

**Social Context, Genes, and Number of Sexual Partners
Among Male Youth**

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ABSTRACT

Over 20 years of research has repeatedly noted that sociological models are generally less predictive of black male sexual behavior than their white counterparts'. None of the prevailing sociological theories (social control, strain, and cultural norm) seems to be able to explain the empirical puzzle. In this article, we describe an analysis of interaction between the *DAT1* gene and socioeconomic-cultural factors (SCF). By introducing the 40-bp variable number of tandem repeats (VNTR) in the dopamine transporter gene (*DAT1*) in the DNA samples collected from about 900 black and white individuals in the National Longitudinal Study of Adolescent Health, we have made important contributions to the understanding of the sociological puzzle. The gene by SCF interaction analysis has revealed a rich set of socioeconomic-cultural predictors of number of sex partners at both individual and contextual levels, particularly for African American males. These SCF findings are only visible in the gene-SCF interaction analysis in which the SCF effects are allowed to be moderated by the *DAT1* genetic variants. Our empirical analysis has lent support for all three theoretical perspectives: social control, strain, and norm theories. None of the three theories is dominant. Social control is important for both black and white males, but particularly important for white males. Strain seems to be confined to African American males. Contrary to general expectation, the cultural norm explanation is only supported in the white male sample and not in the black male sample.

INTRODUCTION

The number of sexual partners is an important indicator of the risk of contracting a sexually transmitted disease (STD), including HIV (Kost and Forrest 1992; Cates and Stone 1992). In the United States, STDs disproportionately affect youth. Of the estimated 12 million new STD infections that occur each year in the United States, three million occur among people younger than 20, and another four million occur among those aged 20-25 (Kassler and Cates 1992). Adolescents are more susceptible to STDs than adults because they have a higher probability of having multiple sexual partners (Institute of Medicine 1997). STDs also disproportionately affect different ethnic groups. Recent data from the National Longitudinal Study of Adolescent Health (Add Health) indicate that more than 20 percent of African Americans have a STD compared to three percent of whites and eight percent of Hispanics (Brückner and Bearman 2005).

Over 20 years of research has repeatedly noted that sociological models are generally less predictive of African American, especially African American male sexual behavior than their white, Hispanic, and Asian counterparts'. The relationship between religiosity and sexual behavior tends to be considerably weaker among African American youth than among whites (Benson, Donahue, and Erickson 1989). Social control theory, strain theory, and cultural theory are three main theoretical perspectives upon which sociologists have relied in the studies of sexual behavior in adolescence and young adulthood.

In this study, we investigated whether introducing a genetic variant in the analysis of risky sexual behavior would give us some fresh leverage for cracking the empirical puzzle and breaking the theoretical doldrums. The data source employed is the DNA sample of about 900 black and white males in the National Longitudinal Study of Adolescent Health

(Add Health). The genetic variant, the 40-bp variable number of tandem repeats¹ (VNTR) in the dopamine transporter gene (*DAT1*) has been shown to be associated with self-reported number of sexual partners among the male Add Health participants. Our analysis focused on how a sociological model explains the within- rather than between-ethnicity variations in number of sexual partners. The genotypic information was not used to form a competing biological model. Rather, the information was used to advance our sociological understanding of sexual behavior. Our analysis on the interactions between *DAT1* and socioeconomic-cultural factors (SCF) has gained important insights into the empirical and theoretical understanding of sexual partnering, especially in the case of African American males.

BACKGRUND

Sociological Theory on Sexual Behaviors

Social control theory, strain theory, and cultural theory are three main theoretical perspectives upon sociologists have relied in the studies of sexual behavior in adolescence and young adulthood. Each theory has different prediction. As the descriptor suggests, a cultural perspective emphasizes within-group norms as primary influences of sexual behavior. Consequently, SCF including religiosity (at both individual and contextual levels) and family structure are expected to be unrelated or weakly related to number of sexual partners. Within social control and strain perspectives, however, SES measures are expected

¹ Variable number of tandem repeats, 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 DNA sequence 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, and SNPs are classes of DNA polymorphisms.

to be important predictors of sexual decisions. But the direction of the prediction differs between the two theories. Social control theory expects individuals to behave in step with the traditional preferences of social institutions such as the church and the family. It predicts that individuals who attend church frequently and who live in an intact family and/or a more religious community have fewer sexual partners. This prediction should hold for both white and black participants under social control theory. The prediction of strain theory, in contrast, would depend on the individual's position in a social hierarchy. For instance, its predictions for the white individuals are similar to those by social control theory. But for black individuals who are generally occupying a lower position in a social ladder, hence the strain, social control would be much less effective or non-effective.

The choice of socioeconomic-cultural measures that were included in regression analysis was guided by the three sociological theories. For social control theory, we examined the effects of family structure, individual-level religiosity, and religion at the contextual level; for strain theory, we investigated the effects of socio-structural factors such as ethnicity, level of education, and contextual-level poverty and education; for cultural norm theory, we tested the effect of prevailing sexual practices in schools.

Genes and Risky Sexual Behavior

Molecular Genetics and their Potential Usefulness for Sociologists. 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 alleles² of a single gene (Risch 2000; Botstein and Risch 2003). Examples of such human outcomes include Huntington's disease, cystic fibrosis, hereditary non-polyposis colon cancer, and

² Different forms (different DNA sequence) of a gene are called alleles which 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.

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, environmental factors, and the interactions between the two. In addition to contributing to work that focuses on genetic influences, sociologists may also be interested in incorporating advances in molecular genetics into sociological thinking. Genes may be an important component of human outcomes that interest social scientists. Taking genetic heritage into account promises an improved understanding of social outcomes and the roles of social context.

The Dopamine Transporter Gene and Number of Sexual Partners. The neurotransmitter³ dopamine has been shown to facilitate male sexual activity in all investigated species including rodents and humans (Dominguez and Hull 2005). Melis and Argiolas (1995)' findings suggest a major role for dopaminergic receptors in both the preparatory and consummatory phase of male sexual behavior; but their role in female sexual behavior is less conclusive.

Though the specific functions that dopamine plays are not entirely understood, evidence has been cumulating 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*⁴ release of dopamine in the nucleus accumbens (Kalivas 2002). *DAT1* is thus an important component for the maintenance of normal dopaminergic neurotransmission.

³ Neurotransmitters are chemicals that allow the movement of information from one neuron across the gap between it and the adjacent neuron.

⁴ *In vitro*, within glass in Latin, is an experimental method where the experiment is performed in a test tube, or outside a living organism or cell.

Vandenbergh et al. (1992) identified a polymorphic 40 bp variable number of tandem repeats (VNTR) in the transcribed portion of the *DAT1* gene which is most commonly observed repeat 9 (*DAT1**9R) to 10 times (*DAT1**10R). One study found that human subjects homozygous for the 10R allele exhibited significantly lower dopamine transporter binding than carriers of the 9R allele (Jacobson et al 2000) although the findings from another study are inconsistent (Heize et al 2000). A number of studies have demonstrated an association between the 10R allele and attention deficit hyperactivity disorder (ADHD) (Cook et al 1995, Daly et al 1999, Gill et al 1997, Waldman et al. 1998, Cornish et al 2005). The *DAT1**9R allele was reported to be associated with both a lower score in novelty seeking and a greater success in smoking cessation (Sabol et al 1999). Although no study seems to have focused on the *DAT1* variants and number of sexual partners, the link is plausible because of the central role of dopamine in motor activity and reward-seeking behavior.

Gene by SCF Interactions. 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 et al. 1977; Kendler 2001; Hunter 2005). In this study, we tested whether genetic variants in *DAT1* moderate the effects of social control, social strain, or cultural norms. For example, social controls in the form of religiosity may protect against risky sexual behavior only for certain genotypes and not for others. Such a protective effect can only be revealed when an analysis of gene-religiosity interaction is carried out.

METHODS AND DATA

The data source for our analysis is the sibling sub-sample of about 900 black and white participants in the National Longitudinal Study of Adolescent Health (Add Health), a nationally representative sample of more than 20,000 adolescents in grades 7-12 in 1994-5 in the United States (Harris et al. 2003). Our dependent variable is number of sexual partners. In

2002 third wave data collection, DNA data were collected for genetic variables. A 40 bp Variable Number Tandem Repeat (VNTR) polymorphism in the 3' untranslated region of the DAT1 gene has been genotyped with a modified method of Vandenberg et al (1992). This VNTR ranges from 3 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 21% and 76% of all alleles, respectively. Our analysis used only individuals with genotypes⁵ of one 10R, two 10Rs, and two 9Rs. The individuals with other genotypes (about 2%) are excluded from the analysis.

Socioeconomic-Cultural Measures we used include church attendance, family structure, marriage/cohabitation parental education. Our analysis included four measures at the contextual level: poverty at the neighborhood level, % college degree of residents aged 25 or older at neighborhood, church adherents/capita represents the percent of church adherents in the county, and % had sex by 16 stands for the percent of students having had sexual intercourse by age 16 in the school.

We carried out the analysis of gene-SCF interactions separately for white and black samples. Our main statistical tool was a Poisson regression model since number of sexual partners is a count variable.

RESULTS AND CONCLUSIONS

In this paper, we discovered that a number of SCF measures (2 biological parents, religious service attendance, proportion holding a college degree in neighborhood, and church adherents in county), once interacting with a *DAT1* polymorphism, are significantly related to number of sexual partners in the black male sample. In contrast, only one SCF measure

⁵ 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 it refers to what combination of alleles the individual carries.

(proportion had sex by 16 in school) was found to interact with the *DATI* genotype for number of sex partners in the white male sample. All the five SCF measures have a considerably larger effect on number of sex partners for the 9R/9R genotype than for the Any10R genotype. Without the interaction analysis or examining the effects of the SCF measures by genotype, these SCF effects would be masked.

Our empirical findings have a number of important theoretical implications and may help break the theoretical doldrums in the area of research on sexual behavior. All three theoretical perspectives found some support in the empirical findings. The frequency of religious service church attendance has a strong social control effect and this effect is much more prominent for the 9R/9R genotype than for the Any10R genotype. Our gene-SNF interaction analysis has unveiled an underlying story that is invisible when the relationship between religious service attendance and number of partner report is examined for African American male youth without considering genotype.

The normative explanation seems to be supported by the result related to ‘proportion in school had sex by 16’ in the white male sample. Individuals in a school with a higher proportion having sex by 16 reported substantially higher number of sex partners than those in a school with a lower proportion. The effect is about twice as large for the 9R/9R genotype than for the Any10R genotype. We obtained the finding on the normative explanation after these social structural measures were controlled for. In our analysis, it is in the white rather than black sample that the evidence for a normative explanation emerges.

Neither social control nor the norm theory can explain three of the five gene-SCF interaction terms we discovered. Two biological parents, proportion holding a college degree in neighborhood, and number of church adherents/capita all have a larger effect for 9R/9R than Any10R; however, the directions of the effects of these social control measures for 9R/9R are opposite to the predictions of the social control theory. Apparently, the three

socioeconomic-cultural factors are ‘anomalously’ associated with higher numbers of reported sex partners.

An explanation has been put forward that the congregations actually function as “structured opportunities” to meet and acquire sexual partners, especially for males (Browning and Olinger-Wilbon 2003). Alternatively, we propose to interpret these anomalous results using (1) the classic strain theory and (2) the characteristics of African American marriage market. The strain theory we applied to our analysis is somewhat more general than the one typically described in sociological literature (e.g. Gottfredson and Hirschi 1990). Strain theory is often used to explain the illegal behavior of those who share the universal aspiration for material success, but who, because of social stratification, discard legitimate means and resort to illegitimate means. The strain is created because of the disjuncture between the culturally shared goals and the structured inability to reach the goals.

To summarize, by introducing measures of genetic variants, we have made important contribution to the understanding of the sociological puzzle of male sexual behavior empirically and theoretically. The gene by SCF interaction analysis has revealed a rich set of socioeconomic-normative predictors of number of sex partners at both individual and contextual levels, particularly for African American males. These SCF findings are only visible in the interaction analysis in which the SCF effects are allowed to be moderated by the *DAT1* genetic variants.

Our empirical analysis has lent support for all three theoretical perspectives: the social control, strain, and norm theories. None of the three theories is dominant. Social control is important for both black and white males, but particularly important for white males. Strain seems to be confined to African American males. Contrary to expectation, norm theory is only supported in the white male sample rather than the black male sample.

Our findings beg the question why socioeconomic-cultural effects tend to be larger for the 9R/9R genotype than the Any10R genotype. This is observed in all five significant interaction terms and for both blacks and whites. We know that the Any10R genotype reports higher numbers of sex partners than the 9R/9R genotype. Combining these results suggests that socioeconomic-cultural effects are larger for the more behaviorally ‘conservative’ genotype. These behavioral conservatives may have more room to be malleable than the genetically more radical type. This reasoning can be tested as a hypothesis for other genes and other risky behaviors.

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Table 1. Descriptive statistics: Mean (standard deviation)

	Mean	S.D	Mean	S.D	Mean	S.D
	W+B male		White male		Black male	
Allele Proportion						
10R (480)	0.753		0.741		0.791	
Genotype Proportion						
Any 10R (480)	0.944	0.230	0.942	0.234	0.950	0.219
Ethnicity/age						
White	0.772	0.420				
Black	0.228	0.420				
Age (18-20)	21.42		19.73		27.14	
Age (21-23)	57.04		58.61		51.76	
Age (24-26)	21.53		21.66		21.11	
2 bio parents/parent education						
2 biological parents	0.612	0.488	0.682	0.466	0.372	0.485
High school	0.293	0.456	0.279	0.449	0.342	0.475
< high school	0.050	0.219	0.034	0.182	0.106	0.308
Some college	0.210	0.407	0.211	0.408	0.206	0.405
≥ college	0.405	0.491	0.445	0.497	0.271	0.446
Missing on education	0.041	0.199	0.031	0.174	0.075	0.265
Marriage/Cohabitation						
Single	0.584	0.493	0.580	0.494	0.598	0.492
Cohabited and married	0.071	0.257	0.077	0.267	0.050	0.219
Married, not cohabited	0.061	0.239	0.071	0.257	0.025	0.157
Cohabited, not married	0.279	0.449	0.267	0.443	0.322	0.468
Church Attendance						
Weekly or more	0.168	0.374	0.147	0.354	0.241	0.429
Contextual characteristics						
Poverty: < 11.6 %	0.557	0.497	0.636	0.481	0.286	0.453
Poverty: 11.6%-23.9%	0.204	0.403	0.208	0.406	0.191	0.394
Poverty: ≥ 23.9 %	0.176	0.381	0.091	0.287	0.467	0.500
Missing on poverty	0.063	0.243	0.065	0.247	0.055	0.229
% College degree	0.224	0.146	0.237	0.149	0.178	0.126
Church adherents/capita	55.9	14.7	54.4	14.3	61.0	14.9
% had sex by 16	42.4	11.0	41.0	11.2	46.8	8.8
No. of Persons	882		676		199	

Table 2. GEE Poisson models of number of sexual partners: Interactions between socioeconomic-cultural factors and dopamine transporter – Add Health Wave III White males

	2 bio parents	Church attendance	% college Degree	Church adherents/capita	% had sex by 16
	e^{β} (P-value)	e^{β} (P-value)	e^{β} (P-value)	e^{β} (P-value)	e^{β} (P-value)
Intercept	2.43(0.124)	2.47(0.046)*	2.87(0.114)	2.37(0.304)	0.36(0.239)
Dopamine transporter					
Any 10R	1.57(0.346)	1.55(0.079)+	1.33(0.621)	1.61(0.551)	11.34(0.003)**
Age group					
Age (24-26)	---	---	---	---	---
Age (18-20)	0.64(0.011)*	0.64(0.010)*	0.64(0.011)*	0.64(0.011)*	0.64(0.010)*
Age (21-23)	0.86(0.310)	0.86(0.303)	0.86(0.316)	0.86(0.310)	0.87(0.329)
2 bio /parent education					
2 biological parents	0.94(0.896)	0.97(0.797)	0.97(0.800)	0.97(0.795)	0.97(0.803)
High school	---	---	---	---	---
< high school	1.15(0.647)	1.14(0.659)	1.15(0.649)	1.15(0.648)	1.14(0.660)
Some college	1.15(0.404)	1.15(0.416)	1.16(0.399)	1.15(0.404)	1.15(0.417)
>=college	1.13(0.429)	1.13(0.432)	1.13(0.429)	1.13(0.428)	1.12(0.441)
Missing on education	1.32(0.353)	1.31(0.357)	1.32(0.351)	1.32(0.353)	1.31(0.357)
Marriage/Cohabitation					
Single	---	---	---	---	---
Cohabited and married	1.46(0.029)*	1.46(0.029)*	1.47(0.027)*	1.46(0.029)*	1.47(0.026)*
Married, not Cohabited	0.91(0.609)	0.91(0.601)	0.91(0.619)	0.91(0.602)	0.91(0.624)
Cohabited, not married	1.58(0.000)***	1.58(0.000)***	1.59(0.000)***	1.58(0.000)***	1.59(0.000)***
Church Attendance					
Weekly or more	0.41(<.0001)***	0.26(0.018)*	0.41(<.0001)***	0.41(<.0001)***	0.41(<.0001)***
Contextual Characteristics					
Poverty: < 11.6 %	---	---	---	---	---
Poverty: 11.6%-23.9%	0.79(0.089)+	0.79(0.090)+	0.79(0.092)+	0.79(0.090)+	0.80(0.095)+
Poverty: >=23.9	1.04(0.856)	1.04(0.842)	1.04(0.846)	1.04(0.856)	1.06(0.770)
Poverty: Missing	0.96(0.818)	0.96(0.813)	0.96(0.820)	0.96(0.819)	0.97(0.847)
% College degree	0.95(0.903)	0.96(0.906)	0.45(0.626)	0.95(0.902)	0.97(0.940)
Church adherents/capita	0.99(0.518)	0.99(0.520)	0.99(0.514)	0.99(0.826)	0.99(0.516)
% Had sex by 16	1.01(0.011)*	1.01(0.011)*	1.01(0.011)*	1.01(0.011)*	1.06(0.002)**
Any10R ×					
2 biological parents	1.03(0.949)				
Church attendance		1.57(0.439)			
% college degree			2.17(0.647)		
Church adherents/capita				0.986(0.991)	
% had sex by 16					0.95(0.014)*
Number of persons	674	674	674	674	674

+ : significant at 0.10; * : 0.05; ** : 0.01; *** : 0.001.

Table 3. GEE Poisson models of number of sexual partners: Interactions between socioeconomic-cultural factors and dopamine transporter – Add Health Wave III Black males

	2 bio parents	Church attendance	% College degree	Church adherents/capita	% had sex by 16
	e^{β} (P-value)	e^{β} (P-value)	e^{β} (P-value)	e^{β} (P-value)	e^{β} (P-value)
Intercept	4.43(0.081)+	11.52(0.005)**	5.39(0.062)+	0.32(0.533)	58.58(0.053)+
Dopamine transporter					
Any 10R	4.36(0.001)***	1.58(0.194)	3.84(0.013)*	63.77(0.029)*	0.31(0.534)
Age group					
Age (24-26)					
Age (18-20)	0.49(0.004)**	0.47(0.002)**	0.48(0.003)**	0.49*0.004)**	0.48(0.003)**
Age (21-23)	0.67(0.059)*	0.66(0.052)+	0.67(0.059)+	0.67(0.065)*	0.67(0.058)+
2 bio /parent education					
2 biological parents	3.76(0.030)*	0.98(0.934)	0.98(0.909)	0.96(0.855)	0.98(0.927)
High school					
< high school	0.89(0.667)	0.88(0.648)	0.88(0.638)	0.88(0.648)	0.88(0.651)
Some college	1.40(0.138)	1.42(0.119)	1.39(0.140)	1.38(0.155)	1.42(0.126)
>=college	0.92(0.709)	0.91(0.675)	0.90(0.655)	0.91(0.675)	0.91(0.685)
Missing on education	0.93(0.816)	0.91(0.742)	0.91(0.744)	0.93(0.793)	0.92(0.783)
Marriage/Cohabitation					
Single					
Cohabited and married	0.87(0.648)	0.91(0.737)	0.93(0.800)	0.87(0.653)	0.93(0.806)
Married, not cohabited	0.47(0.167)	0.48(0.174)	0.48(0.173)	0.48(0.171)	0.49(0.179)
Cohabited, not married	1.30(0.137)	1.304(0.134)	1.28(0.167)	1.29(0.151)	1.31(0.125)
Church Attendance					
Weekly or more	0.70(0.127)	0.07(<.0001)***	0.69(0.110)	0.70(0.121)	0.69(0.112)
Contextual Characteristics					
Poverty: < 11.6 %					
Poverty: 11.6%-23.9%	0.49(0.004)**	0.50(0.005)**	0.51(0.006)**	0.50(0.005)**	0.51(0.005)**
Poverty: >=23.9	0.56(0.022)*	0.59(0.030)*	0.57(0.023)*	0.56(0.022)*	0.58(0.027)*
Poverty: Missing	0.51(0.050)*	0.52(0.058)+	0.52(0.057)+	0.52(0.054)+	0.52(0.056)+
% College degree	0.76(0.739)	0.88(0.877)	7.99(0.027)*	0.70(0.663)	0.84(0.823)
Church adherents/capita	0.99(0.812)	0.99(0.872)	0.99(0.766)	1.06(0.047)*	0.99(0.861)
% Had sex by 16	1.00(0.868)	1.00(0.898)	1.00(0.907)	1.00(0.909)	0.97(0.340)
Any10R ×					
2 biological parents	0.25(0.037)*				
Church attendance		10.16(<.0001)***			
% college degree			0.08(0.014)*		
Church adherents/capita				0.95(0.045)*	
% had sex by 16					1.04(0.314)
Number of persons	199	199	199	199	199

+: significant at 0.10; *: 0.05; **: 0.01; ***: 0.001.