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Original article

Frequency of Truancy at High School: Evidence for Genetic and Twin Specific Shared Environmental Influences

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Abstract

Purpose: The purpose of this study was to examine the relative influence of genetic and environmental factors on variation in truancy during high school. We examined the significance of genetic and shared and nonshared environmental influences. In addition, we tested for the presence of environmental factors specifically shared by twins, but not by their siblings.

Methods: A threshold model was used to analyze data from 4,835 twins and their non-twin siblings.

Results: Results showed a higher prevalence of truancy for males (38% vs. 29%) and an increase in prevalence with age ($\beta = -.53$). Individual differences in frequency of truancy were partly explained by genetic influences ($h^2 = 45\%$); for twins, the environmental variance was partitioned into 25% shared by twins, and 30% nonshared, whereas for singletons all environmental variance was nonshared (i.e., 55%).

Conclusions: Prevalence of truancy was higher for boys than for girls and it increased with age. Genetic and environmental influences accounted for the variance in frequency of truancy. Part of the shared environment represents influences that are shared by twins but not by non-twin siblings.

Keywords: Truancy; Antisocial behavior; Extended family design; Threshold model; Specific twin environment; Genetic influences; Statistical power

Truancy, defined as the illicit absence from school during 1 or more hours or days, is frequent from early adolescence onward. A total of 13% of Dutch high school students report skipping 1 or more hours of school during the past 2 months [1]. Among adolescents from the United States 11% of 8^{th}-grade students, 16% of 10^{th}-grade students, and 35% of 12^{th}-grade students reported skipping 1 or more days of school during the past month [2]. Truancy has been identified as one of the 10 most serious educational problems in the United States [3]. It has been linked to a range of negative outcomes such as substance use [4–6], poor performance at school [7,8], dropping out of school [9,10], and psychiatric disorders [11,12]. For example, adolescents who skipped school were three to six times more likely to use substances than adolescents who did not skip school [6]. Frequency of truancy has found to be negatively correlated with performance at school, even after controlling for verbal ability and personality [7]. Egger et al [11] found that one-quarter of children who skipped classes had at least one psychiatric disorder compared with 6.8% of children who never skipped classes. They found independent relationships between truancy and conduct disorder, oppositional defiant disorder, and depression. These findings clearly make truancy a topic of major concern.

Truancy is not an isolated behavior as it occurs in a broader context of antisocial behavior (ASB) [13]. Research in the field of ASB has started to focus on aggressive versus nonaggressive ASB [14–16], with truancy being a part of the latter [13]. In the present study, we focused on truancy because ASB is especially likely to occur in situations of unsupervised and unstructured time with peers [18,19]. Truancy is distinct from other nonaggressive ASB because it provides such a context in which adolescents are especially likely to

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initiate various kinds of ASB [4]. Indeed, truancy was found to be a first sign and powerful predictor of both aggressive and nonaggressive ASB with truants being more likely further penetrating the juvenile justice system [3], and with truancy increasing the odds of initiation of drug use [4]. Because truancy provides a context for the onset of various kinds of ASB, preventing high school students from truancy might prevent them from engaging in other kinds of ASB as well. From a clinical perspective it is therefore important to understand the etiology of truancy. The causes of individual differences in frequency of truancy, however, are understudied. Therefore, the aim of the present study was to examine the relative influence of genetic and environmental factors on frequency of truancy.

There are sex differences in prevalence of truancy. In the Netherlands, 44% of adolescent boys and 35% of girls reported to skip school during lifetime [1]. The same pattern of sex differences has been found for other types of nonaggressive ASB with higher prevalence in boys than in girls [14,16,20].

One behavior genetic study examined genetic influence on individual differences in truancy and found that the variation could be completely accounted for by shared (73%) and nonshared (27%) environmental influences [15]. However, the authors stated to interpret this result with caution, because the parameter estimates were based on a small prevalence of truancy. Genetic and shared environmental factors have been found to account for a substantial part of variation in nonaggressive ASB [15–17,20].

Truancy and other types of nonaggressive ASB are often performed together with peers [21,22], and twins are likely to grow up within the same peer group [23,24]. Rowe [25] reported that nonaggressive ASB is often performed together with a co-twin; he found that 61% of female twins and 79% of male twins reported committing one or more delinquent acts together with their co-twin. These high levels of co-action in twin pairs may be explained by environmental influences that are shared by twin pairs and not by other members of the family. In other words, the existence of a specific twin environment is plausible for frequency of truancy. However, the possible influence of environmental factors specifically shared by twins on variation in frequency of truancy or other types of ASB has not been studied before.

The relative influence of genetic, shared, and nonshared environmental influences explaining variation in nonaggressive ASB differs between boys and girls. For example, variation in rule breaking behavior in boys was explained by genetic influences (79%), whereas in girls, both genetic (56%) and shared environmental factors (23%) contributed to variation in rule-breaking behavior [14]. This finding may indicate that genetic influences are more penetrant in truancy behavior in males as well.

In the present study, we investigated self-reported truancy, either current or retrospective, in a large sample of twins and their non-twin siblings. We examined the relative influence of genetic and environmental factors on frequency of truancy and whether the relative influence of these factors differed between males and females. Because of the large sample size, this was the first study able to reliably estimate genetic and environmental influences on frequency of truancy. The addition of non-twin siblings to the classical MZ-DZ twin design, offers several advantages: i.e., it increases statistical power to distinguish between additive genetic effects and shared environmental effects [26] and allows testing of differences in prevalence between twins and singletons. Moreover, because of the addition of non-twin siblings, it was possible to distinguish between environmental factors especially shared by twins and those shared by non-twin siblings. The classical twin design assumes that MZ twins are not treated more equal than DZ twins.

Methods

Subjects

Participants were registered with the Netherlands Twin Registry (NTR), kept by the Department of Biological Psychology at the Vrije Universiteit in Amsterdam. The data collection was part of an ongoing, large scale longitudinal study. Since 1991, families with adolescent and young adult twins were assessed every 2–3 years. In 1995, data on frequency of truancy were collected in twins and one or two additional non-twin siblings. Questionnaires were sent to participating families by mail, including two questionnaires for non-twin siblings. If there were more than two non-twin siblings in the family, those siblings who were closest in age to the twins were asked to participate. The response rate was 64%. Part of the non-response was due to the possibility that the addresses in our database were not up to date for all participants. Twins and siblings who were newly and voluntarily registered, who had participated in other data collection waves, and who were older were more likely to complete the questionnaire. In total, 4,889 twins and their non-twin siblings participated in the 1995 survey. The sample was representative of the general Dutch population with regard to educational level of the parents: 13.9% of fathers and 15.3% of mothers had a basic education at elementary school, 61.8% of fathers and 72.5% of mothers had a high school education, and 24.3% of fathers and 12.1% of mothers had a college or university education [27]. In the same age group of the general population, these percentages were 16.9%, 60.6%, and 22.5% for men respectively, and 21.5%, 64.4%, and 13.9% for women [28]. Participants came from all regions of the Netherlands, including both rural and urban areas. The exact procedures have been described in detail elsewhere [29,30].

One twin pair was excluded from the analyses because of unknown zygosity and one triplet was excluded. All participating non-twin siblings were included in the analyses regardless of age except for 32 nonbiological siblings and another 17 siblings who had not reached high school age. This resulted in a total sample of 4,835 twins and non-twin

Table 1
Sample characteristics

Characteristic	N		N
Total sample	4,835	MZM	283
Twins	3,406 (44% m)	DZM	232
Non-twin siblings	1,429 (49% m)	MZF	438
Total families	1,722	DZF	279
Families with twins only	441 (26%)	DOSMF	263
Families with twins + 1 sibling	1,133 (66%)	DOSFM	227
Families with twins + 2 siblings	148 (8%)	Incomplete pairs	38
	Range	Mean	SD
Age twins	14.27–28.25	19.78	3.12
Age siblings	12.01–39.47	22.26	4.97
Age difference twins and siblings	–	3.84	2.34

m = male; MZM = monozygotic male twin pairs; DZM = dizygotic male twin pairs; MZF = monozygotic female twin pairs; DZF = dizygotic female twin pairs; DOSMF = opposite-sex twin pairs with males born first; DOSFM = opposite-sex twin pairs with females born first; SD = standard deviation.

siblings. The characteristics of the sample are presented in Table 1. At the time of data collection 24% of the sample was in high school. A possible explanation for the overrepresentation of female MZ twin pairs is that MZ twins and females are generally more inclined to participate in research of the NTR. For 477 twin pairs (27.7%), zygosity was determined based on blood group or DNA typing. Blood group analysis was based on 13 red cell blood group antigens. When a twin pair had one or more differences in the blood grouping profile, that twin pair was designated to be a dizygotic twin pair. This is an accurate method to assess zygosity based on blood group analysis [31]. Zygosity for the remaining same-gender twin pairs was determined on the basis of questionnaire items. The correspondence between questionnaire and DNA based zygosity was 97% [32].

Measures

To assess frequency of truancy, subjects were asked how often they skipped lessons during a whole day while in high school. Answers could be provided on a six-point scale. The distribution of the scale was: never (67%), one to two times (14%), three to four times (7%), five to 10 times (5%), 11–20 times (3%), and more than 20 times (4%). Because the distribution of the data was very skewed and few subjects indicated to skip lessons during a whole day more than 10 times, scores on frequency of truancy were classified into two distinct categories: 0 = never, 1 = one or more times.

Statistical analyses

Structural equation modeling was used to examine the relative contributions of genetic and environmental influences to frequency of truancy. A threshold model with one threshold was fitted to the raw ordinal data using the software package Mx [33]. The threshold model which is a special application of structural equation modeling, assumes that a trait, measured as dichotomous, has an underlying liability with a continuous and normal distribution with a unit variance. The threshold (expressed in z-values), which is based on the prevalence of the two categories in the sample, represents the value in the latent distribution above which a given individual will endorse the next category. In the latent truancy distribution this means that a lower value of the threshold represents higher prevalence of truancy.

The amount of variance in the underlying liability was modeled as a function of additive genetic (A), shared environmental (C), and nonshared environmental effects (E) which can be estimated by considering the different level of genetic relatedness between MZ and DZ twin pairs and non-twin siblings. MZ twin pairs are genetically identical, whereas DZ twin pairs and non-twin siblings share, on average, 50% of their segregating genes. The amount of variance because of environmental effects shared by twins (T) is obtained by allowing the environmental variances to be more highly correlated among twins than among non-twin siblings [34]. The presence of environmental influences shared specifically by twins implies that twin pairs share more of their environment than non-twin siblings.

Mx was used to estimate thresholds and tetrachoric correlations in a saturated model. When the MZ correlation is higher than the DZ and the non-twin sibling correlation, it is inferred that genetic variation influences individual differences in liability. A DZ correlation higher than half the MZ correlation implies shared environmental effects. When the DZ correlation is higher than the sibling correlation a specific environment might exist which is shared by twins but not by non-twin siblings. The remaining variation is attributed to environmental effects which are not shared by family members. The nonshared environmental variance component also includes measurement error variance.

The data were structured into entire family units consisting of two to four individuals (i.e., two twins and one or two additional siblings) with missing sibling data for families without siblings. As a first step, in a saturated model the threshold for the twins and the non-twin siblings was estimated and the correlations between twin–twin pairs, twin–sibling pairs, and sibling–sibling pairs. Because of the broad age range in our sample we adjusted for possible age effects on the prevalence of truancy by modeling age as a covariate on the threshold. The model for the prevalence of truancy consists of an intercept independent of age, which we call the threshold, plus the effect of age as in a regression equation. Consequently, the threshold can be different between groups (e.g., between twins and siblings), although the actual prevalence might be the same as a consequence of age differences between the groups. The threshold could differ as a function of sex. Within a series of nested models we first tested the significance of the age effect on the threshold by testing whether fixing the beta-weight to zero led to a significant deterioration of model fit. Second, we tested whether the threshold is equal across zygosity groups, twins and siblings, and sex by constraining the corresponding thresholds to be equal. Finally, we tested whether twin correlations were equal across MZ and DZ twins, and DZ twins and siblings by constraining the corresponding twin correlations to be equal.

Next, genetic models were fitted to the data. We started with testing a full ACTE model (Figure 1) against the saturated model (i.e., model without any constraints). In the ACTE model the shared environment (represented by C) is perfectly correlated in both twins and their non-twin siblings, whereas the environment shared specifically by twins (represented by T) is perfectly correlated only by twins [34]. Because twins and their non-twin siblings are differently influenced by their shared environment (i.e., twins share more environment than their non-twin siblings) the model assumes that twins and siblings will differ in correlation, but not in variance [34]. Modeling the variance component T this way implies that the magnitude of T will contribute to the variance of siblings too. The model implies that the environmental factors comprised within T are part of the non-shared environmental variance for non-twin siblings. Sex differences in the relative influence of the variance components A,C,T, and E were assessed by testing whether constraining all parameter estimates of males and females to be equal resulted in a significant deterioration of model fit. Subsequently, the statistical significance of the variance components A, C, and T was assessed by testing whether fixing the corresponding parameter estimate to zero resulted in a significant deterioration of model fit.

The fit of the different models was compared by means of the log-likelihood ratio test (LRT). The difference in minus two times the log-likelihood (-2LL) between two nested models has a Chi-square distribution with the degrees of freedom (df) equaling the difference in df between the two models. If a value of $p > .05$ was obtained from the chi-square test, the fit of the constrained model was not significantly worse than the fit of the more complex model. In this case, the constrained model was kept as the most parsimonious and best fitting model. The fit of the genetic models was also compared to the saturated model by means of Akaike's Information Criterion, keeping the model with the lowest AIC as the best-fitting model [33].

A statistical power analysis was performed to test whether we had sufficient power to detect sex differences in the magnitude of variance components (power estimate should exceed .80). Following the procedure described by Neale and Cardon [35], we calculated the power based on the sample size and different family constellations in our study.

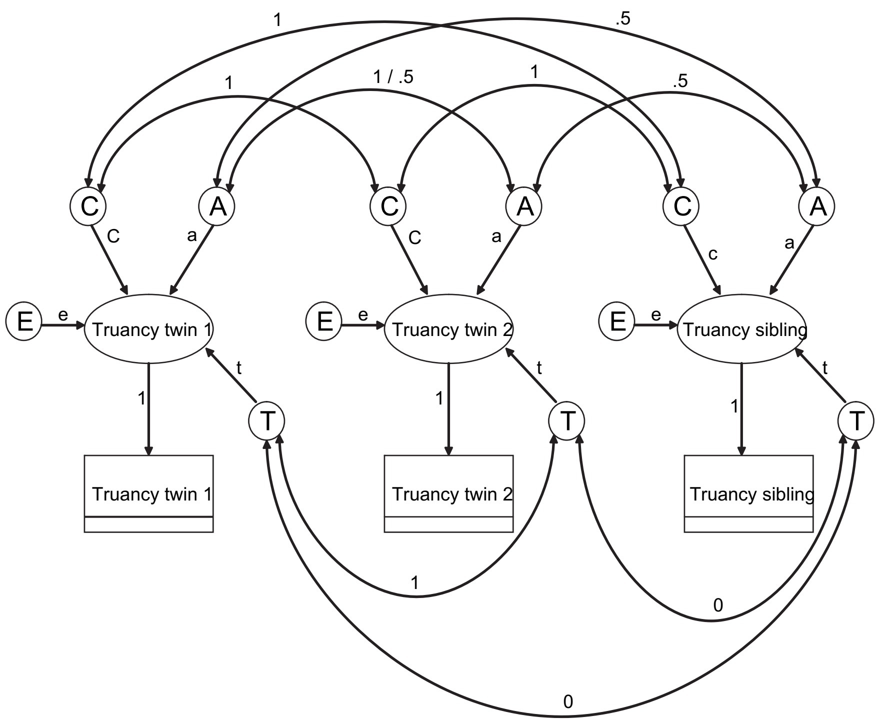

Figure 1. Univariate threshold model with one threshold for frequency of truancy.

Table 2
Fitting results for the saturated model of frequency of truancy

Model	vs.	–2LL	df	χ^2	Δdf	*p*
1. Saturated model	–	5,598.00	4,762	–	–	–
2. Significance of age effect	1	5,717.51	4,763	119.5	1	<.01
3. Threshold MZM = DZM and MZF = DZF	1	5,599.43	4,764	1.428	2	.490
4. Threshold MZM = DZM = DOSM and MZF = DZF = DOSF	3	5,599.58	4,766	.148	2	.929
5. Threshold MZM = DZM = DOSM = brother and MZF = DZF = DOSF = sister	4	5,616.17	4,768	16.59	2	<.01
6. Threshold equal for male and female twins	4	5,626.67	4,767	27.09	1	<.01
7. Threshold equal for brothers and sisters	4	5,609.19	4,767	9.61	1	<.01
8. Correlation MZM = DZM and MZF = DZF	4	5,605.74	4,768	6.162	2	.046
9. Correlation DZM = brothers; DZF = sisters and DOS = brother-sister	4	5,621.41	4,769	21.83	3	<.01

vs. = versus; –2LL = –2 log likelihood; df = degrees of freedom; Δdf = degrees of freedom of χ^2 test; MZM = monozygotic male twin pairs; DZM = dizygotic male twin pairs; MZF = monozygotic female twin pairs; DZF = dizygotic female twin pairs; DOS = opposite-sex twin pairs; DOSM = male twins of opposite-sex twin pairs; DOSF = female twins of opposite-sex twin pairs; brothers = male twin-brother pair and brother-brother pair; sisters = female twin-sister pair and sister-sister pair; brother-sister = male twin-sister pair, female twin-brother pair, brother-sister pair.

The simulated power was based on the estimates of the variance components in the full ACTE model. The estimated power is supplied by Mx.

Results

The results of the saturated model are presented in Table 2. There was a significant negative effect of age on the threshold (β = -.53), meaning that the prevalence of truancy increased with age (model 2). The threshold was equal for MZ and DZ (model 3), and DOS twins (model 4). The threshold was different for twins and non-twin siblings (model 5) and for male and female twins (model 6) and siblings (model 7). The prevalence of truancy was 38% for male twins, 36% for male siblings and 29% for female twins and siblings. This prevalence is similar to the prevalence of individuals of the same age group in the general Dutch population [1] and to what was reported in other studies [4,12].

Twin correlations are presented in Table 3. MZ twin correlations were higher than DZ correlations suggesting that individual differences in liability to truancy are influenced by genes (model 8). MZ twin correlations were less than twice the DZ twin correlations, suggesting that the shared environment also has an influence. Sibling correlations were lower than DZ twin correlations (model 9). This suggests a specific twin environment for liability to truancy and therefore we started our genetic modeling with an ACTE model in which T represents a specific twin environment.

Results of genetic model fitting are presented in Table 4. In model 2, we tested a full ACTE model in which the variance components were estimated for males and females separately. The full genetic model provided a good fit compared to the saturated model. In model 3, we tested whether there were sex differences in the magnitude of the variance components by constraining the ACTE model of males and females to be equal. There appeared to be no significant sex differences in the magnitude of the variance components explaining variation in liability to truancy.

In models 4 till 6, we tested whether fixing the specific twin environmental, the shared environmental, or the genetic parameter estimate to zero would lead to a significant deterioration in model fit. The specific twin environmental variance component was statistically significant. The effect of the shared environment was *not* statistically significant, and additive genetic effects were significant. The LRT tests and the AIC pointed to the ATE model as the best fitting model in which 45% of the variance in liability to truancy could be explained by genetic influences and 55% by nonshared environmental influences. 25% of the environmental influences are specifically shared by twins.

Results from the statistical power analysis indicated that there was not sufficient power to detect sex differences in the magnitude of the variance components as given in Table 4. Based on the sample size and different family constellations we had a power of .49 to detect these gender differences.

Table 3
Twin correlations and confidence intervals for frequency of truancy

	r	CI
MZM	.64	.49–.76
DZM	.42	.23–.60
MZF	.73	.62–.78
DZF	.59	.41–.73
DOS	.46	.32–.58
Brothers	.28	.14–.41
Sisters	.24	.11–.35
Brother-sister	.21	.12–.30

r = correlation coefficient; CI = 95% confidence interval; MZM = monozygotic male twin pairs; DZM = dizygotic male twin pairs; MZF = monozygotic female twin pairs; DZF = dizygotic female twin pairs; DOS = opposite-sex twin pairs; brothers = male twin-brother pair and brother–brother pair; Sisters = female twin-sister pair and sister–sister pair; brother-sister = male twin-sister pair, female twin-brother pair, brother–sister pair.

Table 4
Univariate model fitting results for frequency of truancy

Model	vs.[1]	–2LL	df	χ^2	Δdf	*p*	*AIC* [2]	A	C	T	E
1. Sat.	–	5,598.00	4,762	–	–	–	–	–	–	–	–
2. ACTE											
Males	1	5,599.71	4,766	5.539	8	.699	–6.29	.48 (.01–.66)	.02 (.00–.31)	.15 (.03–.32)	.35 (.24–.46)
Females								.25 (.00–.58)	.11 (.00–.31)	.36 (.17–.54)	.28 (.19–.38)
3. ACTE	2	5,603.28	4,770	3.568	4	.468	–10.72	.41 (.18–.57)	.03 (.00–.17)	.25 (.14–.36)	.31 (.24–.39)
4. ACE	3	5,625.20	4,771	21.92	1	<.01	9.20	.67 (.55–.74)	.00 (.00–.07)	–	.33 (.26–.40)
5. ATE	**3**	**5,603.43**	**4,771**	**.148**	**1**	**.700**	**–12.57**	**.45 (.34–.57)**	**–**	**.25 (.14–.35)**	**.30 (.24–.37)**
6. CTE	3	5,614.63	4,771	11.35	1	<.01	–1.37	–	.24 (.16–.30)	.34 (.26–.43)	.42 (.36–.49)

–2LL = –2 log likelihood; df = degrees of freedom; Δdf = degrees of freedom of χ^2 test; *AIC* = Akaike's Information Criterion; A = genetic variance component; C = shared environmental variance component; T = specific twin environmental variance component; E = nonshared environmental variance component; Sat. = Saturated model.

Boldface type indicates best-fitting model.

[1] Applies only to chi-square tests

[2] Every model was compared with the saturated model.

Discussion

In a large sample of Dutch twins and their non-twin siblings we found that the prevalence of truancy was higher for boys than for girls and that it increases with age indicating that older subjects in our sample reported to skip classes to a larger extent than younger subjects. Overall, 45% of the variance in liability to truancy was accounted for by genetic influences and 55% by environmental influences. Part of the shared environment represents influences that are shared by twins but not by non-twin siblings. In twins 45% of the variance could be accounted for by genetic influences, 25% by environmental influences shared specifically by twins and 30% by nonshared environmental influences. Environmental influences shared by all members of the family were insignificant. Because of a lack of power no sex differences in the magnitude of variance components were found.

The results link partly back to the outcomes of previous research on frequency of truancy and nonaggressive ASB in which truancy represents a distinct behavior [3]. Our finding that boys are more often truants is in line with what we expected based on previous research. It has previously been found that the prevalence of truancy [1] and nonaggressive ASB [14,16,20] is higher in males.

Our results suggest that both genetic and environmental variation play an important role in the etiology of truancy. The magnitude of genetic influences on frequency of truancy appeared to be similar to the heritabilities found for nonaggressive ASB in other studies [15,17], which is in line with our expectation because truancy occurs in a broader context of nonaggressive ASB [13]. The influence of environment shared by *all* family members (i.e., C) was insignificant which is not in line with other studies regarding truancy [15] and nonaggressive ASB [14,16,17,20]. However, we found that a significant proportion of the environmental factors that explain variation in frequency of truancy are specifically shared by twins. These environmental factors can not be explained by age differences between twins and siblings, because they remained significant after adjusting for age effects on the prevalence of truancy. Given that twins share classrooms in many cases they are more likely to skip classes together than regular siblings who do not share classrooms or at least less often than twins. More generally, individuals being in the same situation show similar behaviors. Twins are more likely to be in the same situation than regular siblings. This is likely not only to hold for truancy but for many other behaviors as well. For example, it has previously been demonstrated that delinquent acts are often performed by twins together with a co-twin [25]. It is plausible that previous findings of environmental influences shared by all family members explaining variation in nonaggressive ASB in fact represent environmental influences specifically shared by individuals in the same situation (in our case twins). Because previous studies did not include non-twin siblings they were not able to detect this specific environmental effect for other environmental effects. An important implication for future research with regard to frequency of truancy and related behaviors is that environmental influences shared specifically by twins should be assessed by adding non-twin siblings to the classical twin study.

Participants ranged between 12 and 39 years, so many of the twins and siblings already reached an age at which they left high school. As a consequence, reports of frequency of truancy may be biased because participants who were still in high school may have had less chance for truancy and those who already left high school may not remember exactly how often they skipped school while in high school [36]. To overcome this bias, we adjusted for age effects on the prevalence of truancy in the genetic models. Additional analyses indicated that there was no specific effect of being in high school versus being not in high school on the prevalence of truancy in addition to the age effect. Moreover, genetic and environmental influences on frequency of truancy were found not to differ between participants who were still in high school compared to those who already left high school (i.e., current vs. retrospective reports).

A couple of limitations of the present study should be mentioned. First, frequency of truancy was assessed by self-report. This may lead to a bias because participants may be more reluctant to provide true information about frequency of truancy because it is deviant behavior. The prevalence of truancy may therefore be underestimated [37,38]. Future research with regard to truancy should therefore use other informants like teachers or other school agents who may have a more objective view on students' frequency of truancy. Second, frequency of truancy was analyzed as a dichotomous variable, whereas analyzing it as an ordinal variable with 3 or more categories may have provided more information. The genetic and environmental architecture of frequency of truancy might be different between participants skipping classes occasionally and those skipping classes frequently. Making use of larger samples with twins and non-twin siblings, future studies should investigate whether this is the case with regard to truancy and other ASB.

On the basis of the present data the conclusion seems justified that genetic, nonshared environmental, and environmental influences shared specifically by twins play a role in the etiology of truancy. Because truancy occurs in a broader context of nonaggressive ASB, it is plausible that a genetic liability towards truancy applies to other nonaggressive ASB as well. Since truancy is a first sign and powerful predictor of ASB [3] and truancy provides a context of unsupervised and unstructured time with peers in which ASB is likely to be initiated [4], an important implication of these results is that preventing high school students from truancy is also likely to prevent them from the onset of other kinds of ASB. The influence of environmental factors specifically shared by twins on frequency of truancy emphasizes that truancy is performed together with classmates and other peers. Therefore, another implication of the present study is that prevention of truancy should focus on high school students skipping classes together rather than on the individual truant.

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