



## Genetic and environmental influences on being expelled and suspended from school



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### ABSTRACT

There has been a significant amount of interest in understanding some of the key issues related to school suspensions and expulsions. One of the more intriguing and studied of these issues has to do with factors that contribute to variation in school disciplinary sanctions. To date, however, no research has examined the genetic architecture to either suspensions or expulsions. The current study addresses this gap in the literature by analyzing a sample of twin pairs drawn from the National Longitudinal Study of Adolescent to Adult Health (Add Health). The results of the analyses revealed that shared and nonshared environmental factors accounted for the variation in suspensions. Genetic influences, in contrast, were the dominant source of variation for expulsions. We conclude by discussing the implications of our findings and avenues for future research.

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There has been a considerable amount of interest in unpacking the various factors related to school suspensions and expulsions. Research has, for instance, focused on black–white differences in rates of suspensions and expulsions (Wright, Morgan, Coyne, Beaver, & Barnes, 2014), whether various policies lead to changes in the rates of suspensions and expulsions (Cornell, Gregory, & Fan, 2011), and the various consequences associated with being suspended or expelled (Rocque & Paternoster, 2011). Yet, one of the more elusive issues focuses on variation in the underlying etiological processes that contribute to variation in suspension and/or expulsion. Numerous explanations have been advanced, including discrimination by teachers, prejudicial views held by school administrators, and differential involvement in behaviors that violate school policies, to name just a few (Kinsler, 2011; Moore, 2002; Wright et al., 2014). What is noticeably absent from this line of research is information on the potential influence of genetic factors on explaining individual differences in school suspensions and expulsions. This gap in the existing literature is all the more surprising when juxtaposed against the fact that previous research has shown that nearly every human phenotype, including problem behavior, is at least partially influenced by genetic factors (Polderman et al., 2015).

The results generated from this body of research have revealed consistently that genetic factors explain about 50% of the variance in most phenotypes. This finding is so well established that it has been dubbed the first law of behavior genetics (Turkheimer, 2000). The remaining variance not accounted for by genetic influences is attributable to non-genetic environmental effects (and error). Two types of environmental influence can account for environmental variance: shared environmental influences and nonshared environmental influences. Shared environments are environments that are the same between siblings and that make siblings more similar phenotypically. Nonshared environments, in contrast, are environments and non-genetic factors that cause siblings to be different from each other. Collectively, the genetic effect (referred to as heritability) along with shared and nonshared environmental influences (i.e., non-genetic influences) account for 100% of the variance in all phenotypes.

Given that these genetic and environmental effects are so well established, some may question whether it is necessary to conduct additional univariate studies on the genetic and environmental basis of human behaviors. There is a reason to suspect, however, that suspensions and expulsions may have different etiologies and thus be differentially affected by genetic and environmental influences. Suspensions, for example, can be driven by school-specific policies and differential enforcement by teachers and administrators (e.g., Cornell et al., 2011). Stated differently, environmental factors somewhat outside the control

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of youth might affect the probability that a child or adolescent is suspended from school. Moreover, suspensions, when compared to expulsions, tend to be associated with less serious types of misconduct. These are often minor forms of misbehavior that are age-normative and, on average, under less genetic influence when compared against more serious types of misconduct (Barnes, Beaver, & Boutwell, 2011).

In comparison, there is less discretion when it comes to policies related to expulsions. Expulsions are driven, at least in part, by more serious types of behaviors, such as physical fighting, possession of a deadly weapon, threatening conduct, and the selling of drugs at school. Behaviors that lead to expulsions are thus likely to be significantly more serious when compared to those that result in a suspension. Additionally, previous research has revealed that genetic influences are more heavily involved in the development of more serious forms of antisocial behavior relative to less serious forms of antisocial behavior (Barnes et al., 2011). This suggests that genetic influences may be more likely to underlie the etiology of expulsions compared to suspensions.

To test this possibility, we employ the well-known twin-based research design. With the twin-based research design, the phenotypic similarity of monozygotic (MZ) twins is compared to the phenotypic similarity of dizygotic (DZ) twins. Given that MZ twins share twice as much genetic material as DZ twins, and both types of twins are assumed to share relatively equal environments—an assumption that recent research has indicated is typically upheld (Barnes et al., 2014)—then the only reason that MZ twins should be more similar to one another than DZ twins is because of genetic influences (Plomin, DeFries, Knopik, & Neiderhiser, 2013). As the similarity of MZ twins increases relative to DZ twins, then the genetic effect increases, too. The twin-based research design has been used in thousands of studies, the assumptions that accompany this design have been tested and retested, and overall patterns of findings have been replicated using other types of research designs (e.g., adoption research designs). Against this backdrop, there is reason to suspect that the twin-based method is among the most robust research designs employed in the social and behavioral sciences.

## 1. Methods

### 1.1. Sample

Data for this study were drawn from the National Longitudinal Study of Adolescent to Adult Health (Add Health; Udry, 2003). The Add Health is a four-wave prospective study of a nationally representative sample of American adolescents who were attending middle or high school during the 1994–1995 school year. The first wave of questionnaires—known as the wave 1 in-school surveys—was administered during a regular school day to nearly 90,000 adolescents. In order to gather additional information, a subsample of youth along with their primary caregiver was selected to be re-interviewed in their homes. In total, 20,745 youths participated in the wave 1 in-home component. Approximately 1.5 years later, the second round of interviews was completed with 14,738 of the youths. The final two waves of data were collected in 2001–2002 ( $n = 15,197$ ) and 2007–2008 ( $n = 15,701$ ), respectively (Harris et al., 2003). Given that few respondents were still in high school at wave 3, the current study employs data from only the first two waves of the Add Health.

Embedded within the Add Health data are a number of subsamples. One of these subsamples includes twins that can be used for quantitative genetic analysis (Harris, Halpern, Smolen, & Haberstick, 2006). Twins were oversampled for inclusion in the study. Specifically, during wave 1 interviews, respondents were asked whether they had a co-twin. If they responded affirmatively, then their co-twin was also included in the sample. Overall, close to 800 twin pairs were included in the Add Health data. After removing cases with missing data and after eliminating cases with unknown zygosity, the final analytical sample consisted of 289 MZ twin pairs (578 individuals) and 248 same-sex DZ twin pairs (496 individuals).

### 1.2. Measures

#### 1.2.1. Suspension

Three measures of suspension were used in the current study. First, during wave 1 interviews, respondents were asked whether they had ever received an out-of-school suspension. Responses to this question were coded dichotomously, such that 0 = *never suspended* and 1 = *suspended*. Second, during wave 2 interviews, respondents were again asked if they had received an out-of-school suspension but this time they were asked to report only those incidences that occurred during the current school year (if the interview was conducted in the summer, they were asked about the preceding school year). Responses were once again coded dichotomously, wherein 0 = *not suspended* and 1 = *suspended*. Third, these two dichotomous suspension variables were summed together and then dichotomized to arrive at a lifetime measure of suspension. With this coding scheme, 0 = *never suspended* and 1 = *suspended at least one time*.

#### 1.2.2. Expulsion

Three measures of expulsion were analyzed in this study and they were measured in much the same way as the suspension variables. First, during wave 1 interviews, respondents were asked whether they had ever been expelled from school. Responses to this question were coded dichotomously, such that 0 = *not expelled* and 1 = *expelled*. Second, during wave 2 interviews, respondents were asked whether they had been expelled in the current school year (if the interview was conducted in the summer, they were asked about the preceding school year). Responses were once again coded dichotomously with 0 = *not expelled* and 1 = *expelled*. Third, these two dichotomous expulsion variables were summed together and then dichotomized to create a lifetime measure of expulsion, where 0 = *never expelled* and 1 = *expelled at least one time*. Table 1 presents the prevalence of both suspensions and expulsions, separated according to twin zygosity type.

### 1.3. Plan of analysis

The analysis for the current study followed a two-step process. First, logistic regression models were estimated by zygosity to determine whether there is an association between one twin having been suspended (expelled) and the odds that their co-twin had been suspended (expelled). If there is a genetic effect on being suspended (expelled), then the association for MZ twins should be significantly greater than the association for DZ twins. Second, to more formally estimate the genetic, shared environmental, and nonshared environmental influences on expulsions and suspensions, liability threshold versions of the ACE model were estimated for each of the examined outcomes using the statistical software program *Mplus* (Muthén & Muthén, 2010).

The liability threshold model is a biometric model fitting technique that is similar to the traditional univariate ACE model, but is acceptable for both categorical and dichotomous outcome measures (Prescott, 2004). The liability threshold model decomposes the variance in each of the examined outcome measures into three latent estimates: genetic influences (symbolized as A), shared environmental influences (symbolized as C), and nonshared environmental influences (symbolized as E).

**Table 1**  
Prevalence of suspensions and expulsions by zygosity.

	MZ twins	DZ twins
Suspension (wave 1)	23.6%	30.2%
Suspension (wave 2)	12.9%	11.3%
Expulsion (wave 1)	4.6%	5.5%
Expulsion (wave 2)	2.1%	2.5%
Ever suspended	26.5%	30.0%
Ever expelled	6.3%	5.7%
N (pairs)	289	248
N (individuals)	578	496

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