Evidence for Genetic Influence on Both Cross-Situation and Situation-Specific Components of Behavior

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An assumption often made in the study of personality and in social psychology is that methods variance and situation-specific effects, as key components of measured behavioral variance, are environmental effects. The results of the present research refute that assumption. Nine measures—three traits measured in each of three ways—were obtained at age 24 months for twin sibships participating in the Louisville Twin Study. This report describes a new model that captures the unique information potentially available in such data, by combining multitrait-multimethod and twin-family analytic designs. The results indicated significant genetic influence on methods—situation components of variance along with genetic influence on traits. The findings support heuristics that include both situation-specific patterns of behavior and cross-situational consistencies.

In this report we present novel results from application of a new structural model to unique, multitrait-multimethod (MTMM) twin-family data. The model combines MTMM and quantitative genetic analytic research designs. Several longstanding questions in the study of human behavioral variability are brought into focus. These questions have provoked debate and scholarly conceptual polarization, although attempts at synthesis, in more recent years, have been the norm. Together, the questions pertain to a larger theme (see Epstein, 1979) that might be described as trait theory under attack in the general fields of temperament and personality research and in social psychology. In polarized form, the questions include the following:

1. Is there a universal, or nomothetic, organization of traits (e.g., a general personality factor structure) such that each person's behavior can be predicted consistently from his or her trait position as plotted in the universal multidimensional trait space, or is the organization of personality primarily idiosyncratic, or idiographic, such that the person, not the trait, is the unit of study, each having a uniquely structured behavioral repertoire for responding to various kinds of situations (i.e., Bem & Allen, 1974; Rushton, Jackson, & Paunonen, 1981)?

2. Do concepts of behavioral traits, or the cross-situational consistencies of individuals, have enough predictive utility to justify their study, or does the research literature reflect more justification for the study of situations as determinants of behavior (e.g., Blass, 1984; Milgram, 1963; Mischel, 1968)?

3. When temperament, personality, or both are studied empirically, do the measures reflect actual characteristics of persons or are such measures primarily capturing aspects of relationships and interactions among persons (e.g., Goldsmith, Bradshaw, & Rieser-Danner, 1986; Goldsmith et al., 1987; Stevenson-Hinde, 1986; Stevenson-Hinde & Hinde, 1986; Vaughn & others, 1992)?

This report describes the application of a model developed specifically to reflect the uniquely informative aspects of combined MTMM and twin-family data. The model specification is described along with its application to nine measures of twin and sibling toddler temperament. In brief, the twin-sibship data to which the model was applied consisted of nine measures—three traits measured in each of three ways. Two different labo...
The convergent and discriminant validity among measures of temperament in early childhood has already been examined at the phenotypic level by several researchers (see, e.g., Goldsmith, Rieser-Danner, & Briggs, 1991, and references therein). Ours is the first report, however, to analyze the genetic and environmental relationships among MTMM measures. In so doing, we show that the information provided by twin-family data shed light on the origins of situational effects.

The new structural model was developed and applied with two purposes in mind: (a) to clarify the latent genetic and environmental relationships among various measures of temperament in early childhood and (b) to explore the analytic utility of the combined MTMM and twin-family model to estimate directly, and thus control for statistically, possible methods artifacts. This would enhance the reliability of the genetic and environmental trait structure estimates and clarify the nature of any methods artifacts uncovered.

Combining Two Analytic Strategies

The classical twin method refers to the comparative study of identical and fraternal twin pairs (Eaves, Eysenck, & Martin, 1989; Jinks & Fulker, 1970; Neale & Cardon, 1992). The variance effects that typically are estimated are those of additive genetic action, shared or common family environment, and non-shared or specific environment unique to the individual. When single-born siblings of twins or other single-born sibling pairs are also measured, special twin effects can be assessed. Such twin effects are defined as influences on twins, but not siblings, that lead to increased similarity within twin pairs relative to the similarity within sibling pairs. Twin effects might stem, for example, from twins' sharing family or other life events at exactly the same age. When special twin effects are detected, they can be accounted for statistically, thus preventing such effects from limiting the generalizability of the findings. The twin-family method is particularly helpful in the multivariate case because it enables the differentiation and clarification of latent genetic and environmental factors that are the sources of phenotypic correlations among measures (Eaves & Gale, 1974; Fulker, 1978; Phillips, Fulker, & Rose, 1987) or even among specific test items (Heath & Martin, 1990). In particular, the genetic factor structures need not be the same as environmental factor structures, and the clarification of these components of trait variance and covariance can serve as improvements on trait investigations that rely solely on phenotypic factor analytic descriptions.

MTMM measurement (Campbell & Fiske, 1959) is another powerful approach to the study of human behavior. It is uniquely designed to address key measurement issues, such as convergent and discriminant validity (Althauser, 1974; Alwin, 1974; Werts & Linn, 1970). Specific maximum-likelihood factorial models have been developed to estimate methods and trait effects and to test their significance (Jöreskog, 1971).

Widaman (1985) presented a general taxonomy of MTMM models that was extended by Marsh (1989) to include variations of a model proposed by Kenny (1979). In Kenny's model, methods factors are replaced by modeled correlations among measure-specific (or unique) factors that correspond to measures obtained by like methods. Kenny and Kashy (1992) referred to this as the correlated uniqueness model, and it is a special case of model 4E in Marsh's (1989) list. The consensus trend that has emerged (Kenny & Kashy, 1992; Marsh, 1989) favors (a) applying the correlated uniqueness model and (b) avoiding trait-methods factor correlations. In the nine-variate case, involving three traits and three methods, however, the correlated uniqueness model is equivalent to Widaman's (1985) model 4D, which specifies three intercorrelated trait factors, three intercorrelated methods factors, and nine measure-specific residual variances—one for each variable.

Psychometric Utility

The initial expectations about the analytic utility of the combined MTMM-quantitative genetic model were focused on psychometric and methodological factors. Reliable differences among mothers for general response sets should appear as a shared environmental methods effect for the parental report measures because such effects would be shared by both types of twins as well as their siblings. Differences of state in mothers, on the other hand, would appear as a twin methods questionnaire factor because the twin questionnaires were usually completed on the same day. State covariation in twin pairs themselves, reflected in twin covariation due to same day of testing, likewise, would be detected as twin methods effects for the two laboratory settings—methods. Because, for each of two laboratory evaluations, each twin's behavior was rated by different staff members, methods effects attributable to differences among testers would be revealed as nonshared environmental methods factors for the two laboratory settings.

Furthermore, it is conceivable that mothers of identical twins might tend to minimize, as either a perceptual or reporting bias, differences between their identical twin children relative to parental evaluations of similarities and contrasts between fraternal twin or nontwin sibling pair offspring. If such biases were reflected in individual parental questionnaire reports of each child's behavior, such parental biases could be expected to emerge as a genetic methods factor for the parental report measures because the effect would be to increase the apparent similarity of identical twins relative to fraternal twin or sibling pairs.

Alternatively, if mothers of identical twins tended to maximize perceived differences between their identical twin children (e.g., see Plomin, Willerman, & Loehlin, 1976) in their questionnaire reports, such biases would not be readily discerned from the results of applying the model in its current form. This type of bias could be expected to decrease the absolute values of the loadings of the parental report measures on genetic trait factors, because such effects would lower the similarity of the reports within identical twin pairs relative to the similarity of the twins' rated behaviors from objective laboratory assessment. These biases could also be reflected by increases in the loadings of the nonshared environmental methods factor for the parental report measures, because they would reduce the absolute similarity within identical twin pairs for those measures only. Such biases would also probably reduce the fit of the model because they would be expected to increase (identical) twin variance.
while decreasing the covariance. This type of effect (increasing variance, decreasing covariance) would require a different kind of model specification, similar to that of models of twin contrast effects, such as Carey’s twin interaction model (Carey, 1986; see also Carey, 1992; Phillips & Matheny, 1995).

Method

Participants

The Louisville Twin Study, an ongoing program of research now in its fourth decade, combines both the twin-family and MTMM approaches within an overall program of longitudinal tracking of development from infancy to adulthood (Falkner, 1957; Matheny, 1983, 1989; Phillips & Matheny, 1990; Vandenberg, Stafford, & Brown, 1968; Wilson, 1972, 1978). The twin-siblings in this research have participated in a systematic laboratory-based assessment of infant and toddler temperament involving visits to the research laboratory at 6, 9, 12, 18, 24, and 30 months of age. The present study addressed measures obtained at age 24 months from 318 twin children and 28 siblings of twins, all born between 1978 and 1988. This sample was 52% female and 48% male; 44% were identical twins, and 28% each were same-sexed and opposite-sexed fraternal.

Zygosity determination for same-sexed pairs was based on assay of 20 blood cell antigens or, more recently, on genotyping at seven or more highly polymorphic DNA markers.

Procedures and Measures

From each of three methods of assessment—standardized playroom vignettes, cognitive testing, and parental questionnaire, as detailed below—analyses were conducted by using three aspects of temperament: hedonic emotional tone, activity level, and sociability.

Playroom vignettes. During a visit to the laboratory, each child, unaccompanied by relatives, was engaged in a prearranged sequence of nine consecutive, standardized play routines presented by a staff interactionist (Matheny & Wilson, 1981). The play vignettes, which were age appropriate and moderately challenging, provided a standardized protocol for assessing each child’s responses and behavior. Examples of vignettes used at age 24 months are: an imitative game, role-play with a puppet, and activities with a small mechanical dog that barks while moving toward the child. Each playroom vignette was videotaped for 2 min, providing a total of 18 min of videotaped play activity. Afterwards, the videotape was rated by a staff member, who was not the interactionist, for several aspects of the child’s behavior during each 2-min segment. In the case of twins, each twin’s behavior was rated by a different staff member. Interrater reliabilities were determined periodically. For the temperament ratings discussed in this report, the average reliabilities were: hedonic emotional tone, .95; activity level, .85; and sociability, .88. More detailed descriptions of the organization of vignettes and videotaping formats can be found in Matheny and Wilson (1981), Matheny, Wilson, and Nuss (1984), and Matheny (1991).

Playroom ratings of emotional tone during each of the nine 2-min play vignettes were averaged to yield a playroom (PL) emotional tone (ET) score (ET-PL) for each child. Likewise, nine playroom activity level ratings were combined into an activity (AC) score (AC-PL), and nine sociability-to-interactionist ratings were averaged to yield a playroom sociability (SO) score (SO-PL).

Cognitive testing. At each visit, the child, accompanied by a parent, was also administered the Bayley Scales of Infant Development (Bayley, 1969) in a highly structured cognitive testing session that took place in a testing room. A component of the Bayley Scales, the Infant Behavior Record (IB), is a set of ratings about the child’s behavior during testing that is completed by the examiner after testing. The members of a twin pair do not have same Bayley examiner–IB rating. The IB rating scales included in the analyses reported here were Emotional Tone (ET-IB), Activity (AC-IB), and Sociability-to-Examiner (SO-IB). Interrater reliabilities for the IB were determined periodically. The average reliabilities were: Emotional Tone, .89; Activity, .80; and Sociability-to-Examiner, .82.

Parental questionnaire. A third set of temperament measures was obtained from mothers who completed the Toddler Temperament Scale (TS) of Carey and colleagues (Pullard, McDevitt, & Carey, 1984). The TS questionnaire is based on nine temperament characteristics identified in the New York Longitudinal Study (Thomas, Chess, Birch, Hertzig, & Korn, 1963). The three TS scale scores chosen for the present analyses were Mood (most closely matched in content to the emotional tone measures and designated ET-TS), Activity (AC-TS), and Approach (most closely matched in content to sociability and designated SO-TS).

Mothers usually completed the questionnaires at home and returned them by mail within a few weeks after a laboratory visit. The one-month, test–retest reliabilities for the temperament measures analyzed here, as reported by Pullard et al. (1984), are between .87 and .89. The nine measures selected for analysis putatively reflect three traits measured in each of three ways: (a) Emotional tone, measured in the playroom (ET-PL), on the IB (ET-IB), and from the mother’s ratings on the TS Mood Scale (ET-TS); (b) activity, measured in the playroom (AC-PL), on the IB (AC-IB), and from the mother’s ratings on the TS Activity Scale (AC-TS); and (c) sociability, measured in the playroom (SO-PL), on the IB (SO-IB), and from the mother’s ratings on the TS Approach Scale (SO-TS).

It should be noted that mood (ET-TS) was not designed to be the exact same construct as emotional tone and that approach (ET-TS) was not designed to be the exact same construct as sociability. The content overlap between mood and emotional tone and between approach and sociability, however, were deemed to be sufficiently high to test such convergences in the analyses.

The nine measures were standardized within gender prior to analyses. Although investigations of patterned behavioral consistencies and differences between boys and girls should be carried out, the sample size here was insufficient to examine gender-specific and gender-common aspects of genetic and environmental influences for the nine-variate twin-sibling data.

Five of the measures were transformed by ranking the scores within gender prior to standardization to lessen distributional nonnormality. These were ET-PL, ET-IB, AC-IB, SO-PL, and SO-IB. The average correlation between the ranked, standardized scores and the raw scores was .95. The loss of information from the transformations was deemed acceptable in light of the consequences of inappropriately applying models to nonnormal data. For the maximum-likelihood methods used in these analyses, failure to satisfy the assumption of multivariate normality at a reasonable level invalidates inferences based on the statistical properties of the chi-square distribution and may also result in unacceptably biased parameter estimates (see Hopper, 1986, and references therein).

Model

Figure 1 presents a diagram of the MTMM model as applied to the nine temperament measures. Each of the nine measures was hypothesized to be a trait–method unit (Campbell & Fiske, 1959, p. 81)—that is, the weighted sum of the effects of a latent, unmeasured trait in the person (ET, AC, or SO), a method (PL, IB, or TS), and an error term or residual—which has been omitted from Figure 1 for the sake of visual simplicity. As can be seen in Figure 1, factor correlations were estimated among the three latent traits—ET, AC, and SO—as well as between the two laboratory methods factors—PL and IB—within each of the genetic and environmental structures to which the MTMM model was applied.

Figure 2 shows a diagram of the components of the genetic—environ-
Figure 1. Multitrait-multimethod model applied to three traits each measured in three ways. Residuals are omitted from the diagram. Traits: ET = emotional tone; AC = activity; SO = sociability. Methods: PL = playroom vignettes; IB = Infant Behavior Record; TS = Toddler Temperament Scale.

Figure 2. Multivariate path diagram of the component matrices of the genetic-environmental model for a single individual. The component matrices are detailed in Table 1. $F_T$ = effects shared by a twin pair but not by siblings; $F_G$ = genetic factors; $F_{CE}$ = shared family environmental factors; $F_{SE}$ = nonshared environmental factors; $P$ = observed measures for an individual. $\theta$, $\lambda$, $\eta$, and $\psi$ represent path matrices.

Figure 3. Multivariate path diagram of the estimated components of resemblance for a twin pair. The component matrices are detailed in Table 1. $F_T$ = effects shared by a twin pair but not by siblings; $F_G$ = genetic factors; $F_{CE}$ = shared family environmental factors; $F_{SE}$ = nonshared environmental factors; $P$ = observed measures for an individual. $\theta$, $\lambda$, $\eta$, and $\psi$ represent path matrices.

Table 1: Variable and Parameter Matrices

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>$P$</td>
<td>Vector</td>
<td>Observed measures</td>
</tr>
<tr>
<td>$F_H$</td>
<td>Vector</td>
<td>Additive genetic factors</td>
</tr>
<tr>
<td>$F_{CE}$</td>
<td>Vector</td>
<td>Shared environmental factors</td>
</tr>
<tr>
<td>$F_{SE}$</td>
<td>Vector</td>
<td>Nonshared environmental factors</td>
</tr>
<tr>
<td>$F_T$</td>
<td>Vector</td>
<td>Twin factors</td>
</tr>
</tbody>
</table>

The symbol $\pi$ is used to denote the proportion of additive genetic effects that are identical in the members of a sibling or twin pair because of common ancestry, which for identical twins is 1.0 (for a single genotype) and for fraternal twins and full siblings is 0.5, on average. This is also referred to as the additive genetic correlation between siblings, twins, or both.

The way in which the MTMM and quantitative genetic strategies were combined in the model designed for the present analyses was by specifying the MTMM model presented in Figure 1 as the structure of the factor pattern (path) matrices shown in Figures 2 and 3. When applied to the genetic-environmental model, factor correlations among traits and methods can be specified within exogenous genetic and environmental factor correlation matrices (e.g., $C_{FG}$ for $F_G$ factors, $C_{FSE}$ for $F_{SE}$ factors).
The model is similar to one described by Heath, Neale, Kessler, Eaves, and Kendler (1992) because both combine psychometric and quantitative genetic models. The model presented here, however, does not require the postulation of latent phenotypes, but it can be modified to test for a (parsimonious) latent phenotypic structure by constraining each of the path matrices shown in Figure 2 to differ from each other only by a set of constant scalars.

Table 2 lists the modeling equations for the expected sources of variance and covariance in the twin—sibling families.

**Estimation Algorithm**

In the usual case, structural models are applied to observed summary statistics, such as correlation or covariance matrices generated from complete data from all cases. In the analyses reported here, the case is a twin—sibling. Too few data for siblings were available to construct sibling covariance matrices of order 27 or 36 for the pair of twins plus one or two siblings, respectively, each measured on nine variables. Instead, the models were applied to each family's vector of data by means of the maximum-likelihood pedigree algorithm (Lange, Westlake, & Spence, 1976). A log-likelihood was calculated for each sibling, and these were summed across the whole sample:

$$L_i = -1/2 \ln | \Sigma_i | - 1/2 (X_i - \mu)^T \Sigma_i^{-1} (X_i - \mu),$$

where for the $i$th pedigree, $\Sigma$ represents the matrix of observed covariances among family scores, $X$ is the vector of observed family data, and $\mu$ is a vector of expected means. In model comparisons involving large samples, twice the difference between two log-likelihoods is distributed asymptotically as chi-square with degrees of freedom equal to the difference in the number of free parameters used in fitting the two comparison models. Following Hopper and Mathews (1982), a test of the assumption of multivariate normality underlying the use of the log-likelihood sum, based on the Anderson-Darling statistic (Stephens, 1974), was applied. Maximum-likelihood estimates were obtained by minimizing the negative of the sum of all families' log-likelihoods, by using the MINUIT (James & Roos, 1989) optimization software along with user-supplied routines.

A major advantage afforded by the pedigree method is that all available data can be included in the analyses, and missing data do not result in the loss of a case. In addition, a portion of the likelihood for each family can be used to test the assumption of multivariate normality in the data (Hopper & Mathews, 1982; Phillips & Fulker, 1989; Phillips & Matheny, 1990) by means of the Anderson-Darling statistic (Stephens, 1974). This is especially important in pedigree applications because no other indicator of goodness of fit, such as the likelihood ratio statistic, is available for the initial model that is tried.

**Table 2**

<table>
<thead>
<tr>
<th>Matrix</th>
<th>Expectation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Within-person (twin)</td>
<td>$\lambda C_{xh} \lambda' + \eta C_{yeh} \eta' + \psi C_{zeh} \psi' + \Theta C_{tth} \Theta'$</td>
</tr>
<tr>
<td>Within-person (nontwin)</td>
<td>$\lambda C_{xh} \lambda' + \eta C_{yeh} \eta' + \beta C_{zeh} \beta'$</td>
</tr>
<tr>
<td>Identical twins</td>
<td>$\lambda C_{xh} \lambda' + \eta C_{yeh} \eta' + \beta C_{zeh} \beta'$</td>
</tr>
<tr>
<td>Fraternal twins</td>
<td>$\lambda C_{xh} \lambda' + \eta C_{yeh} \eta' + \Theta C_{tth} \Theta'$</td>
</tr>
<tr>
<td>Siblings</td>
<td>$\lambda C_{FG} \lambda' + \eta C_{EG} \eta'$</td>
</tr>
</tbody>
</table>

Note. FT = effects shared by a twin pair but not by siblings; FG = genetic factors; FCE = shared family environmental factors; FSE = nonshared environmental factors; $\theta$, $\lambda$, $\eta$, and $\psi$ represent path matrices; $C$ = covariance matrix.

**Descriptive Full Model**

Before testing the combined MTMM/genetic—environmental model, the unconstrained latent genetic and environmental covariance matrices were estimated. This is the equivalent of a saturated or full model that, in the usual modeling case, would be fitted to complete covariance structures. Rather than estimating the individual elements of the latent covariance structures, a Cholesky decomposition was applied such that each of the path matrices shown in Figure 2 was patterned as a lower triangular Cholesky (decomposition) matrix of estimates, and the covariances among latent factors were set to zero. The Cholesky technique is a convenience that ensures positive-definite expected covariance structures.

**Results**

Two sets of tests of homogeneity of variances and covariances were conducted before combining data across gender: (a) among the three types of fraternal twin pair types (same-sexed male and female pairs and opposite-sexed pairs) and (b) between male and female identical twin pairs. No significant differences were found for any of the nine temperament measures. For fraternal twins, chi-square statistics ($df = 7$) averaged 7.33 and ranged between 0.95 and 13.75. For identical twins, the average chi-square ($df = 4$) was 1.79, and the range was 0.38 to 4.98.

The results of the full modeling series applied to the data are listed in Table 3. The application of the full Cholesky decomposition within path matrices $\lambda$, $\eta$, $\psi$, and $\theta$ yielded a negative log-likelihood (-LL) of 955.80. The Anderson-Darling statistic indicated acceptable multivariate normality ($A^2 = 1.89, p > .10$), as did the Anderson-Darling statistics for all subsequent models.

All Cholesky factor patterns except that for nonshared environmental effects yielded latent component covariance matrices that were less than full rank. The genetic factor pattern contained five nonzero factors that accounted for 36% of the variance of the measures. In striking contrast, the shared environmental factor pattern contained two nonzero factors accounting for 6% of the variance, and the twin effects factor pattern had three nonzero factors accounting for 8% of the variance. The remaining 50% of the total variance among the nine measures was accounted for by nonshared environmental effects.

Each of these types of influence on familial covariation (genetic, shared family environmental, and special twin effects) was tested separately. Genetic influence on the nine measures was significant, Model 2, $\chi^2(45) = 62.29, p < 0.05$. However, both shared family environment, Model 3, $\chi^2(45) = 3.38, p > 0.99$, and special twin effects, Model 4, $\chi^2(45) = 11.72, p > 0.99$, were strongly rejected. Both shared environmental and special twin effects parameters could also be dropped simultaneously from the model, Model 5, $\chi^2(90) = 23.88, p > 0.99$. Next, all off-diagonal elements of the path matrix $\psi$ were set to zero. This model failed unconditionally, Model 6, $\chi^2(36) = 171.64, p < 0.001$, indicating that the observed correlations among the measures could be attributed, at least in part, to nonshared environmental effects.

The second series of models reflected the application of the MTMM model factors of Figure 1 as the genetic and nonshared environmental factors of Figures 2 and 3. All MTMM factors, for both traits and methods, were modeled in both the genetic...
Table 3  
Modeling Results

<table>
<thead>
<tr>
<th>Model</th>
<th>-LL</th>
<th>NPAR</th>
<th>$\chi^2$</th>
<th>df</th>
<th>$p$</th>
<th>Versus</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Full Cholesky</td>
<td>955.80</td>
<td>180</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2. No genetic</td>
<td>986.95</td>
<td>135</td>
<td>62.29</td>
<td>45</td>
<td>&lt;.05</td>
<td>1</td>
</tr>
<tr>
<td>3. No shared environmental*</td>
<td>957.49</td>
<td>135</td>
<td>3.38</td>
<td>45</td>
<td>&gt;.99</td>
<td>1</td>
</tr>
<tr>
<td>4. No twin effects*</td>
<td>961.66</td>
<td>135</td>
<td>11.72</td>
<td>45</td>
<td>&gt;.99</td>
<td>1</td>
</tr>
<tr>
<td>5. No shared environmental and no twin combined*</td>
<td>967.74</td>
<td>90</td>
<td>23.88</td>
<td>90</td>
<td>&gt;.99</td>
<td>1</td>
</tr>
<tr>
<td>6. Nonshared diagonal</td>
<td>1041.62</td>
<td>144</td>
<td>171.64</td>
<td>36</td>
<td>&lt;.001</td>
<td>1</td>
</tr>
<tr>
<td>7. Genetic and nonshared: MTMM*</td>
<td>985.65</td>
<td>62</td>
<td>35.83</td>
<td>28</td>
<td>&gt;.10</td>
<td>5</td>
</tr>
<tr>
<td>8. Genetic and nonshared $r_{ET,SO} = 1$*</td>
<td>986.91</td>
<td>58</td>
<td>2.51</td>
<td>4</td>
<td>&gt;.60</td>
<td>7</td>
</tr>
<tr>
<td>9. No genetic methods</td>
<td>1006.99</td>
<td>48</td>
<td>40.18</td>
<td>10</td>
<td>&lt;.001</td>
<td>8</td>
</tr>
<tr>
<td>10. No genetic traits</td>
<td>1010.07</td>
<td>48</td>
<td>46.33</td>
<td>10</td>
<td>&gt;.99</td>
<td>8</td>
</tr>
<tr>
<td>11. No genetic specifics</td>
<td>999.30</td>
<td>49</td>
<td>24.79</td>
<td>9</td>
<td>&lt;.005</td>
<td>8</td>
</tr>
<tr>
<td>12. No nonshared environmental traits</td>
<td>996.82</td>
<td>48</td>
<td>19.83</td>
<td>10</td>
<td>&lt;.05</td>
<td>8</td>
</tr>
<tr>
<td>13. No nonshared environmental methods</td>
<td>1027.71</td>
<td>48</td>
<td>81.60</td>
<td>10</td>
<td>&lt;.001</td>
<td>8</td>
</tr>
<tr>
<td>14. Genetic $r_{ET,SO,AC} = 1$*</td>
<td>988.09</td>
<td>57</td>
<td>2.36</td>
<td>1</td>
<td>&gt;.10</td>
<td>8</td>
</tr>
</tbody>
</table>

Note:  
- LL = sample negative log-likelihood; NPAR = number of free parameters; MTMM = multitrait-multimethod; ET = emotional tone; SO = sociability; AC = activity.  
* Increasingly parsimonious models that could not be rejected.

and nonshared environmental factor patterns exactly as diagrammed in Figure 1 for each factor pattern. This set of constraints was not significantly different from the reduced descriptive Cholesky decomposition in Model 5. Several of the estimated factor correlations, however, exceeded 1.0, particularly between ET and SO, suggesting an empirically unidentified model. To remedy this, a model was tested in which ET and SO were specified as a single latent trait factor in the genetic and nonshared environmental matrices. This reduced model gave a quite acceptable fit, Model 8, $\chi^2(4) = 2.51, p > 0.60$. All parameter estimates in Model 8 were well within the expected bounds of -1.0 to 1.0. The difference between this model and that of Figure 1 is that all three trait factors (ET, AC, and SO) as shown in the figure would be combined into a single factor, with which three arrows would go into the three ET measures, three arrows would go into the three SO measures, and three arrows would go into the three AC measures. Alternatively, the diagram could be modified such that all the correlations among the ET, AC, and SO factors, shown in Figure 1 as double-headed arrows, would be fixed at 1.0.

The quite surprising result from application of Models 7 and 8 was that substantial loadings appeared for the all of the genetic factors designed to allow for methods effects, for both parental questionnaire and laboratory settings, in addition to the loadings representing the less surprising influence of nonshared environmental methods effects. These methods or situation-specific genetic loadings were not small, and, as a group, they were quite significant, Model 9, $\chi^2(10) = 40.18, p < .001$.

Genetic influence on traits also could not be dropped from the model, Model 10, $\chi^2(10) = 46.33, p < .001$, nor could the genetic test-specific uniquenesses be deleted, Model 11, $\chi^2(9) = 24.79, p < .005$. Nonshared environmental trait factors were also significant, Model 12, $\chi^2(10) = 19.83, p < .05$, as were nonshared environmental methods effects, Model 13, $\chi^2(10) = 81.60, p < .001$. Finally, genetic trait factors ET/ SO and AC were combined into a single factor, the equivalent of setting the genetic trait factor correlation to 1.0. This model could not be rejected, Model 14, $\chi^2(1) = 2.36, p > .10$. We have labeled this general, genetic, cross-situation temperament factor *vivacity*. The difference between this model and that of Figure 1 is that all three trait factors (ET, AC, and SO) as shown in the figure would be combined into a single factor, vivacity, from which three arrows would go into the three ET measures, three arrows would go into the three SO measures, and three arrows would go into the three AC measures. Alternatively, the diagram could be modified such that all the correlations among the ET, AC, and SO factors, shown in Figure 1 as double-headed arrows, would be fixed at 1.0.

Model 14 factor pattern estimates are presented in Table 4. The estimated correlation between genetic situation-specific laboratory factors PL and IB was .66. Nonshared environmental factor correlations were .19 between trait factors ET/ SO and AC and .24 between laboratory factors PL and IB. All the measures except ET-TS (mood measured by the Toddler Temperament Scale) showed moderate loadings on the single genetic vivacity factor. One end on this dimension defines a child who tends to be positive in affect, active, and sociable across situations. In contrast, the genetic loading for activity on the IB factor is in the opposite direction, and one pole of this dimension describes a child who is positive in affect, sociable, and low in activity during cognitive testing. The more salient aspects of the PL and TS genetic factors tend to be ET and SO, particularly for PL.

The ET/ SO factor in the nonshared environmental loading matrix appears to be largely a TS factor, with modest, but significant, loadings from laboratory measures. The AC factor in this matrix is dominated by the PL loading. The nonshared environmental methods factors are well defined, and the negative loading for AC on the IB factor parallels the pattern seen in the genetic factor pattern.

Table 5 lists the proportions of the total variance of the nine measures accounted for by genetic and nonshared environmental effects, listed separately by factor type: (a) cross-situational consistencies, that is, trait factors; (b) situation-specific, or methods factors; and (c) residual test-specific factors unique to each measure. Across these three behavioral aspects, the percentage distributions of genetic and nonshared environmental
factors are strikingly similar, yielding essentially an equal apportionment of total variance effects between genetic and nonshared environmental factors. Situation-specific/methods factors accounted for the greatest proportion of total variance (41%), and cross-situational/trait factors accounted for the least (25%).

Table 6 shows the estimated genetic and nonshared environmental correlations among the nine measures, with proportions of variance given on the diagonal. Estimated heritabilities range from 26% for SO-IB to 79% for ET-TS.

**Discussion**

The results presented here indicate that individual differences in responding to specific situations, usually assumed to be environmental effects, are influenced by genetic factors. The results also suggest that average levels of sociability, emotional tone, and activity in early childhood are influenced by the same or overlapping genes and that, separate from these genetic factors, there are genetic factors that influence situation-specific responding for more than one characteristic in that particular situation. Two children, for example, showing similar overall average levels of sociability, emotional tone, and activity, may diverge in their behavioral patterns in the Bayley test-taking situation such that one child becomes more sociable and positive (and less active) than usual during the Bayley test, whereas the other becomes less sociable and positive (and more active) than usual during the Bayley test.

Individual differences for situational effects have been referred to by researchers before (e.g., Matheny & Dolan, 1975). The broad implication of our findings is that analysis-of-variance-based research designs, in which trait and situational main effects are examined along with tests for trait–situation interactions (see, e.g., Blass, 1991, and references therein), should be reexamined and extended. In particular, it would seem that the focus on situational main effects has resulted in a neglect of individual differences in situation-specific responding. The existence of genetically based situational-specific individual differences, along with unequivocal support for individual differences for general traits, also suggests that variable, although not necessarily idiosyncratic, organizations of personality, temperament, or both are distinct possibilities. Although the number of such idiographic behavioral organizations could extend theoretically to infinity, it is more likely that a large percentage of individuals could be described reliably by a manageable number of such organizational schemas of situation-general and situation-specific responding, which would be more consistent with person-centered approaches. It is also noteworthy that differential situation-specific patterns of responding have been conceptualized and investigated recently in regard to the development of several forms of shyness, fearfulness, and inhibition in children (see Asendorpf, 1989, 1990, and references therein). Furthermore, an increasing number of researchers are investigating individual differences in trait-like, generalized cross-situational variability or consistency (e.g., Baumeister & Tice, 1988) as well as individual differences in patterns of responding (Tellegen, 1988; Tellegen, Kamp, & Watson, 1982; Waller & Reise, 1992; see also Paunonen & Jackson, 1985).

It must also be highlighted that the observed correlations among ET, SO, and AC for 24-month-old children appear to be attributable in part to the pleiotropic effects of a single set of genes. Previous phenotypic factor analyses of Louisville Twin Study data indicated a trait labeled tractability (Matheny et al., 1984), which differs somewhat from the genetically defined trait described in this report. The difference is that the tractability dimension from phenotypic factor studies did not include activity. Our combined quantitative genetic–MTMM analyses shed light on this because the opposite signs shown for activity in the factor patterns (positive loading on the genetic trait factor and negative loadings on both the genetic and nonshared environmental IB and TS factors) would tend to cancel out in factor analyses of phenotypes. We have chosen a new descriptor for the genetically defined trait—vivacity—to capture the nonpassivity reflected in the positive sociable end of this dimension. The lack

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Table 4

**Final Model Estimates: Standardized Factor Loadings \times 100**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Vivacity</th>
<th>PL</th>
<th>IB</th>
<th>TS</th>
<th>Spec</th>
</tr>
</thead>
<tbody>
<tr>
<td>ET-PL</td>
<td>38</td>
<td>44</td>
<td></td>
<td></td>
<td>39</td>
</tr>
<tr>
<td>ET-IB</td>
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<td></td>
<td>66</td>
<td></td>
<td>0</td>
</tr>
<tr>
<td>ET-TS</td>
<td>-1</td>
<td></td>
<td></td>
<td>58</td>
<td>68</td>
</tr>
<tr>
<td>AC-PL</td>
<td>46</td>
<td>5</td>
<td></td>
<td></td>
<td>36</td>
</tr>
<tr>
<td>AC-IB</td>
<td>51</td>
<td></td>
<td>-39</td>
<td></td>
<td>0</td>
</tr>
<tr>
<td>AC-TS</td>
<td>40</td>
<td></td>
<td></td>
<td>-22</td>
<td>71</td>
</tr>
<tr>
<td>SO-PL</td>
<td>33</td>
<td>56</td>
<td></td>
<td></td>
<td>23</td>
</tr>
<tr>
<td>SO-IB</td>
<td>28</td>
<td></td>
<td>38</td>
<td></td>
<td>19</td>
</tr>
<tr>
<td>SO-TS</td>
<td>42</td>
<td></td>
<td></td>
<td>48</td>
<td>0</td>
</tr>
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</table>

<table>
<thead>
<tr>
<th>ET/SO</th>
<th>AC</th>
<th>PL</th>
<th>IB</th>
<th>TS</th>
<th>Spec</th>
</tr>
</thead>
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<tr>
<td>ET-PL</td>
<td>17</td>
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<tr>
<td>ET-IB</td>
<td>2</td>
<td></td>
<td>67</td>
<td></td>
<td>22</td>
</tr>
<tr>
<td>ET-TS</td>
<td>30</td>
<td></td>
<td></td>
<td>32</td>
<td>11</td>
</tr>
<tr>
<td>AC-PL</td>
<td>74</td>
<td>33</td>
<td></td>
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<td>0</td>
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<tr>
<td>AC-IB</td>
<td>3</td>
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<td>-25</td>
<td></td>
<td>73</td>
</tr>
<tr>
<td>AC-TS</td>
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<td></td>
<td></td>
<td>-28</td>
<td>45</td>
</tr>
<tr>
<td>SO-PL</td>
<td>7</td>
<td>41</td>
<td></td>
<td></td>
<td>60</td>
</tr>
<tr>
<td>SO-IB</td>
<td>7</td>
<td></td>
<td>45</td>
<td></td>
<td>73</td>
</tr>
<tr>
<td>SO-TS</td>
<td>66</td>
<td></td>
<td></td>
<td>-41</td>
<td>0</td>
</tr>
</tbody>
</table>

Note. The specifics form a diagonal in each actual factor pattern, not a column as shown here. Dashes indicate loading fixed at zero. Factor correlations: Genetic, PL with IB = 0.66; nonshared environmental, ET/SO with AC = 0.19, PL with IB = 0.24, ET = emotional tone; AC = activity; SO = sociability; PL = playroom, IB = Bayley Infant Behavior Record; TS = Toddler Temperament Scale; Spec = Specifics; ET/SO = combined factor for ET and SO.

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Table 5

**Proportions of Variance**

<table>
<thead>
<tr>
<th>Methods–source</th>
<th>Cross-situations</th>
<th>Situation specific</th>
<th>Test specific</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genetic</td>
<td>13</td>
<td>21</td>
<td>15</td>
<td>49</td>
</tr>
<tr>
<td>Nonshared environmental</td>
<td>12</td>
<td>20</td>
<td>19</td>
<td>51</td>
</tr>
<tr>
<td>Total</td>
<td>25</td>
<td>41</td>
<td>34</td>
<td>100</td>
</tr>
</tbody>
</table>
of detectable discriminant validity in our results among the separate temperament constructs, at the genetic level, is consistent with previous findings by Goldsmith et al. (1991) of weaker than expected discriminant validity of temperament questionnaires at the phenotypic level. Increased sample size, however, may yield sufficient statistical power to differentiate significantly among the genetic trait factors, thus nullifying our current genetic vivacity factor by decomposing it into its component traits.

Other aspects of the genetic factor pattern in Table 4 are also noteworthy. An artifactual genetic methods factor may be indicated for the parental questionnaire report. Had we not found evidence for independent situation-specific genetic influence on behavior in each of the two laboratory settings, we could infer that the TS genetic methods factor suggested a response bias on the part of mothers of monozygotic twins, minimizing within-pair differences, as described above. The possibility of similar bias on the part of staff raters, however, is precluded by the fact that the members of a twin pair had different raters. Given that the results suggest genetic influence on laboratory situations effects, we must consider the possibility that the parental questionnaire also reflects a genetic situation-specific effect, say, that of home life. The interpretation of the genetic methods—situations factor for the parent questionnaire thus remains unclear.

The TS Mood measure, from the parental questionnaire report, did not correspond at the genetic level with hedonic emotional tone as measured in laboratory settings. The nonshared ET trait loadings are also small. These results suggest that the TS Mood measure taps a somewhat different construct at age 24 months.

The nonshared environmental trait factors were each dominated by a single measure. Two of these, emotional tone and sociability, largely reflected the TS questionnaire scales Mood and Approach, respectively. The nonshared environmental activity factor was dominated by the playroom measure. Although significantly different from zero, the other nonshared environment trait loadings were generally quite small, indicating that they contributed little to the correlations among the measures. The nonshared methods loadings, on the other hand, were moderate to large. These factors include measurement variance attributable to individual raters for the PL and IB laboratory methods factors. They also may reflect actual nonshared situation-specific environmental influences. Future studies of the longitudinal persistence of these various effects should help to clarify some of them.

It must be emphasized that inferences about overlap or independence among various genetic factors reflect statistical genetic aspects of the data but not necessarily the exact forms of gene action, pleiotropic effects, and biological structures. The genetic factor pattern in our final model reflects the genetic correlations among the nine measures, which are not significantly different from the genetic correlations estimated from the full model Cholesky decomposition. Carey (1988), however, has distinguished between statistical genetic correlations and biological pleiotropisms in polygenic systems, showing that statistical genetic correlations do not necessarily reflect the exact nature and relationships among genes. Knowledge of such relationships must await the identification of the genes themselves and elucidation of the pathways from genotypes to measured behavioral phenotypes.

This report illustrates that combined MTMM and quantitative genetic research strategies provide a useful method for clarifying the genetically based dimensions of temperament and personality. Aspects of temperament in young children are understood to be more visible, relative to older individuals, and are thought to provide the foundation for later personality development. As the sample size in the Louisville Twin Study temperament research program increases we will extend our combined model to reflect longitudinal—developmental patterns in the MTMM twin—family data. Increased sample size will also facilitate inclusion of additional measures, such as cognitive data, other aspects of temperament, or other methods of temperament and later personality assessment to provide a broader view of the underlying structure of behavioral development.

References


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