Heritability of DUI Convictions: A Twin Study of Driving Under the Influence of Alcohol

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Background: The study was undertaken to assess the relative contributions of genetic and environmental influences on drunk-driving. *Methods:* Driving records of a cohort of male and female twins ($N = 17{,}360$) from the Mid-Atlantic Twin Registry were examined. Structural equation models were used to estimate the *magnitude* of genetic and environmental effects on male and female phenotypes, and test for gender differences. *Results:* There were significant gender and age effects. Compared with females, males were five times more likely to engage in driving under the influence. Among persons aged 21–49 years, the risk for drunk-driving was eight times that for those aged 50+ years and five times greater than those ≤20 years. In both males and females, aged 21–49 years, a large proportion (57%) of the variance in drunk-driving was due to genetic factors and the remaining 43% due to individual specific environmental influences. *Conclusions:* Drunk-driving is under significant genetic influence in both males and females. Our findings suggest that a different set of genes influence DUIs in men and women.

∎ **Keywords:** DUI, twins, gender differences

The World Health Organization (WHO) has identified driving under the influence of alcohol as a major factor responsible for road traffic injuries worldwide (WHO, 2003). In the USA, motor vehicle crashes are the third leading cause of death, resulting in more than 40,000 fatalities each year. In 2002, there were 6.3 million traffic crashes with more than 2.9 million people sustaining injuries and nearly 43,000 fatalities (National Highway Traffic Safety Administration, 2002). Forty-one percent of all fatalities recorded that year were alcohol-related. The enormous impact of drunk-driving makes the study of the causal factors involved in driving under the influence an urgent priority.

Temperance boards were originally established in Sweden in 1916 to register individuals with alcoholism or sentinel events due to alcohol. The Temperance Board data have been used by researchers in a variety of ways, including evaluation of the influence of heritability on alcohol-related events (Kendler et al., 1997). Data from the Temperance Board registration of male–male twin pairs showed five subtypes of alcoholism, three of which included drunk-driving (Kendler et al., 1998). For the three subtypes of alcoholism that included a history of drunk-driving (i.e., Early onset — Multiple registrant, Single cause registrant — Drive [SCR-Drive], and Late onset — Multiple registrant),

the hazard rate of Temperament Board registrations was higher in monozygotic twins as compared to dizygotic twins, consistent with a genetic influence on DUI.

It is recognized that alcoholism is clinically and etiologically heterogeneous. Genetic analyses have showed that subtypes of drunk-driving such as public drunkenness and alcohol-related crime significantly predicted Temperance Board Registration in the co-twin of 5,177 male twin pairs. These associations were higher in MZ versus DZ twins — evidence for a substantial genetic role in these different subtypes. A probandwise concordance rate of 0.23 for monozygotic twins and 0.09 for dizygotic twins was reported specifically for drunk-driving (Kendler et al., 1998). Approximately 41% of the variance in alcohol-related driving was attributable to genetic influences. Of the total genetic variance, 26% was attributable to a

common genetic factor that influenced public drunkenness and other alcohol-related crime and 14% was specific to drunk-driving. There was a small familial environmental effect of 8% that was shared with the other two alcohol-related behaviors (Kendler et al., 1998).

A recent analysis of DUI behavior from the U.S. National Longitudinal Study of Adolescent Health (ADD Health; Beaver & Barnes, 2012) reported heritability estimates of 53% with the remaining variation accounted for by non-shared environmental factors. These estimates were based upon self-reported data.

The present study was undertaken to assess the relative contributions of genetic, shared, and individual specific environmental effects on drunk-driving in a large US sample of male and female twins from the Mid-Atlantic Twin Registry (MATR). One of the methodological issues in the study of genetic and environmental factors in alcohol-related outcomes has been the validity of the data. Alcohol-related outcomes are often based on self-report and therefore subject to bias. We obtained actual driving records to avert the potential bias of self-reported data. Our goal was to compare the findings with the prior analyses from the Swedish cohort and National Longitudinal study and to elucidate any significant gender differences in the etiology of drunk-driving using data from opposite-sex twin pairs.

Methods

Participants represented a cohort of twins, aged 18–67. The MATR is a population-based registry of over 75,000 twin pairs ascertained through birth records (Lilley & Silberg, 2013). For evaluating the effects of heritability on the likelihood of driving under the influence of alcohol, Virginia driving records were matched with the twin pairs available from the registry by the Department of Motor Vehicles. To protect confidentiality, no personal identifiers resulting from the DMV match were retained. Driving while intoxicated, drinking while operating a motor vehicle, driving under the influence of alcohol, or refusing blood alcohol/breath test were considered 'drunk-driving' or DUI.

Study Sample

The total number of twin-pairs with DMV records was 13,267. There were 8,680 twin-pairs where zygosity information was available for both twins. The breakdown showed 2,619 MZ pairs and 6,061 DZ pairs. Of the MZ pairs 1,256 were males and 1,363 were females. There were 1,051 male DZ pairs, 1,114 female DZ pairs, and 3,896 DZ opposite-sex pairs.

Statistical Analyses

Genetic analyses. Standard biometrical genetic model-fitting methods were used to decompose the observed vari-

ation in drunk-driving in terms of additive genetic (A), shared environmental (C), and non-shared or unique environmental (E) risks. Additive gene action (A) reflects the additive or average effect of individual alleles at genetic loci influencing a trait or behavior. Common environmental effects (C) describe influences that make family members more alike compared to random pairs of individuals. Non-shared or unique environmental risks (E) capture aspects of the environment that are unique to each individual and are therefore uncorrelated between twins. Since MZ twin pairs are genetically identical, the additive genetic correlation is fixed to 1.0. The additive genetic correlation for DZ twin pairs is fixed to 0.5 because on average DZ twin pairs share only half their genes in common. Non-shared environmental effects (E) are by definition uncorrelated and also include measurement error, including short-term fluctuations of the environment. An MZ correlation that is about twice the DZ correlation suggests the presence of an underlying genetic influence that is additive in nature. A DZ correlation that is greater than half the MZ correlation suggests common environmental influences. An MZ correlation that is less than 1 suggests the presence of specific or unique environmental influences.

The model can be extended to allow for heterogeneity between the sexes in the relative contributions of the three sources of variance and to permit a test of sex differences in which genes contribute to risk for DUI (Neale & Cardon, 1992). Limitations, extensions, and assumptions of the model have been widely discussed. Principal assumptions are: additive gene action, random mating, and equal environmental correlations in MZ and DZ twins (Eaves et al., 1989).

Tetrachoric correlations were computed from 2×2 contingency tables of conviction status in MZ and DZ same-sex and opposite-sex twin pairs. This estimation assumes an underlying, normally distributed liability to the trait due to genetic and environmental factors (Neale & Cardon, 1992). Because driving under the influence is coded as present or absent ('0' or '1'), the data for model fitting was analyzed using the raw ordinal data option in the Mx software package (Neale et al., 2003). This approach assumes that the observed ordinal categories within each variable are an imprecise measure of an underlying latent normal liability distribution, and that this liability distribution has one or more threshold values that discriminate between the categories. Thresholds can be conceived of as cut points along a standard normal distribution that classifies individuals in terms of a probability or risk of endorsing one of two or more discrete (ordinal) categories.

Structural Equation Modeling

The contribution of genetic and environmental factors to drunk-driving was estimated using structural equation analysis with the statistical program Mx. Several alternative

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TABLE 1

Cross-Tabulation of Drunk-Driving Convictions by Age Goup and Gender

Age* group	Drunk-driving conviction			Total
	No	Yes	Prevalence	
≤20 years				
Males	2,048	41	1.96	2,089
Females	2,086	12	0.57	2,098
Total	4,134	53	1.27	4,187
21–49 years				
Males	3,857	405	9.50	4,262
Females	4,778	105	2.15	4,883
Total	8,635	510	5.58	9,145
≥50 years				
Males	2,128	32	1.48	2,160
Females	1,865	3	0.16	1,868
Total	3,993	35	0.87	4,028
Total	16,762	598	3.44	17,360

TABLE 2

Tetrachoric Correlations for Drunk-Driving Convictions in MZ and DZ Twins Aged 21–49 Years

Zygosity group	Number of twin pairs	Correlation	LL of correlation	UL of correlation
MZM	688	0.54	0.34	0.72
DZM	459	0.18	-0.07	0.42
MZF	834	0.58	0.29	0.86
DZF	648	0.35	-0.11	0.80
DOS	1,882	-0.01	-0.21	0.18

Note: MZM = monozygotic male twin pairs; DZM = dizygotic male twin pairs; MZF = monozygotic female twin pairs; DZF = dizygotic female twin pairs; DOS = dizygotic opposite-sex pairs; LL = Lower 95% confidence limit; UL = Upper 95% confidence limit.

sex-limitation models, using all six zygosity groups (MZ-males, MZ-females, DZ-male, DZ females, DOS-MF (DZ opposite-sex pairs where the first twin is a male and the second twin a female), and DOS-FM (DZ opposite-sex pairs where the first twin is a female and the second twin a male)), were used to test hypotheses about etiology and of possible gender effects underlying the influence of genetic and environmental factors on drunk-driving.

The general sex-limitation model tests whether the magnitude of genetic and environmental effects are the same for male and females. Using the opposite-sex twins, the more restricted sex-limitation model tests whether or not it is the same set of genes or shared environmental experiences that influence a trait in males and females (Eaves et al., 1978; Neale & Cardon, 1992).

Maximum likelihood estimates of model parameters and likelihood ratio tests of alternative hypotheses were obtained. The *p* value of the associated chi-square statistic was used to evaluate the fit of the model. The model that fits the data well is the one that has a non-significant *p* value for the chi-squared (χ^2) goodness-of-fit statistic. Another indicator of fit is Akaike's information criterion (AIC) defined as χ^2 minus twice the degrees of freedom (*df*). Models with low AIC values indicate a more parsimonious explanation of the data. Because it is biologically rare to have genetic dominance in the absence of additive genetic effects the DE model was not considered. In the classical study of twins reared together, genetic dominance (D) and shared environment (C) are completely confounded, making it impossible to estimate both parameters simultaneously.

Results

Prevalence Rates

Table 1 shows a total of 598 DUI convictions — 53 convictions in persons under 21 years, 510 in persons aged between 21 and 49 years, and 35 in persons aged 50+ years. Overall prevalence of DUI convictions over an 11-year period was 3.4%. The age group with the highest prevalence (5.6%) was the 21- to 49-year-olds. In all age groups, the prevalence for males was greater than that for females.

We found significant gender differences in DUI convictions. Compared with females, males were approximately five times more likely to engage in drunk-driving. Relative to persons aged 50 and above, twins in the age range 21–49 years had greater than eight times the risk for drunk-driving. For persons less than 21 years old, there was a 1.7-fold increase in risk above that for persons 50 years old and above. Compared with twins less than 21 years old, twins aged 21–49 years old had five times the risk for drunk-driving conviction.

Genetic Analyses

Due to a low prevalence of drunk-driving convictions in those under the legal age (<21 years) and those aged 50 years or more, these age groups were excluded from the genetic analysis. There were 4,511 twin pairs between the ages of 21 to 49 years.

Twin Correlations

The twin correlations for DUIs and their 95% confidence intervals for the five zygosity groups are presented in Table 2. Among same-sex male pairs, MZ twin correlations were approximately twice that of the DZ twin pairs. The MZ and DZ male–male pair correlations were 0.54 and 0.18, respectively. The female correlations were 0.58 for MZ twins and 0.35 for DZ twin pairs. The DZ opposite-sex correlation was -0.01. The correlation patterns for MZ and DZ twin pairs, especially the DZ opposite-sex twins, suggest there may be etiological differences in the causes of DUI in males and females.

Model Fitting

In fitting structural equation models to the data we assumed the thresholds or prevalence for driving under the influence to be different in males and females. We sought to: (1) estimate the relative role of additive genetic, shared
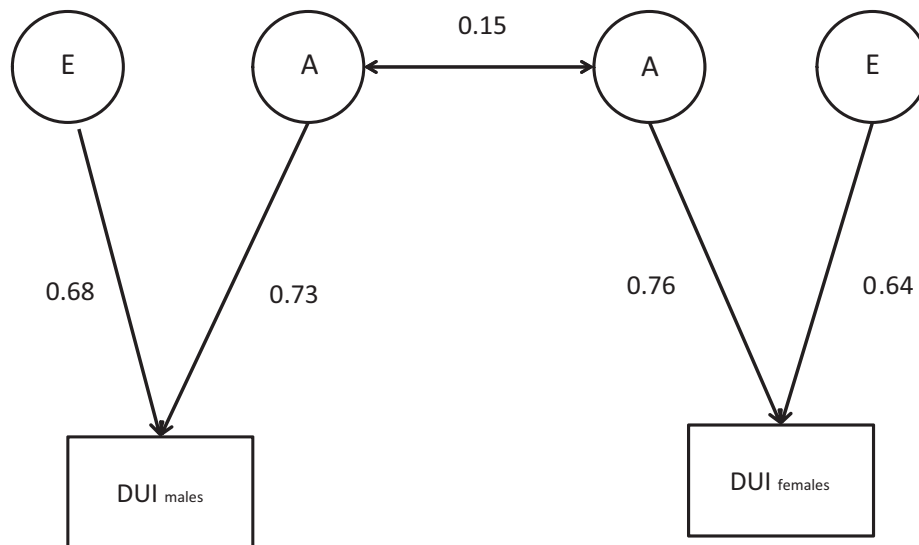
FIGURE 1

Additive genetic (A) and unique environmental (E) parameter estimates and additive genetic correlation for DUIs in male and female twins. Path diagram is shown for DZ opposite-sex twin pairs.

environmental, and individual specific environmental factors on DUIs in males and females; (2) test for differences in the magnitude of these components in males and females; and (3) determine whether the same genes influence the trait for the two sexes.

DUI Convictions in MZ and DZ Twins

We fit a model that assumed that different genes affect DUIs in males in females and permit the magnitude of the variance components to be different in the two sexes. There was little difference in the fit of a model that allowed the estimates of the genetic and individual specific environmental factors to be the same in males and females. According to AIC a model that constrained the genetic correlation, r_g, to 0.5, did not provide as good a fit as a model that freed the genetic correlation in opposite-sex pairs. This suggests that there may be a different set of genes influencing DUIs in males and females.

We show the parameter estimates for males and females, and the genetic correlation between them in Figure 1. In females the standardized components of variance showed that 58% of the variance in DUI conviction was due to additive genetic influence and 42% of the variance due to unique environmental effects. For males the estimates were 54% and 46%, respectively. The genetic correlation r_g between opposite-sex twins was estimated at 0.15. There was no effect of the shared environment.

Discussion

Using actual driving conviction records linked to a large twin registry, we found a significant genetic component to drunk-driving among 21- to 49-year-old males and females. The prevalence of drunk-driving for males and females could not be constrained to be equal. For male MZ twin pairs, the tetrachoric correlations were 0.54 and 0.18 in DZ male twins. Female MZ twins had a twin correlation of 0.58 and DZ female twin pairs, 0.35. There was nearly a zero correlation in opposite-sex twin pairs.

The results of model fitting indicated that a large proportion (57%) of the variance in drunk-driving was due to genetic factors and the remaining variance (43%) due to individual specific environmental influences. Although both the Swedish and US ADD Health samples obtain significant heritability for drunk-driving, our estimate of 57% is higher than that reported. However, given the relatively low prevalence and analysis of binary outcomes, these estimates are expected to lie within a broad interval of confidence.

There are additional risk factors involved in DUIs, such as the personality traits of risk-taking, antisociality, and sensation-seeking, which all have a higher male-to-female ratio. This is in concert with the well-known fact that the rate of alcoholism is higher in males than in females. Risk-taking has been implicated as a major factor underlying motor vehicle crashes (Eysenck, 1990; Zuckerman & Kuhlman, 2000). Numerous studies have reported moderate to significant correlations between sensation-seeking and risky driving behavior, including driving under the influence of alcohol (Dahlen et al., 2005). A review of 18 studies reported a significant association between sensation-seeking and drunk-driving in 13 studies, and a stronger association in men (Jonah, 1997).

Twin studies have indicated a genetic basis for sensation-seeking to be the underlying causal factor in risky behavior. Nearly half of the genetic variance for willingness to drive while drunk is due to genetic effects influencing the personality trait of extraversion (Martin & Boomsma, 1989). Other factors that have been associated with drunk-driving are impulsiveness (Ryb et al., 2006), psychopathic deviance (MacDonald & Pedersen, 1990), drug use problems (Lapham et al., 2001), and neurocognitive impairment (Ouimet et al., 2007). All of these factors have a strong genetic etiology. The twin correlations for antisocial personality disorder of 0.52 in MZ and 0.24 in DZ young adult twins are nearly identical to those for drunk-driving, also showing a substantial genetic influence (Silberg et al., 2007). Given the finding of gender differences in the causes of DUI, and differences in the personality factors that underlie them, studies of any genetic association between DUIs and personality in males and females is an important area of study.

A few limitations from this study deserve special mention. First, there were a relatively small number of twin matches in this study. Nevertheless, the twin correlations in the sample we used are comparable to those reported previously in the Swedish population (Kendler et al., 1997). This is the first study, to our knowledge, of using actual driving conviction records paired with twin pairs to evaluate the genetic influence on drunk-driving. Nonetheless, since the DMV only keeps records on DUI convictions for 11 years, we would not have been able to identify twins who had DUI convictions for longer periods of time. Another important limitation is the relatively small differences in the fit of the models. The small study sample size may have magnified subtle differences in the data and would require replications in other population samples.

This study of a large twin registry using actual driving conviction records provides important insights for future exploration. Further studies of the genetic influence on driving under the influence should include the need for replication in other population samples, conducting studies using larger sample sizes, and studying the differences between personality traits that may account for the difference in genetic effect in drunk-driving between men and women.

Acknowledgments

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