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# Parenting as Phenotype: A Behavioral Genetic Approach to Understanding Parenting

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## Parenting as Phenotype: A Behavioral Genetic Approach to Understanding Parenting

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### SYNOPSIS

This article discusses the behavioral genetic (BG) approach to parenting. Parenting is considered a phenotype that can be influenced by nature and nurture. Genetic contributions to parenting are conceptualized as evidence of genotype-environment correlation ( $r_{GE}$ ). Early BG studies focused on demonstrating that some parenting dimensions were heritable due to passive and evocative  $r_{GE}$  processes. Current studies are investigating moderators and mediators of genetic and environmental contributions to parenting. The paper uses parent and child report data on parental warmth from the Twins, Adoptees, Peers, and Siblings (TAPS) study to illustrate the BG approach. Results show that heritability is significant for parent and child reports, but environmental influences differ by information source. Three questions are addressed concerning the BG approach to parenting: What is the nature of parenting? How does the approach inform parenting practice and interventions? What are the future directions?

### INTRODUCTION

Our work focuses on understanding how genetic and environmental factors contribute to individual differences in parenting behavior. It is guided by the behavioral genetic (BG) approach that views parenting behaviors not as pure environmental phenomena, but as “phenotypes” that can be influenced by nature and nurture (McGuire, 2003). Phenotypes are measured behaviors or traits, such as depression or, in our case, parental warmth. BG studies on the “nature of nurture” show that many measures of the child’s environment are heritable (Plomin, 1994). Significant genetic contributions to “environmental” measures are conceptualized as genotype-environment correlation.

#### Genotype-Environment Correlation ( $r_{GE}$ )

Genotype-environment correlation ( $r_{GE}$ ) and genotype  $\times$  environment interaction ( $G \times E$ ) are forms of genotype-environment interplay (see Horowitz, Marceau, & Neiderhiser, 2011; Jaffee & Price, 2007; McGuire, 2003; Plomin, 1994).  $G \times E$  occurs when the environment moderates the expression of a genotype or when environmental influences differ by genotype.  $r_{GE}$  is a bidirectional link between individual differences in genotypes and environmental experiences. An example of a  $G \times E$  interaction would be parental negativity having a greater influence on children with difficult temperaments. An example of  $r_{GE}$  would be parental negativity and children’s difficult temperament sharing a genetic basis.

There are three types of *r*GE processes: passive, evocative, and active (McGuire, 2003). Passive *r*GE occurs when family members share both environments and genes. For instance, biologically related family members may participate in social activities together because parents and their genetically related children share genes related to the heritable trait of extraversion. Here, genetic and environmental contributions to behavior are confounded. Evocative *r*GE processes refer to the extent to which genetically linked traits in individuals elicit responses from others in the environment. For instance, parents may be more controlling towards children high in activity level, another heritable trait. Active *r*GE processes refer to the extent to which people seek out environments that are correlated with their genetically linked traits. For example, active children may seek out physical activities for themselves, creating opportunities to increase their health and their parents' health. Studies of the heritability of parenting currently focus on passive and evocative processes because active *r*GE is difficult to detect without longitudinal data.

### Estimating $h^2$ (and $c^2$ ) of Parenting

BG studies are designed to disentangle the genetic and environmental components in passive *r*GE processes. Kinship designs allow researchers to separate phenotypic variability into three components of variance:  $h^2$ ,  $c^2$ , and  $e^2$  (see Plomin, DeFries, McClearn, & McGuffin, 2008, for details about BG methods). The  $h^2$  statistic represents heritability and estimates the degree to which individual differences in a phenotype are associated with individual differences in genotypes within a population. Heritability can be further separated into additive ( $a^2$ ) and nonadditive ( $d^2$ ) genetic variance. Additive genetic variance is the result of alleles at multiple loci adding up in their contributions to behavior. Nonadditive genetic variance is due to higher-order interactions across alleles and would contribute to behavioral similarity only in the MZ twin pairs, who share all of their genes. Most kinship designs do not have the power to detect both  $a^2$  and  $d^2$  along with the environmental effects; consequently, most studies of the heritability of parenting are studies of additive genetic contributions to parenting. The  $c^2$  statistic estimates the degree to which individual differences in a phenotype are associated with family similarity after controlling for genetic similarity. Researchers often refer to this statistic as “common environment” or “shared environment” because it was assumed to be due to shared family experiences. The  $e^2$  statistic estimates the degree to which family members are not similar in a phenotype, and includes measurement error. Researchers often refer to this statistic as “nonshared environment” because it was assumed to be due to dissimilar family experiences. BG analyses of behaviors/traits, however, do not directly capture environmental processes. If family members respond differently to a “common” environment (e.g., family economic hardship), the impact of the experience would be found in  $e^2$ , not  $c^2$ . If different circumstances lead family members to the same outcome (e.g., depression),  $c^2$  would be significant for the outcome, not  $e^2$ . Consequently, BG researchers have begun measuring the environment directly to better understand G-E interplay.

Most kinship designs involve twins, biologically related families, and adoptive families, and each design has strengths and weaknesses (McGuire, 2003; Plomin et al., 2008). The twin design includes monozygotic (MZ) twins and dizygotic (DZ) twins. MZ twins result from the division of a single fertilized egg and share all genes. DZ twins result from the separate fertilization of two eggs by separate sperm and share (on average in the population) 50% of their segregating genes. Family designs include parents and their genetically related children, who share 50% of their inherited genes, and full siblings (FS) who, like DZ twins, result from the separate fertilization of two eggs, but at different points in time, and share 50% of their segregating genes (on average in the population). Adoption designs include either family members reared together who are not genetically related to each other or family members who are genetically related and were adopted into different families.

Extended kinship designs may include stepsiblings, nieces/nephews, and cousins. Our study, the Twin, Adoptees, Peers, and Siblings (TAPS) study, uses a design that combines the traditional twin, family, and adoption designs with two novel additions: virtual twins (VT) and friend-friend (FF) pairs (McGuire, Segal, Gill, Whitlow, & Clausen, 2010). VTs are same-aged, genetically unrelated pairs reared together since infancy who replicate the rearing situation of twins without genetic relatedness. The FF pairs were not used directly in our BG analyses, but they help us understand the potential role of shared social factors.

Heritability is significant when kinship similarity in the measured phenotype is associated with genetic similarity. In the TAPS sample, significant additive genetic influence ( $a^2$ ) would be found if the sibling interclass correlations followed this pattern: MZ twins > DZ twins = FS pair > VT pairs. If the correlations are high and do not differ significantly across the pairs, then  $c^2$  will be significant. The VT pair correlation, in particular, should be significant because adoptive sibling correlations are considered direct estimates of common environment.  $E^2$  includes error, but will also be significant when intraclass correlations are not high across kinship pairs. A significant correlation for the FF pairs could indicate that social factors may be contributing to parenting behavior.

BG designs also vary by target of the study (Horowitz et al., 2011; McGuire, 2003). In parent-based BG designs, the target sample is the parents in the family and these designs assess passive  $rGE$  contributions to parents' behavior towards their children. Significant  $c^2$  would mean that the parents were similar to their own co-twins/siblings in their parenting behavior, after controlling for genetic similarity. In child-based designs, the target sample is the children in the family and these designs assess evocative  $rGE$  contributions to parenting behavior towards them. Significant  $c^2$  here would mean that the twins/siblings were receiving similar kinds of parenting, after controlling for genetic similarity. New designs combine the parent-based and child-based designs into one (Horowitz et al., 2011); for example, the children-of-twins design includes adult twins and their children. Our research focuses on understanding child effects (e.g., evocative  $rGE$  processes) in family relationships during middle childhood, a time when children spend a great deal of time in the family. Consequently, our study is a child-based design.

### BG Analysis of Parental Warmth using TAPS

Early child-based studies showed significant heritability for parenting measures, but the results differ by dimension (McGuire, 2003). Kendler and Baker (2007) conducted a meta-analysis of the 55 independent studies of genetic contributions to environmental measures, including 22 studies that focused on measures of parenting. Using data from 12 studies that were child-based, they found that the weighted heritabilities were highest for parental warmth (34-37%), followed by protectiveness (20-26%) and control (12-17%). The ten parent-based BG studies of parenting also showed higher heritabilities for parental warmth (35%) compared to other parenting dimensions (19-23%). Although most studies relied on self-report data, the available data across all 22 studies suggested that heritability is higher for self-reports (.29%) compared to observer reports (14%). Thus, dimension and information source appear to moderate genetic contributions to parenting behavior, although some source differences may be due to methodological issues such as reporter biases or reactivity (Kendler & Baker, 2007).

In this article, we use data from the TAPS study to illustrate how the BG approach can be used to test moderators of  $rGE$ . We focus on parental warmth because we are interested in positive aspects of family experiences due to their links to children's well-being (McGuire et al., 2010). Research suggests that family members can have different experiences even in the same relationship (McGuire, 2001). Consequently, we tested for evidence of evocative  $rGE$  across two different reporters: parents and children. Neiderhiser and colleagues (2004)

conducted a similar analysis using the NEAD project data. The NEAD study is a child-based BG design that includes adolescent twins, full siblings, and stepsiblings. Their results showed significant  $a^2$  and  $c^2$  for mothers' reports of their positivity (i.e., closeness and affection) towards their children, but the significant  $a^2$  was mostly due to low similarity for the genetically unrelated stepsiblings ( $r_j = .12$ ), with the other sibling pairs showing high correlations ( $r_{fs} = .94$  to  $.56$ ). Teenaged siblings' reports of their mothers' positivity toward them were attributed to  $e^2$ .

Our analysis using TAPS data extends the work by Neiderhiser and colleagues (2004) in four ways: (1) it focuses on the more specific dimension (i.e., parental warmth) rather than a broad dimension (i.e., parental positivity) because specific measures may show different results (Jaffee & Price, 2007); (2) it was conducted when the children were in middle childhood and common environmental influences may be greater for middle childhood compared to adolescence (see Burt, 2009); (3) it included VTs who are genetically unrelated, but the same age, thus decreasing the chances that hypothesized low sibling similarity for these pairs would be due to age differences within the pair: and (4) it included FF pairs to see if social background factors contributed to parenting. Based on Neiderhiser et al. and other studies of parental positivity, we expected parental reports to show significant  $a^2$  and  $c^2$ . We tested to see if the differences between our study and Neiderhiser et al. would result in higher  $a^2$  and  $c^2$  estimates for the children's reports.

The TAPS participants were 300 child-child dyads and their parents. Most of the families (79%) lived near metropolitan areas in the Western United States; however, the VT families were from multiple regions across the United States. Family income ranged from less than \$10,000 to \$300,000 or higher, and parental education ranged from 8<sup>th</sup> grade to graduate education, with most families in the middle-class range. The breakdown for parents' reports of children's ethnicity was: 62.8% White, non-Hispanic ancestry, 20.6% mixed ancestry (including White/Hispanic), 7.4% Latino/Hispanic ancestry, 3.8% Asian ancestry, 3.3% African ancestry, and 2% marked "other" or did not respond. The percentage of children of White, non-Hispanic heritage compared to children of other heritages did not differ across dyad type. Most of the families were two-parent, never-divorced families (79%), followed by single-parent families (16%), stepfamilies (3%), and cohabitating or domestic partners (1%).

Both participating children had to meet strict criteria: (1) be 7 to 13 years old, (2) be in a twin or sibling relationship, and (3) be free of disabilities or handicaps that would prevent them from completing the measures (see McGuire et al., 2010, for details about recruitment and screening processes). The average age of the children in the study was 10.1 years ( $SD = 1.4$  years). Forty-six percent of the children were boys ( $n = 254$ ) and this ratio did not differ by dyad type. The average age of the parent completing the parenting measure was 41.7 years ( $SD = 6.4$  years), and the average age of the co-parent was 44.2 ( $SD = 6.5$  years).

The TAPS design included five dyad types that varied in genetic relatedness, as noted above. The first two dyad types were twin pairs: 54 MZ twins and 86 DZ twins (52 same-sex pairs and 34 opposite-sex pairs). The zygosity of the MZ and same-sex DZ twin pairs was established by comparative examination of 13 short tandem repeat (STR) DNA markers. The third dyad type consisted of the 69 FS pairs (36 same-sex pairs and 33 opposite sex pairs). The FS pairs were genetically related pairs within 4 years of age of each other. The average age difference between the siblings was 26.9 months ( $SD = 10.4$ ) with a range of 12 to 50 months. The fourth dyad type was the VT pairs (16 same-sex pairs and 27 opposite-sex pairs). The VT pairs were genetically unrelated, same-aged siblings. They consisted of either one adopted and one biological child, or two adoptees who had to fulfill additional criteria: (1) the siblings had to be within 9 months of each other in age; (2) the

children had to have been reared together since they were 1 year of age; and (3) the children had to have been in the same school grade, but could have attended separate classes or schools. The average age difference for the VTs was 3 months ( $SD = 2.6$  months) with a range of 0 to 9 months. A fifth dyad, FF pairs, was included in the TAPS study as a comparison group ( $n = 48$  pairs). The FF pairs were required to be same-sex. The average age difference for the FF pairs was 6.3 months ( $SD = 6.4$ ) with a range of 0 to 33 months.

After obtaining consent from all participants, family members were interviewed in their homes by trained testers as part of a 2- to 3-hr assessment. One parent (which was the mother in 99% of the families) and the two children completed the same measure, an 8-item scale that is based on the "acceptance-rejection" subscale of the Children's Report of Parent Behavior Inventory (CRPBI; Schaefer, 1965). Versions of Schaefer's measure have been used in previous BG studies of parenting (McGuire, 2003). The scale used in our study asked if the target is accepting, is able to comfort, shows positive affect, and understands the child. Children were interviewed to ensure that they understood the questions. The target parent (mostly mothers) completed the measure as part of a packet of questionnaires. Cronbach alphas were .86 for both children's reports and .80 and .84 for parents' reports of their warmth toward Sibling 1 and Sibling 2, respectively.

Our data analytic strategy began with calculating sibling intraclass correlations for child and parent reports of parental warmth for the four sibling dyads after controlling for age and sex of the child. We then used a model-fitting approach with covariance matrices because it provides a more powerful analysis of sibling resemblance compared to examining patterns of correlations. (FF pairs are excluded from these analyses.) Model-fitting analyzes the data for different sibling types simultaneously, tests for the fit of the model, makes assumptions explicit, and permits tests of alternative models. In this study, univariate maximum-likelihood model-fitting analyses were performed using LISREL 8 (Jöreskog & Sörbom, 1996). A univariate ACE model was used to estimate additive genetic (A), common environment (C), and nonshared environment (E) (plus error) contributions to variance in the parental warmth (see Figure 1). Based on a behavioral genetic approach, the correlation between additive genetic effects (A) for the two siblings is hypothesized to be 1 for MZ twins and .5 for DZ twins and .5 for full siblings and 0 for VT pairs. The common environmental path (C) is hypothesized to be 1 for all pairs because they live in the same home. The nonshared environmental path (E) is hypothesized to be 0 for all pairs because it reflects the degree to which the pairs are not similar. The patterns in the covariance matrices were compared to this hypothesized model. A model was fit to the data to that constrained the three parameters to be equal for the child and parent reports of parental warmth.

The ACE model contains additional assumptions: negligible nonadditive genetic variance ( $d^2$ ), no assortative mating, no selective placement of adopted siblings, and equal shared environment across sibling groups. As mentioned above,  $d^2$  is the result of higher-order interactions across alleles. The current study could be underestimating heritability and overestimating nonshared environment if  $d^2$  is present. Assortative mating means that people mate with others who are similar to them in the trait being studied, and selective placement means that adoptees were placed in homes with parents with similar physical or behavioral characteristics; both of these situations would mean that genetic and environmental influences were confounded in the current design and could result in overestimating heritability. The equal environment assumption states that the dyad types do not differ from each other on environmental factors that influence variability in the behavior being studied. Research suggests that MZ twins are treated more similarly compared to DZ twins (McGuire, 2001, 2003); however, studies of families where parents of twins are mistaken about their children's zygosity have shown that parents respond to twins' based on their actual zygosity, not their perceived zygosity (McGuire, 2003). Thus, differences in

social experiences across twin dyads are unequal for genetic, not environmental, reasons (Plomin et al., 2008). Still, a violation of this assumption could result in overestimating heritability. It will be important to test these assumptions in future studies and to replicate any results using different types of kinship designs.

Table 1 shows the sibling intraclass correlations for child and parent reports of parental warmth. The pattern suggests significant heritability and nonshared environment for the child reports, with MZ twins twice as similar as DZ twins coupled with low similarity for the other pairs. The results also showed significant heritability and common environment for the parent reports, with high sibling similarity across the dyads coupled with lower correlations for the FS and VT pairs. The TAPS parent-report data show a similar pattern as the NEAD data reported in Neiderhiser et al. (2004), with a low sibling intraclass correlation for the genetically unrelated pair ( $r_i = .39$ ) and high correlations for the other pairs. The TAPS child report data, however, showed a pattern that was closer to an additive genetic pattern (i.e.,  $MZ > DZ = FS > VT$ ) when compared to the NEAD child-report data. Specifically, intraclass correlations in TAPS showed the following pattern:  $MZ > DZ > FS = VT$ . The lower than expected correlation for the FS pairs may be due to the fact that they are different-aged pairs. The model fitting analyses confirmed our interpretations of the intraclass correlations, with both reports showing significant heritability (Table 2). A model that constrained the three parameters to be the same for child and parent reports did not fit the data,  $X^2(21) = 235.45, p < .001$ .

We found evidence of evocative  $rGE$  in both the parent and child reports. Parents are partially reacting to children's genetically influenced characteristics. The findings are consistent with our perspective that parenting is a phenotype that is a reflection of nature and nurture and not an assessment of "pure" nurture (McGuire, 2003). Our results also suggest that parents are not just reacting to their children's heritable characteristics. The common environment parameter ( $c^2$ ) was higher for parents' reports and the nonshared environmental parameter ( $e^2$ ) was higher for children's reports. These differences could be due to measurement error, but they may also reflect unique experiences for the parents and children during encounters involving the expression of parental warmth. Children may experience warmth differently even when parents display similar levels of warmth toward the children in the family (i.e., all children in the family receive love and care). The significant nonshared environment found for children's reports in TAPS is consistent with research on siblings' differential experiences in families (McGuire, 2001). The significant shared environment effect for parents' reports of their warmth could be due to social background factors; the approaching significant intraclass correlation for the FF pairs supports the exploration of social background or cultural similarity (i.e., social homogamy) in future BG studies of parenting. The significant shared environment effect in our child-based design may also be due to the influence of parents' own genotypes on their parenting. Parent-based designs indicated that parental reports of positive parenting are heritable, which would be seen in the  $c^2$  parameter in the child-based design (Neiderhiser et al., 2004).

## DISCUSSION OF THE BG APPROACH TO PARENTING

Our article used data from the TAPS study to explore one potential moderator of genetic and environmental contributions to parental warmth: information source or perspective. Our child-based design was novel because it combined traditional BG designs with two novel additions: virtual twins and friend-friend pairs. We found evidence for evocative  $rGE$  in both reports, but environmental contributions differed for parents and children. Below, we address three questions concerning parenting to further clarify how the BG approach informs parenting research.

### What Does the BG Approach Reveal about the Nature of Parenting?

The BG approach does not tell us which parenting behaviors are optimal. Instead, researchers often use the BG approach in conjunction with theories about the nature of parenting. Our work is based on attachment and evolutionary theories that assume that positive family experiences, such as warmth and trust, are good for family members because they promote survival and well-being (McGuire et al., 2010). The BG approach also does not tell us if dimensions of parenting are universal. Heritability and shared environment estimates can vary across populations; consequently, it is important that researchers not assume that genetic contributions are evidence of universality (McGuire, 2003). To our knowledge, there are no studies that examine the heritability of parenting across multiple cultures. BG studies within Western cultures indicate that parental warmth, control, and responsiveness are different dimensions because they show differential heritability or shared environmental influences (Kendler & Baker, 2007; McGuire, 2003). Our findings suggest, however, that parental warmth is a different experience for children and parents in the same family.

### How does the BG Approach Inform Parenting Practice and Interventions?

Molecular genetic studies of parenting in humans have increased significantly in the last few years (Jaffee & Price, 2007). Exciting work is being conducted using these techniques with other animals as well as humans (see Jensen & Champagne, 2012). The molecular genetic approach does not rely on components of variance estimated indirectly in populations to investigate gene-environment interplay. Instead, investigators examine links between variability in a gene (i.e., the alleles) and variability in trait or behavior in a sample of individuals. It is a more fine-grained analysis that does not require a kinship design. Using molecular genetic techniques, researchers will be able to uncover specific processes that link individual differences in genes to physiological processes to parenting behavior, which improves our ability to intervene in distressed family circumstances. Kinship studies are still needed, however. Kinship studies can detect the presence of passive  $rGE$  in links between parenting and outcome measures and provide candidates for molecular genetic work. Parenting researchers can use kinship designs to uncover non-genetic environmental influences that have a stable impact on children's development (see Bornstein, 2012; Conger, Schofield, & Nepl, 2012) by controlling for genetic factors until candidate genes are discovered (Burt, 2009).

### What are the Future Directions for BG Research on Parenting?

Molecular genetic studies will increase in the future in parenting research. Kinship studies can be improved to better inform the parenting literature while the search for genes linked to parenting behavior continues. The next step in our own research is to test for mediators of genetic contributions to parents' and children's perceptions of parental warmth (e.g., emotional stability) and to examine links with other positive family experience (e.g., sibling intimacy) and children's well-being (e.g., self-esteem). Future BG studies need to address limitations of the TAPS study and other BG studies. For instance, as with many studies of  $rGE$ , our study did not have the statistical power to examine multiple moderators (e.g., reporter  $\times$  sex composition of the dyad; Jaffee & Price, 2007). In addition, we were not able to examine how genetic and environmental contributions change over time (Kendler & Baker, 2007).

Current BG studies use complex designs to understand moderators and mediators of genetic and environmental contributions to parenting. Some researchers are combining parent and child-based designs, while others are examining how heritability changes across target parent (mothers versus fathers), age and sex of the children, and developmental context (Horowitz et al., 2011; Kendler & Baker, 2007). Behavioral studies of parenting are no



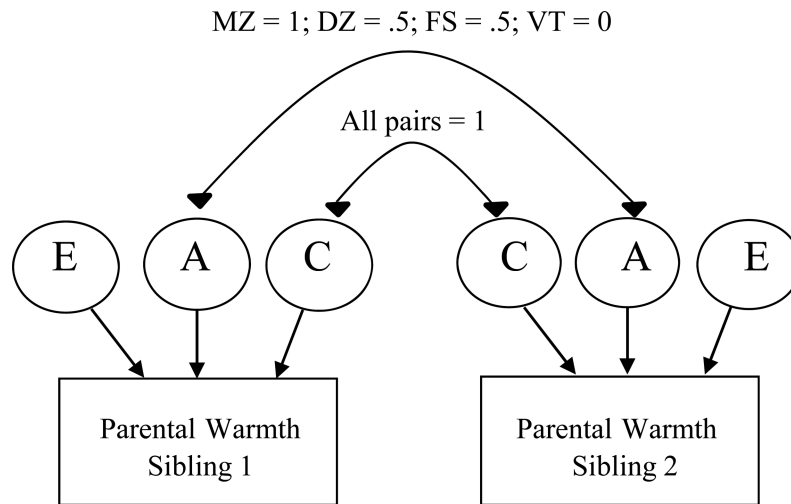
longer just estimating heritability. They are investigating how *r*GE changes across other levels of “E” (which parent or reporter) or “G” (the child's biological age, sex, or temperament characteristics). These efforts would be aided by collaborations between behavioral geneticists and parenting researchers from many theoretical backgrounds. Studies that combine expertise from both the “nature” and “nurture” side would be an important step in understanding the interplay between them.

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**Figure 1.**

Univariate behavioral genetic model. A = Additive genetic variance; C = common environmental variance; E = nonshared environmental variance plus measurement error. The correlation for the path for A for Sibling 1 and Sibling 2 is determined by genetic relatedness of the pair. MZ = monozygotic twin pairs; DZ = dizygotic twin pairs; FS = Full sibling pairs; VT = virtual twin pairs. The correlation for the Path for C for Sibling 1 and Sibling 2 is set to 1 for all pairs because they were all raised together.

**TABLE 1**  
 Sibling and Friend Intraclass Correlations for Child and Parent Reports of Parental Warmth by Dyad Type

|                  | MZ                | DZ                | FS                | VT                | FF                |
|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| <i>n</i> (dyads) | 54                | 86                | 69                | 43                | 48                |
| Child Report     | .44 <sup>**</sup> | .28 <sup>**</sup> | .12               | .13               | -.13              |
| Parent Report    | .73 <sup>**</sup> | .78 <sup>**</sup> | .72 <sup>**</sup> | .39 <sup>**</sup> | .27 <sup>**</sup> |

Note: MZ = monozygotic twin pairs; DZ = dizygotic twin pairs; FS = Full sibling pairs VT = virtual twin pairs; FF = friend-friend pairs.

<sup>\*\*</sup> *p* < .001.

Variance Components with Confidence Intervals and  $\chi^2$  Values from the ACE Model-fitting Results for Child and Parent Report of Parental Warmth.

TABLE 2

|               | Variance Components <sup>a</sup> |                   |                  | Model    |    |     |
|---------------|----------------------------------|-------------------|------------------|----------|----|-----|
|               | a <sup>2</sup>                   | c <sup>2</sup>    | e <sup>2</sup>   | $\chi^2$ | df | p   |
| Child Report  | .33<br>(.16,.50)                 | .19<br>(-.04,.42) | .48<br>(.40,.56) | 8.69     | 9  | .50 |
| Parent Report | .29<br>(.19,.38)                 | .44<br>(.38,.51)  | .27<br>(.23,.31) | 14.78    | 9  | .10 |

Note

<sup>a</sup>Includes 90% confident intervals. a<sup>2</sup> = additive genetic variance; c<sup>2</sup> = common environment variance; e<sup>2</sup> = nonshared environmental variance and error.

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p < .001