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ORIGINAL RESEARCH

Parent–Offspring Similarity for Drinking: A Longitudinal Adoption Study

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Abstract Parent–offspring resemblance for drinking was investigated in a sample of 409 adopted and 208 non-adopted families participating in the Sibling Interaction and Behavior Study. Drinking data was available for 1,229 offspring, assessed longitudinally up to three times in the age range from 10 to 28 years. A single drinking index was computed from four items measuring quantity, frequency and density of drinking. As expected, the mean drinking index increased with age, was greater in males as compared to females (although not at the younger ages), but did not vary significantly by adoption status. Parent–offspring correlation in drinking did not vary significantly by either offspring or parent gender but did differ significantly by adoption status. In adopted families, the parent–offspring correlation was statistically significant at all ages but decreased for the oldest age group (age 22–28). In non-adopted families, the parent–offspring correlation was statistically significant at all ages and increased in the oldest age group. Findings imply that genetic influences on drinking behavior increase with age while shared family environment influences decline, especially during the transition from late-adolescence to early adulthood.

Keywords Adoption study · Drinking behavior · Shared environmental influence · Parent–offspring correlation

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Introduction

One of the most salient characteristics of drinking behavior is that it is strongly developmentally graded (Masten et al. 2008). Many individuals start to drink in early or middle-adolescence, and adolescent initiation is typically followed by a period of rapid escalation in drinking that peaks sometime in late-adolescence or early-adulthood (Schulenberg and Maggs 2002). For most individuals, the attainment of middle-age is marked by a moderation in their drinking behavior (Muthén and Muthén 2000). Importantly, milestones in the development of drinking have important prognostic significance. For example, initiation of drinking in early-adolescence is associated with a substantially increased risk of alcoholism in adulthood (Grant and Dawson 1997; McGue and Iacono 2005; McGue et al. 2001), and rapid escalation of drinking in late-adolescence is an important indicator of future vulnerability (Tucker et al. 2005). There is a clear need to understand the developmental basis of drinking behavior.

Behavioral genetics has made important contributions to understanding the development of drinking behavior. There is a substantial body of research showing that drinking behavior is moderately heritable (Dick et al. 2009). Importantly, the magnitude of genetic influences on drinking, much like drinking behavior itself, may be developmentally graded (McGue and Irons 2013). An influential longitudinal study of adolescent Finnish twins, for example, reported that the heritability of the frequency of alcohol use increased from 33 % at age 16 to 50 % at age 18.5 (Rose et al. 2001). The magnitude of shared environmental influences (i.e., those environmental factors that contribute to twin similarity) decreased from 37 to 14 % over the same age period. An analysis of retrospective reports of alcohol use (as well as caffeine, nicotine, and cannabis use) from a sample of nearly

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1,800 pairs of male twins, similarly reported that the magnitude of genetic influences increased with age while the magnitude of shared environmental influences declined (Kendler et al. 2008).

A pattern of increasing heritability and decreasing shared environmental influence rather than being specific to drinking appears to characterize a broad range of behavioral traits. A meta-analysis of cross-sectional twin studies, reported age-related increases in the heritability of externalizing behaviors, IQ, social attitudes, and symptoms of depression and anxiety (Bergen et al. 2007). Individual twin studies have reported similar age-related increases in heritability as well as decreases in the contribution of shared environmental influences for traits as diverse as aspects of brain anatomy (Lenroot and Giedd 2008), features of the parent–child relationship (Ludeke et al. 2013), weight and body mass index (Dubois et al. 2012), and religiousness (Koenig et al. 2008). The age-related decline in shared environmental influences is hypothesized to be due to the diminishing impact of the rearing home as individuals age. The age-related increase in genetic influences is hypothesized to be attributable to active gene–environment correlational processes. That is, as individuals get older they gain increasing control over the environments they experience and exert that control in a way that is consistent with, and so amplifies, the phenotypic effect of their underlying genetically influenced dispositions (Scarr and McCartney 1983).

Although the behavioral genetic literature is consistent in implicating age-related increases in heritability and decreases in shared environmental influences, the existing research is largely limited to studies of twins and is predominantly cross-sectional or if longitudinal spans only a narrow age range. It is important to determine whether the same pattern holds with other behavioral genetic designs. John Loehlin has made many contributions to the field of behavioral genetics, but certainly one of his most enduring contributions has been in the use of adoption studies to address important behavioral genetic questions. The Texas Adoption Project (TAP) is one of the pioneering adoption studies in psychology and one of the unique features of the TAP is its longitudinal design. Most notably, TAP has been the basis for longitudinal investigations into genetic and environmental contributions to stability and change in IQ (Loehlin et al. 1989), personality (Loehlin et al. 1990), and social outcomes in adulthood (Loehlin et al. 2007).

In the current paper we carry on the tradition established by John Loehlin with TAP by undertaking a longitudinal analysis of parent–offspring resemblance for alcohol consumption in a sample of adopted and non-adopted families. How parent–offspring resemblance for drinking changes over adolescence and early adulthood has important implications for understanding the development of drinking problems, especially given the prominence social modeling plays in several theories of alcoholism (Bandura 1999; Marlatt 1996). Nonetheless, there is a relatively small number of studies of parent–offspring resemblance in drinking where the assessment is based on self-report rather than offspring report of their parents' drinking and very few of these are longitudinal. The current study is based on the Sibling Interaction and Behavior Study (SIBS), a longitudinal study of 409 adopted and 208 non-adopted (i.e., genetically related) families that spans early adolescence through early adulthood. The study is designed to test the following three hypotheses:

1. There is parent–offspring resemblance for drinking in adopted families, implicating shared environmental influences.
2. Parent–offspring similarity for drinking is greater in non-adopted as compared to adopted families, implicating genetic influences.
3. Parent–offspring similarity in drinking is moderated by offspring age such that in non-adopted families there is increasing parent–offspring similarity in drinking with age but in adopted families there is decreasing similarity.

Method

Sample

The sample was drawn from participants in the SIBS, a longitudinal study of the development of substance use and related mental disorders in adopted and non-adopted youth (McGue et al. 2007). The intake SIBS sample consisted of 409 adopted and 208 non-adopted families, with each family consisting of a pair of adolescent siblings and their parents. Adopted families were recruited through three large Minnesota (MN) adoption agencies. Eligibility included having an adopted child between the ages of 11 and 21 years at the time of the intake assessment who had been permanently placed into the adoptive home prior to age 2 years (mean = 4.7 months, SD = 3.4 months, with 96 % placed prior to 1 year of age), and a second adolescent in the home who was not biologically related to the adopted adolescent. In 124 of the adopted families, the second adolescent was a biological child of one or both parents. We do not have information on the biological parents of the adopted participants in SIBS. Non-adopted families were ascertained through publicly available MN birth certificates and were recruited to match the adopted sample in terms of age and sex. Offspring in the non-adopted families were full biological siblings and no more than 5 years apart in age. Participation rates among eligible

families at intake were not significantly different between non-adoptive (57 %) and adoptive (63 %) families. Consistent with MN state demographics, the vast majority of the parents (>95 %) in both adopted and non-adopted families were white. Similarly, 95 % of the non-adopted offspring were white. In contrast, the majority of the adopted offspring were non-white, with 67 % of East Asian (specifically Korean) ancestry, and 12 % with various other ethnic backgrounds. Although the adopted and non-adopted samples are consequently not matched for ethnicity, in previous analyses of SIBS data ethnicity was not associated with outcome (Keyes et al. 2013). Comparisons of non-adoptive parents' education and marital status to 2000 census data show that they were generally representative of MN families with two children. A detailed overview of study recruitment and participation has been provided elsewhere (McGue et al. 2007).

The offspring in the SIBS sample completed three longitudinal assessments. The intake assessment was completed by 1,232 offspring with a mean (SD) age of 14.9 years (1.9). The first follow-up was completed by 1,158 (94.0 %) offspring at an average age of 18.3 (2.1), and the second follow-up was completed by 1,126 (91.4 %) offspring at an average age of 22.4 (1.9). Parent data used in the current analysis was all based on the intake assessment, as both parents did not participate in subsequent assessments.

Measures

A composite drinking index was derived from four self-report drinking items: (1) frequency of alcohol use in the previous 12 months (scored on a scale from 0 = never to 5 = at least once a day), (2) typical number of drinks consumed per drinking session in the previous 12 months (scored on a scale from 0 = never to 6 = 30 or more), (3) maximum number of alcoholic drinks consumed in a 24-h period (scored on a scale from 0 = never to 6 = 30 or more), and 4) total number of times intoxicated from alcohol (scored on a scale from 0 = never to 6 = 50 or more). Responses to these items were obtained from two separate assessments. The first assessment was a computerized substance use (CSU) inventory in which the respondent reported on their use of nicotine, alcohol and other drugs. The CSU was completed in a private room by all participants age 18 years and younger. The second assessment was based on a customized form of the Substance Abuse Module (SAM), an expansion to the World Health Organization's Composite International Diagnostic Interview (Robins et al. 1987). The SAM assessment was administered by trained interviewers to all participants age 16 years and older. Initially, we formed a composite drinking scale by summing the four index items in each of the two assessments. The internal consistency reliability estimates were 0.96 and 0.94 for the CSU index at the intake and first follow-up assessments respectively, and 0.92, 0.90 and 0.83 for the SAM index at the intake, first follow-up, and second follow-up assessments respectively (because the youngest participant at the second follow-up was 19 years old, none was administered the CSU).

At the intake and first follow-up assessments, participants between the ages of 16 and 18 completed both the SAM and CSU, allowing us to assess the consistency of responses across the two formats. The correlation between the two indexes was 0.88 (N = 321) at intake and 0.91 (N = 800) at first follow-up, indicating a very high degree of convergence across the two indexes. To make the two alternative forms of the drinking index fully commensurate, integrate the two assessments when participants completed both, and obtain an estimate of the composite score when individuals were missing a specific item, we used item response theory and integrated data analysis methods (Hussong et al. 2013) to estimate a common latent trait. The resulting drinking index scores from the IRT analysis were linearly transformed so that non-drinkers received the lowest index score of 0, and the standard deviation for the index score for offspring participants at first follow-up was set to 1.0.

Methods of analysis

Parent–offspring correlations for the drinking index were estimated using maximum likelihood methods as implemented in Mx (Neale et al. 2003). Multiple models were fit in order to test whether correlations varied significantly by offspring gender, parent gender, and adoption status. Alternative models were compared using the χ^2 likelihood ratio test and the Akaike Information Criteria (AIC = $\chi^2 - 2df$).

Results

Descriptive analysis

Table 1 provides descriptive statistics on the drinking index as well as age at assessment for participating offspring at the three assessment stages and their parents at intake. Not all offspring participating at a given assessment provided the information needed to compute their drinking index. Offspring drinking data was available for 1,229 (out of 1,232 participants) at intake, 1,143 (out of 1,158 participants) at the first follow-up, and 1,089 (out of 1,126 participants) at the second follow-up. In order to assess the potential effects of sample attrition, we compared those who had valid drinking data at the two follow-ups to those

Table 1 Descriptive information on age and drinking index in adopted and non-adopted families

	Adopted		Non-adopted	
	Female	Male	Female	Male
Offspring intake				
N	381	308	292	248
Age				
Mean	15.0	14.9	14.9	14.9
(SD)	(2.1)	(1.7)	(2.0)	(1.8)
Index				
Mean	0.47	0.34	0.46	0.42
(SD)	(0.79)	(0.72)	(0.79)	(0.82)
Offspring follow-up 1				
N	362	287	265	229
Age				
Mean	18.5	18.1	18.3	18.2
(SD)	(2.3)	(1.9)	(2.0)	(1.9)
Index				
Mean	1.28	1.39	1.23	1.47
(SD)	(0.91)	(1.06)	(0.99)	(1.06)
Offspring follow-up 2				
N	356	258	261	214
Age				
Mean	22.5	22.4	22.2	22.3
(SD)	(2.0)	(1.6)	(1.8)	(1.8)
Index				
Mean	1.83	2.15	1.82	2.10
(SD)	(0.68)	(0.75)	(0.67)	(0.82)
Parent intake				
N	407	374	207	177
Age				
Mean	47.9	49.3	44.1	45.9
(SD)	(3.6)	(3.7)	(4.2)	(4.9)
Index				
Mean	1.57	1.92	1.64	1.99
(SD)	(0.42)	(0.48)	(0.49)	(0.58)

Parent data was obtained at the intake assessment of their offspring; female parent column gives data for mothers and male column gives data for fathers

who did not (either because they did not participate in the assessment or because they did not complete the drinking assessment) on their intake drinking index as well as the

Fig. 1 The relationship between drinking and age in males and females. Plotted is all observed drinking index data, in which case there are up to three observations for participating offspring but only one observation for participating parents. The *curves* give the lowess-averaged values with the *shaded areas* giving the associated 95 % confidence intervals. The oldest offspring was assessed at age 28 years; the youngest parent at age 35

drinking indexes of their mothers and fathers. At the first follow-up, those with drinking data did not differ significantly from those without on either their intake drinking index or their parents' intake drinking indexes (all standardized mean differences <0.25 in absolute value; all $p > 0.05$). At the second follow-up, those with drinking data had moderately higher intake drinking scores than those without drinking data (standardized mean difference of 0.24, $p < 0.01$), but there was no difference in their parents' drinking scores. Attrition analysis thus suggests minimal bias in loss to follow-up with a slight over-representation of those with higher intake drinking scores at the second follow-up.

Among offspring, age at assessment and the drinking index did not vary significantly by adoption status at any of the three assessments (all standardized mean differences <0.10 in absolute value; all $p > 0.05$). The association of sex with the drinking index increased across assessments. The standardized mean difference (positive indicating greater male mean) was −0.13 ($p = 0.04$) at intake, 0.16 ($p < 0.01$) at first follow-up, 0.41 ($p < 0.001$) at second

Table 2 Mean (SD) drinking index and sample size in age-restructured offspring sample

Age group	Female offspring		Male offspring	
	Adopted	Non-adopted	Adopted	Non-adopted
10–12	0.02 (0.16)	0.03 (0.21)	0.00 (0.00)	0.00 (0.00)
	N = 50	N = 38	N = 50	N = 38
13–15	0.38 (0.74)	0.32 (0.69)	0.23 (0.60)	0.29 (0.70)
	N = 251	N = 186	N = 238	N = 178
16–18	1.02 (0.91)	1.01 (0.93)	1.22 (1.03)	1.25 (1.02)
	N = 269	N = 214	N = 223	N = 186
19–21	1.72 (0.75)	1.68 (0.83)	2.02 (0.86)	2.00 (0.86)
	N = 265	N = 215	N = 155	N = 164
21–24	1.89 (0.61)	1.94 (0.52)	2.23 (0.61)	2.26 (0.73)
	N = 202	N = 132	N = 173	N = 100
25–28	1.82 (0.53)	2.02 (0.40)	2.31 (0.28)	2.07 (0.79)
	N = 48	N = 20	N = 14	N = 25

follow-up in the offspring sample. Among parents, who only participated at the intake assessment, the standardized mean sex difference was 0.68 ($p < 0.001$). Adopted parents were significantly older than non-adopted parents (by an average of 3.8 years for mothers and 3.4 years for fathers), but adopted and non-adopted parents did not vary significantly in the drinking index. A plot of all of the drinking index data by assessment age is given in Fig. 1, which provides a sense for the variability that exists in the data as well as the relationship of the drinking index with age and sex.

We investigated parent–offspring resemblance as a function of the offsprings' age at assessment rather than as a function of the three assessments (i.e., intake and the two follow-ups). To do this, it was necessary to restructure the offspring drinking data. Specifically, a drinking phenotype was created for each of the following three-year age blocks chosen to ensure that across the multiple assessments no participant had more than one observation within any given block: (1) 10–12, (2) 13–15, (3) 16–18, (4) 19–21, (5) 21–24, and (6) 25–28. The up to three drinking assessments for each offspring were allocated to the appropriate age block, with the drinking index coded as missing for the remaining blocks for that individual. Table 2 provides descriptive data for the restructured drinking data. Several general observations are notable. First, the restructured data show the same pattern of mean differences evident with the original data; i.e., little difference by adoption status and greater drinking by males as compared top females at the older but not the younger ages. Second, consistent with other epidemiological research (Johnston et al. 2014; Windle et al. 2008), there is very little drinking

Table 3 Correlations in offspring drinking index over time

	Age at assessment				
	13–15	16–18	19–21	21–24	25–28
13–15	1.0				
16–18	0.30	1.0			
19–21	0.23	0.52	1.0		
21–24	0.19	0.45	0.62	1.0	
25–28	NA	0.43	0.56	0.65	1.0

NA Not available because there are no cases observed in this cell

reported in the youngest age group (10–12). Because there can be no meaningful parent–offspring correlation where there is little offspring drinking, the 10–12 age data was dropped in subsequent analysis.

Table 3 gives the correlations in drinking index over time. As expected, the longer the retest interval the lower the phenotypic correlations, and the stability of the drinking index increases with age. In general, the stability correlations are moderate in magnitude, suggesting that there is substantial re-ordering of individual differences in drinking over time, especially at the younger ages.

Parent–offspring correlation

We estimated both the individual parent–offspring correlation as well as the midparent–offspring correlation as a function of age using Mx. Because the number of observations in the 25–28 age-group was relatively small, correlations for this age-group were constrained to be equal to correlations for the next youngest age group, 22–24. Table 4 gives model-fit statistics. For the parent–offspring correlation, there was no evidence (by χ^2 test and AIC) that correlations varied by offspring sex (Model 2 vs. Model 1) or for mothers versus fathers (Model 3 vs. Model 2). However, Model 4, which placed the added constraint that the correlations for adopted offspring equaled those for non-adopted offspring fit poorly. Model-fitting results were similar for the midparent–offspring correlation. That is, the midparent–offspring correlation did not differ significantly by offspring sex (Model 2 vs. Model 1) but did differ significantly for adopted and non-adopted offspring (Model 3 vs. Model 2).

The parent–offspring and mid-parent offspring correlations for the best-fitting model (i.e., no difference by offspring sex or for mother versus father but differences as a function of adoption status) are plotted in Figs. 2a, b, respectively. All correlations in both the adopted and non-adopted sample are significantly different from 0. As a follow-up to the finding of an overall significant difference between the adopted and non-adopted correlations, we

Table 4 Model fit statistics

Model #	Equal parent–offspring correlation by:			Model-fit indexes				
	Female = male	Mother = father	Adopted = biological	−2lnL	df	χ^2 (df)	*p*	AIC
Parent–offspring correlation:								
1	No	No	No	9680.1	5466			
2	Yes	No	No	9701.6	5482	21.6 (16)	0.16	−10.4
3	Yes	Yes	No	9708.4	5490	28.4 (24)	0.24	−19.6
4	Yes	Yes	Yes	9722.2	5494	42.2 (28)	0.04	−13.8
Midparent–offspring correlation:								
1	No	NR	No	11070.3	4392			
2	Yes	NR	No	11081.4	4400	11.4 (8)	0.18	−4.6
3	Yes	NR	Yes	11094.3	4404	24.3 (12)	0.02	0.3

Model 1 in both cases is the base model against which the other models are compared. NR = not relevant as there is not a separate father-offspring and mother-offspring correlation here

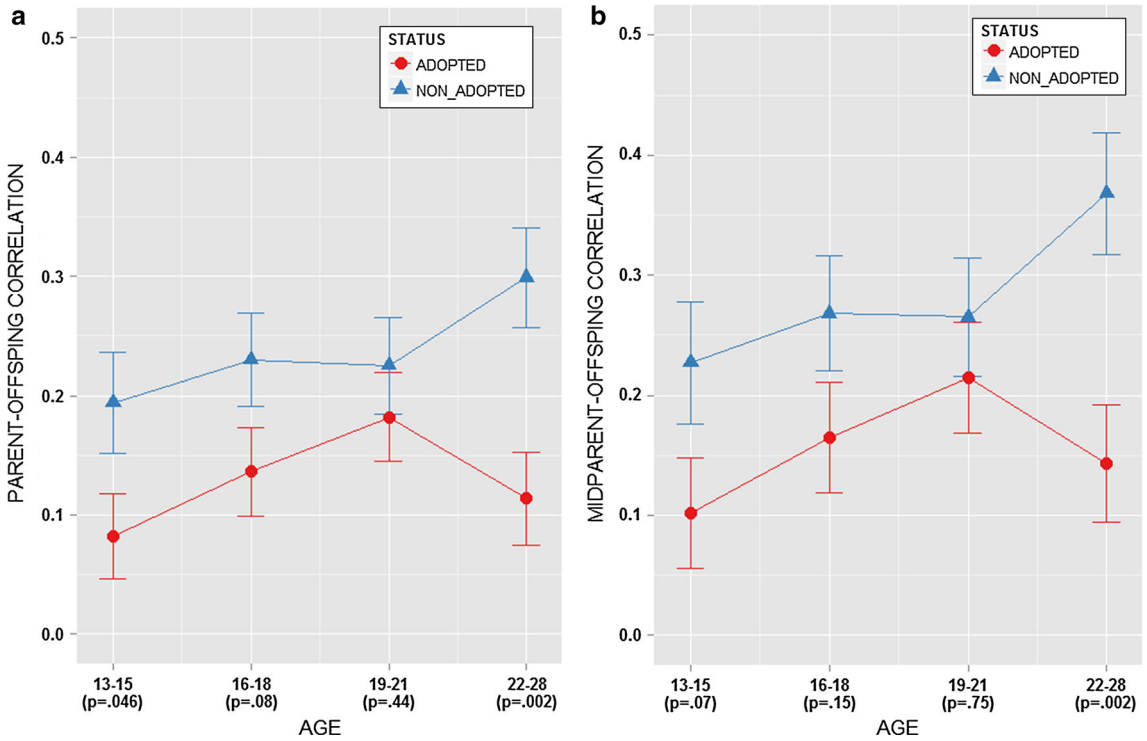

Fig. 2 **a** Estimated parent–offspring correlation as a function of offspring age in adopted and non-adopted families. The *error bars* demarcate one standard error; the *p*-values below the age-group label give the significance of the difference between the adopted and non-adopted correlations. **b** Estimated midparent–offspring correlation as a function of offspring age in adopted and non-adopted families. The *error bars* demarcate one standard error; the *p*-values below the age-group label give the significance of the difference between the adopted and non-adopted correlations

compared the adopted and non-adopted correlations at each age block by likelihood-ratio $\chi^2$and report the resulting *p* value in the figures. In both the adopted and non-adopted sample, the parent–offspring correlation increases with age through age 19–21. Through that age, the non-adopted correlation is consistently greater than the adopted correlation, although the difference is statistically significant in only one case (marginally with $p = 0.046$ for the parent–offspring correlation at age 13–15). The correlation pattern is quite different at the oldest age (22–28). In this age group, the non-adopted correlation continues to increase but the adopted correlation declines relative to

earlier ages. Both the parent–offspring and midparent–offspring correlations are significantly greater among non-adopted as compared to adopted offspring (in both cases $p = 0.002$).

Discussion

Longitudinal analysis of parent–offspring resemblance in a sample of 409 adopted and 208 non-adopted families led to the following major findings: (1) There is significant parent–offspring resemblance for drinking in adopted families, implicating the importance of shared environmental influences on drinking. (2) Parent–offspring resemblance for drinking is greater among non-adopted, genetically related, pairs than among adopted pairs, implicating the importance of genetic influences. (3) Parent–offspring resemblance in drinking increases into early adulthood in genetically-related pairs but declines at the oldest ages studied in adopted pairs.

Before discussing the significance of each of these findings, it is important to acknowledge the limitations of the current investigation. First, our sample of adopted and non-adopted families originated from a single U.S. state. As a consequence, the sample of non-adopted families is primarily of European ancestry whereas the adopted offspring are primarily of East Asian or other ancestral backgrounds. Although we have not found consistent evidence of ethnicity effects in SIBS, the generalizability of the findings here to other ethnic groups is uncertain. Second, adopted families are not representative of all families with children. In particular, there is concern that restriction of range in the adoptive family environment might attenuate inferences about the importance of shared environmental factors (Stoolmiller 1999). Although we cannot completely rule out the possibility of restriction of range in the adopted families, it is important to note that there were no significant differences in the drinking index in adopted and non-adopted parents (Table 1).

Our finding of significant parent–offspring resemblance in adopted families provides strong support for the hypothesis that the family environment influences drinking behavior, at least through adolescence. For many psychological traits, there exists a large body of behavioral genetic research suggesting that the shared family environment has little if any effect (Plomin and Daniels 1987). Recently however, there has been a reconsideration of the role of the shared environment with evidence emerging for the existence of shared environmental influences on some psychological traits, especially those related to rule-breaking behavior and intellectual achievement (Buchanan et al. 2009; Burt 2009). Here we provide additional evidence for shared environmental influences using a novel longitudinal adoption study design. Although our research allows us to establish the existence of shared environmental influences on drinking, at least through late adolescence, it does not allow us to determine the basis for the parent–offspring association. That is, while the significant adopted parent–offspring correlation in drinking is certainly consistent with a social learning effect, it may also arise because parents who drink heavily engage in parenting behaviors that increase the likelihood that their children drink heavily (Latendresse et al. 2008) or from some other factor.

Given the substantial behavioral genetic research literature that exists, our finding significant parent–offspring resemblance for drinking in non-adopted families is not unexpected. Nonetheless, as mentioned above the relevant literature is overwhelmingly based on twin studies; there are surprisingly few parent–offspring studies of drinking. This is particularly the case for studies in which parents' drinking was assessed by self-report rather than by offspring report, so that the current study adds importantly to our understanding of the degree to which parents and their offspring resemble each other in their drinking. Previous research based on parent-reported drinking has found modest parent–offspring correlations, typically in the 0.1–0.25 range (Kendler et al. 2013; White et al. 2000). We observe similarly modest parent–offspring correlations throughout adolescence. Interestingly, we found that the non-adopted parent–offspring correlation continues to increase through early adulthood, to 0.30 for single parent–offspring and 0.37 for midparent–offspring. This increase is consistent with the increase in genetic influences on drinking that has been reported in studies of twins (Kendler et al. 2008; Rose et al. 2001). What is perhaps most surprising here is that parents resemble their genetic children more at an age when they are likely to no longer be living at home than at an earlier age when they were.

The increase in the non-adopted parent–offspring correlation we observed in the oldest age group (22–28) stands in contrast to the decrease in the adopted parent–offspring correlation we observed at this age. The decline in adopted parent–offspring correlation reflects the diminishing impact the rearing environment has on drinking behavior and is consistent with a broad behavioral genetic literature showing that shared environmental influences decline with age, especially during the transition from late adolescence to early adulthood (Plomin and Daniels 1987). Yet although our study finds a declining impact of the environmental consequences of parent drinking, it is important to recognize that the impact of parent drinking in the 22–28 age group is not zero; the adopted parent–offspring correlation in this age group is statistically significant although modest in magnitude. An important question is whether the adopted parent drinking effect will endure to older ages or continue to diminish.

In summary, a longitudinal investigation of 409 adopted and 208 non-adopted families revealed moderate parent–offspring correlation in drinking. The parent–offspring correlation did not vary by offspring or parent gender but was greater in non-adopted as compared to adopted parent–offspring pairs. Importantly, parent–offspring resemblance for drinking increased in non-adopted pairs but decreased in adopted pairs in the oldest age group (22–28 years). These data are consistent with an increasing influence of genetic factors and decreasing influence of the home environment during the transition from adolescence to early adulthood.

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Conflict of interest The authors declare that they have no conflicts of interest.

Human and Animal Rights and Informed Consent The SIBS protocol was reviewed and approved by the Institutional Review Board at the University of Minnesota. Written informed assent or consent was obtained from all participants, with parents providing written consent for their minor children.

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