

## 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

**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

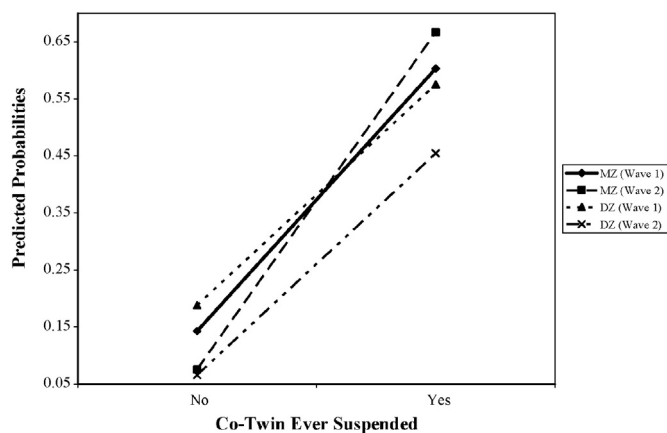
E). The A component of the model provides a latent estimate of the proportion of the variance in the outcome measure that can be explained by additive genetic influences. The C component provides a latent estimate of the proportion of the variance in the examined outcome that can be explained by shared environmental influences that make siblings more similar (e.g., SES and school policies). The E component provides a latent estimate of the proportion of the variance in the outcome measure that is explained by unique or nonshared environmental influences that make siblings different from one another (e.g., different peer groups), and also includes error. All three factors cumulatively explain 100% of the variance in the examined outcome measure.

## 2. Results

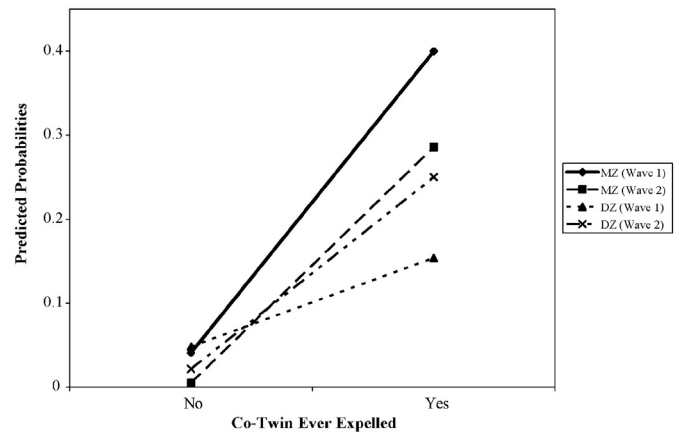
The analysis began by estimating binary logistic regression models for suspensions at wave 1 and wave 2. The results of these models are presented as predicted probabilities, conditional on co-twin suspension status and zygosity. The estimates are presented in Fig. 1. As can be seen, the odds ratios (ORs)—which are provided in the figure caption—are all larger for MZ twins compared to DZ twins, suggesting that there could be a genetic effect on the probability of suspension. Importantly, however, the predicted probabilities of being suspended are largely comparable for MZ and DZ twins.

Next, the same models were calculated except that the wave 1 and wave 2 expulsion variables were used instead of the suspension variables. The results of the logistic regression models are presented in Fig. 2. For these variables, the ORs are all larger for MZ twins than for DZ twins. The predicted probabilities clearly indicated that the effect of having an MZ co-twin who was expelled increased the predicted probability of being expelled more when compared to the effect of having a DZ co-twin who was expelled. This pattern of results is consistent with a partial genetic explanation for the odds of expulsion.

The last set of logistic regression models examined the composite measures of ever being suspended or ever being expelled. The results of these models are presented in Fig. 3 and show a pattern of results that is consistent with the wave-specific findings. Specifically, the ORs and predicted probabilities for the ever suspended variable are comparable for MZ and DZ twins, suggesting genetic influences on being suspended are minimal. For expulsions, the OR is greater for MZ twins than for DZ twins, which is reflected in the drastically different predicted probabilities of being expelled between both types of twins. This latter finding therefore suggests a potential genetic effect on being expelled.



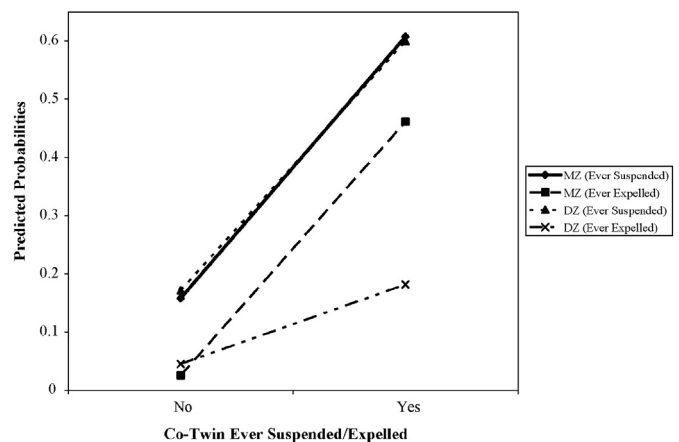
**Fig. 1.** Predicted probabilities of being suspended based on zygosity and whether co-twin had been suspended. Notes: MZ twins (wave 1):  $b = 2.210$ ,  $SE = .322$ ,  $OR = 9.120$ ,  $p < .001$ ; MZ twins (wave 2):  $b = 3.202$ ,  $SE = .515$ ,  $OR = 24.571$ ,  $p < .001$ ; DZ twins (wave 1):  $b = 1.765$ ,  $SE = .308$ ,  $OR = 5.843$ ,  $p < .001$ ; DZ twins (wave 2):  $b = 2.470$ ,  $SE = .530$ ,  $OR = 11.818$ ,  $p < .001$ .



**Fig. 2.** Predicted probabilities of being expelled based on zygosity and whether co-twin had been expelled. Notes: MZ twins (wave 1):  $b = 2.750$ ,  $SE = .715$ ,  $OR = 15.636$ ,  $p < .001$ ; MZ twins (wave 2):  $b = 4.392$ ,  $SE = 1.306$ ,  $OR = 80.800$ ,  $p < .001$ ; DZ twins (wave 1):  $b = 1.277$ ,  $SE = .829$ ,  $OR = 3.587$ ,  $p = .123$ ; DZ twins (wave 2):  $b = 2.714$ ,  $SE = 1.260$ ,  $OR = 15.083$ ,  $p < .05$ .

Last, liability threshold models were conducted to estimate the genetic, shared environmental, and nonshared environmental influences on the suspension and expulsion measures. Several goodness of fit statistics were estimated to evaluate model fit. More specifically, the Comparative Fit Index (CFI), the Tucker–Lewis Index (TLI), and the Root Mean Square Error of Approximation (RMSEA) were estimated. Model fit was assessed using results from all of the estimated statistics using criteria specified by Hu and Bentler (1999). A model that fits the data well should report CFI and TLI values of .95 or greater and RMSEA values of .06 or smaller. Wald's difference in coefficient test was used to maximize model parsimony and compare nested models alongside baseline models. Chi-square statistics were calculated to examine whether the prevalence of suspensions and expulsions varied significantly by zygosity (see Table 1). The results revealed that the chi-square values were non-significant for wave 1 and wave 2 expulsions, wave 2 suspensions, the ever suspended measure, and the ever expelled measure. The only chi-square statistic that was significant was for wave 1 suspensions (chi-square = 5.80,  $df = 1$ ,  $p = .02$ ).

The results of the liability threshold models and corresponding model fit statistics are presented in Table 2. As can be seen, the wave-specific suspension measures were not influenced by genetic factors, but rather by a combination of shared environmental influences (between 64%



**Fig. 3.** Predicted probabilities of ever being suspended/expelled based on zygosity and whether co-twin had ever been suspended/expelled. Notes: MZ twins (ever suspended):  $b = 2.110$ ,  $SE = .360$ ,  $OR = 8.246$ ,  $p < .001$ ; MZ twins (ever expelled):  $b = 3.489$ ,  $SE = .717$ ,  $OR = 32.743$ ,  $p < .001$ ; DZ twins (ever suspended):  $b = 1.980$ ,  $SE = .358$ ,  $OR = 7.239$ ,  $p < .001$ ; DZ twins (ever expelled):  $b = 1.546$ ,  $SE = .861$ ,  $OR = 4.694$ ,  $p = .073$ .

**Table 2**  
ACE model parameter estimates and fit statistics for suspensions and expulsions.

	Parameter estimates			Model fit statistics				
	A	C	E	$\chi^2$	$\Delta\chi^2$	CFI	TLI	RMSEA
<i>Suspension (wave 1)</i>								
ACE	.18	.50**	.32**	7.18		.971	.981	.072
AE	.59	.00	.08	15.87	8.04**	.918	.959	.105
CE	.00	.64**	.36**	7.70	.72	.975	.987	.059
E	.00	.00	1.00**	167.11	147.17**	.000	.553	.348
<i>Suspension (wave 2)</i>								
ACE	.27	.54*	.19**	1.39		1.00	1.007	.000
AE	.86**	.00	.14*	7.38	5.39*	.979	.990	.060
CE	.00	.77**	.23**	2.49	1.03	1.000	1.005	.000
E	.00	.00	1.00**	181.11	164.11**	.000	.565	.388
<i>Expulsion (wave 1)</i>								
ACE	.64*	.00	.36*	1.05		1.000	1.068	.000
AE	.64**	.00	.36*	1.23	.00	1.000	1.072	.000
CE	.00	.54**	.46**	2.93	5.98*	1.000	1.028	.000
E	.00	.00	1.00**	23.37	21.31**	.048	.619	.117
<i>Expulsion (wave 2)</i>								
ACE	.54	.30	.16	1.72		1.000	1.022	.000
AE	.86**	.00	.14	2.00	.30	1.000	1.026	.000
CE	.00	.78**	.22	2.52	.78	1.000	1.019	.000
E	.00	.00	1.00**	45.06	41.10**	.000	.590	.185
<i>Ever suspended</i>								
ACE	.04	.62**	.34**	2.06		1.000	1.005	.000
AE	.78**	.00	.22**	13.91	10.76**	.918	.959	.103
CE	.00	.65**	.35**	2.03	.04	1.000	1.008	.000
E	.00	.00	1.00**	135.71	123.32**	.000	.569	.335
<i>Ever expelled</i>								
ACE	.80**	.00	.20*	.46		1.000	1.026	.000
AE	.80**	.00	.20*	.61	.00	1.000	1.026	.000
CE	.00	.73**	.27**	3.78	66.92**	1.000	1.002	.000
E	.00	.00	1.00**	71.40	66.93**	.000	.591	.239

Chi-square difference tests were performed using Wald's test of parameter constraints. Note: Best-fitting model are bold-typed.

\*  $p < .05$ .

\*\*  $p < .01$ .

and 77% of the variance) and nonshared environmental influences (between 23% and 36% of the variance). A different pattern of findings emerged for the wave-specific expulsion measures. Specifically, genetic factors explaining 64% of the variance in the liability for expulsion at wave 1 and 86% of the variance in the liability at wave 2. The remaining variance in liability was attributable to nonshared environmental sources of variance. In the final models, measures assessing ever being suspended and ever being expelled were analyzed and the results revealed that 65% of the variance in liability of ever being suspended was the result of shared environmental factors, while the remaining 35% of the variance was the result of nonshared environmental factors. With respect to ever being expelled, ACE model parameter estimates from the best-fitting model suggested that 80% of the variance in liability was due to genetic factors, while the remaining 20% of the variance in liability was the result of nonshared environmental factors.

### 3. Discussion

During the past decade, we have seen a resurgence of research examining some of the key factors related to youth who receive serious school sanctions, particularly suspensions and expulsions. Despite the amount of research devoted to this topic, to date there has not been any research examining the genetic architecture of these types of disciplinary outcomes. The current study addressed this gap in the literature by analyzing a sample of twin pairs drawn from the Add Health. The results of our analyses revealed two broad findings. First, the results revealed that variation in suspensions was not influenced by genetic factors, but rather was the result of shared and nonshared environmental effects. This is a particularly interesting finding given that virtually

every human phenotype, at least to some extent, is impacted by genetic factors (Polderman et al., 2015). We revisit this finding momentarily. Second, and in direct contrast, were the results from the analysis of expulsion. These results suggested genetic factors accounted for most of the variance in liability for expulsion, with nonshared environmental influences accounting for the remaining variance.

Now to address the question: What accounts for these somewhat disparate findings in regard to the genetic and environmental contributors to suspensions and expulsions? As previously mentioned, suspensions are often reserved for less serious offenses and may be guided more by school-specific policies. Suspensions might also be the result of subjective assessments and enforced at the discretion of teachers and school administrators. Expulsions, however, are often reserved for the most serious types of behavior and for students who display disruptive and serious misconduct repeatedly. Not only are these types of behaviors under strong genetic influence (Barnes et al., 2011), but teachers and administrators likely have less discretionary oversight in administering punishments in such instances as most of the time they fall under zero-tolerance policies. If this is the case, then the end result is that individual behavior may drive expulsions to a greater extent than it does for suspensions, suggesting that genetic factors are more likely to underlie the former.

These findings have potential important ramifications for current research on suspensions and expulsions. Using the current findings as a backdrop, it appears as though expulsions are driven by individual behavior, not by some type of widespread discriminatory nature of school administrators. Variation in suspensions, however, is driven more by environmental influences. Much more research is needed on this topic in order to unpack the specific shared and nonshared environmental factors that are involved in creating variation in suspensions. Until such research is conducted, it is impossible to identify the specific environmental factors that are related to school suspensions among youth.

Although our study is the first to estimate genetic and environmental influences on suspensions and expulsions, there are a number of limitations that should be addressed in future studies. First, the measures of suspensions and expulsions were based on self-reports, not on school administration data. As a result, there is the possibility that these estimates are not entirely accurate. But we have little reason to suspect systematic bias given that self-reports of arrest (a much more serious outcome, meaning it is *more* likely to show bias than self-reports of suspensions or expulsions) tend to provide an accurate picture of offenders' arrest histories (Pollock, Menard, Elliott, & Huizinga, 2015). Second, the analyses were based on a sample of twins and thus the generalizability of these estimates remains in question. With that said, research exists showing that the twin sample of the Add Health is not significantly different from the nationally representative sample of the Add Health (Barnes & Boutwell, 2013). Last, the current analysis was only able to decompose variance in suspensions and expulsions without providing any information regarding the specific genetic polymorphisms, the specific shared environments, and the specific nonshared environments that might be accounting for this variance. Future research would benefit greatly from identifying these sources of variance.

Before concluding, it is important to note that just because expulsions are under significant genetic influence does not mean that these behaviors are inevitable outcomes for those who are genetically predisposed for being expelled. Genetic influences can be exacerbated or dampened depending on exposure to different types of environments (Rutter, 2006). Certain school and classroom environments may suppress or, conversely, may exacerbate antisocial predispositions. Beginning to identify which environments—particularly those found within the school—might be able to attenuate genetic effects could go a long way towards reducing problem behavior at school and, as a consequence, expulsions. In order for this to be achieved, the possibility that genetic influences are at play should be given full consideration in future studies on the causes of suspensions and expulsions.



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