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A Behavior–Genetic Study of Parenting Quality, Infant Attachment Security, and Their Covariation in a Nationally Representative Sample

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A number of relatively small–sample, genetically sensitive studies of infant attachment security have been published in the past several years that challenge the view that all psychological phenotypes are heritable and that environmental influences on child development—to the extent that they can be detected—serve to make siblings dissimilar. Using the twin subsample (N = 485 same-sex pairs) of the nationally representative Early Childhood Longitudinal Study—Birth Cohort, the authors provide evidence that parenting quality and infant attachment security observed at 24 months, as well as their covariation, are a product of shared and nonshared environmental (but not genetic) variation among children. In contrast, genetic differences between infants played a prominent role in explaining observations of temperamental dependency.

Keywords: infant attachment security, behavior–genetic, shared environment, temperamental dependency

In the past several years, a number of genetically sensitive studies of infant attachment security have been published that challenge what has become conventional wisdom among many behavior–genetic researchers and other commentators (Bouchard, 2004; Harris, 1995; Rowe, 1994; Scarr, 1992; Turkheimer, 2000): that all psychological phenotypes are heritable and that environmental influences on child development—to the extent that they can be detected—serve to make siblings dissimilar (Plomin & Daniels, 1987).[1] Results in this literature have been remarkably consistent. For example, in virtually all relevant twin studies of infants and preschoolers (e.g., Bakermans-Kranenburg, van IJzendoorn, Bokhorst, & Schuengel, 2004; Bokhorst et al., 2003; Fearon et al., 2006; O'Connor & Croft, 2001; Ricciuti, 1993), the estimated additive genetic effects on security were modest and often close to zero. Moreover, there was evidence in each of those studies of substantial shared and nonshared environmental influences on the development of attachment security (for a detailed review, see Bokhorst et al., 2003). Similarly, studies of the intergenerational transmission of attachment-related experience in biologically unrelated dyads (e.g., Dozier, Stovall, Albus, & Bates, 2001; Veríssimo & Salvaterra, 2006) have revealed no evidence that genetic variation plays a role in the development of attachment security in the early life course.

In the most recent publication in this area (Fearon et al., 2006), investigators moved beyond simple univariate behavior–genetic models to show that the covariance between parental sensitivity and attachment security in infancy was accounted for by shared and nonshared environmental (but not genetic) influences. This particular analysis—the first of its kind—was especially important in that it offered evidence that the mechanisms underlying the predictive significance of what is viewed as the primary antecedent of infant attachment security (i.e., observed parenting quality; De Wolff & van IJzendoorn, 1997) are nongenetic in origin. Specifically, Fearon et al. (2006) demonstrated, as expected, that a large majority of the covariation between maternal sensitivity and infant security could be accounted for by shared environmental variation, such that when sensitivity was shared by siblings, it was positively associated with infant security. Interestingly and unexpectedly, however, these investigators also determined that when sensitivity was not shared within families, the target of such sensitivity was actually significantly less likely to be secure (this effect was detected as a negative nonshared environmental correlation, which has the effect of suppressing the association between sensitivity and security).

Although such results are provocative, one of the major limitations of this work to date is that it has been based on modest-sized samples of unknown representativeness. For example, the largest such study (Bokhorst et al., 2003) combined two small convenience samples, yielding a total of only 57 monozygotic and 100 dizygotic twin pairs (19 of whom were opposite-sex). In addition,

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[1] We acknowledge that not all psychologists who use behavior–genetic methods would endorse this view. Nonetheless, we regard it as a consensus statement for many behavior–genetic researchers and developmental psychologists. For example, Rutter (2002) concluded "any dispassionate reading of the literature leads to the inescapable conclusion that genetic factors play a substantial role in the origins . . . of all psychological traits" (p. 2), and Turkheimer's (2000) "laws of behavior-genetics" state that "genetic variance is an important component of variation for all behavioral outcomes, but variation among families is not" (p. 160).

almost all of the published reports in this literature (i.e., Bakermans-Kranenburg et al., 2004; Bokhorst et al., 2003; Fearon et al., 2006) are based on the same sample (or subsamples thereof), albeit with different emphases (i.e., mother–child security, father–child security, and the covariance of parental sensitivity and attachment security). Finally, no behavior–genetic twin study to date has measured attachment security in the home as assessed by trained observers (but see Bakermans-Kranenburg et al., 2004, which examined mothers' reports of father–child attachment security and dependency on the basis of the Attachment Q-Sort [Waters and Deane, 1985]).

In the current report, we address questions related to the generalizability of behavior–genetic findings of minimal genetic influence on the development of infant attachment security by revisiting the twin subsample (N = 485 same-sex twin pairs) of the Early Childhood Longitudinal Study—Birth Cohort (ECLS–B), an ongoing study of the 2001 birth cohort. The present study extends previously published analyses based on the 9-month ECLS–B assessment (Roisman & Fraley, 2006) through an examination of whether observations of infant attachment security, parenting quality, and their covariation during the ECLS–B 24-month home assessment were largely the product of shared as well as nonshared experiences with primary caregivers, consistent with the expectation of many attachment theorists (e.g., Weinfield, Sroufe, Egeland, & Carlson, 1999).

In contrast, as would be expected given that temperament is theorized to have its roots in part in genetic differences (Rothbart & Bates, 1998), we also examined whether genetic variation accounted for observations of temperamental dependency. We examined temperamental dependency for several reasons. First, it is well established in behavior–genetic research that genetic differences among infants play a prominent role in accounting for observations of temperamental dependency, whereas differences among families do not (e.g., Bakermans-Kranenburg et al., 2004). If we were unable to replicate this result with the ECLS–B sample, it might be claimed that the current investigation was simply based on an unusual sample. Second, the current study relied on an adaptation of the Attachment Q-Set (Waters, 1995), which produces two conceptually distinct dimensions, one reflecting secure base behavior (i.e., attachment security) and the other temperamental dependency, marked by excessive separation-distress proneness (see also Belsky & Rovine, 1987, for a similar distinction). Whereas these dimensions are weakly correlated (negatively) in children around the age of 1 year (Bakermans-Kranenburg et al., 2004), they tend to be more strongly negatively associated in older samples (Vaughn & Bost, 1999). Given that we expected to find that attachment security and temperamental dependency would be moderately correlated by age 2, we reasoned that evidence for a differential behavior–genetic etiology of these constructs would be especially compelling.

Method

Participants

The Early Childhood Longitudinal Study—Birth Cohort (ECLS–B) is based on a nationally representative probability sample, initially consisting of 10,688 parents of children born in 2001 who have been tracked longitudinally thus far from 9 to 24 months. Children were sampled for the study via registered births from the U.S. National Center for Health Statistics, and the target population for the study consisted of all children born in 2001, with three exceptions: children who died before the age of 9 months ($<$ 0.7%), children born to parents younger than age 15 ($<$ 0.2%), and children adopted prior to the age of 9 months (unknown percentage). Several subsamples, including twins, were oversampled in ECLS–B to increase analytic power. More detailed information regarding recruitment of the cohort is available in Bethel, Green, Nord, Kalton, and West (2005).

Participants for the current study were drawn from the twin subsample (N = 485 same-sex twin pairs) of the ECLS–B who participated in a 24-month assessment of this cohort.[2] In addition to being of established zygosity (determined by parent and ECLS–B staff report) and the same sex, twin pairs were included in the current analysis if they met two criteria: (a) both twins participated in the ECLS–B, and (b) they resided in the same home. At the ECLS–B 24-month assessment, twin zygosity was ascertained both by parental report (as at 9 months; see Roisman & Fraley, 2006) and via a composite ECLS–B staff and parent assessment of zygosity. For the latter composite, ECLS–B staff and participating parents completed a set of standard questions used to determine zygosity for same-sex twins demonstrated to converge strongly ($\geq$ 95%) with results of genetic testing that are widely used in behavior–genetic work (Goldsmith, 1991), including probes about whether twins differed in terms of hair texture, shades of hair colors, eye color, complexion, facial appearance, and shape of ear lobes. As might be expected, the simple parent-report method and the official ECLS–B composite yielded somewhat different totals of monozygotic (MZ) and dizygotic (DZ) co-twin pairs at age 24 months (77% agreement, κ = .46, $p <$ .001; parent report: n_{MZ} = 168, n_{DZ} = 311, and 6 pairs of unknown zygosity; ECLS–B staff and parent composite ratings: n_{MZ} = 120 and n_{DZ} = 365). As such—and consistent with ECLS–B recommendations—all analyses are presented twice, using each assessment of zygosity (note that the pattern of results was identical to what is described in this report when only the subset of participants for whom ECLS–B and parent-reported zygosity were in agreement were analyzed).

The diverse subsample of twin pairs that is the focus of this study was 58.1% European American; 16.1% African American; 18% Hispanic; 3.7% Asian, Hawaiian, or Pacific Islander; 0.6% American Indian or Native Alaskan; and 3.5% multiracial. In addition, this subsample represents the entire range of the socioeconomic spectrum (M = 3.2, SD = 1.4; range = 1, [lowest quintile] to 5 [highest quintile]), as assessed by a socioeconomic status composite variable consisting of measures of parental education and occupation and household income. Finally, MZ and DZ twin pairs were roughly half male and half female, and sampling was not based on whether the twins were MZ or DZ. Therefore, the MZ versus same-sex DZ distribution described above is simply a feature of prevalence in the 2001 birth cohort, despite the fact that,

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[2] This analysis was based on the ECLS–B Longitudinal 9-Month–2-Year Restricted Use Data File. This data set and ECLS–B methods and sampling documentation manuals can be requested at no charge through the U.S. Department of Education National Center for Education Statistics Web site at http://nces.ed.gov/ecls/Birth.asp

typically, a third of all twin births are MZ, same-sex DZ, and opposite-sex DZ (G. Mulligan, personal communication, April 17, 2006).

Procedures

All measures used in the current study derive from a 2^+-hr home visit with the twins completed close to their second birthdays. Specifically, the measure of parenting quality was based on a videotaped semistructured interaction during the 24-month assessment (only one twin was present in the room at a time, although a single caregiver took part in interactions with both Twin A and Twin B), and these videos were coded subsequently by individuals not involved with data collection who were also blind to data from the co-twin interaction. In contrast, the attachment security and temperamental dependency measure was completed after the home visit by the interviewer who conducted the assessment. It should be noted that the videotaped parenting quality measured focused on *parental* behavior in a standard, semistructured context, whereas the attachment security/temperamental dependency measure focused on the *children's* behavior in relation to the parent across the entire home visit, which consisted of parent questionnaires, the Bayley assessment of cognitive and motor development, the Two Bags Task, and physical measurements.

Measures

Parenting quality. As a direct measure of socioemotional functioning, ECLS–B staff administered the Two-Bags Task during the 24-month home visit. The videotaped Two Bags Task is a simplified version of the Three Bags Task administered in other national studies (e.g., the National Institute of Child Health and Human Development Study of Early Child Care) that involves a semistructured interaction between primary caregivers and target children. More specifically, caregivers were instructed to play for approximately 10 min with two different sets of toys (one bag contained a set of toy dishes and the other a children's picture book). As in prior work, a number of parent and child rating scales were coded from videotapes by ECLS–B staff. In the current analysis, we focused on the a priori scale Parental Supportiveness, a composite of the Parent Sensitivity, Parental Stimulation of Cognitive Development, and Parental Positive Regard scales (correlations among these scales were all in excess of .50). We used this composite and this particular paradigm for assessing parenting quality because of its comparability with methods used in prior research establishing associations between parenting quality and infant attachment security (De Wolff & van IJzendoorn, 1997).

To ascertain reliability in the ECLS–B on the Two Bags test, four members from the Westat child development staff were initially trained to 90% agreement with four individuals responsible for training coders of the Three Bags Task from the Early Head Start Research and Evaluation Project. (Westat is a statistical survey research organization.) These Westat staff members in turn served as supervisors for ECLS–B training and coding of the Two Bag Task at the 24-month assessment. Reliability with Westat supervisors was obtained on a weekly basis, and coders averaged 95.95% agreement with supervisors (across nine coders, reliability ranged from 95% to over 97%). As mentioned previously, coders were blind to ratings from co-twin interactions.

Infant attachment security and temperamental dependency. Infant attachment security and temperamental dependency were assessed using the Toddler Attachment Sort–45 (TAS-45), a revision of the Attachment Q-Sort (AQS; Waters, 1995) designed by ECLS–B staff. Like the AQS, the TAS-45 is a Q-set consisting of descriptors that are sorted by trained observers into a forced distribution from least to most characteristic of target participants' behavior. Specifically, the TAS-45 consists of 45 cards describing the target children's behavior. Later, these distributions were correlated with two criterion sorts, one reflecting prototypically secure and the other prototypically dependent children (as rated by experts in child development). Through this process, each participant received scores on security and dependency ranging from -1 (*not at all secure/dependent*) to 1 (*prototypically secure/dependent*; these scores reflect the correlation of a given participant's score with each prototype). Prototypically secure children used caregivers as a secure base of exploration and as a safe haven when distressed, whereas prototypically dependent children showed evidence of high levels of clingy, demanding, and fussy behavior, as well as excessive distress upon separation. As stated in the introduction, the security dimension is thought to characterize the quality of the child's attachment relationship with the target caregiver, whereas the dependency construct is meant to reflect the child's distress proneness, an aspect of temperament; the security and dependency dimensions are weakly correlated at age 1 but come to be more strongly negatively associated over time (Vaughn & Bost, 1999). In the current sample, security and dependency were correlated $-.39$ ($p < .001$), suggesting, as expected, that these are overlapping but not redundant constructs by age 24 months.[3]

Before data collection commenced, ECLS–B staff were trained extensively in the use of the TAS-45 with a set of three self-administered, computer-based training modules and a 20-page manual. Each coder had to pass a quiz related to each module with a score of 80% or greater. Trainees were also asked to complete TAS-45 coding of three videos. Scoring on these practice tapes was compared with standardized results, and the average agreement rate across trainees was 82% (trainees were deemed certified on the TAS-45 if they scored at or above 80%). It should be noted that though the TAS-45 is essentially a short form of the AQS, because TAS-45 was designed specifically for the ECLS–B study, this study is, to our knowledge, the first investigation to examine its validity (i.e., in relation to observed parenting quality).

Biometric Modeling: Univariate Analyses

To examine the sources of individual differences in each variable of interest, we estimated the parameters of the ACE —a commonly used biometric model in the behavioral–genetics literature (see Neale & Cardon, 1992). According to this model, variation in an outcome arises from three latent sources: additive

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[3] Although somewhat beyond the scope of this article, we conducted an exploratory behavior–genetic decomposition of this negative correlation between temperamental dependency and attachment security. The most parsimonious account of the data was the full behavior–genetic model (ACE) for both ECLS–B staff/parent–rated and parent-reported zygosity.

genetic variation (A), variation in environments shared between siblings (C), and variation in environments not shared between siblings (E). The additive genetic component represents the degree to which genetic variability contributes to variation in the outcome of interest and can be expressed mathematically as $A = 2 \times (r\text{MZ} - r\text{DZ})$, in which r represents correlation. The shared environment component represents the degree to which variation common to siblings contributes to the outcome of interest (i.e., $C = r\text{MZ} - A$). Finally, the nonshared effect represents the degree to which variation not shared by siblings contributes to the outcome of interest (i.e., $E = 1 - A - C$). The nonshared environment component also reflects random measurement errors (see Neale & Cardon, 1992, for relevant figures).

We estimated the parameters of the ACE model using the computer program Mx (Neale, Boker, Xie, & Maes, 1999) and evaluated the fit of the model using several statistics, including chi-square, the Akaike's information criterion (AIC; Akaike, 1983), and the root-mean-square error of approximation (RMSEA). Chi-square is a commonly used statistic for quantifying model fit; higher values of chi-square indicate larger deviations between the model's implied values and the empirical ones. AIC is proportional to the chi-square statistic (it is equal to $\chi^2 - 2 \times df$), but it is designed to benefit more parsimonious models. Smaller AIC values indicate a better fit. The RMSEA represents the degree of error involved in reproducing the observed covariance matrix from the estimated model. Smaller values indicate better model performance. A well-fitting model should have a nonsignificant chi-square, a low AIC, and a low RMSEA (RMSEAs $\leq .06$ indicate acceptable fit; Hu & Bentler, 1998).

In addition to evaluating the full ACE model for each outcome of interest, we also constrained certain paths to 0 as a way of determining whether the data can be explained just as well by assuming that one or more variance components are irrelevant in explaining variation in a given outcome. In the analyses that we report later, we evaluated all possible submodels of the full ACE model: AE (i.e., a model that does not assume a role of shared environmental factors), CE (i.e., a model that assumes no additive genetic effects), and E (i.e., a model that assumes that all phenotypic variation is due to nonshared environmental factors). In cases in which removing one or more components did not significantly diminish the fit of the model, we focused on the more parsimonious model.

Biometric Modeling: Bivariate Analysis

Using the bivariate behavior–genetic ACE model (see Fearon et al., 2006), we also used the Mx statistical software package (Neale et al., 1999) to decompose genetic and environmental influences on the covariance between parenting quality and infant attachment security. These analyses compare the pattern and magnitude of within-sibling correlations (e.g., the effect of Twin A's parenting quality on Twin A's security) and cross-sibling correlations (e.g., the effect of Twin A's parenting quality on Twin B's security) to the expected values of the general bivariate model. If cross-sibling effects are larger for MZ twins than for DZ twins, the covariation between the two variables can be described as genetically mediated, reflected in a significant genetic correlation between the constructs (r_A). In contrast, to the extent that within- and cross-sibling correlations are significant and do not differ between MZ and DZ twins, the covariation of interest is mediated by the shared environment, which is reflected in a significant shared environmental correlation (r_C). Finally, if the within-twin correlation is larger than the cross-twin correlation, this indicates that the association between variables emerges from experiences not shared between siblings (under this scenario, a significant nonshared environmental correlation, r_E, would be detected by the model).

Note that this analysis also yields estimates of a_{PQ}, a_{AS}, c_{PQ}, c_{AS}, e_{PQ}, and e_{AS}, coefficients representing genetic (a), shared environmental (c), and nonshared environmental (e) paths to parenting quality (PQ) and attachment security (AS). The amount of genetic, shared environmental, and nonshared environmental variance common to parenting quality and infant attachment security can be estimated by multiplying the paths for parenting quality ($a_{\text{parenting quality}}$, $c_{\text{parenting quality}}$, $e_{\text{parenting quality}}$), attachment security ($a_{\text{attachment security}}$, $c_{\text{attachment security}}$, $e_{\text{attachment security}}$), and the correlation between the two (r_A, r_C, r_E) separately for A, C, and E. The proportion of the phenotypic correlation that is accounted for each of these sources can be estimated by dividing each of the resulting scores by the phenotypic correlation. As with univariate analyses, bivariate model fitting allows for tests of the goodness of fit of the ACE model and its submodels with the chi-square, AIC, and RMSEA criteria outlined earlier.

Results

Biometric Modeling: Univariate Analyses

To evaluate the relative contribution of genetic, shared environmental, and nonshared environmental sources of variance, we estimated the parameters of the full ACE model (with 95% confidence intervals [CI] for A, C, and E), as well as the various derivatives of it. Each set of analyses was based on the variance–covariance matrix for MZ and DZ twins (the number of twin pairs, *n*s, for MZ and DZ varies somewhat in these analyses depending on participation in each part of 24-month assessment; see tables). In addition, in each table, we present results based on the ECLS–B staff/parent composite rating of zygosity and parent reports of zygosity separately.

Parenting quality. Table 1 reports the results of the model-fitting analyses for the full ACE model and its submodels. As can be seen, in the full ACE models the contribution of additive genetic variance to parenting quality was virtually 0 (A = .04, 95% CI = .00, .17, in the ECLS–B staff/parent–reported zygosity analysis; A = .00, 95% CI = .00, .11, in the parent-reported zygosity analysis). In contrast, C and E respectively accounted for 77% (95% CI = 66%, 83%) and 19% (95% CI = 14%, 25%) of the variance in parenting quality in the ECLS–B staff/parent–reported zygosity analysis and 79% (95% CI = 70%, 83%) and 21% (95% CI = 16%, 25%) of the variance in parenting quality in the parent-reported zygosity analysis. Moreover, when the additive genetic component of the model was constrained to equal 0, the constrained model (CE) was able to explain the data just as well as the full ACE model.

Attachment security. Table 2 reports the results of the model-fitting analyses for the full ACE model and its submodels for observations of infant attachment security. As can be seen, in the full ACE models the contribution of additive genetic variance to attachment security was small to modest (A = .17, 95% CI = .00,

Table 1

Estimates of the Contribution of Additive Genetic, Shared Environmental, and Nonshared Environmental Sources of Variance to Variation in Parenting Quality

	Model fit					Nested model comparisons			Variance components		
Model	χ^2	*df*	*p*	AIC	RMSEA	χ^2_{diff}	*df*	*p*	A	C	E
					ECLS–B staff/parent–rated zygosity[a]						
ACE	2.619	3	.454	−3.381	.032	—	—	—	.04	.77	.19
AE	95.107	4	<.001	87.107	.285	92.488	1	<.001	.84	—	.16
CE	**2.913**	**4**	**.573**	**−5.087**	**.018**	**0.294**	**1**	**.588**	—	**.79**	**.21**
E	311.588	5	<.001	301.588	.627	308.269	2	<.001	—	—	1.00
					Parent-reported zygosity[b]						
ACE	2.906	3	.406	−3.904	.047	—	—	—	.00	.79	.21
AE	92.748	4	<.001	84.748	.304	89.842	1	<.001	.81	—	.19
CE	**2.906**	**4**	**.574**	**−5.094**	**.031**	**<0.000**	**1**	**.999**	—	**.79**	**.21**
E	307.165	5	<.001	297.165	.628	304.259	2	<.001	—	—	1.00

Note. The statistics for the nested model comparisons test the difference in fit obtained when specific sources of variation in the full ACE (A = additive genetic effect; C = shared environmental effect; E = nonshared environmental effect) model are constrained to 0. The most parsimonious model in each set is highlighted in bold. ECLS–B = Early Childhood Longitudinal Study—Birth Cohort; AIC = Akaike's information criterion; RMSEA = root-mean-square error of approximation; A = additive genetic effects; C = shared environmental factors; E = nonshared environmental factors; AE = model that assumes no role for shared environmental factors; CE = model that assumes no additive genetic effects; E = model that assumes all phenotypic variation stems from nonshared environmental factors; MZ = monozygotic twin pairs; DZ = dizygotic twin pairs.

[a] *n*MZ = 78; *n*DZ = 234.

[b] *n*MZ = 98; *n*DZ = 211.

.35, in the ECLS–B staff/parent–reported zygosity analysis; A = .03, 95% CI = .00, .22, in the parent-reported zygosity analysis). In contrast, C and E respectively accounted for 53% (95% CI = 38%, 66%) and 30% (95% CI = 24%, 40%) of the variance in attachment security in the ECLS–B staff/parent–reported zygosity analysis and 61% (95% CI = 46%, 68%) and 36% (95% CI = 29%, 43%) of the variance in attachment security in the parent-reported zygosity analysis. In fact, when the additive genetic component of the model was constrained to equal 0, the constrained model (CE) was able to explain the data just as well as the full model.

Table 2

Estimates of the Contribution of Additive Genetic, Shared Environmental, and Nonshared Environmental Sources of Variance to Variation in Attachment Security

	Model fit					Nested model comparisons			Variance components		
Model	χ^2	*df*	*p*	AIC	RMSEA	χ^2_{diff}	*df*	*p*	A	C	E
					ECLS–B staff/parent–rated zygosity[a]						
ACE	0.970	3	.808	−5.030	.000	—	—	—	.17	.53	.30
AE	38.957	4	<.001	30.957	.160	37.987	1	<.001	.75	—	.25
CE	**3.644**	**4**	**.456**	**−4.356**	**.019**	**2.674**	**1**	**.102**	—	**.63**	**.37**
E	237.967	5	<.001	227.967	.473	236.997	2	<.001	—	—	1
					Parent-reported zygosity[b]						
ACE	1.930	3	.587	−4.070	.004	—	—	—	.03	.61	.36
AE	45.840	4	<.001	37.840	.175	43.910	1	<.001	.69	—	.31
CE	**2.028**	**4**	**.731**	**−5.972**	**.000**	**0.098**	**1**	**.754**	—	**.63**	**.37**
E	231.673	5	<.001	221.673	.452	229.743	2	<.001	—	—	1

Note. The statistics for the nested model comparisons test the difference in fit obtained when specific sources of variation in the full ACE (A = additive genetic effect; C = shared environmental effect; E = nonshared environmental effect) model are constrained to 0. The most parsimonious model in each set is highlighted in bold. ECLS–B = Early Childhood Longitudinal Study—Birth Cohort; AIC = Akaike's information criterion; RMSEA = root-mean-square error of approximation; A = additive genetic effects; C = shared environmental factors; E = nonshared environmental factors; AE = model that assumes no role for shared environmental factors; CE = model that assumes no additive genetic effects; E = model that assumes all phenotypic variation stems from nonshared environmental factors; MZ = monozygotic twin pairs; DZ = dizygotic twin pairs.

[a] *n*MZ = 116; *n*DZ = 345.

[b] nMZ = 157; *n*DZ = 298.

Table 3

Estimates of the Contribution of Additive Genetic, Shared Environmental, and Nonshared Environmental Sources of Variance to Variation in Temperamental Dependency

	Model fit					Nested model comparisons			Variance components		
Model	χ^2	*df*	*p*	AIC	RMSEA	χ^2_{diff}	*df*	*p*	A	C	E
					ECLS–B staff/parent–rated zygosity[a]						
ACE	1.094	3	.779	−4.096	.000	—	—	—	.61	.02	.37
AE	**1.129**	**4**	**.890**	**−6.871**	**.000**	**0.035**	**1**	**.852**	**.63**	—	**.37**
CE	17.501	4	.002	9.501	.139	16.047	1	<.001	—	.41	.59
E	101.001	5	<.001	91.001	.332	99.907	2	<.001	—	—	1
					Parent−reported zygosity[b]						
ACE	1.846	3	.605	−4.154	.000	—	—	—	.43	.11	.46
AE	**2.788**	**4**	**.594**	**−5.212**	**.000**	**0.942**	**1**	**.332**	**.56**	—	**.44**
CE	10.722	4	.030	2.722	.091	8.876	1	.003	—	.41	.59
E	94.429	5	<.001	84.429	.296	92.583	2	<.001	—	—	1

Note. The statistics for the nested model comparisons test the difference in fit obtained when specific sources of variation in the full ACE (A = additive genetic effect; C = shared environmental effect; E = nonshared environmental effect) model are constrained to 0. The most parsimonious model in each set is highlighted in bold. ECLS–B = Early Childhood Longitudinal Study—Birth Cohort; AIC = Akaike's information criterion; RMSEA = root-mean-square error of approximation; A = additive genetic effects; C = shared environmental factors; E = nonshared environmental factors; AE = model that assumes no role for shared environmental factors; CE = model that assumes no additive genetic effects; E = model that assumes all phenotypic variation stems from nonshared environmental factors; MZ = monozygotic twin pairs; DZ = dizygotic twin pairs.

[a] *n*MZ = 116; *n*DZ = 345.

[b] *n*MZ = 157, *n*DZ = 298.

Temperamental dependency. Table 3 reports the results of the model-fitting analyses for the full ACE model and its submodels for observer ratings of dependency. Consistent with what has been reported before in the literature (e.g., Bakermans-Kranenburg et al., 2004), there was evidence in both sets of analyses of a sizable genetic and nonshared environmental component to ratings of temperamental dependency but negligible evidence of a shared environmental component. Specifically, for the full ACE model, A = .61 (95% CI = .33, .71), C = .02 (95% CI = .00, .22), and E = .37 (95% CI = .29, .48) in the ECLS–B staff/parent–reported zygosity analysis and A = .43 (95% CI = .15, .63), C = .11 (95% CI = .00, .33), and E = .46 (95% CI = .37, .56) in the parent-reported zygosity analysis. Consistent with these results, constraining the shared environmental component to equal 0 (AE) led to the most parsimonious account of these data.

Biometric Modeling: Bivariate Analyses

The phenotypic correlation between parenting quality and attachment security was .19 ($p < .05$, adjusted due to the nonindependence of twin data), which is comparable to the meta-analytic effect identified by De Wolff and van IJzendoorn (1997; i.e., r = .24).[4] To evaluate the relative contribution of genetic, shared environmental, and nonshared environmental sources of variance to this covariation, we estimated the parameters of the full bivariate ACE model, as well as the various derivatives of it. Each set of analyses was based on the variance–covariance matrix for MZ and DZ twins. In addition, in each table we present results based on the ECLS–B staff/parent–reported composite rating of zygosity and parent reports of zygosity separately.

Table 4 reports the results of the model-fitting analyses for the full ACE model and its submodels for the covariation between parenting quality and attachment security. As can be seen, in both sets of analyses the most parsimonious account of these data involves shared and nonshared environmental components. The estimated coefficients for the CE model based on the ECLS–B zygosity composite were as follows: r_C =.226, r_E = .107, $c_{\text{parenting quality}}$ = .892, $c_{\text{attachment security}}$, = .823, $e_{\text{parenting quality}}$, = .452, and $e_{\text{attachment security}}$ = .568 (r_A, $a_{\text{parenting quality}}$, and $a_{\text{attachment security}}$ were constrained to 0). Per the path analytic tracing rules described earlier, the percentage of phenotypic variance accounted for by variation in shared environment was (.892 × .823 × .226 = .166/.193 =) 86%, and the percentage of phenotypic variance accounted for by nonshared environment was (.452 × .568 × .107 = .027/.193 =) 14%. The coefficients based on parent reports of zygosity were similar: r_C =.225, r_E = .113, $c_{\text{parenting quality}}$ = .892, $c_{\text{attachment security}}$, = .822, $e_{\text{parenting quality}}$, = .453, and $e_{\text{attachment security}}$ = .570 (r_A, $a_{\text{parenting quality}}$, and $a_{\text{attachment security}}$ were constrained to 0). The percentage of phenotypic variance accounted for by variation in shared environment was (.892 × .822 × .225 = .165/.194 =) 85%, and the percentage of phenotypic variance accounted for by nonshared environment was (.453 × .570 × .113 = .029/.194 =) 15%. Although these results are highly consistent with those presented by Fearon et al. (2006), it is important to note that the nonshared environmental correlation between maternal sensitivity and attachment security was negative in that study, whereas it was positive in the current work (see Discussion below).

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[4] The correlation was .193 for ECLS–B staff/parent–rated zygosity and .194 for parent-reported zygosity, which resulted from slightly different sample sizes (several twins could not be identified as MZ or DZ by parents; see Methods).

Table 4
Fit Indices for the Bivariate ACE Model of the Covariation Between Parenting Quality and Attachment Security at 24 Months

	Model fit					Nested model comparisons		
Model	χ^2	*df*	*p*	AIC	RMSEA	χ^2_{diff}	*df*	*p*
ECLS–B staff/parent–rated zygosity[a]								
ACE	11.743	11	.383	−10.257	.016	—	—	—
AE	142.674	14	<.001	114.674	.183	130.931	3	<.001
CE	**13.671**	**14**	**.474**	**−14.329**	**.005**	**1.928**	**3**	**.587**
E	502.396	17	<.001	468.396	.434	490.653	6	<.001
Parent−reported zygosity[b]								
ACE	20.096	11	.044	−1.904	.079	—	—	—
AE	170.791	14	<.001	142.791	.219	150.695	3	<.001
CE	**20.096**	**14**	**.127**	**−7.904**	**.057**	**<.0.000**	**3**	**.999**
E	501.273	17	<.001	467.273	.425	481.177	6	<.001

Note. The statistics for the nested model comparisons test the difference in fit obtained when specific sources of variation in the full ACE (A = additive genetic effect; C = shared environmental effect; E = nonshared environmental effect) model are constrained to 0. The most parsimonious model in each set is highlighted in bold. ECLS–B = Early Childhood Longitudinal Study—Birth Cohort; AIC = Akaike's information criterion; RMSEA = root-mean-square error of approximation; AE = model that assumes no role for shared environmental factors; CE = model that assumes no additive genetic effects; E = model that assumes all phenotypic variation stems from nonshared environmental factors; MZ = monozygotic twin pairs; DZ = dizygotic twin pairs.

[a] *n*MZ = 78; *n*DZ = 230.

[b] *n*MZ = 98; *n*DZ = 207.

Discussion

Revisiting the twin subsample from the nationally representative ECLS–B, an ongoing longitudinal investigation of the 2001 American birth cohort, we found that the current study replicated evidence from groundbreaking genetically informed studies that observations of parenting quality and infant attachment security in the early life course, as well as their covariation, are a product of shared and nonshared environmental (but not genetic) variation among children (Bakermans-Kranenburg et al., 2004; Bokhorst et al., 2003; Dozier et al., 2001; Fearon et al., 2006; O'Connor & Croft, 2001). This is the first study to have shown this result with attachment security data drawn from home observations by trained coders.

Consistent with the first behavior–genetic study of the association between parenting quality and infant security (Fearon et al., 2006), we found evidence that a large majority of the association between maternal sensitivity and infant security was accounted for by shared environmental variation, such that when sensitivity was shared within families, it was positively associated with infant security. However, in contrast to Fearon et al.'s (2006) study, but somewhat more in line with the expectations of attachment theory, the results of this study suggest that even when sensitivity is not shared within families, the target of such sensitivity is probabilistically more likely to be secure. Like Fearon et al. (2006), we found no evidence that covariation between parenting quality and security could be accounted for by genetic variation between children.

In contrast—but as expected—genetic differences between infants played a prominent role in accounting for observations of temperamental dependency. We nonetheless caution the reader that, although we expected and found that temperamental dependency was heritable, it does not necessarily follow that temperament is in any sense genetically determined. First, as has been emphasized by Partridge (2005), heritability coefficients reflect "both genotypic and epigenotypic variance" (p. 987). Second, much of the variation in temperamental dependency was accounted for the nonshared environment (i.e., experiences not shared by siblings within a given family).

As an extension of a prior behavior–genetic investigation based on the ECLS–B 9-month assessment (Roisman & Fraley, 2006), the current study reaffirms an important exception to the claim that individual differences in all psychological phenotypes are heritable and that shared environmental factors are relatively inconsequential for that variation (Turkheimer, 2000). Similarly, it demonstrates how behavior–genetic research designs have the potential to provide among the strongest support for socialization theories, even those that posit that genetic variation plays little or no role in the development of a given phenotype. We caution, nonetheless, that a large number of developmentally significant variables have been demonstrated to be heritable in quantitative behavior–genetic studies, even those historically viewed as direct measures of the environment (Rutter, 2002). In particular, we would be remiss in not mentioning that genetic differences between adolescents explain variation in the quality of parenting in adolescence, at least in some domains (Neiderhiser et al., 2004).

Given this state of affairs, we believe it crucial that developmental psychologists take seriously the fact that shared environments and shared genes are inextricably confounded within all studies involving between-family comparisons. As we have stated previously, although we are skeptical of claims regarding the far-reaching role of genetic variation in understanding all individual differences, we are equally surprised by the tendency of some developmental researchers to be somewhat dismissive about research in quantitative behavioral genetics. To be sure, numerous caveats and assumptions attach to all behavior–genetic decompositions of variance (Gottlieb, 1995; Greenberg, 2005; Partridge, 2005). Nonetheless, the only way to rule out the potential confounding effects of genetic variability is by taking that variability into account, and behavior–genetic designs offer one way to do so.

Like all other genetically informed studies of infant attachment security and its correlates, this investigation made use of a child-based behavior–genetic design. Although ECLS–B data suggest that genetic variability among infants is not associated with variation in the quality of parenting, infant attachment security, and their covariation, it could be that a study of MZ and DZ adults would yield contrasting results with a parent-based design, such as the Children of Twins approach (D'Onofrio et al., 2005; see also Neiderhiser et al., 2004). If it were determined that the quality of infant attachment security reliably covaries with genetic variability among parents, for example, a claim could be still made for the role of passive genetic processes in the development of infant security (Neiderhiser et al, 2004).

A second limitation relates to the use of a new assessment of attachment security (and temperamental dependency), the Toddler Attachment Security Q-Set (TAS-45). First, TAS-45 data were provided by research assistants who completed sorts for both twins. Ideally, participants would have been rated by different trained coders. Second, although the TAS-45 was based on Waters' (1995) well-validated Attachment Q-Set (AQS), relatively little is known about how it performs relative to the AQS. That said, the data presented herein suggesting that TAS-45 attachment security is as strongly associated with parenting quality as the meta-analytic effect documented by De Wolff and van IJzendoorn (1997) represents promising evidence of its validity.

Finally, questions remain about what causal factors lead secure parents to have secure children, given that observations of parenting quality are only moderately correlated with ratings of infant attachment security (De Wolff & van IJzendoorn, 1997) as well as evidence documented here and elsewhere (Bakermans-Kranenburg et al., 2004; Bokhorst et al., 2003; Fearon et al., 2006; O'Connor & Croft, 2001) that nonshared environmental processes account for a substantial proportion of the variation in infant attachment security (as well as its covariation with parenting quality).[5] We concur with Fearon et al. (2006) that this latter finding presents a serious challenge to attachment researchers who, until recently, have almost exclusively focused on identifying the antecedents of attachment security in variation in parenting experiences assumed to be largely shared within families. Thus, in a somewhat paradoxical twist of fate, genetically informed research may have provided one of the more useful pieces of evidence in the search to identify the precise environmental mechanisms governing the development of attachment security in the early life course.

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[5] We suspect that the meta-analytic estimate of the magnitude of the association between parenting quality and infant attachment security is an underestimate of the true effect since most studies tend to use relatively brief assessments of parenting quality (e.g., 10 min in the present study). Nonetheless, even if this is true, behavior–genetic analyses suggest that a substantial proportion of the variation in parenting quality, infant attachment security, and their covariation emerges from nongenetic sources of variation specific to children (rather than shared among siblings within families).

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