increasingly becomes accepted and even expected. Unlike much criminal activity, adolescent sexual activity is largely victimless. Though we consider social control theory useful, it will not be the overarching theory for our analysis.

Demographic and individual characteristics such as age, marriage and cohabitation experience, religiosity, cognitive test score, and physical maturity are also included as controls. Individuals who marry young and who are in a stable marriage are expected to have fewer sexual partners. Religion is considered to affect beliefs, attitudes, and behaviors through the mechanisms of social control, social support, and values or identity (Wallace and Williams 1997). Religious influences coming from families, church youth groups, and community norms can have an impact on adolescent behavior.

Traditionally, religious institutions in the United States promote certain types of sexual ideologies, which are characterized by abstinence, procreation, and celibacy, and which are intended to assert social influences and control over sexual behavior by prescribing behavioral standards and proscribing sexual activities. In contrast to these more traditional sexual ideologies, American popular culture and mass media are perceived to actively promote a sexual ideology characterized by pleasure (DeLamater 1989).

A higher level of cognitive development generally operates as a protective factor against early sexual activity during adolescence (Halpern et al. 2000). Physical maturity is found to predict early sexual debut among adolescents (Udry and Billy 1987; Capaldi, Crosby, and Stoolmiller 1996). Gagnon and Simon (1973) argue that when an adolescent male develops musculature, a beard, body hair, and mature genitals, he responds to the social expectations of peers and parents by developing a role as a potential sexual partner.

Genetics-Informed Sociology

Advances in molecular genetics and consensus on importance of environment.—Intense efforts in molecular genetics over the past two decades have discovered more than a thousand genes responsible for Mendelian human outcomes—outcomes mostly determined by alleles of a single gene (Risch 2000; Botstein and Risch 2003).² Examples of such human outcomes

² Different forms (different DNA sequences) of a gene, called alleles, may be found at a given location on members of a homologous set of chromosomes. Structural variations between alleles may lead to different phenotypes for a given trait.

include Huntington's disease, cystic fibrosis, hereditary nonpolyposis colon cancer, and heritable breast cancers. Molecular genetic efforts have been much less successful on non-Mendelian or complex human outcomes. Many of these outcomes, including reading disability, smoking, alcohol use, drug use, and obesity, are of interest to sociologists. The links between genetic heritage and complex human outcomes are enormously complicated, typically involving multiple genes, numerous environmental factors, and the interactions between the two.

As reviewed briefly above, it was not until recently that the genetics community produced persuasive evidence for the association between genetic variants and complex human outcomes. Two fundamental technological breakthroughs paved the way for the discoveries: the HapMap data that reduce genotyping of redundant SNPs (single nucleotide polymorphisms, which are a type of genetic marker) and high throughput genotyping.

The genetics community has increasingly expressed the consensus that social scientists' expertise in social contexts is essential for understanding many complex human diseases. The success of the Human Genome Project (Collins, Morgan, and Patrinos 2003) and the HapMap Project (International HapMap Consortium 2005) is improving the design and effectiveness of genetic studies of complex outcomes.³ These advances, however, do not lessen the need for understanding the social environmental component of the puzzles. On the contrary, inadequate understanding of social environments has become a bottleneck for the rapid technological advances in molecular genetics. The HapMap project (International HapMap Consortium 2005), the National Human Genome Research Institute (Collins et al. 2003), and the Committee on Gene-Environment Interactions for Health Outcomes at the Institute of Medicine in the National Academies of Sciences (Hernandez and Blazer 2006) called for heavy investment in information on social and cultural exposures and in longitudinal studies of adequate size that could obtain such information.

In what ways can genetics inform sociology?—A fundamental insight of genetics-informed sociology is that individuals may possess dissimilar genetic predispositions at birth for certain traits and behaviors. Because genetic sequences are formed at conception and remain largely unchanged throughout life, genetic effects are not confounded by social contextual and other environmental influences. Genetic sequences, however, are not

³ The International HapMap Project is a multicountry endeavor to identify and catalog genetic similarities and differences in human beings. The project is a collaboration among scientists and funding agencies from Japan, the United Kingdom, Canada, China, Nigeria, and the United States.

immune to social contextual influences before conception. For example, assortative mating likely plays a significant role in DNA sequence arrangement.

There are a number of specific areas in which knowledge of genetic dispositions may advance sociology. First, measures of genetic predispositions may increase a sociological model's predictive power. Adding genetic information may enrich sociological models and deepen the general understanding of human outcomes under study. Second, genetic measures can isolate purer effects of social contexts from genetic confounders. Many effects of social contexts yielded by conventionally sociological models may be overestimated because of genetic confounding. For example, conventionally estimated effects of social origin (measured by parental education, parental occupation, and parental income) on children's educational attainment may not be purely environmental. Because parents and children share 50% of genetic material, the transmission from parents to children is both social and genetic. This is the so-called gene-environment correlation. In this case, parental genetic effects and parental environmental effects are correlated and entangled. Purer effects of social origin can be estimated to the extent that relevant genetic measures that are correlated with parental measures are included in the analysis.

The crucial question is not whether genes are predictive of a human outcome, but whether the genes are correlated with social contexts. If the two are uncorrelated, genetic information improves prediction, but does not confound the estimates of social contextual effects. The current difficulty with this strategy is that many of the relevant genetic measures are unknown. The control for the confounding will not be adequate if only isolated genetic variants are taken into account.

Third, for the reason just described, gene-environment interaction analysis will likely remain a more fruitful vehicle for some time to come for social scientists whose primary interest is to understand effects of social contexts. Gene-environment interaction refers to the principle that an environment may influence how sensitive we are to the effects of a genotype and vice versa (Plomin, Defries, and Loehlin 1977; Kendler 2001; Hunter 2005). A biological example of this comes from individuals with the Δ -32 deletion in the *CCR5* gene; these individuals have lower rates of HIV infection and slower disease progression than those without the deletion when exposed to similar environmental conditions (Smith et al. 1997). This example illustrates how environmental exposure is mitigated by genotype.

A social science example comes from Caspi et al. (2002), who found that a functional polymorphism in the monoamine oxidase A (*MAOA*) gene modifies the effect of maltreatment on violent behavior. Only maltreated children with a genotype generating low levels of *MAOA* expres-

sion tended to develop the violent behavior problem. Maltreated children with a genotype that produced high levels of *MAOA* activity were less affected. The main effect of *MAOA* was not observed. This case shows how the manifestation of a genotype effect depends on a social context.

Ignoring information on genetic dispositions may lower our ability to discern the effect of a social context. Individuals with different genetic dispositions may respond to the same social context differently. In such a case, a social theory that assumes a uniform social influence on all individuals would not be able to measure up against empirical data. For example, suppose that there are two alleles (A and B) at one genetic locus: 10% of the sample have A and the other 90% have B. Suppose that only individuals with A are responsive to an environmental influence. Then if the genetic variation is ignored, the environmental effect, which is an average over A individuals and much more numerous B individuals, will likely remain hidden from the analysis. Our findings on gene-environment interaction between the *DAT1* gene and cognitive ability (described below) provide a case in point.

Finally, sociologists may be interested in genetic influences themselves on social behaviors. For many human outcomes (e.g., obesity and hypertension), sociological analysis is understandably more interested in the influences of social contexts than the other causes of the outcomes. This preference may change in studies whose purpose is to understand social behaviors (e.g., popularity, social isolation, and serial divorces). In such cases, the influences of social contexts may not be the only focal point of sociological analysis. Genetic causes may be of additional importance because of sociologists' interest in the outcomes.

THE DOPAMINE TRANSPORTER GENE AND PATTERN OF SEXUAL PARTNERING

Both animal and human studies have demonstrated a genetic basis for sexual behavior. A study based on 1,600 female twin pairs reported an estimated heritability of 0.40 for the self-reported number of sexual partners (Cherkas et al. 2004). Another study based on pairs of full siblings, half-siblings, cousins, and a small number of same-sex twins from the National Longitudinal Study of Youth identified a genetic contribution (heritability) to age at first sex in the all-ethnicities sample (0.37), the white sample (0.51), and the male sample (0.54) (Rodgers, Rowe, and Buster 1999). Evidence for age at first sex is also reported from the National Longitudinal Study of Adolescent Health (Add Health); the evidence is based on both a biometrical analysis of twins and an association with the variants of the *DRD4* gene (Guo and Tong 2006).

The neurotransmitter dopamine has been shown to facilitate male sexual activity in all investigated species, including rodents and humans (Dominguez and Hull 2005).⁴ Melis and Argiolas's (1995) findings suggest a major role for dopaminergic receptors in both the preparatory and consummatory phases of male sexual behavior, but their role in female sexual behavior is less conclusive. Hull, Meisel, and Sachs (2002) discussed three mechanisms through which male sexual behavior is affected by dopamine among rats: dopamine increases male sexual arousal and courtship behavior, enhances the motor acts of mounting behavior, and facilitates genital response to stimulation.

The soluble carrier family 6 dopamine transporter member three gene (*DAT*; locus symbol *SLC6A3*) codes for a dopamine transporter protein (DAT), which limits the level and duration of dopamine receptor activation (Bannon and Whitty 1995). For decades, major investigations have targeted the role of dopaminergic neurotransmission in complex behaviors involving addition and reward (Bressan and Crippa 2005). Though the specific functions that dopamine performs are not entirely understood, evidence has been accumulating for an important role of dopamine in the regulation of the additive and rewarding behaviors. A number of animal studies demonstrate that natural rewarding stimuli such as food, drink, and sex increase the *in vivo* release of dopamine in the nucleus accumbens (Kalivas 2002). A mouse model that had knocked out the dopamine transporter gene established the central importance of a dopamine transporter in controlling synaptic dopamine levels, as well as its role as an obligatory target for the behavioral and biochemical action of amphetamine and cocaine (Giros et al. 1996).⁵ *DAT1* is thus an important component for the maintenance of normal dopaminergic neurotransmission.

Vandenberg et al. (1992) identified a polymorphic 40-bp variable number of tandem repeats (VNTR) in the *DAT1* gene, which is most commonly observed to repeat 9 (*DAT1**9R) to 10 times (*DAT1**10R).⁶ Biochemical

⁴ Neurotransmitters are chemicals that allow the movement of information from one neuron across the gap between it and the adjacent neuron.

⁵ The gene knockout is created by selectively disabling a specific target gene in a particular type of cells, called embryonic stem cells. The technique has been used to make several thousand different knockout mice. Knockout mice have become one of the most useful scientific tools in helping to understand the human genome and its roles in disease.

⁶ VNTR is a chromosomal locus at which a particular repetitive sequence is present in different numbers in different individuals of a population. Most of our DNA sequence is identical to the DNA sequences of others. However, there are inherited regions of DNA that can vary from one individual to another. Variations in DNA sequence among individuals are termed *polymorphisms*. Sequences with a high degree of polymorphism are very useful for DNA analysis, which often attempts to link human outcomes to variations in DNA sequence. VNTR, STR (short tandem repeat), and SNP are classes of DNA polymorphisms.

functional analysis shows that the *DAT1**9R allele is associated with lower levels of DAT than the 10 allele (Fuke et al. 2001; Fuke, Sasagawa, and Ishiura 2005; VanNess, Owens, and Kilts 2005). A number of studies have demonstrated an association between the 10R allele and attention deficit hyperactivity disorder (ADHD) (Cook et al. 1995; Gill et al. 1997; Waldman et al. 1998; Daly et al. 1999; Cornish et al. 2005). The *DAT1**9R allele was reported to be associated with both a lower score in novelty seeking and greater success in smoking cessation (Sabol et al. 1999; Cornish et al. 2005).

GENDER AND PATTERN OF SEXUAL PARTNERING

In this study, we focus on male patterns of sexual partnering, and we justify the focus theoretically and empirically. Males and females differ substantially with respect to patterns of sexual partnering. Males of most mammalian species show a strong desire for variety in sexual partners. In the laboratory, this phenomenon has been referred to as the Coolidge effect (Wilson, Kuehn, and Beach 1963; Bermant, Lott, and Anderson 1968; Bermant 1976). The Coolidge effect was first observed among rats. The same effect is more striking in farm animals such as sheep and cattle (Wilson 1992). Studies based on self-reports among human subjects found that partner variety is of greater interest to male adolescents (Small, Silverberg, and Kerns 1993), male college students (Clark and Hatfield 1989), and male adults (Carroll, Volk, and Hyde 1985; Simpson and Gangestad 1991; Buss and Schmitt 1993; Oliver and Hyde 1993; McBurney, Zapp, and Streeter 2005) than to their female counterparts.

Two broad theoretical approaches have been developed to explain the gender differences in number of sexual partners or, more generally, the gender differences in reproductive strategies: the evolutionary theory and the social control of human sexuality. The evolutionary theory argues that the differences in the relative costs and benefits of sexual behaviors between the two genders over the course of the evolutionary process have produced the gender differences in mating predispositions (Maynard 1977; Symons 1979; Hrdy 1981; Geary 1998).

Social theories have emphasized social regulation of human sexuality as a source for gender differences in sexual behavior (DeLamater 1981, 1989). Social theories argue that the gender differences are at least partially due to double sexual standards, because men traditionally enjoy more power than women in virtually all the major institutions: politics, religion, economics, and family. Our focus on males is further justified by our empirical findings that the *DAT1* gene is not associated with number of sexual partners among females in our sample (as shown in an analysis

below). This initial contingency table analysis is confirmed by regression analysis (data not shown).

METHODS AND DATA

Data Source

The data source for our analysis is Add Health, a nationally representative sample of more than 20,000 adolescents in grades 7–12 in 1994–95 in the United States (Harris et al. 2003). Add Health is longitudinal; the respondents have since been followed by two additional in-home interviews in 1995–96 (wave 2) and 2002 (wave 3). Add Health is school based, and the adolescents were from 134 schools. The school sample was stratified by region, ethnic mix, size, urbanicity (urban/suburban/rural), and school type (public/private/parochial).

Data were collected from adolescents and from their parents, siblings, friends, peers, fellow students, and school administrators. Existing national data sources about neighborhoods and communities have been incorporated. In wave 3 in 2002, DNA samples were collected from a subset of about 2,500 siblings. Our study uses the approximately 680 white male participants whose analysis information is available. Our gene-environment interaction analysis focuses on white males because of the small sizes of the other ethnic groups, especially the small size of the *DAT1**9R/9R subcategory. Only 10 individuals in the African-American sample are in this subcategory. The white male sample contains 39 9R/9Rs.

Measures

Number of sexual partners.—At wave 3, the respondents ages 18–26 were asked the question, “With how many partners have you ever had vaginal intercourse, even if only once?” As with any survey of sensitive private information, reporting accuracy is a concern. To protect confidentiality, reduce nonresponses, and increase reporting accuracy, this section of the interview was self-administered by audio-CASI (computer-assisted self-interview). The sensitive question was read to respondents through audio headphones. Respondents were given instructions by the computer on how to complete their answers. The technique has been shown to reduce the disparity between men and women in the reported number of sex partners (Tourangeau and Smith 1996).

As in most surveys that ask about number of sexual partners (Smith 1992), the number of female partners reported by males exceeds the number of male partners reported by females in Add Health, with an overall male-female ratio of 1.3 to 1. Because heterosexual intercourse involves

a male and a female, in a closed population the total number of copulations for males must equal those for females; the total number of sexual partners for males must also equal those for females. There are a number of explanations that may potentially account for the higher reported male-to-female ratio. The male and female respondents in our Add Health sibling sample may refer to different sets of sexual partners. A small number of females may have a large number of partners, and these females are less likely to respond to social survey. Finally, the males may have overreported.

DNA preparation and genotyping.—At wave 3, in collaboration with the Institute for Behavioral Genetics in Boulder, Colorado, Add Health collected, extracted, and quantified DNA samples from the sibling subsample. Genomic DNA was isolated from buccal cells using a modification of published methods (Lench, Stanier, and Williamson 1988; Meulenbelt et al. 1995; Freeman et al. 1997).⁷ Microsatellite and VNTR polymorphisms were done using fluorescent primers that were analyzed on an ABI capillary electrophoresis instrument.⁸

A 40-bp VNTR polymorphism in the 3' untranslated region of the *DAT1* gene has been genotyped with a modification of the method of Vandenberg et al. (1992). This VNTR ranges from three to 11 copies, with the 9-repeat (9R or 440 bp) and 10-repeat (10R or 480 bp) polymorphisms being the two most common alleles (Doucette-Stamm et al. 1995). In the Add Health sibling sample, the 9R and 10R account for about 24.5% and 74.2% of all alleles, respectively. Our analysis used only individuals with genotypes of one 10R, two 10Rs, and two 9Rs.⁹ The individuals with other genotypes (about 2%) are excluded from the analysis. In our analysis sample, 94.2% and 5.8% of the white respondents possess Any10R and 9R/9R genotypes, respectively. A chi-square test for the polymorphism reveals no deviation from the Hardy-Weinberg equilibrium.

Social contextual and individual measures.—Family structure is a variable of four categories: families with two biological parents, single-parent families, stepparent families, and other types of families, including families with adopted and foster children. In our final models, we use a two-category variable of the presence or absence of *two biological parents*. Parental education also has four categories: *less than (<) high school, high*

⁷ Buccal cells are the cells from the inner lining of the mouth. These cells are routinely shed and replaced by new cells. As the old cells die, they accumulate in the saliva in the mouth and can easily be collected by a simple procedure using mouthwash.

⁸ The additional details on DNA collection and genotyping are provided at the Add Health Web site (<http://www.cpc.unc.edu/projects/addhealth/>).

⁹ In general, the genotype is the specific genetic makeup (the specific genome) of an individual. Here we refer to an individual's genotype with regard to a particular gene of interest and the combination of alleles that the individual carries.

school diploma, *some college*, and at least a college degree (\geq *college*). Add Health measures the level of education from both the mother and the father of a respondent. We use the higher of the two when both are available.

Our analysis includes three measures at the contextual level. Poverty at the neighborhood level is measured by the proportion of families living below the official poverty line in a census block group, which is the smallest geographic area for which the census bureau publishes sample data. In 1990, block groups averaged 452 housing units or 1,100 individuals. The block groups are divided into low-poverty, median-poverty, and high-poverty categories. The two cutoff points for the three categories are 11.6% (the median proportion of families in a block group living below the poverty line) and 23.9% (the 75th percentile). *Church adherents per capita* represents the percentage of church adherents in the county, and *%had sex by 16* stands for the percentage of students in the respondent's school having had sexual intercourse by age 16.

Our measure of marital and cohabitation experience includes categories for respondents who are single, who have cohabited and been married, who have only been married, and who have only been in a cohabiting relationship. *Church attendance* measures attendance frequency with the categories never, less than monthly, less than weekly, and weekly or more. To reduce the number of parameters that need to be estimated in the interaction analysis, we use a two-category variable of attending religious service weekly or more and attending religious service less than weekly or never.

The Add Health Peabody Picture Vocabulary Test (PVT) is a slightly shortened version of the standard Peabody Picture Vocabulary Test (Rice and Brown 1967; Lubin, Larsen, and Matarazzo 1984), which is usually considered a verbal IQ test. In our main regression analysis, the variable *PVT* is standardized into a *Z*-score by subtracting every PVT score from the sample mean and then dividing the result by its standard deviation. *Physical maturity* is a dummy variable constructed from the wave-1 question of whether the adolescent's physical development is more advanced than that of other boys of the same age. Table 1 provides the mean or proportion and associated standard deviation of these variables.

Number of Sexual Partners

TABLE 1
DESCRIPTIVE STATISTICS FOR WHITE MALES ($N = 674$)

	Mean/Proportion	SD
%10R (480) allele751	.432
%Any10R (480) genotype942	.234
Individual and family traits:		
Age 18–20	19.73	39.79
Age 21–23	58.61	49.25
Age 24–26	21.66	41.19
Two biological parents682	.466
High school279	.449
< high school034	.182
Some college211	.408
≥ college445	.497
Missing data on education031	.174
Single580	.494
Cohabited and married077	.267
Married, not cohabited071	.257
Cohabited, not married267	.443
Church attendance147	.354
PVT00	1.00
Physical maturity545	.498
Contextual characteristics:		
Poverty < 11.6%636	.481
Poverty 11.6%–23.9%208	.406
Poverty ≥ 23.9%091	.287
Missing data on poverty065	.247
Church adherents per capita	54.4	14.3
%had sex by 16	41.0	11.2

Statistical Models

We carried out the analysis of gene-environment interactions via the GEE (generalized estimating equations) Poisson regression model. Equation (1) describes the basic regression model for the interaction analysis:

$$E(Y_{ij}|x_{ij}) = \exp [\beta_0 + \beta_1 \text{ANY10R}_{ij} + \beta_2 SC_{ij} + \beta_3 (\text{ANY10R} \times sc)_{ij} + \beta_4 \text{AGE}_{ij}], \quad (1)$$

where $E(Y_{ij}|x_{ij})$ is the expected number of sexual partners for individual i in sibling cluster j given the individual's characteristics x_{ij} ; ANY10R_{ij} is one of the two genotypes in the *DAT1* VNTR polymorphism under investigation for the individual; SC_{ij} is a column vector denoting social contextual measures; β_1 and β_2 (a row vector) represent the effects of ANY10R_{ij} and SC_{ij} , respectively; and $(\text{ANY10R} \times sc)_{ij}$ is a product of ANY10R and a single social contextual measure. The exposure for number

of sexual partners was explicitly adjusted by the age categorical variable. The dependence among the siblings is addressed by the GEE (Liang and Zeger 1986), which has long been established in the statistical literature as a standard approach for addressing correlated data. The GEE models were implemented using SAS.

RESULTS

Mean Number of Sexual Partners by Genotype, Gender, and Age

Table 2 shows the mean number of sexual partners by genotype and age group for all males, all females, and white males. Among the males, the 10R allele is associated with a higher number of sexual partners. In the younger male group, ages 18–22, possessing one or two copies of 10R approximately doubles the number of partners. In the older male group, ages 23–26, possessing one or two copies of 10R increases the number of partners from about four to seven. As expected, age is positively related to the number of reported partners, but there does not seem to be an interaction between age and the effect of the *DAT1* variants; that is, the effect of *DAT1* does not seem to vary across the life stages of adolescence and young adulthood.

Among females, the 10R allele is not associated with a higher number of sexual partners. This is the case in both age groups, suggesting an interaction between *DAT1* and gender. The same relationship between the *DAT1* variants and number of sexual partners observed among all males is also observed among white males. In the rest of the article, we will only describe results from the white male sample.

Regression Results

The three models of sexual partners in table 3 establish the main effect of the Any10R genotype. The first GEE model controls for age group and addresses the sibling structure of the data so that the statistical significance of a genotype effect can be tested. In the first model, those with the *DAT1**Any10R genotype report 93% ($\exp(0.66) = 1.93$) more sexual partners than those with the *DAT1**9R/9R genotype.

The second and third models in table 3 include a set of social contextual factors as well as individual controls. In the third model, those with the *DAT1**Any10R genotype report 60% more sexual partners than those with the *DAT1**9R/9R genotype. Compared with the basic first GEE model, the genotype effect obtained after adding social contextual and individual factors is reduced, but the level of significance remains about the same. The second model does not include the genotype Any10R. Its coefficients

Number of Sexual Partners

TABLE 2
MEAN NUMBER OF SEXUAL PARTNERS BY GENOTYPE,
GENDER, AND AGE GROUP

Gender/Age Group	9R/9R	9R/10R	10R/10R
All males:			
18–22	2.42 (33)	4.92 (243)	5.29 (415)
23–26	4.08 (25)	6.85 (158)	7.07 (289)
All females:			
18–22	4.12 (42)	4.44 (263)	3.56 (481)
23–26	4.60 (20)	5.80 (164)	4.60 (317)
White males:			
18–22	2.24 (21)	5.19 (224)	4.91 (164)
23–26	3.78 (18)	6.21 (145)	7.05 (109)

NOTE.—Numbers in parentheses are sample sizes.

and standard errors are rather similar to those in the third model, suggesting moderate correlations between Any10R and the included social contextual and individual factors.

In the full model, church attendance is strongly and negatively related to number of sexual partners. Those who attend religious services at least weekly report about 60% [$1 - \exp(-0.90)$] fewer sexual partners than those who never attend religious services or attend religious services less than weekly. Marital status and cohabitation experience are also significantly related to number of sexual partners. Those who have only cohabited report the highest number of sexual partners (58% higher than those who are single), followed by those who have cohabited and married, those who are single, and those who have only been married. Physical maturity at wave 1 is associated with a larger number of partners. Only one contextual measure significantly predicts number of sexual partners: a 1% increase in the proportion of students in school having had sex by age 16 raises the number of partners by about 2.1%.

Because the reference category of *DAT1**9R/9R has only about 6% of the white sample, it is more appropriate to refer to 9R/9R as the protective genotype than to refer to Any10R as the risky genotype. Given that about 94% of the sample falls into the Any10R category, the average number of sexual partners for Any10R should be close to the sample mean. Re-estimating the protective effect by coding 9R/9R as 1 and Any10R as 0 (the reference category) yields the coefficient of -0.468 , which is exactly the same in value, but has an opposite sign. The *t*-ratio remains the same as well. Thus, according to the full model in table 3, the 9R/9Rs report only about 63% as many sexual partners as the Any10Rs.

Table 4 explores the interactive effects of the dopamine transporter gene and a number of social contextual and individual nongenetic (we

TABLE 3
GEE POISSON MODELS OF NUMBER OF SEXUAL PARTNERS: MAIN EFFECTS
OF DOPAMINE TRANSPORTER AND MULTILEVELS OF SOCIAL CONTEXTS
FOR WHITE MALES

	<i>DAT1</i> + AGE	SOCIAL CONTEXTS	
		No <i>DAT1</i>	+ <i>DAT1</i>
Intercept	1.29*** (.28)	1.344*** (.374)	.904* (.438)
Any10R dopamine transporter66* (.26)468* (.227)
Individual and family traits:			
Ages 24–26
Ages 18–20	-.60*** (.17)	-.549** (.181)	-.537** (.181)
Ages 21–23	-.21 (.15)	-.194 (.153)	-.187 (.151)
Two biological parents		-.048 (.12)	-.063 (.122)
High school
< high school01 (.308)	.03 (.309)
Some college091 (.171)	.11 (.17)
≥ college129 (.148)	.132 (.148)
Missing data on education331 (.313)	.312 (.313)
Single
Cohabited and married351 (.19)	.339 (.189)
Married, not cohabited		-.185 (.201)	-.185 (.202)
Cohabited, not married439** (.135)	.44** (.134)
Church attendance		-.901*** (.193)	-.896*** (.192)
PVT		-.049 (.057)	-.044 (.057)
Physical maturity279* (.113)	.288* (.113)
Contextual characteristics:			
Poverty < 11.6%
Poverty 11.6%–23.9%		-.239 (.139)	-.238 (.139)
Poverty ≥ 23.9%092 (.206)	.08 (.206)
Poverty data missing041 (.19)	.036 (.189)
Church adherents per capita ...		-.4 (.428)	-.358 (.428)
%had sex by 16		1.214* (.524)	1.128* (.534)

NOTES.—*N* = 674. Numbers in parentheses are SEs. Ellipses indicate that the variable is a reference category; a blank cell indicates that the variable was not included in the model.

* *P* > .05.

** *P* > .01.

*** *P* > .001.

assume) characteristics. The first three of the four models in table 4 each add a single interaction term to the full main-effect model in table 3. In the last model, all three interaction terms are added simultaneously. The first model examines the interaction between Any10R and the proportion in school having had sex by age 16; the second, the interaction between Any10R and standardized PVT *Z*-score; and the third, the interaction between Any10R and physical maturity at wave 1. All three interaction terms as well as their corresponding main effects are significant in the first three models. PVT *Z*-score is not significant in the main-effect model

TABLE 4
GEE POISSON MODELS OF NUMBER OF SEXUAL PARTNERS: INTERACTIONS BETWEEN SOCIOECONOMIC-CULTURAL FACTORS AND
DOPAMINE TRANSPORTER FOR WHITE MALES

	%had sex by 16	PVT	Physical Maturity	All Three
Intercept	-.868 (.789)	.971* (.418)	.437 (.406)	-.348 (.629)
Any10R dopamine transporter	2.318** (.724)	.43* (.18)	.954*** (.208)	1.795*** (.595)
Individual and family traits:				
Ages 24-26
Ages 18-20	-.537** (.18)	-.54** (.179)	-.529** (.181)	-.535** (.18)
Ages 21-23	-.177 (.152)	-.183 (.15)	-.183 (.152)	-.176 (.151)
Two biological parents	-.061 (.122)	-.065 (.123)	-.061 (.121)	-.063 (.122)
High school
< high school034 (.307)	.026 (.308)	.03 (.308)	.027 (.307)
Some college108 (.169)	.103 (.17)	.109 (.17)	.102 (.17)
≥ college129 (.148)	.129 (.149)	.129 (.148)	.127 (.148)
Missing data on education311 (.312)	.315 (.313)	.311 (.312)	.313 (.312)
Single
Cohabited and married347 (.188)	.34 (.188)	.341 (.189)	.346 (.188)
Married, not cohabited	-.176 (.2)	-.172 (.2)	-.175 (.202)	-.161 (.201)
Cohabited, not married447*** (.133)	.436*** (.132)	.442 ***(.134)	.442 ***(.132)

TABLE 4 (Continued)

	%had sex by 16	PVT	Physical Maturity	All Three
Church attendance	-.894*** (.192)	-.9*** (.192)	-.904*** (.192)	-.902*** (.193)
PVT	-.04 (.057)	-.57* (.236)	-.044 (.057)	-.396 (.241)
Physical maturity28* (.114)	.287* (.114)	.876*** (.262)	.586** (.19)
Contextual characteristics:				
Poverty < 11.6%
Poverty 11.6%–23.9%	-.229 (.138)	-.224 (.139)	-.238 (.138)	-.224 (.139)
Poverty ≥ 23.9%101 (.206)	.093 (.206)	.083 (.206)	.104 (.206)
Poverty data missing045 (.189)	.046 (.189)	.034 (.189)	.047 (.188)
Church adherents per capita	-.36 (.429)	-.353 (.429)	-.354 (.428)	-.351 (.43)
%had sex by 16	5.404** (1.662)	1.055* (.527)	1.092* (.536)	3.613** (1.369)
Any10R ×:				
%had sex by 16	-4.471* (1.744)			-2.673 (1.49)
PVT538* (.243)		.363 (.252)
Physical maturity			-.603* (.292)	-.311 (.225)

NOTES.— $N = 674$. Numbers in parentheses are SEs. Ellipses indicate that the variable is a reference category; a blank cell indicates that the variable was not included in the model.

* $P > .05$.

** $P > .01$.

*** $P > .001$.

in table 3, but its main effect and interaction effect are both statistically significant in table 4.

When all three interaction terms are estimated in the same model, only the interaction term involving %had sex by 16 is marginally significant. The lack of statistical power is probably a major factor in the nonsignificance of the multiple interaction terms in the last model in table 4. In the discussion and conclusion section below, only the models with a single interaction term are interpreted.

Profiling Individuals with 9R/9R and Any10R

In this section, we provide a profile for individuals with the 9R/9R genotype and the Any10R genotype. Our data have established a protective effect of 9R/9R relative to Any10R with respect to number of sexual partners. But are the 9R/9Rs systematically different from the Any10Rs in family SES, academic performance, cognitive ability, religiosity, physical maturity, and popularity among peers? Is the 9R/9R genotype also protective of other risky health behaviors in addition to pattern of sexual partnering?

These questions are explored preliminarily in table 5, which reports the mean or proportion of individual characteristics, parental characteristics, and health behaviors for both 9R/9R and Any10R. All measures of characteristics and behaviors are from Add Health wave 1 or the earliest wave at which the data are available. The results based on other waves are similar and are not presented. To perform statistical significance tests, we regress each characteristic on Any10R, controlling for age when appropriate. The regression model is linear, logit, or Poisson depending on the distribution of a particular characteristic. The GEE regression framework is used to handle the sibling clustering in the Add Health sample (Liang and Zeger 1986). Table 5 reports the regression coefficient for Any10R and the associated *t*-ratio.

The similarities and differences between individuals with 9R/9R and individuals with Any10R are systematic. The 9R/9Rs do not differ significantly from the Any10Rs in age, physical maturity, church attendance, number of friend nominations received (*popularity received*), number of friend nominations sent (*popularity sent*), and how sensitive they are to other people's feelings. The two groups are not different in family SES as measured by the presence of two biological parents and whether at least one parent has a college degree. The 9R/9Rs, however, have a higher cognitive ability, as measured by PVT *Z*-score (108.5 vs. 104.8), and a higher GPA (3.08 vs. 2.75) than the Any10Rs.

It turns out that the 9R/9Rs not only have fewer sexual partners, but also have fewer binge drinking days (about 50% fewer), smoke far fewer

TABLE 5
COMPARING THE 9R/9R AND ANY10R GENOTYPES FOR WHITE MALES

	MEAN		β	<i>t</i> -RATIO	MODEL
	9R/9R	Any10R			
Individual characteristics:					
Age ^a	15.77	15.65	.009	.03	Linear
Physical maturity ^a62	.54	-.34	-1.00	Logit
GPA ^a	3.08	2.75	-.39	-2.98**	Linear
Cognitive ability (PVT)	108.5	104.8	-3.33	-1.96*	Linear
Church attendance40	.35	-.20	-.73	Logit
Popularity received	5.48	5.34	.001	.00	Linear
Popularity sent	4.74	4.81	.003	.00	Linear
Sensitive to other people's feelings ^b	2.07	1.98	-.047	-.69	Linear
Parental characteristics:					
Two biological parents65	.68	.001	.001	Logit
%parents having college degree77	.66	-.31	-1.19	Logit
Risky health behaviors:					
No. sexual partners	2.94	5.66	.69	2.59**	Poisson
Binge drinking days41	.81	.71	1.99*	Poisson
No. cigarettes per day ^a62	2.74	2.18	4.56***	Poisson
Frequency of seatbelt use ^a	3.37	2.92	-.46	-2.97**	Linear
Delinquency summary scale	1.22	2.00	.87	1.99*	Linear
Delinquency items:					
Burglarize building ^a025	.067	.038	1.33	Linear
Use or threaten with weapon ^a025	.070	.045	1.53	Linear
Sell marijuana or other drugs10	.14	.032	.38	Linear
Steal items worth < \$50 ^a25	.38	.18	1.17	Linear
Take part in group fight ^a15	.25	.11	1.67	Linear
Deliberately damage property of others25	.36	.13	1.38	Linear
Seriously injure someone ^a25	.29	.054	.52	Linear
Carry weapon to school ^a05	.081	.033	.83	Linear
Self injured and treated by doctor or nurse05	.15	.10	2.61**	Linear
Pulled knife/gun on someone ^a00	.055	.049	4.78***	Linear
Shot/stabbed someone ^a00	.02	.02	3.20**	Linear
Carry weapon to school ^a075	.12	.045	.76	Linear

NOTE.—*N* = 674.

^a From wave-1 survey.

^b From wave-2 survey.

* *P* > .05.

** *P* > .01.

*** *P* > .001.

cigarettes per day, are more likely to wear a seatbelt when driving or riding in a car, and score lower on the delinquency summary scale than the Any10Rs. All of these differences in risky health behaviors are statistically significant. To unpack the delinquency summary scale, we regress each of the 12 items in a GEE regression on Any10R, controlling for age. Although only three of the 12 items are significant, all of the differences are in the expected directions.

DISCUSSION AND CONCLUSION

Our empirical analysis has yielded a substantial main effect of the VNTR polymorphism in the *DAT1* gene on number of sexual partners among white male adolescents and young adults. This main effect is present in the contingency table analysis (table 2), the initial GEE regression model that controls for age and sibling clustering (table 3), and the full GEE regression model that controls for a set of additional social contextual and individual characteristics (table 3). However, *DAT1* should not be viewed as a sex gene. More appropriately, we consider the effect of the 9R/9R genotype a protective effect relative to the Any10R genotype, to which 94% of the sample belong.

The full model in table 3 points to the importance of multiple levels of social contexts. Marriage and frequent church attendance on the part of the individual both reduce the number of sexual partners. The proportion of the students in school having had sex by age 16 is significantly and positively associated with number of sexual partners.

Profiling the 9R/9R and Any10R individuals has uncovered intriguing similarities and differences between the two groups. The groups seem to have similar family background. They do not differ in age, physical maturity, religiosity, or popularity. The 9R/9Rs have a slightly higher GPA and a slightly higher cognitive ability score, and they are less likely to engage in risky health behaviors than the Any10Rs, including having multiple sexual partners, binge drinking, smoking, not wearing a seatbelt when riding or driving a car, and other delinquent and criminal acts. These findings provide further support for the protective effect of 9R/9R and suggest that the protective effect may go beyond the pattern of sexual partnering. Are individuals with 9R/9R straight arrows who are behaviorally more conservative than the population average?

Interpreting gene-environment interactions is not always straightforward. When a genotype interacts with a social context measure, it means that the genotype effect and the social context effect depend on each other. The interaction can be viewed from two angles. One reveals how a social-context effect varies by genotype—that is, a social-context effect may be

weaker or stronger for one genotype than for another. The other angle examines how a genotype effect differs across social-contextual categories. Both may be interesting to sociologists.

Figure 1 was created to assist in the interpretation of gene-environment interactions for the regression results presented in table 4. Part A describes the interaction between the genotype effect and the effect of the prevailing sexual norm in school. It plots the predicted number of sexual partners against %had sex by 16 for two genotypes (Any10R and 9R/9R). The values of the other variables in the regression equation are set at the sample means.

The main-effect model in table 3 indicates a protective effect of 9R/9R relative to the large majority in the Any10R genotype. Part A of figure 1 suggests that the protective effect depends on %had sex by 16. The effect diminishes as the proportion increases. The protective effect disappears completely as the proportion approaches 0.50; 0.41 is the average proportion in the sample (table 1).

The interpretation could also focus on the effect of the prevailing sexual practice in school. Part A of figure 1 confirms the positive relationship between number of sexual partners and %had sex by 16. The relationship seems to hold for both genotypes; however, the effect of the prevailing sexual practice in school is much larger on the 9R/9R genotype than on the Any10R genotype. Roughly, when %had sex by 16 increases from 0.3 to 0.5, the predicted number of partners for 9R/9R increases from 1.5 to 5, while the predicted number of partners for Any10R only increases from 4.5 to 5.5.

Although the social normative explanation is supported, its significance is difficult to evaluate. Several authors (Furstenberg et al. 1987; Lauritsen 1994) point out that the apparent normative differences may merely reflect the differences in the underlying social structure. To control for differences in social structural conditions, we have included in all models variables for family structure and parental education at the individual level and prevalence of poverty and number of church adherents per capita at the contextual level. A normative explanation persists after these social structural measures are controlled for.

Four decades of data in multiple national studies show continuing long-term trends in the United States toward increased acceptance of premarital sex and unmarried cohabitation (Thornton and Young-DeMarco 2001). Udry (1996) reasons that in contemporary industrial societies, individual behavior is increasingly more influenced by biological differences reflecting inherent behavioral predispositions and less influenced by societal pressures to conform. Our empirical data provide evidence for this reasoning, but also point to a more complicated picture. The relative importance of biology and environment may be a function of genotype.

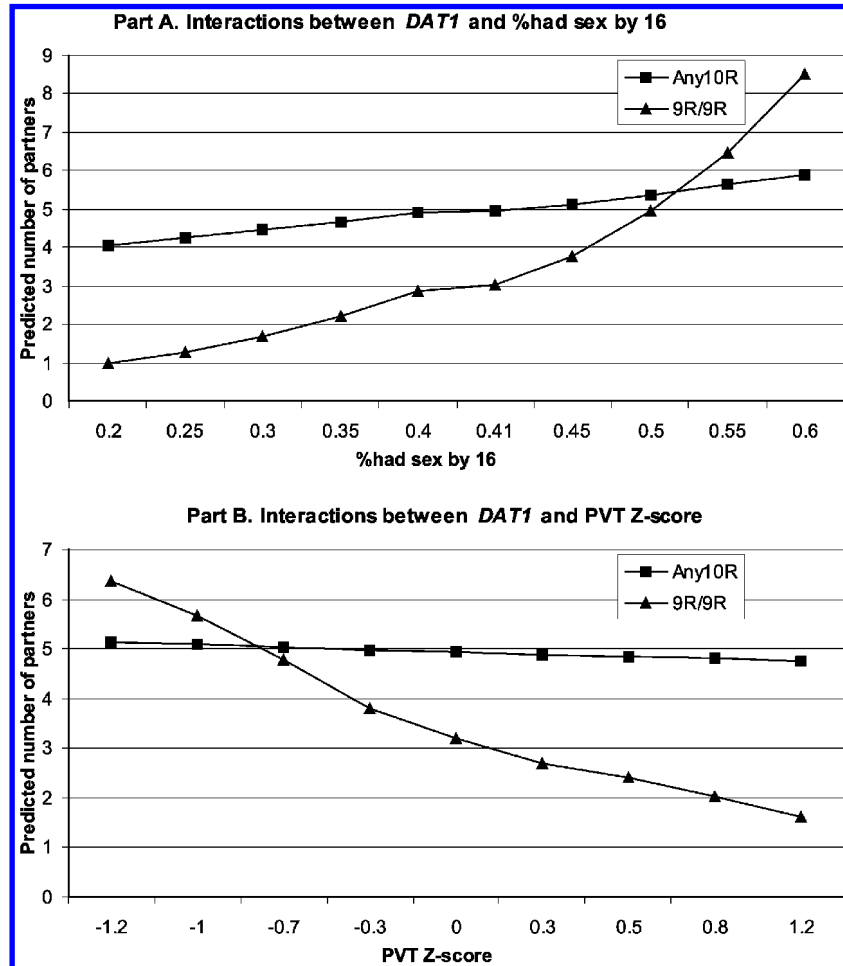


FIG. 1.—Interpretations of gene-environment interactions for number of sexual partners, for results in table 4.

The Any10Rs that account for 94% of the sample are only slightly affected by social pressure, while the behavior of the 9R/9Rs varies dramatically as social pressure shifts (fig. 1, pt. A).

Part B of figure 1 describes the interaction between genotype and cognitive ability. The protective effect of 9R/9R is, again, conditional on another factor: cognitive ability. The protective effect of 9R/9R tends to hold at the medium-range or high levels of cognitive ability. At low levels of cognitive ability, the protective effect of 9R/9R is not observed.

It is interesting to note that while cognitive ability is not significantly

related to number of partners in the main-effect model in table 3, both the main effect of cognitive ability and its interaction with Any10R turn significant in the interaction model in table 4. This apparent paradox can be explained by the interaction described in figure 1, part B, which shows that the protective effect of high cognitive ability only holds among those with the 9R/9R genotype. The protective effect is not present among the Any10Rs. In this case, the gene-environment interaction analysis has unveiled an underlying story that is invisible when the relationship between cognitive ability and number of partners is examined without considering genotype.

The gene-environment interaction involving cognitive ability seems to be a case of low intelligence trumping genetics. The behaviorally conservative 9R/9R genotype may be generally more averse to risks and more concerned about the consequences of unwanted pregnancy and STDs than the Any10R genotype. But those 9R/9Rs with lower cognitive ability may miscalculate and especially underestimate the risks involved, thus reducing or eliminating the protective genotype effect. However, if cognitive ability is subject to important genetic influences, the *DAT1* by cognitive ability interaction would be partially a gene-gene interaction.

Study participants who consider themselves more physically mature report a higher number of partners; however, the proportional increase for the 9R/9R genotype is larger (1.4 times more) than for the Any10R genotype (0.35 times more).

The gene-environment interaction results beg the more general question of why social contextual and individual effects tend to be larger for the 9R/9R genotype than the Any10R genotype. This pattern is observed in the interaction analysis involving both prevailing sexual practice in school and cognitive ability. Are social contextual effects generally larger for the more behaviorally conservative genotype? This can be tested explicitly for other genes and other risky behaviors. If the hypothesis is supported empirically, the next question is, Are individuals who are less risk-prone more likely to conform to social pressure and more easily shaped by other individual characteristics than the average crowd?

We hope that our most significant and lasting contribution will be the introduction of the approach of genetics-informed sociology—a contribution that goes beyond the case of male sexual behavior. The approach advocates capitalizing on genetic information in a study of sociological influences. Individuals with dissimilar genetic predispositions may be more or less sensitive to the same social influence. Understanding a social influence may depend upon understanding genetic heritage.

There are a number of specific ways a sociological analysis may benefit from genetic information. Caspi et al. (2002) show that the riskier genotype in the *MAOA* gene is not sufficient to lead to antisocial behavior. It is the

combination of both the riskier genotype and abuse in childhood that gives rise to antisocial behavior.

The results from table 3 have lent support for the influence of social contexts. When a gene-environment interaction is allowed, however, the story becomes more complicated. The interaction that involves %had sex by 16 suggests that the protective effect of 9R/9R tends to be lost in schools in which higher proportions of students start having sex early. The interaction that includes cognitive ability exhibits a protective effect of 9R/9R that tends to be present at higher levels of cognitive ability. The protective effect of cognitive ability is only visible in the interaction analysis in which the *DAT1* variant is allowed to interact with the effect of cognitive ability. If we had ignored genetic information, the protective effect of cognitive ability would have gone undetected.

Genetics-informed sociological analysis has ramifications for theory building. For certain human traits and behaviors, the “one size” of a single social theory may not fit all. Explaining a trait or behavior may require a theory that accommodates the complex interplay between socioeconomic-cultural influences and individual genetic predispositions.

False positive findings are a huge concern in the genetics community. Evidence that links genetic variants and human phenotypes typically needs to be replicated multiple times to be considered particularly convincing. Thus far, geneticists have been primarily interested in the main effects of genes. Sociologists are structurally or intrinsically more interested in gene-environment interactions than main effects. Interaction results are considerably more difficult to estimate than main effects. A low statistical power is almost always an issue. Even when the sample is reasonably large, a key category could be small. Thus, the first waves of genetic results based on sociological data must be viewed with caution. The experience in the genetics community shows that multiple replication is an essential step for reducing false positive findings. The results presented in this article are based on about 1/6 of the Add Health sample. We are planning a replication of our current results when the DNA data and the related genotyping for the entire Add Health sample ($N \approx 15,000$) become available.

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