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The influence of three genes on whether adolescents use contraception, United States 1994-2002

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Abstract

In a further contribution to recent investigations of the relevance of genetic processes for demographic outcomes, we investigate genetic associations with whether adolescents use contraception. Using data from the National Longitudinal Study of Adolescent Health, we find that variants in the dopamine transporter gene DAT1, the dopamine receptor gene DRD2, and the monoamine oxidase gene MAOA are associated with unprotected sexual intercourse. Consistent with previous analyses of these data, the genotypes DRD2*A1/A2, DRD2*A2/A2, DAT1*9R/10R, and MAOA*2R/ are associated with higher odds of unprotected sexual intercourse than other genotypes at these loci. The DRD2 associations apply to both men and women, whereas the other associations apply to women only. These results are robust to controls for population stratification by continental ancestry, do not vary by contraceptive type, and are consistent with previous research showing that these genetic variants are associated with higher rates of impulsivity.

Keywords

adolescents; contraception; genetics; DRD2; DAT1; MAOA

Introduction

A number of health processes of interest to demographers have been linked to genetic variants involved in the regulation of neurotransmitters in the human brain. For instance, an analysis of data on adolescents in the United States demonstrated that timing of first sexual intercourse is associated with variation in the DRD4 gene in all races and ethnicities (Guo and Tong 2006). Similarly, research has linked variations in mental health (Caspi et al. 2002) and health behaviors (e.g., Salamone 1994) to different genetic variants that regulate neurotransmitter function. These findings illustrate the potential for genetic influences on a wide range of demographic processes.

To contribute to this line of research we investigated the association of genes regulating the experience of psychological reward—the dopamine transporter gene *DAT1*, the dopamine receptor gene *DRD2*, and the monoamine oxidase gene *MAOA*— with whether adolescents used a contraceptive when they last engaged in sexual intercourse. We concluded that variation in these genes was associated with large differences in the odds of reporting unprotected last coitus. We further concluded that these associations were not limited to particular contraceptive types, and were not mere artifacts of the differential frequency of genetic variants by ancestral group.

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Because many readers of this Journal may be unfamiliar with some of the genetic and biological concepts discussed in the paper, we provide an appendix that contains definitions of those genetic terms we have used that seem least likely to be familiar. Additionally, many terms are briefly clarified parenthetically in the text the first time they are used. For those interested in learning more about the use of genetic data and concepts in social science research, we refer the reader to the large number of recent special issues of journals on the subject (e.g., Guo 2006, 2008; Bearman 2008; Blum 2010).

Previous studies on contraceptive use

In spite of recent declines, teenage childbearing is still more prevalent in the United States than in most other developed countries. Twenty-two per cent of women have had a child before age 20 in the United States, whereas the figure is only 15 per cent in Great Britain, 11 per cent in Canada, 6 per cent in France, and 4 per cent in Sweden (Singh and Darroch 2000; Singh et al. 2001). The large majority of early pregnancies and births are unintended (Henshaw 1998; Abma et al. 2004) and most births to adolescent mothers take place outside marriage (Franzetta et al. 2006).

Among teens and young adults, unintended pregnancies are the result of either unprotected sexual intercourse or contraceptive failure (Brown and Eisenberg 1995; Glei 1999), and the former is by far the strongest risk factor. Those who forgo contraceptives are significantly more likely to become pregnant than those who sometimes or always use contraceptives. Adolescents in the United States initiate sexual intercourse at about the same age as adolescents in most other developed countries, but US adolescents are less likely to use contraceptives. Twenty-five and twenty per cent of women in the US report unprotected first and most recent coitus, respectively (Singh et al. 2001). In contrast, the corresponding figures are 11 and 12 per cent for France, 21 and 4 per cent for Great Britain, and 22 and 7 per cent for Sweden.

Unintended pregnancies can have serious consequences, perhaps forcing adolescents and young adults into unwanted marriages, limiting their educational and career opportunities, and sometimes predisposing them to long-term dependence on the support of welfare agencies. Differential rates of unintended pregnancy among racial and ethnic minorities contribute to disparities in socioeconomic and health prospects of both parents and children. These and other consequences of unintended pregnancies point to a compelling need for research on the full range of factors that influence contraceptive use.

Previous studies have demonstrated the importance of a number of factors that influence contraceptive use at the family, individual, and partner level. Adolescents aged 15-17 report lower rates of use than older youths (Glei 1999). Racial and ethnic minorities, especially Hispanics, on average report lower levels of use (Ford et al. 2001). Higher levels of parents' education and living with two biological parents predict a higher likelihood of use (Manning et al. 2000). Frequency of church attendance is shown to be associated with timing of first sexual intercourse, but not necessarily with contraceptive use (Manlove et al. 2006). Knowledge of contraception, the way it is perceived, and relevant attitudes are shown to be important predictors of use (Schuster et al. 1998; Ryan et al. 2007), while Manlove et al. (2004) show that many relationship characteristics and partner attributes are significantly related to females', but not to males', contraceptive use. Psychological factors will also be relevant since the opportunity for coitus sometimes occurs unexpectedly, and individuals may have to decide whether to proceed with it in the absence of an effective contraceptive option. Finally, consistent contraceptive availability is required for consistent contraceptive use (e.g., Longmore et al. 2003).

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Genetic propensities for non-use of contraception

In addition to demonstrating the importance of individual, family, and partner influences on contraceptive use, Manlove et al. (2004) observe that its use or non-use by the individual is relatively stable over time, and suggest that this is due to unmeasured propensities of the individual. In this and following sections, we outline why genetic variation in individual propensities could plausibly contribute to the explanation of whether contraception is used. Although no previous study has attempted to link genetic variants to contraceptive use, available evidence suggests that links between contraceptive behavior and the *DAT1, DRD2* and *MAOA* genes are plausible.

While it has long been clear that no gene controls behavior directly, certain genes do affect behavior via neurotransmitters in the brain such as dopamine and serotonin. Neurotransmitters function by transmitting signals across the synapse (connection) between brain cells. Biochemical work suggests that neurotransmitters are involved in the regulation of 'pleasure' behaviors such as sexual intercourse, substance abuse (especially alcohol consumption), binge eating, novelty seeking, and risk taking (Salamone 1994). These neurotransmitters may affect behaviour by modulating its psychological rewards (Blum et al. 1996). Because neurotransmitters regulate the experience of pleasure, genes such as *DAT1, DRD2*, and *MAOA,* which influence neurotransmitter function, they are potentially important in the explanation of patterns of pleasurable behaviors such as coitus.

A key concept in this connection is impulsivity. Impulsivity is often measured using the 'delay discounting task', which assesses an individual's preference for a lesser reward with a nearer time horizon over a larger reward later in time (Ainslie 1975; Eisenberg et al. 2007a). The involvement of neurotransmitters in impulsivity has been demonstrated in animal models (Cardinal et al. 2001; Isles et al. 2004; van Gaalen et al. 2006; Winstanley et al. 2006), and is supported by neuroimaging studies in humans (McClure et al. 2004). Impulsivity could plausibly influence contraceptive behaviour in number of ways. For instance, it could influence the frequency of coitus and the type of relationship in which it occurs, which are associated with contraceptive use patterns. Impulsivity could also influence the odds of use contraception in any relationship context. More immediately, it could influence the likelihood of a person keeping contraceptives available and of forgoing sexual intercourse if they were not available.

To summarize, neurotransmitter function appears to influence impulsivity, which may plausibly influence the odds of using contraceptives during sexual intercourse. For these reasons we thought it likely that variation in genes regulating neurotransmitter function—such as *DAT1, DRD2*, and *MAOA*—would be associated with contraceptive use. As well as investigating this association, we investigated differentials in the association of these genes by contraceptive type, in the belief that contraceptive methods that were coitus-dependent might be more strongly related to processes governing impulsivity than those that were not.

Hypotheses

The DAT1 gene

Given current knowledge of the functioning of the dopamine transporter gene (*DAT1*) and previously published analyses using the National Longitudinal Study of Adolescent Health (Add Health) dataset, we expected that the *DAT1* gene would be related to contraceptive behaviour among adolescents in the United States. The *DAT1* gene codes for a dopamine transporter protein, which limits the level and duration of dopamine receptor activation (Bannon and Whitty 1995). The central importance of the dopamine transporter in controlling synaptic dopamine levels was established by a study that selectively disabled the *DAT1* gene in laboratory mice (Giros et al. 1996). Because dopamine and other

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neurotransmitters regulate reward and impulsivity and *DAT1* regulates their function, we predicted that variation in the functioning of this gene would influence contraceptive behavior.

Vandenbergh et al. (1992) first discovered the major alleles (variations) in *DAT1*, identifying a 40-base-pair (bp) repeat in the gene, which repeats serially, with the number of such repeated sequences varying between individuals. The most common variants in this gene repeat such a sequence 9 (*DAT1**9R) or 10 times (*DAT1**10R). Furthermore, the number of repeated sequences at this locus influences the biochemical functioning of the gene: the *DAT1**9R allele is associated with lower levels of dopamine transporter (DAT) in comparison to the 10R allele (Fuke et al. 2001; Fuke et al. 2005; VanNess et al. 2005).

This variability in biochemical functioning is behaviorally consequential. For instance, the *DAT1**10R allele is linked to 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) and the *DAT1**9R allele is associated with both a lower score in novelty seeking and a greater success in smoking cessation (Sabol et al. 1999). Similarly, previous research using the Add Health dataset supports the association of *DAT1* with risky behaviour. For instance, relative to the *DAT1**10R/10R and *DAT1**9R/10R genotypes, men with the *DAT1**9R/9R genotype scored considerably lower on scales measuring propensity for serious and violent delinquency (Guo et al. 2008c) and reported fewer sexual partners (Guo et al. 2008b). In short, the DAT1*9R allele seems to be associated with a broadly conservative pattern of behaviour. We therefore posed the following hypothesis:

> Hypothesis 1: individuals with the DAT1*9R/9R genotype are less likely to engage in unprotected sexual intercourse than individuals with the DAT1*10R/10R genotype or the DAT1*9R/10R genotype.

The DRD2 gene

We also expected that variations in the dopamine D2 receptor (*DRD2*) gene would be related to differences in adolescent contraceptive behavior. This gene regulates the functioning of dopamine receptors along brain synapses, and therefore potentially influences the effect of this pleasure-regulating neurotransmitter. To the extent that differences in the pleasurable effects of dopamine could influence a tendency to engage in potentially risky sexual behavior, functional variation in this gene could plausibly influence contraceptive use.

Civelli and colleagues were the first to clone a *DRD2* gene (Bunzow et al. 1988) and the first to describe variation in the structure of the gene. The two alleles at this locus (known as the TaqI polymorphism) are the result of variability in a single nucleotide in the gene, which takes the form of either a T or C nucleotide, resulting in two different alleles (known as A1 and A2). This is known as a single nucleotide polymorphism, or SNP. Although recent research has shown that the TaqI polymorphism is actually located in a neighboring gene known as the ankyrin repeat and kinase domain containing-1 (ANKK1) gene (Neville et al. 2004), this genetic variant is still believed to influence dopamine function (Laakso et al 2005).

Despite the obvious theoretical relevance of this gene for the regulation of neurotransmitter function, findings about the connection of *DRD2* to behavioral outcomes have been mixed.. For example, although some studies have linked *DRD2**A1 alleles to alcoholism (Noble 1998), others do not find this link (Gorwood et al. 2000). However, previous research using Add Health supports the connection of variation in this gene with risky behavioral outcomes. Compared with the *DRD2**A2/A2 and the *DRD2**A1/A1 genotypes, Guo et al.

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(2008c) found that males with the *DRD2**A1/A2 genotype reported significantly higher scores on scales measuring propensity for serious and violent delinquency. On the basis of these previous findings, we posed another hypothesis:

> Hypothesis 2: Individuals with the DRD2*A1/A2 genotype are more likely to engage in unprotected sexual intercourse than individuals with the DRD2*A1/A1 or DRD2*A2/A2 genotypes.

The MAOA gene

We also expected that differences in the monoamine oxidase A (*MAOA*) gene would be related to variability in contraceptive behavior. *MAOA* has long been a leading candidate gene for studying impulsive and aggressive behaviour in rodents and humans. The gene produces an enzyme (also named MAOA; we differentiate the two by italicizing the gene and not the enzyme) that catalyzes the oxidative deamination (breakdown) of a number of neurotransmitters in the brain, including dopamine. The functioning of this gene is best observed by the effect of its disablement. In a series of studies, Case et al. (1995) and Shih and Thompson (1999) developed mice with a targeted disruption of the *MAOA* gene, and observed an increase in the brain levels of dopamine, serotonin, and norepinephrine, as well as an increase in manifested aggression among the males. These results show that *MAOA*, by breaking down neurotransmitters in brain synapses, functions to regulate the level of these neurotransmitters, and therefore potentially to influence behaviour influenced by neurotransmitter function, such as contraceptive behaviour.

Sabol et al. (1998) first identified a 30-base-pair repeat in *MAOA*, which is known as a variable number tandem repeat (VNTR). Like the polymorphism for *DAT1*, this shows that humans vary in the number of repeated sequences of base observed in their DNA.

As with the *DAT1* gene, variability in the number of repeats in *MAOA* is biochemically consequential, affecting levels of neurotransmitter activity that may be associated with outcomes such as depression and impulsive aggressive behaviour (Brunner et al 1993). Among three of the repeats (2, 3, and 4) in the VNTR they analyzed, Caspi et al. (2002) showed that maltreated children with a 3-repeat allele were more likely to engage in violent behavior than maltreated children with a 4-repeat allele in the *MAOA* gene. Previous work using the Add Health dataset demonstrates that males with a VNTR 2-repeat (2R) in *MAOA* report a level of serious delinquency and violent delinquency in adolescence and young adulthood at least twice as high as those for participants with the other variants. In a biochemical functional analysis, the 2-repeat allele exhibited far levels of promoter activity than the other alleles (Guo et al. 2008a). In light of these findings we posed the following hypothesis:

> Hypothesis 3: individuals with the MAOA*2R genotype are more likely to be engage in unprotected sexual intercourse than those with the other MAOA genotypes.

Gene-sex interactions

We expected sex differences in the associations of genetic variants with contraceptive use for a number of reasons. First, the *MAOA* gene is on the sex-linked X chromosome, of which females possess two copies and males only one. Possession of two copies of the X chromosome increases the odds that, relative to males, females inherit a copy of the *MAOA**2R allele. Table 2 confirms this, showing that 3 per cent of females in the sample have copies of the *MAOA**2R allele whereas only 1 per cent of males do. However, although females are more likely to possess a copy of this allele, it is less likely to be expressed owing to X-inactivation, a process whereby women, who have two X

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chromosomes, randomly inactivate the genes on one of these chromosomes. This process could influence the effect of possession of a *MAOA**2R allele.

A second reason for expecting sex differences in the associations is that the potential consequences of unprotected sexual intercourse differ sharply for the two sexes. For females, unprotected sexual intercourse increases the probability of pregnancy, which may be followed by lengthy periods of child-bearing and child-rearing. In contrast, males may often experience no or fewer consequences of pregnancy. Thus, even if the two sexes are subject to the same genetic propensities for contraceptive use, the fact that females have greater disincentives for risky sexual behavior than males may moderate the effects of any genetic propensities.

Finally, males and females may also differ importantly in sexual behavior more generally. Males of most mammalian species show a stronger desire towards variety in sexual partners than do females. This phenomenon has been referred to as the 'Coolidge Effect' (Wilson et al. 1963; Bermant et al. 1968; Bermant 1976).

Although a sex difference in the effect of genes is likely, its total direction cannot be straightforwardly predicted. The effects of random inactivation, differential costs of childrearing, and differences in sexual behavior more broadly could modulate genetic effects in unpredictable and inseparable ways. In summary, genetic influences on contraceptive behavior may vary by sex owing to differences in the chromosomal structure of each sex as well as differences in broader patterns of sexual behavior and propensities. For these reasons, we analyzed genetic associations with contraceptive use separately by sex, formalized in the following hypothesis:

> Hypothesis 4: Genetic effects may vary by sex.

Variations by contraceptive type

It is possible that genetic effects on contraceptive behaviour varies by type of contraceptive. All contraceptive use requires a degree of planning and a desire to avoid undesired consequences of sexual behavior. However, certain types of contraceptive behavior may be differentially related to impulsivity. Specifically, the decision whether to use a condom can be an impulsive one since the decision is made immediately preceding coitus. In contrast, the decision to use most other modes of effective contraception is made separately from any particular occurrence of coitus. Although other contraceptive methods are coitus-dependent (such as the diaphragm), condom use is by far the most common coitus-dependent method in the Add Health dataset. For this reason and owing to the association of neurotransmitter function with impulsivity, condom use may be differentially related to the functioning of these genes compared with other types of contraceptive use. Therefore we posed the following hypothesis:

> Hypothesis 5: Genetic associations may vary by contraceptive type—specifically, between condom use and other contraceptive methods.

Samples

To test the hypotheses, we used data from the National Longitudinal Study of Adolescent Health (Add Health), which started as a nationally representative sample of more than 20,000 adolescents in grades 7-12 in 1994/5 in the United States (Harris et al. 2009). The respondents have since been followed by two additional in-home interviews in 1995/6 (Wave II) and 2002 (Wave III). Add Health is school-based and the adolescents are from 134 schools. The school sample was stratified by region, ethnic mix, size, urbanicity (urban/suburban/rural), and school type (public/private/parochial).

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A key feature of the Add Health sampling design was an oversample of the siblings of those selected to participate in the survey, known as the genetic subsample. In this subsample, all identified identical twins, fraternal twins, and half-siblings of initial survey respondents were recruited into the study, while a sample of full siblings were recruited when both members of a pair were sampled independently (see http://www.cpc.unc.edu/projects/addhealth/design/wave1/index.html#in-school-sampling-frame-1). Our analysis was based on the 2,574 individuals in the genetic subsample whose buccal (cheek) cell DNA was collected at Wave III in 2002. Our analytical dataset consisted of 2,167 individuals who had experienced sexual intercourse by Wave III and whose genetic and environmental data were available. We employed every wave-individual observation by which the individual in question had experienced sexual intercourse, such that each individual could potentially contribute three observations from Waves I-III of the dataset. Table 1 shows the distribution of the observations by Add Health wave and sex. The 2,167 individuals contributed 4,063 observations, with earlier waves contributing fewer observations since the proportion of the subsample with sexual intercourse experience grew with each additional wave. Of the total sample of 4,063 observations, females contributed 2,092 observations and males 1,971. The repeated measures of the same individual were analysed simultaneously with necessary statistical adjustments (described below).

Measures

In this section we discuss the survey and genetic measures used in our study. In the following sections we discuss and justify our measure of contraceptive use, describe how our genetic data were obtained and coded in our study, and briefly review the range of demographic, social, and behavioral controls we included in our models. These controls were employed to ensure that the genetic associations which were the focus of our analysis were not spurious. Descriptive statistics on all variables used in this analysis are provided in Table 2.

Contraceptive use

In order to connect our findings to the literature on the genetics of risky behavior, we set up our analysis in terms of the *non-use* rather than the more common *use* of contraception. Therefore, although our dependent variable was contraceptive use at last coitus, the category of this variable which we modelled was non-use. For linguistic convenience, we refer to this category as unprotected sexual intercourse (or coitus), by which we mean sexual intercourse in which no effective contraceptive method was used.

Contraceptive use is a sensitive subject and not amenable to direct observation. For this reason Add Health adopted audio-computer-assisted self-interview techniques, which have been showed to increase response rates and reduce biases when sensitive questions are involved (Turner et al. 1998; Des Jarlais et al. 1999; Newman et al. 2002).

Unprotected sexual intercourse at last coitus was measured by the answer to the following yes/no question at Waves I and II: ‘Did you or your partner use any method of birth control when you had sexual intercourse most recently?’ At Wave III, a slight variant of this question was used: ‘The most recent time you had vaginal intercourse, did you or your partner use some form of birth control?’ Respondents were deemed to have engaged in unprotected sexual intercourse if they did not use an effective contraceptive technique at last coitus. A subsequent question then asked respondents to list up to three contraceptive methods that were used at last coitus. We coded all those who reported using coitus interruptus (withdrawal) or the rhythm method as having engaged in unprotected sexual intercourse because these methods are not usually as effective as alternative methods such as

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the pill (e.g., Fu et al 1999). Finally, for some analyses we distinguished between use of condoms and use of other contraceptive methods.

Three measures of contraceptive use are commonly reported in the contraceptive literature: use at first intercourse, patterns of use over time, and use at last intercourse. We selected use at last intercourse for a number of reasons. First, owing to its temporal proximity, it is probably less subject to biases than either recall of use at first intercourse or patterns of contraceptive use. Second, we wished to take advantage of the repeated measures of contraceptive use at Waves I-III in Add Health and examine the role of genetic propensities in contraceptive use across adolescence and young adulthood—an objective that could not be accomplished by the measure of use at first intercourse, which does not vary over time. Third, use at last coitus is less likely than the patterns-of-contraceptive-use indicator to be affected by the individual's total number of coital experiences. For a given probability of use, those with a higher number of experiences are more likely to report inconsistent use, and those with lower numbers to report consistent use or consistent non-use. Fourth, use at last coitus has been shown to be correlated with use at first coitus and use at other times, an association that remains after controls for potential confounders (Kusseling et al. 1995; Shafii et al. 2007).

Genetic measures

As part of Add Health Wave III, buccal cell DNA samples were collected from a subset of the overall sample. Genomic DNA was isolated at the Institute for Behavioral Genetics at the University of Colorado (http://www.cpc.unc.edu/projects/addhealth/) using a modification of published methods (Lench et al. 1988; Meulenbelt et al. 1995; Spitz et al. 1996; Freeman et al. 1997). The average yield of DNA was 58 ± 1 micrograms (μg).

Two types of genetic measure were used in our analysis: 1) functional genetic polymorphisms, which were hypothesized to be linked to contraceptive use, and 2) ancestrally informative markers, which were used to address potential confounding caused by population stratification, a statistical concern described in detail below.

This study examined variants in each of three genes: *DAT1, DRD2*, and *MAOA*. The analysis of *DAT1* focused on three genotypes: 9R/9R, 10R/10R, and 9R/10R; these three genotypes accounted for more than 96% of the analysis sample. *DRD2* has three different genotypes, which are A2/A2 (178/178), A1/A1 (304/304), and A1/A2 (178/304). (The numbers in parentheses refer to the number of base pairs in the allele's genetic sequence.) *MAOA* has five different alleles, with 2, 3, 3.5, 4, or 5 copies of the repeated sequence; the 3 and 4 repeats are much more common than the 2, 3.5, and 5 repeats in human populations. Our analysis investigated the association of the 2R allele among males, and the possession of any 2R allele among females, with contraceptive use. The distributions of genes and self-reported ethnicity did not show any deviation from the Hardy-Weinberg equilibrium (indicating that these genetic factors did not appear to be subject to evolutionary pressures, genetic drift, or other disturbances).

Add Health obtained a panel of 186 ancestrally informative markers, of which 121 were successfully obtained using an Illumina GoldenGate assay for 384 candidate SNPs. This panel was designed for the purpose of the detection and correction of population stratification for genetic association studies (Enoch et al. 2006).

Demographic, family socioeconomic, and knowledge/attitude measures

Race/ethnicity was measured using self-reports of individuals, who were first asked 'Are you of Hispanic or Spanish origin?' and then 'What is your race? You may give more than one answer'. The resultant variable included the categories of Hispanics, African

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Americans, Asians, Native Americans, and Non-Hispanic whites. Any respondent who reported a Hispanic or Latino ethnicity in the survey was coded as Hispanic, and any non-Hispanic who reported African American, Asian, or Native American ethnicity was coded (non-exclusively) in those categories. *Age* in years was measured using data on month and year at interview and birth. For analyses, this variable was dichotomized, with 1 indicating that the individual was less than or equal to age 18 at time of interview and 0 indicating that they were older. The legal age of adulthood may be related to contraceptive use since childbearing increasingly influences contraceptive decisions after age 18. Moreover, Glei (1999) finds that the difference between 17-year-olds and 18-year-olds corresponds to the largest increase in rates of use of effective contraception, suggesting that age 18 is a turning point in life-course patterns of contraceptive use.

Our analysis included a number of other control variables, mostly constructed using Wave I data. Using the household roster data, we inferred *parental structure* and *number of biological siblings* living at home with the respondent. Adolescents were coded as living in one of the following types of family: single parent, two biological parents, one biological parent/one stepparent, or 'other'. Information on *parents' education* came from parents' responses in the Wave-I home interviews to the question, 'How far did you go in school?' We coded this information dichotomously: 1 if the most educated parent attended at least some college, 0 otherwise.

For *parents' income* in thousands of dollars, we used the parents' self-report at the Wave-I interview, without transformation. Reported incomes of $1,000,000 or more were top coded as $999,000. *Frequency of church attendance* was measured with the question 'In the past 12 months, how often did you attend religious services?' 'Once a week or more' was coded 1, other responses were coded 0; these other responses included 'Once a month or more but less than once a week', 'Less than once a month', and 'Never'. *Months since first sexual intercourse* was the length of time in months from time of first sexual intercourse to the interview.

Smoked in last 30 days was coded 1 one if the respondent had smoked in this period and 0 if not or if respondent had indicated that he or she had never smoked. *Drinking frequency* was measured on a scale of how often a respondent had drunk alcohol in the previous 12 months. The scale ranged from 0 to 6 with 0 indicating 'Never,' and 6 indicating 'Every day or almost every day'. Legitimate skips (based on other questions measuring whether the respondent had ever drunk alcohol) were coded as 0. *Expelled from school* was a time-varying self-reported measure of whether a respondent had ever been expelled from school by the date of each of the first three Add Health Waves. *Married at Wave III* was based on self-reported marital history at Wave III. It was coded 1 if the respondent reported having been married or was currently married, and 0 otherwise.

Knowledge and attitude measures included Birth control self-efficacy, Prepared for birth control, Forgo coitus if no birth control, Contraceptive knowledge, and *Contraceptive attitude.* The first three measures were scales that asked respondents to show on a scale of 1 to 5 how sure they were that they could: (i) stop and use contraceptives before sexual intercourse, (ii) plan ahead to have contraceptives available, and (iii) forgo sexual intercourse in the absence of contraceptives. The measure of contraceptive knowledge was the proportion of a series of ten factual questions about contraceptives that the respondent answered correctly (questions H1KQ1A to H1KQ10A in the Add Health codebook). Finally, the measure of contraceptive attitudes was the average score on a battery of seven scales that asked respondents to indicate their attitudes to aspects of contraception on a scale of 1 to 5. (We used all such items in the Add Health survey—H1BC1 to H1BC8 in the codebook—

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except for H1BC6, which reads, 'It is easy for you to get birth control'; unlike the other measures, this item does not directly measure an attitude.)

Statistical methods

Our analysis was undertaken in two stages: an exploratory analysis and a regression analysis. The exploratory analysis investigated the proportion of cases of unprotected sexual intercourse by genotype, life stage, and sex. The regression analysis used a generalized estimating equation (GEE) logistic regression to estimate the association between the genetic polymorphisms and unprotected sexual intercourse:

$$p_{ijt}/\left(1-p_{ijt}\right)=\exp\left(\beta_0+\mathbf{D}_{jit}\beta_1+C_{ji}\beta_2+\mathbf{G}_{jt}\beta_3\right), \quad 1$$

where *i, j,* and *t* index individual, sibling cluster, and Add Health Wave, respectively; p is the probability of unprotected last coitus; **D** is a row vector of demographic covariates; **C** is a row vector of individual, family, and knowledge/attitude measures; and **G** is a row vector of covariates measuring genetic variants in *DAT1, DRD2*, and *MAOA*. GEE methods (Liang and Zeger 1986) have long been established in the statistical literature as a standard way of analyzing data with correlated observations. Finally, although our primary objective was to test the associations of genetic variants with unprotected sexual intercourse, we included a full set of demographic, family, and knowledge/attitude variables in addition to genetic variants in the statistical models. The purpose of doing so was to test whether the genotypes modelled made independent contributions to the explanations of contraceptive use net of a standard social science model of this variable.

Out of about 20 variables used in our regression analysis, the large majority of cases (82 per cent) had missing data for two or fewer variables. Those with the highest proportions of missing data were Parents' income (22.1 per cent), Birth control self-efficacy (17.4 per cent), and Prepared for birth control (16.9 per cent). The proportions missing for other variables were much lower. For the analysis, missing data were imputed using the EM algorithm via SAS's PROC MI. The EM algorithm provides unbiased, maximum-likelihood estimates of missing values through a two-step, iterative process (Dempster et al. 1977; Allison 2001).The missing genetic data were not imputed.

In addition to correlated observations and missing data, population stratification (e.g., Cardon and Palmer 2003) was another potential concern for our analysis. Population stratification occurs when a population consists of multiple subgroups, each with a different allele distribution. This can potentially produce false associations between genetic polymorphisms and an outcome, just as a false statistical association can be produced through confounding. Within each subgroup, the allele may be unrelated to the outcome but nonetheless yield the appearance of an association between them. Because this potential source of bias is not adequately addressed using controls for racial/ethnic background alone, we used the ancestrally informative markers in the Add Health data to control for population stratification via the methods of structured association (Pritchard et al. 2000) and principal components (Price et al. 2006). The proportional bio-ancestral contributions from the structured association approach and the principal components approach were estimated using the software packages STRCTURE and Plink, respectively.

Results

Exploratory results

Table 3 shows the proportion of cases of unprotected last coitus by genotype, sex, and age group. Our hypotheses are supported in ten of the twelve subgroups of sex, age, and genes

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(*DAT1, DRD2*, or *MAOA*), with the exception of results related to the *DAT1* genes for males, especially males older than 18.

In the *DAT1* comparisons, females with the 9R/9R genotype are less likely to report unprotected last coitus for both age groups. For males, however, this pattern was not observed. In the *DRD2* comparisons, those with the heterozygous A1/A2 genotype are the most likely to report unprotected sexual intercourse in all age-sex groups. Those with *MAOA**2R/- genotypes report higher rates of unprotected last coitus than all other *MAOA* genotypes in each sex-age block.

Regression models

The GEE binary regression analysis expanded upon the exploratory results from the contingency table analysis, by taking into account the correlation among the repeated measures over Add Health Waves and within sibling clusters. Table 4 presents the coefficients of the genetic variants estimated in a social science model of unprotected sexual intercourse. The coefficients for males and females were estimated in separate regression models, with separate models employing two different controls for population stratification by ancestry – using controls for race, and using the structured association method (Pritchard et al. 2000). These separate models are labelled 'Race Controls' and 'Structural Controls.' The associations of genetic variants in the *DAT1, DRD2*, and *MAOA* genes with contraceptive behavior were estimated simultaneously. The estimates were similar when the variants of each gene were entered into the model separately (results not shown). For each estimate, we present its exponentiated coefficient to facilitate interpretation, as well as the *t* ratio of the coefficient. The level of statistical significance is also indicated.

The coefficients of genetic variants in Table 4 are consistent with the results from the contingency analysis (Table 3). As before, our hypothesis concerning the *DAT1* gene is supported among females only. Females with the *DAT1**9R/10R genotype have more than twice the odds of having engaged in unprotected sexual intercourse than those with the *DAT1*9R/9R* genotype, which we regarded as a behaviorally conservative genotype. The *DAT1**10R/10R genotype has a coefficient similar to that for *DAT1**9R/10R, but the estimate is not statistically significant.

Depending on the model specification, individuals with the *DRD2**A1/A2 or *DRD2**A2/A2 genotype have about 72-95 per cent (males) and 65-72 per cent (females) higher odds than individuals with the *DRD2**A1/A1 genotype of reporting unprotected last coitus. Thus one or two A2 alleles are associated with a higher risk of unprotected sexual intercourse. Of the *MAOA**2R associations, only the coefficient for females is statistically significant. Females possessing a *MAOA**2R allele have odds of unprotected last coitus about 158-175 per cent higher than the odds of those without a 2R allele.

Even with the inclusion of a number of genetic variables, a number of more traditional social science variables retain significant associations with the probability of unprotected sexual intercourse. Among males, Native Americans have odds of reporting unprotected sexual intercourse 239 per cent higher than those of whites. More hostile attitudes to contraception are associated with 24 per cent higher odds of unprotected sexual intercourse. For married persons, the odds of unprotected sexual intercourse are more than twice as high as those for persons in other forms of relationship. A number of other factors among males predict a lower likelihood of unprotected sexual intercourse: those more knowledgeable about contraceptives have lower odds of unprotected sexual intercourse, and the odds are also lower for those who report that they would forgo intercourse in the absence of available contraception.

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Similar, but distinctive, relationships are observed among females. Those from families with two biological parents have lower odds of reporting unprotected sexual intercourse than do those from nontraditional family structures. Lower odds are also observed for those whose parents who have higher incomes, those who have higher scores on the scale of Contraceptive self-efficacy, and those who report that they would refrain from intercourse if contraception was not available. Lastly, higher odds of unprotected intercourse are observed for those who have been expelled from school, those who have attitudes hostile to contraceptive use, and those who were married by wave 3 of Add Health.

The right-most two columns of Table 4 present the estimates obtained after controlling for population stratification via the method of structured association. On the whole, these estimates do not differ substantially from those in the first two columns, where population stratification is controlled by self-reported race and ethnicity. We also estimated male and female models controlling population stratification via the method of principal components (results not shown). The principal components method yields results substantially identical to those yielded by the structured association method.

Finally, Tables 5 (for females) and 6 (for males) present the results of two logistic GEE models of contraceptive use by type, where the categories of the dependent variable were ‘condom use’, ‘other effective contraceptive use’, and ‘no contraceptive use at last sexual intercourse’. In these logistic regression models, only observations in which the indicated contraceptive outcomes were observed were compared. While multinomial logistic regression is the usual method of analysing unordered dependent variables, no software was available to estimate such models using GEE. The method we used is closely related, but not identical, to GEE multinomial logit regression.

Although these estimates sometimes differ in degree when modelling the two comparisons, overall the genetic associations are substantially similar for condoms and other methods of contraception compared with no effective contraception. The sole exceptions to this generalization are the *DAT1* associations with unprotected sexual intercourse, which are negative for males’ condom use and have either no effect or a small positive one for other contraceptive use. However, none of these odds ratios are statistically significant. Finally, it is notable that the only statistically significant effect of genotypic variation among males is that of the *DRD2**A1/A2 genotype on the condom–none comparison. This is to be expected given that males have more direct control and knowledge over condom than over other types of contraceptive, which are likely to be disproportionately female-controlled.

Discussion and conclusion

Our empirical investigation supports the proposition that genes—specifically the *DAT1, DRD2,* and *MAOA* genes—have a role in regulating neurotransmitter function, and thereby contraceptive use, among adolescents and young adults. There is evidence for four of our five hypotheses about genetic associations and the gene-sex interaction. Our first hypothesis stated that there should be a positive relationship between possession of a *DAT1**9R/10R or *DAT1**10R/10R genotype and the odds of engaging in unprotected sexual intercourse. This hypothesis was supported among females only—females with the *DAT1**9R/10R genotype have odds about twice as high as those with the 9R/9R genotype of engaging in unprotected sexual intercourse. These and all findings remain significant even with the inclusion of a comprehensive set of controls in the model.

Our second hypothesis predicted that individuals with the *DRD2**A1/A2 genotype should report higher rates of unprotected sexual intercourse than those with other *DRD2* genotypes. This hypothesis was supported among both males and females. Males with the *DRD2**A1/

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A2 genotype were estimated to have 91-95 per cent higher odds of reported unprotected sexual intercourse than those with the *DRD2**A1/A1 genotype. Similarly females with this genotype were estimated to have 72 per cent higher odds of unprotected sexual intercourse than those with the *DRD2**A1/A1 genotype.

Our third hypothesis predicted that those with the *MAOA**2R/- genotype would demonstrate higher odds of reporting unprotected sexual intercourse than those with other *MAOA* genotypes. This hypothesis was supported among females only— depending on model specification, females with this genotype were estimated to have 158 to 175 per cent higher odds of reporting unprotected sexual intercourse than those with other *MAOA* genotypes.

Our fourth hypothesis predicted that the associations of these genetic variants with contraceptive behavior might vary by sex in an uncertain direction. This hypothesis was supported: while all three association hypotheses were supported for the females, only one was supported for males. These results suggest that genetic propensities may interact with sex. The specific mechanisms for the gene-sex interaction remain unknown, and should be the subject of future research.

Finally, our fifth hypothesis predicted that the associations of these genes would vary by contraceptive type, specifically that the association for condom use would differ from that for other contraceptive types. This hypothesis was not supported: the associations of genetic variants with these two contraceptive types were very similar for both males and females. We conclude that the genetic associations which we document do not vary significantly by contraceptive type.

A great deal of human genetic research has been plagued by the problems of small sample sizes, population stratification, multiple testing, inappropriate controls, and lack of replicability (Ioannidis et al. 2001; Cardon and Palmer 2003; Ioannidis et al. 2003). Furthermore, although *DRD2* is one of the most investigated genes for psychiatric conditions, considerable inconsistency exists about which allele in *DRD2* is associated with high-risk outcomes (Noble 2003). The source of these disagreements about the nature of *DRD2* effects is not well understood. Many studies (e.g., Eisenberg et al. 2007b) were based on small convenience samples in clinical settings. In contrast, our findings are based on a nationally representative sample with more than 2,000 respondents, and we control for a wide set of individual contraceptive-relevant characteristics.

Although we use only one dataset and replications would be required for greater confidence in these findings, our analysis is relatively free from typical weaknesses in clinically-based genetic studies. To be specific: our analytical sample is reasonably large; our tests are driven by explicit hypotheses; we work with only a small number of genetic polymorphisms (thus minimizing multiple testing concerns); our positive and negative cases come from the same population; and we were able to adjust for potential population stratification using a panel of ancestrally informative markers.

Furthermore, we have re-estimated our models of contraceptive use, employing the entire Add Health sample and without including genetic polymorphisms because they are unavailable for the full sample (results not shown). The estimates of the non-genetic associations based on the full sample are comparable to those based on the Add Health genetic sample, suggesting that our findings may be generalizable to the Add Health full sample.

Nevertheless, our analyses are subject to a number of limitations. While our overall sample is relatively large, the number of observed respondents with certain genotypes is sometimes small. Estimates of these associations may therefore be imprecise. Furthermore, the

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inconsistency of previous research on the associations of *DRD2* with behavioral outcomes suggests that a degree of caution is merited. Our analyses need to be replicated in future research with independent samples.

Finally, establishing genetic associations with contraceptive behavior does not automatically imply a causal relationship, nor does it directly clarify the mechanisms linking genotype with behavior. However, our results are consistent with previous research on the dopaminergic system, the literature on which has established a key role for the system in the production of individual differences in impulsivity. Impulsivity may plausibly influence the odds of obtaining effective contraception, of using the contraceptive obtained, and of forgoing sexual intercourse in the absence of effective contraceptive options. Although we cannot test the connections between genotype and these behaviours directly with our data, we founded our hypotheses on the assumed connections and our findings are largely consistent with our assumptions. However, future research should investigate the connections in more depth and test them against competing explanations for these results.

To summarize: our analysis finds evidence of statistically significant and substantial associations between human genetic variation and the contraceptive behaviour of adolescents and young adults. These genetic effects were estimated side by side with demographic, psychological, environmental, and attitudinal factors, and may partially explain the observation that patterns of contraceptive use are fairly stable over time. These results add to the growing body of evidence of the relevance of biology to a variety of demographic processes.

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APPENDIX: A glossary of genetic and biological concepts and terms

Allele

DNA sequences which vary within a species. Variations between alleles may lead to different phenotypes for a given trait. For instance, there are three variants of the red blood cell type gene A, B, and O, which in different combinations produce the A, B, AB, and O blood types.

Dopamine

A brain chemical that transmits signals between neurons in the brain. This chemical is involved in motivation, reward, and other cognitive functions. Dopamine is a monoamine neurotransmitter (see below).

Enzyme

A groups of chemicals serving as catalysts (which accelerate or decelerate chemical processes) for chemical reactions. For instance, the MAOA enzyme breaks down neurotransmitters in the brain, limiting the duration of their influence on chemical reward.

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Genotype

The observed combination of alleles in an organism at a particular location in the DNA sequence. Excluding the X and Y chromosomes for males, all humans have two copies of every genetic sequence, and these together define the genotype. For instance, someone with an AB blood type has one A allele and one B allele, giving them an A/B genotype.

Hardy-Weinberg equilibrium

A principle stating that the genetic variation in a population will remain constant from one generation to the next in the absence of disturbing factors. In other words, when a gene's distribution is not subject to natural selection, assortative mating, substantial genetic drift, or other pressures, we expect to observe an equilibrium in which the allelic frequencies in one generation approximately match that of the next.

Knock-out mice study

A research design in which mice are genetically engineered to ensure that a certain gene does not function. These studies seek to identify genetic influences through the effect of their absence. For instance, disabling the *MAOA* gene in mice results in increased levels of neurotransmitters in the brain, suggesting that *MAOA* plays a role in regulating the prevalence of these chemicals.

Locus

A specific location in the DNA sequence of a species.

Monoamine neurotransmitters

A group of neurotransmitters including dopamine, norepinephrine, and serotonin.

Neurotransmitters

A category of chemicals which function as the principal 'messenger' chemicals in the brain. These function by modulating, amplifying, or relaying messages between brain neurons.

Nucleotide

The set of molecules from which DNA is constructed. DNA consists of two matching strings of nucleotides arrayed in a double helix. Matching nucleotides in DNA are together known as base pairs. There are four nucleotides in DNA: adenine (A), thymine (T), guanine (G), and cytosine (C). Each nucleotide pairs with another deterministically—A with T and G with C. These are the codes from which all proteins, and therefore cell functions, are produced.

Polymorphism

Variation in a DNA sequence between individuals. This term is a synonym of 'allele.'

Population stratification

A form of confounding whereby the appearance of a direct association of a gene with an outcome may be created spuriously. Certain alleles are more commonly found in some subpopulations than others. If these subpopulations are associated with variability in an

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outcome, the appearance of an association between the alleles and outcomes in question can be created where none exists. For instance, if persons descended from a certain region were more likely to possess the DRD2*A1 allele and (unrelatedly) were more likely to engage in unprotected sexual intercourse, a spurious association between the A1 allele and unprotected sexual intercourse would be observed.

Serotonin

A brain chemical that transmits signals between neurons in the brain, and that is involved in the regulation of pleasure and other cognitive functions. Serotonin is a monoamine neurotransmitter (see above).

Single nucleotide polymorphism (SNP)

Variations in a DNA sequence of base pairs that occur when a lone nucleotide in the base pair sequence varies between individuals. For instance, if a four-nucleotide sequence was typically GGAC but in some members of the species was GAAC, this would be a SNP. This is a type of genetic polymorphism (see above).

Synapses

The space between neuron cells in the brain, in which neurotransmitters such as dopamine are passed to deliver messages between neurons.

Variable Number Tandem Repeat (VNTR)

A location in the genome at which a particular repetitive sequence of base pairs is present with different numbers of repeated sequences in different individuals in a population. For instance, if a given section of DNA is ATGATG in one person and ATGATGATG in another, this is a VNTR.

References

Abma, JC.; Martinez, GM.; Mosher, WD.; Dawson, BS. Teenagers in the United States: Sexual activity, contraceptive use, and childbearing, 2002. National Center for Health Statistics; Hyattsville, MD: 2004.

Ainslie G. Specious reward - behavioral theory of impulsiveness and impulse control. Psychological Bulletin. 1975; 82(4):463–96. [PubMed: 1099599]

Bannon, Michael J.; Whitty, Christopher J. Neurokinin receptor gene-expression in substantia nigra: Localization, regulation, and potential physiological significance. Canadian Journal of Physiology and Pharmacology. 1995; 73(7):866–870. [PubMed: 8846423]

Bearman, Peter. Introduction: Exploring Genetics and Social Structure. The American Journal of Sociology. 2008; 114(S1):v–x.

Bermant, G. Sexual behavior: Hard times with the Coolidge effect. In: Siegel, MH., editor. Psychological research: Inside story. Harper & Row; New York: 1976.

Bermant G, Lott DF, Anderson L. Temporal characteristics of Coolidge effect in male rat copulatory behavior. Journal of Comparative and Physiological Psychology. 1968; 65(3P1):447–452. [PubMed: 5691208]

Blum K, Cull JG, Braverman ER, Comings DE. Reward deficiency syndrome. American Scientist. 1996; 84(2):132–145.

Blum, Nathan J. Introduction. Journal of Developmental & Behavioral Pediatrics. 2010; 31(7):523–524. [PubMed: 20814251]

Brown, Sarah S.; Eisenberg, Leon, editors. The best intentions: Unintended pregnancy and the well-being of children and families. National Academy Press; Washington, D.C.: 1995.

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

Bunzow, James R.; Vantol, Herbert H. M.; Grandy, David K.; Albert, Paul; Salon, John; Christie, MacDonald; Machida, Curtis A.; Neve, Kim A.; Civelli, Oliver. Cloning and expression of a rat D2 dopamine receptor CDNA. Nature. 1988; 6201; 336:783–787. [PubMed: 2974511]

Cardinal, Rudolf N.; Pennicott, David R.; Sugathapala, C. Lakmali; Robbins, Trevor W.; Everitt, Barry J. Impulsive choice induced in rats by lesions of the nucleus accumbens core. Science. 2001; 292(5526):2499–2501. [PubMed: 11375482]

Cardon, Lon R.; Palmer, Lyle J. Population stratification and spurious allelic association. Lancet. 2003; 361(9357):598. [PubMed: 12598158]

Cases O, Seif I, Grimsby J, Gaspar P, Chen K, Pournin S, Muller U, Aguet M, Babinet C, Shih JC, Demaeyer E. Aggressive-behavior and altered amounts of brain-serotonin and norepinephrine in mice lacking MAOA. Science. 1995; 268(5218):1763–1766. [PubMed: 7792602]

Caspi, Avshalom; McClay, Joseph; Moffitt, Terrie E.; Mill, Jonathan; Martin, Judy; Craig, W.; Taylor, Alan; Poulton, Richie. Role of genotype in the cycle of violence in maltreated children. Science. 2002; 297(5582):851–854. [PubMed: 12161658]

Cook, Edwin H.; Stein, Mark A.; Krasowski, Matthew D.; Cox, Nancy J.; Olkon, Deborah M.; Kieffer, John E.; Leventhal, Bennett L. Association of attention-deficit disorder and the dopamine transporter gene. American Journal of Human Genetics. 1995; 56(4):993–998. [PubMed: 7717410]

Cornish KM, Manly T, Savage R, Swanson J, Morisano D, Butler N, Grant C, Cross G, Bentley L, Hollis CP. Association of the dopamine transporter (DAT1) 10/10-repeat genotype with ADHD symptoms and response inhibition in a general population sample. Molecular Psychiatry. 2005; 10(7):686–698. [PubMed: 15809660]

Daly G, Hawi Z, Fitzgerald M, Gill M. Mapping susceptibility loci in attention deficit hyperactivity disorder: Preferential transmission of parental alleles at DAT1, DBH and DRD5 to affected children. Molecular Psychiatry. 1999; 4(2):192–196. [PubMed: 10208453]

Dempster AP, Laird NM, Rubin DB. Maximum likelihood from incomplete data via EM algorithm. Journal of the Royal Statistical Society Series B-Methodological. 1977; 39(1):1–38.

Des Jarlais, Don C.; Paone, Denise; Milliken, Judith; Turner, Charles F.; Miller, Heather; Gribble, James; Shi, QH.; Hagan, H.; Friedman, SR. Audio-computer interviewing to measure risk behaviour for HIV among injecting drug users: A quasi-randomised trial. Lancet. 1999; 353(9165):1657–1661. [PubMed: 10335785]

Eisenberg, Dan T.A.; Campbell, Benjamin; MacKillop, James; Modi, Meera; Dang, David; Lum, J. Koji; Wilson, David S. Polymorphisms in the dopamine D2 and D4 receptor genes and reproductive, sexual and life history behaviors. Evolutionary Psychology. 2007a; 5:696–715.

Eisenberg, Dan T.A.; MacKillop, James; Modi, Meera; Beauchemin, Joshua; Dang, David; Lisman, Stephen A.; Lum, J. Koj; Wilson, David. Examining impulsivity as an endophenotype using a behavioral approach: A DRD2 TaqI a and DRD4 48-bp VNTR association study. Behavioral and Brain Functions. 2007b; 3(2):1–14. [PubMed: 17214890]

Enoch, Mary-Anne; Shen, Pei-Hong; Xu, Ke; Hodgkinson, Colin; Goldman, David. Using ancestry-informative markers to define populations and detect population stratification. Journal of Psychopharmacology. 2006; 20(4 supplement):19–26. [PubMed: 16785266]

Ford, Kathleen; Sohn, Woosung; Lepkowski, James. Characteristics of adolescents' sexual partners and their association with use of condoms and other contraceptive methods. Family Planning Perspectives. 2001; 33(3):100–132. [PubMed: 11407432]

Franzetta, Kerry; Ikramullah, Erum; Manlove, Jennifer; Moore, Kristin Anderson; Cottingham, Sarah. Facts at a glance. Child Trends; Washington, DC: 2006.

Freeman, Bernard; Powell, John; Ball, David; Hill, Linzy; Craig, Ian; Plomin, Robert. DNA by mail: An inexpensive and noninvasive method for collecting DNA samples from widely dispersed populations. Behavior Genetics. 1997; 27(3):251–257. [PubMed: 9210796]

Fu, Haishan; Darroch, Jacquenline E.; Haas, Taylor; Ranjit, Nalini. Contraceptive failure rates: New estimates from the National Survey of Family Growth. Family Planning Perspectives. 1999; 31(2): 56–63. [PubMed: 10224543]

Fuke, Satoshi; Sasagawa, Noboru; Ishiura, Shoichi. Identification and characterization of the hesr1/hey1 as a candidate trans-acting factor on gene expression through the 3′ non-coding

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polymorphic region of the human dopamine transporter (DAT1) gene. Journal of Biochemistry. 2005; 137(2):205–216. [PubMed: 15749835]

Fuke S, Suo S, Takahashi N, Koike H, Sasagawa N, Ishiura S. The VNTR polymorphism of the human dopamine transporter (DAT1) gene affects gene expression. Pharmacogenomics Journal. 2001; 1(2):152–156. [PubMed: 11911442]

Gill M, Daly G, Heron S, Hawi Z, Fitzgerald M. Confirmation of association between attention deficit hyperactivity disorder and a dopamine transporter polymorphism. Molecular Psychiatry. 1997; 2(4):311–313. [PubMed: 9246671]

Giros, Bruno; Jaber, Mohamed; Jones, Sara R.; Wightman, R. Mark; Caron, Marc G. Hyperlocomotion and indifference to cocaine and amphetamine in mice lacking the dopamine transporter. Nature. 1996; 379(6566):606–612. [PubMed: 8628395]

Glei, Dana A. Measuring contraceptive use patterns among teenage and adult women. Family Planning Perspectives. 1999; 31(2):73–80. [PubMed: 10224545]

Gorwood P, Batel P, Gouya L, Courtois F, Feingold J, Ades J. Reappraisal of the association between the DRD2 gene, alcoholism and addiction. European Psychiatry. 2000; 15(2):90–96. [PubMed: 10881204]

Guo, Guang. The linking of sociology and biology. Social Forces. 2006; 85(1):145–149.

Guo, Guang. Introduction to the Special Issue on Society and Genetics. Sociological Methods & Research. 2008; 37(2):159–163.

Guo, Guang; Tong, Yuying. Age at first sexual intercourse, genes, and social context: Evidence from twins and the dopamine D4 receptor gene. Demography. 2006; 43(4):747–769. [PubMed: 17236545]

Guo, Guang; Ou, Xiao-Ming; Roettger, Michael; Shih, Jean C. The VNTR 2 repeat in MAOA and delinquent behavior in adolescence and young adulthood: Associations and MAOA promoter activity. European Journal of Human Genetics. 2008a; 16(5):626–634. [PubMed: 18212819]

Guo, Guang; Tong, Yuying; Cai, Tianji. Gene by social context interactions for number of sexual partners among white male youths: Genetics-informed sociology. American Journal of Sociology. 2008b; 114:S36–S66.

Guo, Guang; Michael Roettger, E.; Cai, Tianji. The integration of genetic propensities into social control models of delinquency and violence among male youths. American Sociological Review. 2008c; 73:543–568.

Harris, KM.; Halpern, CT.; Whitsel, E.; Hussey, J.; Tabor, J.; Entzel, P.; Udry, JR. The national longitudinal study of adolescent health: Research design. 2009. Available online at: http://www.cpc.unc.edu/projects/addhealth/design

Henshaw, Stanley K. Unintended pregnancy in the United States. Family Planning Perspectives. 1998; 30(1):24–46. [PubMed: 9494812]

Hodgkinson, Colin A.; Yuan, Qiaoping; Shen, Pei-Hong; Heinz, Elizabeth; Lobos, Elizabeth A.; Binder, Elizabeth B.; Cubells, Joe; Ehlers, Cindy L.; Gelernter, Joel; Mann, John; Riley, Brien; Roy, Alec; Tabakoff, Boris; Todd, Richard D.; Zhou, Zhifeng; Goldman, David. Addictions biology: Haplotype-based analysis for 130 candidate genes on a single array. Alcohol & Alcoholism. 2008; 43(5):505–515. [PubMed: 18477577]

Ioannidis, John P.A.; Ntzani, Evangelia E.; Trikalinos, Thomas A.; Contopoulos-Ioannidis, Despina G. Replication validity of genetic association studies. Nature Genetics. 2001; 29(3):306–309. [PubMed: 11600885]

Ioannidis, John P. A.; Trikalinos, Thomas A.; Ntzani, Evangelia E.; Contopoulos-Ioannidis, Despina G. Genetic associations in large versus small studies: An empirical assessment. Lancet. 2003; 361(9357):567–571. [PubMed: 12598142]

Isles, Anthony R.; Humby, Trevor; Walters, Eurof; Wilkinson, Lawrence S. Common genetic effects on variation in impulsivity and activity in mice. Journal of Neuroscience. 2004; 24(30):6733–6740. [PubMed: 15282276]

Kusseling FS, Wenger NS, Shapiro MF. Inconsistent contraceptive use among female college-students - implications for intervention. Journal of American College Health. 1995; 43(5):191–195. [PubMed: 7499632]

NIH-PA Author Manuscript

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Aki, Laakso; Pohjalainen, Tiina; Bergman, Jörgen; Kajander, Jaana; Haaparante, Merja; Solin, Olof; Syvälahti, Erkka; Hietala, Jarmo. The A1 allele of the human D2 dopamine receptor gene is associated with increased activity of striatal L-amino acid decarboxylase in healthy subjects. Pharmacogenetics and Genomics. 2005; 15:387–391. [PubMed: 15900211]

Lench, Nicholas; Stanier, Philip; Williamson, Robert. Simple non-invasive method to obtain DNA for gene analysis. Lancet. 1988; 1(8599):1356–1358. [PubMed: 2898042]

Liang, Kung-Yee; Zeger, Scott L. Longitudinal data-analysis using generalized linear-models. Biometrika. 1986; 73(1):13–22.

Manlove, Jennifer; Ryan, Suzanne; Franzetta, Kerry. Contraceptive use and consistency in US teenagers' most recent sexual relationships. Perspectives on Sexual and Reproductive Health. 2004; 36(6):265–275. [PubMed: 15687085]

Manlove, Jennifer S.; Terry-Humen, Elizabeth; Ikramullah, Erum N.; Moore, Kristin A. The role of parent religiosity in teens' transitions to sex and contraception. Journal of Adolescent Health. 2006; 39(4):578–587. [PubMed: 16982394]

Manning, Wendy D.; Longmore, Monica A.; Giordano, Peggy C. The relationship context of contraceptive use at first intercourse. Family Planning Perspectives. 2000; 32(3):104–110. [PubMed: 10894255]

McClure, Samuel M.; Laibson, David I.; Loewenstein, George; Cohen, Jonathan D. Separate neural systems value immediate and delayed monetary rewards. Science. 2004; 306(5695):503–507. [PubMed: 15486304]

Meulenbelt, Ingrid; Droog, Simone; Trommelen, Gerjan J. M.; Boomsma, Dorret I.; Eline Slagboom, P. High-yield noninvasive human genomic DNA isolation method for genetic-studies in geographically dispersed families and populations. American Journal of Human Genetics. 1995; 57(5):1252–1254. [PubMed: 7485180]

Neville, Matt J.; Johnstone, Elaine C.; Walton, Robert T. Identification and characterization of ANKK1: A novel kinase gene closely linked to DRD2 on chromosome band 11q23.1. Human Mutation. 2004; 23(6):540–545. [PubMed: 15146457]

Newman, Jessica Clark; Des Jarlais, Don C.; Turner, Charles F.; Gribble, Jay; Cooley, Phillip; Paone, Denise. The differential effects of face-to-face and computer interview modes. American Journal of Public Health. 2002; 92(2):294–297. [PubMed: 11818309]

Noble, Ernest P. The d-2 dopamine receptor gene: A review of association studies in alcoholism and phenotypes. Alcohol. 1998; 16(1):33–45. [PubMed: 9650634]

Noble, Ernest P. D2 dopamine receptor gene in psychiatric and neurologic disorders and its phenotypes. American Journal of Medical Genetics Part B-Neuropsychiatric Genetics. 2003; 116B(1):103–125.

Price, Alkes L.; Patterson, Nick J.; Plenge, Robert M.; Weinblatt, Michael E.; Shadick, Nancy A.; Reich, David. Principal components analysis corrects for stratification in genome-wide association studies. Nature Genetics. 2006; 38(8):904–909. [PubMed: 16862161]

Pritchard, Jonathan K.; Stephens, Matthew; Rosenberg, Noah A.; Donnelly, Peter. Association mapping in structured populations. American Journal of Human Genetics. 2000; 67(1):170–181. [PubMed: 10827107]

Ryan, Suzanne; Franzetta, Kerry; Manlove, Jennifer. Knowledge, perceptions, and motivations for contraception - influence on teens' contraceptive consistency. Youth & Society. 2007; 39(2):182–208.

Sabol SZ, Hu Stella, Hamer D. A functional polymorphism in the monoamine oxidase A gene promoter. Human Genetics. 1998; 103(3):273–279. [PubMed: 9799080]

Sabol, Sue Z.; Nelson, Mark L.; Fisher, Craig; Gunzerath, Lorraine; Brody, Cindy L.; Hu, Stella; Sirota, Leo A.; Marcus, Stephen E.; Greenberg, Benjamin D.; Lucas, Frank R.; Benjamin, Jonathan; Murphy, Dennis L.; Hamer, Dean H. A genetic association for cigarette smoking behavior. Health Psychology. 1999; 18(1):7–13. [PubMed: 9925040]

Salamone, John D. The involvement of nucleus-accumbens dopamine in appetitive and aversive motivation. Behavioural Brain Research. 1994; 61(2):117–133. [PubMed: 8037860]

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Schuster, Mark A.; Bell, Robert M.; Berry, Sandra H.; Kanouse, David E. Impact of a high school condom availability program on sexual attitudes and behaviors. Family Planning Perspectives. 1998; 30(2):67–72. 88. [PubMed: 9561871]

Shafii, Taraneh; Stovel, Katherine; Holmes, King. Association between condom use at sexual debut and subsequent sexual trajectories: A longitudinal study using biomarkers. American Journal of Public Health. 2007; 97(6):1090–1095. [PubMed: 17463388]

Shih JC, Thompson RF. Monoamine oxidase in neuropsychiatry and behavior. American Journal of Human Genetics. 1999; 65(3):593–898. [PubMed: 10441564]

Singh, Susheela; Darroch, Jacqueline E. Adolescent pregnancy and childbearing: Levels and trends in developed countries. Family Planning Perspectives. 2000; 32(1):14–23. [PubMed: 10710702]

Singh, Susheela; Darroch, Jacqueline E.; Frost, Jennifer J. Socioeconomic disadvantage and adolescent women's sexual and reproductive behavior: The case of five developed countries. Family Planning Perspectives. 2001; 33(6):251–289. [PubMed: 11804434]

Spitz, Elizabeth; Moutier, René; Reed, Terry; Busnel, Marie Claire; Marchaland, Catherine; Roubertoux, Pierre L.; Carlier, Michèle. Comparative diagnoses of twin zygosity by SSLP variant analysis, questionnaire, and dermatoglyphic analysis. Behavior Genetics. 1996; 26(1):55–63. [PubMed: 8852732]

Turner CF, Ku L, Rogers SM, Lindberg LD, Pleck JH, Sonenstein FL. Adolescent sexual behavior, drug use, and violence: Increased reporting with computer survey technology. Science. 1998; 280(5365):867–873. [PubMed: 9572724]

van Gaalen, Marcel M.; Koten, Reinout van; Schoffelmeer, Anton N. M.; Vanderschuren, Louk J. M. J. Critical involvement of dopaminergic neurotransmission in impulsive decision making. Biological Psychiatry. 2006; 60(1):66–73. [PubMed: 16125144]

Vandenbergh, David J.; Persico, Antonio M.; Hawkins, Anita L.; Griffin, Constance A.; Li, Xiang; Jabs, Ethylin W.; Uhl, Goerge R. Human dopamine transporter gene (DAT1) maps to chromosome-5p15.3 and displays a VNTR. Genomics. 1992; 14(4):1104–1106. [PubMed: 1478653]

VanNess, Sidney H.; Owens, Michael J.; Kilts, Clinton D. The variable number of tandem repeats element in DATI regulates in vitro dopamine transporter density. Bmc Genetics. 2005; 6(55)

Waldman ID, Rowe DC, Abramowitz A, Kozel ST, Mohr JH, Sherman SL, Cleveland HH, Sanders ML, Card JHC, Stever C. Association and linkage of the dopamine transporter gene and attention-deficit hyperactivity disorder in children: Heterogeneity owing to diagnostic subtype and severity. American Journal of Human Genetics. 1998; 63(6):1767–1776. [PubMed: 9837830]

Wilson JR, Kuehn RE, Beach FA. Modification in sexual behavior of male rats produced by changing stimulus female. Journal of Comparative and Physiological Psychology. 1963; 56(3):636–644. [PubMed: 14001051]

Winstanley, Catherine A.; Theobald, David E. H.; Dalley, Jeffrey W.; Cardinal, Rudolf N.; Robbins, Trevor W. Double dissociation between serotonergic and dopaminergic modulation of medial prefrontal and orbitofrontal cortex during a test of impulsive choice. Cerebral Cortex. 2006; 16(1): 106–114. [PubMed: 15829733]

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Table 1

Distribution of observations by Add Health wave and sex for a study of genetic influences on adolescents' contraceptive behaviour, United States 1994-2002

	Wave 1	Wave 2	Wave 3	Total number of observations	Number of persons
Male	418	559	1031	1971	1031
Female	418	573	1136	2092	1136
All	836	1132	2167	4110	2167

Source: National Longitudinal Study of Adolescent Health, waves I-III.

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Table 2

Descriptive statistics for all variables used in a study of genetic influences on adolescents' contraceptive behaviour, United States 1994-2002

Variable	Description	Range	Male Mean (SD)		Female Mean (SD)	
Genotype						
*DAT1**9R/9R	=1 if *DAT1* 9R/9R	0-1	0.04	--	0.04	--
*DAT1**9R/10R	=1 if *DAT1* 9R/10R	0-1	0.32	--	0.33	--
*DAT1**10R/10R	=1 if *DAT1* 9R/9R	0-1	0.59	--	0.61	--
*DAT1**-/-	=1 if *DAT1* not 9R/9R, 9R/10R, or 10R/10R	0-1	0.04	--	0.03	--
*DRD2**A1/A1	=1 if *DRD2* A1/A1 (long)	0-1	0.08	--	0.08	--
*DRD2**A2/A2	=1 if *DRD2* A2/A2 (short)	0-1	0.54	--	0.53	--
*DRD2**A1/A2	=1 if *DRD2* A1/A2	0-1	0.39	--	0.38	--
MAOA *2R/−	= 1 if *MAOA* includes 2R allele	0-1	0.01	--	0.03	--
*MAOA**−/−	= 1 of *MAOA* does not include 2R allele	0-1	0.99	--	0.97	--
Demographics						
Age <=18	=1 if R <=18 at time of interview	0-1	0.42	--	0.41	--
African American	=1 if R a non-Hispanic African American (self-report)	0-1	0.22	--	0.22	--
Hispanic	=1 if R Hispanic, of any race (self-report)	0-1	0.16	--	0.15	--
Asian	=1 if R of any Asian race/nationality (self-report)		0.06	--	0.06	--
Native American	=1 if R Native American (self-report)	0-1	0.03	--	0.03	--
Non-Hispanic white	=1 if R a non-Hispanic white (self-report)	0-1	0.52	--	0.54	--
Family						
2 biological parents	=1 if 2 bio. parents live at home	0-1	0.57	--	0.56	--
Parents' income	Parents' yearly income, in $1000s	0 -999	41.69	34.11	45.66	55.12
Parents' education >HS	=1 if parents attended at least some college	0-1	0.37	--	0.33	--
# Siblings	Number of siblings in R's household	0-11	1.90	1.14	2.01	1.17
Behaviour and atttitudes						
Religiosity	=1 if attends church 1/week +	0-1	0.22	--	0.27	--

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Variable	Description	Range	Male Mean (SD)		Female Mean (SD)	
Months since 1st sex	No. months since 1st sexual intercourse	0-197	37.95	30.54	31.56	25.09
Smoked last 30 days	=1 if has smoked a cigarette in last 30 days	0-1	0.41	--	0.37	--
Drinking frequency	in last 12 months: 0=never, 6=every day	0-6	2.23	1.88	1.78	1.60
Expelled from school	=1 if R has ever been expelled from school	0-1	0.11	--	0.05	--
Birth control. self-efficacy	1-5, how sure could stop pre-coitus to use birth ctrl?		3.93	1.08	4.15	1.05
Prepared for birth control.	1-5, how sure could make sure had birth control available pre-coitus?		4.34	0.90	4.50	0.77
Forgo coitus if no birth control available	1-5, how sure could forgo coitus if partner refused birth control?		3.77	1.17	4.38	1.00
Contraceptive knowledge	% of contraceptive knowledge questions answered correctly	0-1	0.63	0.17	0.66	0.16
Contraceptive attitudes	Average score,1-5 for contraceptive attitudes	1-5	2.37	0.85	1.95	0.73
Married at wave 3	=1 if currently married in wave 3 of Add Health	0-1	0.18	--	0.27	--
Sample size				1971	2092	

NOTE: The symbol '–' indicates an unlisted allele (e.g., neither 9R nor 10R for *DAT1* gene).

Source: As for Table 1.

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Table 3

Percentage of cases of unprotected last coitus by sex, age group, and genotype among adolescents, United States 1994-2002

	Males (N=1971)		Females (N=2092)	
Genotype	**Age ≤18 (N)**	**Age >18 (N)**	**Age ≤ 18 (N)**	**Age >18 (N)**
DAT1				
9R/9R	25.71 (35)	30.19 (53)	**27.59 (29)**	**20.37 (54)**
9R/10R	25.29 (257)	23.82 (382)	39.27 (275)	34.07 (408)
10R/10R	29.18 (490)	30.04 (669)	31.60 (519)	31.96 (751)
−/−	20.00 (40)	26.67 (45)	44.44 (27)	20.69 (29)
DRD2				
A1/A1	15.63 (64)	22.22 (90)	29.87 (77)	20.83 (96)
A2/A2	27.70 (444)	25.73 (614)	33.49 (433)	31.14 (684)
A1/A2	**29.30 (314)**	**31.91 (445)**	**36.47 (340)**	**35.28 (462)**
MAOA				
2R/−	**37.50 (16)**	**45.45 (11)**	**58.62 (29)**	**48.39 (31)**
−/−	27.17 (806)	27.68 (1138)	33.50 (821)	31.46 (1211)

Boldface indicates that the results are consistent with the following hypotheses: (1) *DAT1**9R/9R respondents have lower rates of unprotected sex than other *DAT1* genotypes; (2) *DRD2**A1/A2 respondents have higher rates of unprotected sex than other *DRD2* genotypes; and (3)*MAOA**2R respondents have higher rates of unprotected sex than other *MAOA* genotypes. Formal hypothesis tests are presented in Table 4. The symbol '−' indicates an unlisted allele (e.g., neither 9R nor 10R for *DAT1* gene).

Source: As for Table 1.

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Table 4

Associations of genotypes and other variables with adolescents%#x2019; non-use of contraception, by sex: Results of generalized estimating equation logistic regressions with controls for population stratification, United States 1994-2002

	Race controls		Structural controls	
	Males	Females	Males	Females
Variables	e^{β} (t)	e^{β} (t)	e^{β} (t)	e^{β} (t)
Genotype				
DRD2 *A1/A2	1.95 (2.49)*	1.72 (2.53)*	1.91 (2.44)*	1.72 (2.51)*
*DRD2** A2/A2	1.82 (2.23)*	1.65 (2.35)*	1.72 (2.08)*	1.68 (2.44)*
*DRD2** A1/A1 (Ref.)	--	--	--	--
DAT1 *9R/10R	0.72 (1.15)	2.06 (2.21)*	0.77 (0.93)	2.07 (2.22)*
DAT1 *10R/10R	0.77 (0.95)	1.62 (1.50)	0.82 (0.73)	1.59 (1.44)
DAT1 *−/− (Ref.)	0.54 (1.57)	1.91 (1.37)	0.61 (1.18)	1.83 (1.28)
DAT1 *9R/9R	--	--	--	--
*MAOA** 2R/−	1.67 (0.89)	2.75 (2.83)**	1.70 (0.93)	2.58 (2.70)**
*MAOA** −/− (Ref.)	--	--	--	--
Demographics				
Age <=18	0.89 (1.00)	1.08 (0.64)	0.91 (0.82)	1.07 (0.61)
African American	1.20 (1.06)	0.84 (1.06)	--	--
Hispanic	1.20 (1.05)	1.16 (0.88)	--	--
Asian	1.45 (1.51)	1.30 (1.02)	--	--
Native American	3.39 (4.23)**	0.70 (1.36)	--	--
Caucasian (Ref.)	--	--	--	--
Family				
2 biological parents	0.83 (1.49)	0.75 (2.37)*	0.84 (1.36)	0.77 (2.12)*
Parents' income	1.00 (1.16)	1.00 (2.09)*	1.00 (1.33)	1.00 (1.98)*
Parents' education >HS	1.01 (0.08)	0.84 (1.36)	0.98 (0.15)	0.82 (1.56)
Number of siblings	1.01 (0.21)	1.11 (2.17)*	1.02 (0.35)	1.1 (1.99)*
Behaviour and attitudes				
Religiosity	1.22 (1.56)	1.03 (0.24)	1.25 (1.77)†	1.01 (0.09)
Months since 1st sex	1.00 (1.25)	1.00 (2.05)*	1.00 (1.46)	1.00 (1.92)†
Smoked last 30 days	1.26 (1.96)†	1.27 (2.05)*	1.24 (1.83)†	1.29 (2.17)*
Drinking frequency	1.02 (0.72)	0.95 (1.43)	1.02 (0.62)	0.95 (1.37)
Expelled from school	1.36 (1.64)	1.85 (2.51)*	1.41 (1.85)†	1.79 (2.36)*
Birth control self-efficacy	0.95 (0.89)	0.90 (2.02)*	0.95 (0.90)	0.90 (2.00)*
Prepared for birth control	0.90 (1.59)	0.86 (2.00)*	0.89 (1.73)†	0.86 (1.93)†

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	Race controls		Structural controls	
	Males	Females	Males	Females
Variables	**e^{β} (t)**	**e^{β} (t)**	**e^{β} (t)**	**e^{β} (t)**
Forgo coitus if no birth control available	0.89 (2.17) *	0.75 (5.46) **	0.90 (2.17) *	0.75 (5.40) **
Contraceptive knowledge	0.44 (2.58) **	0.99 (0.02)	0.45 (2.54) *	0.98 (0.05)
Contraceptive attitudes	1.24 (3.07) **	1.45 (4.59) **	1.24 (3.01) **	1.44 (4.53) **
Married at Wave 3	1.90(4.42) **	1.84 (4.77) **	1.85 (4.23) **	1.88 (4.90) **
Intercept	0.56 (0.97)	0.70 (0.55)	0.65 (0.67)	0.54 (0.90)
Sample size	1971	2092	1971	2092

† p <0.10;

* p < 0.05;

** p <0.01, two-tailed test

Note: Regression coefficients are presented in exponentiated (odds' ratio) form. Numbers in parantheses are t-statistics. The symbol '-' indicates an unlisted allele (e.g., neither 9R nor 10R for *DAT1* gene).

Source: As for Table 1.

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Table 5

Associations of genotypes and other variables with female adolescents' non-use of contraception, by contraceptive type: Results of generalized estimating equation logistic regressions, United States 1994-2002

	None vs. Condom	None vs. Other
Variables	**e^{β} (t)**	**e^{β} (t)**
Genotype		
*DRD2**A1/A2	1.63(2.02) *	2.07(2.59) **
*DRD2**A2/A2	1.68(2.17) *	1.73(2.01) *
*DRD2**A1/A1		
DAT1 *9R/10R	1.76(1.55)	1.77(1.37)
DAT1 *10R/10R	2.16(2.07) *	2.13(1.80) †
DAT1 *−/−	2.38(1.52)	1.46(0.70)
DAT1 *9R/9R		
*MAOA**2R/−	2.68(2.57) *	5.72(2.42) *
*MAOA**−/−		
Demographics		
Age <=18	0.76(2.13) *	2.60(5.79) **
African American	0.58(2.94) **	2.19(3.28) **
Hispanic	1.08(0.4)	1.21(0.86)
Asian	1.28(0.87)	1.74(1.42)
Native American	0.96(0.11)	0.41(2.62) **
Caucasian		
Family		
2 biological parents	0.77(1.91) †	0.72(2.07)
Parent's income	1.00(2.19) *	1.00(2.76) **
Parents' education >HS	0.83(1.30)	0.88(0.79)
Number of siblings	1.05(0.99)	1.20(2.76) **
Behaviour and attitudes		
Religiosity	1.03(0.23)	1.21(1.06)
Months since 1st sex	1.01(2.63) **	1.00(0.89)
Smoked last 30 days	1.09(0.66)	1.38(2.08) *
Drinking frequency	0.98(0.61)	0.91(1.91) †
Expelled from school	2.13(2.43) *	1.17(0.48)
Birth control self-efficacy	0.88(2.02) *	0.95(0.57)
Prepared for birth control	0.94(0.71)	0.72(2.64) **
Forgo coitus if no birth	0.78(4.49) **	0.75(3.67) **

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	None vs. Condom	None vs. Other
Variables	**e^{β} (t)**	**e^{β} (t)**
control available		
Contraceptive knowledge	0.68(1.01)	0.69(0.77)
Contraceptive attitudes	1.49(4.49) **	1.42(2.97) **
Married at Wave 3	1.91(4.42) **	1.51(2.46) *
Intercept	1.05(0.07)	3.15(1.25)
Sample size	1545	1128

† p <0.10;

* p <0.05;

** p < 0.01, two-tailed test

NOTE: Regression coefficients are presented in exponentiated (odds' ratio) form. Numbers in parantheses are t-statistics. Contraceptive methods considered to be ineffective (coitus interruptus, rhythm method) are categorized as no method. Sample sizes reflect the number of observations who reported one of the two outcome values being analyzed. The symbol odds'-odds' indicates an unlisted allele (e.g., neither 9R nor 10R for *DAT1* gene).

Source: As for Table 1.

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Table 6

Associations of genotypes and other variables with male adolescents' non-use of contraception by contraceptive type: Results of generalized estimating equations logistic regressions, United States 1994-2002

	None vs. Condom	None vs. Other
Variables	**e^{β} (t)**	**e^{β} (t)**
Genotype		
*DRD2*A1/A2*	1.85(2.15)*	1.45(0.92)
*DRD2*A2/A2*	1.68(1.83)†	1.52(1.06)
*DRD2*A1/A1*		
*DAT1 *9R/10R*	0.64(1.37)	1.00(0.00)
*DAT1 *10R/10R*	0.60(1.64)	1.09(0.22)
*DAT1 *–/–*	0.45(1.82)†	0.60(0.86)
*DAT1 *9R/9R*		
*MA OA *2R/–*	1.55(0.72)	1.99(0.64)
MAOA–/–*		
Demographics		
Age <=18	0.57(4.61)*	3.20(5.37)**
African American	0.89(0.61)	2.77(3.74)**
Hispanic	0.99(0.07)	1.95(2.69)**
Asian	1.27(0.85)	1.81(1.75)†
Native American	2.93(3.5)**	4.22(2.76)**
Caucasian		
Family		0.70(1.83)†
2 biological parents	0.89(0.81)	
Parents' income	1.00(0.87)	0.99(1.43)
Parents' education >HS	1.04(0.28)	0.92(0.42)
Number of siblings	1.00(0.07)	0.99(0.12)
Behaviour and attitudes		
Religiosity	1.33(2.09)*	1.02(0.10)
Months since 1st sex	1.00(2.28)*	1.00(0.92)
Smoked last 30 days	1.20(1.46)	1.26(1.27)
Drinking frequency	1.01(0.32)	0.97(0.61)
Expelled from school	1.48(1.91)†	1.24(0.78)
Birth control self-efficacy	0.95(0.86)	0.87(1.54)
Prepared for birth control	0.90(1.43)	0.86(1.44)
Forgo coitus if no birth control available	0.89(2.16)*	0.90(1.19)

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	None vs. Condom	None vs. Other
Variables	**e^{β} (t)**	**e^{β} (t)**
Contraceptive knowledge	0.45(2.34) *	0.31(2.45) *
Contraceptive attitudes	1.36(3.98) **	1.01(0.10)
Married at Wave 3	2.19(4.74) **	1.08(0.37)
Intercept	1.13(0.17)	9.84(2.48) *
Sample size	1492	852

† $p < 0.10$;

* $p < 0.05$;

** $p < 0.01$, two-tailed test

NOTE: Regression coefficients are presented in exponentiated (odds ratio) form. Numbers in parantheses are t-statistics. Contraceptive methods considered to be ineffective (coitus interruptus, rhythm method) are categorized as no method. Sample sizes reflect the number of observations who reported one of the two outcome values being analyzed. The symbol '-' indicates an unlisted allele (e.g., neither 9R nor 10R for *DAT1* gene).

Source: As for Table 1.