Sources of Structure: Genetic, Environmental, and Artifactual Influences on the Covariation of Personality Traits

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ABSTRACT The phenotypic structure of personality traits has been well described, but it has not yet been explained causally. Behavior genetic covariance analyses can identify the underlying causes of phenotypic structure; previous behavior genetic research has suggested that the effects from both genetic and nonshared environmental influences mirror the phenotype. However, nonshared environmental effects are usually estimated as a residual

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term that may also include systematic bias, such as that introduced by implicit personality theory. To reduce that bias, we supplemented data from Canadian and German twin studies with cross-observer correlations on the Revised NEO Personality Inventory. The hypothesized five-factor structure was found in both the phenotypic and genetic/familial covariances. When the residual covariance was decomposed into true nonshared environmental influences and method bias, only the latter showed the five-factor structure. True nonshared environmental influences are not structured as genetic influences are, although there was some suggestion that they do affect two personality dimensions, Conscientiousness and Love. These data reaffirm the value of behavior genetic analyses for research on the underlying causes of personality traits.

For decades, personality psychologists worked to define the phenotypic structure of personality—the pattern of covariation of observed personality traits (Goldberg, 1993). The present near-consensus on the Five-Factor Model (FFM; McCrae & John, 1992) has allowed researchers to proceed to a new question: What accounts for the observed structure? Personality traits are known to be substantially inherited (Loehlin, 1992), but can genetics alone explain the covariation of traits, or is the phenotypic FFM the net result of combined genetic and environmental influences?

The answer to that question has always been relevant to developmentalists and clinicians who seek to understand the origins of personality, but it has taken on particular importance in the era of molecular genetics (Plomin & Caspi, 1998). Identifying the particular genes associated with any single trait has been likened to finding "many tiny needles in the haystacks" (Plomin, 1990, p. 187), and this daunting search must be guided by an understanding of the origins of personality structure. Cloninger, Adolfsson, and Svrakic (1996) have argued that "traits derived by factor analysis at the phenotypic level, such as extraversion . . . are likely to be composites of aetiologically heterogeneous facets" that may not be optimal guides for "unraveling the genetics and neurobiology underlying human personality" (p. 3). Indeed, it would make little sense to look for the genes responsible for extraversion if extraversion were merely a cluster of genetically unrelated traits inculcated by certain patterns of child rearing.

But are the facets of extraversion (and other phenotypic factors) in fact genetically unrelated? It might seem that molecular genetics itself would offer the most direct answers to such questions, but, to date, progress in that field has been halting. Early reports of specific genes linked to personality traits (Benjamin et al., 1996; Lesch et al., 1996) have not been consistently replicated (Flory et al., 1999; Vandenbergh et al., 1997). At present, it appears more realistic to rely on the well-established methods of behavior genetics.

Genetic Covariance Analyses

Conventional behavior genetics analyses attempt to determine the proportion of variance in a trait attributable to genetic and environmental influences. More recently, attention has been focused on the genetic and environmental sources of covariance among different traits (e.g., Carey & DiLalla, 1994; Jang & Livesley, 1999). For example, Eley (1997) investigated the possibility that the well-known correlation between anxiety and depression might be due to shared genes that influence both these dispositions. Such analyses can be extended to examine the intercorrelations among many traits, and factor analysis (e.g., Livesley, Jang, & Vernon, 1998) can summarize the structure of genetic and environmental influences on personality just as it summarizes the structure of traits themselves. Genetic covariance analyses might be used to ask whether and to what degree the FFM is the result of genetic and environmental influences.

Personality psychologists have frequently assumed that different traits and trait factors had different sources (Strelau, 1987). In particular, the classic distinction between temperament and character assumed that some traits (such as Neuroticism and Extraversion) were primarily the result of nature, whereas others (such as Agreeableness and Conscientiousness) reflected socialization and personal experience (cf. Cloninger, Przybeck, Svrakic, & Wetzel, 1994). This appealing dichotomy has been called into question by recent evidence that traits from all five major personality factors are moderately to strongly heritable (Jang, Livesley, & Vernon, 1996), but the heritability of individual traits does not speak directly to the heritability of their patterns of covariance. Traits such as dutifulness, order, and achievement striving might each individually be partly heritable, but their covariation in defining the Conscientiousness factor might be due entirely to environmental influences such as religious training or parental encouragement.

Depending on the research design, behavior genetics analyses can estimate contributions from additive and non-additive (dominant-recessive) genetic influences, shared environmental influences (e.g., perinatal, common family and community influences on both twins), and nonshared environmental influences (experiences unique to each twin). Nonshared environmental influences have become a focus of interest in behavior genetics because they appear to have as much influence on personality as do genes, and a far greater influence than shared environmental influences (Bouchard, 1994; Plomin, Chipuer, & Neiderhiser, 1994). This is a puzzling finding, because most personality theories have stressed environmental influences (such as parental role models and educational opportunities) that are generally shared, and because it is far from clear why the causal impact of an experience should depend on whether or not it is shared by family members.

A number of researchers have attempted to identify specific circumstances or experiences that uniquely shape the personality of one of a pair of twins (e.g., Baker & Daniels, 1990; Hetherington, Reiss, & Plomin, 1994; Vernon, Jang, Harris, & McCarthy, 1997), and arguments have been made concerning the importance of birth order (Sulloway, 1996) and peer influences (Harris, 1998). But although some of these findings are suggestive and the arguments provocative, it is fair to say that researchers have not yet documented major nonshared environmental influences on personality. One possible reason for this is that much of the reported effect may be spurious.

Nonshared environmental influences are normally calculated as a residual—that is, they are what remains when genetic and shared environmental influences are removed. One crucial consequence of this procedure is that the nonshared environment term includes both random error and systematic bias along with any true nonshared environmental influence. Random error contributes to unreliability, and behavior geneticists sometimes refine their estimates by expressing heritabilities in terms of the proportion of reliable variance (e.g., Jang, McCrae, Angleitner, Riemann, & Livesley, 1998). Systematic bias is a form of method variance and can only be controlled in studies that include multimethod personality assessments (e.g., Riemann, Angleitner, & Strelau, 1997)—a design still rare in behavior genetics research. In the present study we attempt to separate true nonshared environmental effects from artifacts of method bias in analyses of trait covariance.

The Puzzle of Parallel Structures

An example of genetic covariance analysis was published by Loehlin (1987), who analyzed the structure of item clusters from the California Psychological Inventory (CPI; Gough, 1987) in samples of monozygotic (MZ) and dizygotic (DZ) twins. Using formulas that parallel the wellknown formulas for estimating the heritability of single traits, Loehlin derived three matrices that represented the covariance among different traits, due to genes, shared environment, and nonshared environment. When these matrices were factored, four factors emerged from analyses of genetic covariance that could be interpreted as variants of the FFM factors of Neuroticism, Extraversion, Openness, and Conscientiousness (items measuring the fifth factor, Agreeableness, are rare in the CPI; see McCrae, Costa, & Piedmont, 1993). Two quite different factors emerged in the analysis of shared environmental effects: family problems and masculinity/ femininity; the former is not an aspect of personality per se, and the latter is probably an artifact of the exclusive use of same-sex twins in this study (Loehlin, 1987).¹

Three interpretable factors were found in the analysis of the nonshared environmental covariance matrix, which, as in the genetic analysis, resembled Neuroticism, Extraversion, and Conscientiousness. Thus, the nonshared environmental influences appeared to mirror most of the genetic influences. This is not an isolated finding: Livesley, Jang, and Vernon (1998) found similar structures in genetic and nonshared environmental components of traits related to personality disorders, and Plomin, DeFries, and McClearn (1990, p. 236) noted that, across a range of studies, "the structure of genetic influences seems to be similar to the structure of [nonshared] environmental influences."

Plomin et al. (1990) also pointed out that this phenomenon is surprising: "Most of us would probably predict different patterns of genetic and environmental influences" (p. 236). The fact that the pattern of nonshared

1. This interpretation may not be obvious. As Loehlin (1987) explained, "Since the study excluded unlike-sex fraternal twin pairs, all of the biological variation associated with sex lies between pairs for both kinds of twin, and thus necessarily is confounded with shared environmental effects" (p. 143). Said another way, same-sex twins will tend to resemble each other in any sex-related variable whether they are DZ or MZ; because shared environmental effects are calculated as twice the DZ correlation minus the MZ correlation, effects that apply equally to both types of twins will appear to contribute to shared environmental effects.

environmental influences seems to duplicate the pattern of genetic influences might perhaps be explained by hypothesizing that each personality factor represents the effects of a neuropsychic structure that is initially defined by genes and subsequently modified by experience. But that hypothesis returns us to a question raised earlier: If these presumed neuropsychic structures are so malleable that all five can be modified by nonshared experiences, why are none of them affected by shared experiences?

An alternative explanation would call attention to the error-ofmeasurement components of the nonshared environment term. Random error would not, of course, create any replicable structure, but systematic bias could. It has been known for decades that there are in fact systematic biases in personality judgments, and the structure of those biases is known as *implicit personality theory* (IPT; Borkenau, 1992).

In an early demonstration of IPT, Passini and Norman (1966) asked students to rate the personalities of complete strangers. Although each individual rating was presumably an arbitrary guess, Passini and Norman found that guessing followed a clear pattern: Students who supposed that the strangers were talkative also imagined that they were sociable and cheerful; across a range of targets, these associations defined an Extraversion factor. Factor analysis of all the ratings showed a structure very close to the FFM.

Some researchers concluded from such studies that personality trait structure was nothing but a projection of semantic biases onto person perceptions (Shweder, 1975). But a variety of studies have since confirmed that personality traits are veridical (e.g., Woodruffe, 1985), and the parallel between the FFM and IPT is easily understandable: IPT closely resembles the real structure of personality because individuals have learned, with reasonable accuracy, the true associations between traits (c.f., Sneed, McCrae, & Funder, 1998). Students guess that a stranger who is talkative is also sociable, because, in fact, talkative people are usually sociable.

In ratings of strangers the observed structure must represent IPT because it cannot be influenced by the (unknown) true personalities of the targets. But the structure of self-reports and ratings of well-known targets is also likely to include some degree of IPT bias. Cross-observer correlations on personality traits typically range from .4 to .6 (McCrae & Costa, 1989), well below scale reliability. The method variance that accounts for the discrepancy between reliability and validity is probably

structured in terms of IPT. For example, two observers may agree that a target is sociable but disagree on just how sociable the target is. The observer who gives a higher rating for sociability is also likely to give a higher rating for cheerfulness and talkativeness. Thus, part of the covariance of these traits may be attributable to systematic biases in person perception, which result in correlated errors in individual judgments.

If these biases do indeed take the form of IPT, then similarities in structure between genetic covariance and nonshared environmental covariance could be due entirely to the presence of IPT bias in the latter. That hypothesis is testable but only by designing a new way of estimating nonshared environmental influences that is free of IPT.

Estimating the Components of Trait Covariances

The classic design for genetic covariance analysis (e.g., Loehlin, 1987) in reared-together twin samples requires three correlation matrices: The phenotypic correlation matrix, **R**, which is based on the self-reports of a sample of twins; the mean cross-correlation matrix of a subsample of MZ twins, **Rmz**, and the mean cross-correlation matrix of a subsample of DZ twins, **Rdz**. (Cross-correlation matrices consist of correlations of Trait X in Twin A with Trait Y in Twin B and of Trait Y in Twin A with Trait X in Twin B; the average of these two is the mean cross-correlation.)

As Loehlin (1987) noted, the classic assumption that MZ twins share all their genes, whereas DZ twins share, on average, only half, makes it possible to estimate covariance matrices from these three. Specifically, the genetic covariance matrix (Cg), shared environmental covariance matrix (Cs), and nonshared environmental covariance matrix (Cns) can be estimated as follows:

1) Cg = 2*(Rmz - Rdz);

2)
$$Cs = 2*Rdz - Rmz;$$

and

3) Cns = R - Rmz.

Note that all these are estimated covariance matrices; we discuss their diagonal values and strategies for factoring them in the Analyses section.

As Rowe (1982) pointed out, the cross-correlation matrices in this design (**Rmz** and **Rdz**) ought to be relatively free of IPT bias, "since the correlations represent the association between traits independently reported by two individuals [Twin A and Twin B]" (p. 1072); the biases in one twin would likely not be shared by the other.² It follows that **Cg** and **Cs** should also be relatively free of IPT bias. **Cns**, however, involves the matrix **R**, which is a monomethod correlation matrix potentially contaminated by IPT bias.

To produce an IPT-free **Cns** matrix, we need an estimate of the intercorrelation of phenotypic traits which is itself IPT-free, and this can only be obtained from a heteromethod matrix in which traits are independently assessed by two different methods. The most convenient source of such a matrix comes from mean cross-correlations between two raters of the same target individuals. In the present article we will employ a matrix of self/spouse correlations, **Rss**. In principle, **Rss** reflects genetic, shared environmental, and true nonshared environmental influences along with random error, but it excludes systematic biases, which are unlikely to be shared by self and spouse. Table 1 presents a model of the sources of variance in the observed correlation matrices.

Together, **R** and **Rss** can be used to estimate covariance among traits due to IPT bias,

4) **Cipt = R – Rss**;

and **Rss** can replace **R** in the computation of an IPT-free nonshared environmental covariance matrix **Cns**', estimated as

5) Cns' = Rss - Rmz.

Note that in these formulas the conventional **Cns** has been decomposed into bias and true nonshared influence:

6) $\mathbf{Cns} = (\mathbf{Cipt} + \mathbf{Cns'}) = (\mathbf{R} - \mathbf{Rss} + \mathbf{Rss} - \mathbf{Rmz}) = (\mathbf{R} - \mathbf{Rmz}).$

Factor analyses generally require large samples, and that is especially so when the matrices factored are based on difference scores. In this study

2. If IPT bias is itself heritable or due to shared environmental effects, than MZ and DZ cross-correlations would also be contaminated with IPT bias, as would matrices derived from them. There is at present no evidence for such effects, and the present article assumes that, if they exist, they are small.

Table 1
A Model of Sources of Variance in Four Correlation Matrices

$\mathbf{R} = \mathbf{G} + \mathbf{E}\mathbf{s} + \mathbf{E}\mathbf{n}\mathbf{s} + \mathbf{IPT} + \mathbf{\epsilon}$
$\mathbf{Rmz} = \mathbf{G} + \mathbf{Es} + \mathbf{\varepsilon}$
$\mathbf{R}\mathbf{d}\mathbf{z} = \frac{1}{2}\mathbf{G} + \mathbf{E}\mathbf{s} + \mathbf{\varepsilon}$
$\mathbf{Rss} = \mathbf{G} + \mathbf{Es} + \mathbf{Ens} + \mathbf{\epsilon},$
where $G =$ genetic influences, $Es =$ shared environmental influences, Ens
= nonshared environmental influences, IPT = influence of implicit

personality theory, and ε = random error.

we conduct the primary analyses in a sample that combines German and Canadian twin samples. Previous analyses (Jang et al., 1998) suggest that, despite differences of language and culture, the two samples are sufficiently similar in genetic and environmental influences to justify combining them; averaging the two correlation matrices eliminates any effects due to mean level differences. The combined sample is used in a series of analyses that compare the structure of covariance matrices with the FFM. Previous research suggests that we should replicate the FFM in the phenotypic covariance of traits (R and Rss), the genetic covariance (Cg), the nonshared environmental covariance including IPT bias (Cns), and (as Passini & Norman, 1966, found) in pure measures of IPT bias (Cipt). We hypothesize that we will replicate the FFM neither in the shared environmental covariance, Cs, because shared environment usually plays little or no role in shaping personality, nor in the IPT-free nonshared covariances, Cns', because that would lead to the puzzling parallelism noted above.

However, a failure to find the FFM does not mean that there is no structure at all. Subsequent analyses will therefore examine alternative factor solutions. Analyses will be conducted in parallel on two random subsamples; factor congruence will be used to identify a replicable factor solution (cf. Everett, 1983).

Ideally, the **Rss** matrix would be obtained from self- and spouse ratings of the twins. Those data are not, however, available. Instead, we employ self/spouse data from two American samples, on the assumption that self/spouse correlations are likely to be very similar across samples, whether or not the targets happen to be twins. Future research should include multiple observer ratings on the twins in the study.

Statistical Approach

Most contemporary behavior geneticists employ versions of structural equation modeling, such as confirmatory factor analysis (CFA), to conduct multivariate behavior genetic analyses (Neale & Cardon, 1992). These techniques were designed to provide both parameter estimates and statistical tests of significance. Unfortunately, the tests appear to be highly sensitive to both sample size and violations of assumptions (Hu, Bentler, & Kano, 1992). Furthermore, when dealing with complex structures, CFA—with its usual reliance on chi-square as the primary fit index—may reject highly replicable structures (McCrae, Zonderman, Costa, Bond, & Paunonen, 1996). Technical problems are frequently encountered when large matrices are factored, and CFA is not appropriate for situations in which data exploration is required.

In the present study we adopt an alternative approach. We begin with simple cross-twin correlations, which are appropriate because nonadditive genetic effects have not been found in analyses of NEO-PI-R scales in these samples (Jang et al., 1998). Exploratory factor analyses are supplemented with targeted rotations, and both Varimax and orthogonal Procrustes solutions are evaluated by congruence coefficients (Haven & ten Berge, 1977). Although oblique Procrustes rotation can severely distort interpretation of data through capitalization on chance (Horn, 1967), orthogonal Procrustes rotation is much less susceptible to these problems. Monte Carlo simulations (McCrae et al., 1996) demonstrate that high congruence coefficients are extremely rare when random data are rotated by orthogonal Procrustes rotation.

Procrustes rotation is a form of confirmatory factor analysis, in which observed matrices are rotated toward a target matrix—in this case, the phenotypic FFM as seen in American normative data (Costa & McCrae, 1992). It is possible that the underlying sources of covariance form some other structures. To differentiate these from chance, we must look for replicable structures, and, for that purpose, systematic comparisons of factor structures from random halves of the sample will be examined (cf. Everett, 1983). Replicable structures might be used as targets for confirmatory analyses in future studies.

METHOD

Participants

Participants were 709 monozygotic (MZ) and 444 dizygotic (DZ) volunteer general population twin pairs from Canada and Germany. The Canadian data and portions of the German data have been published previously and are described in Jang et al. (1998).

Canadian twins. The Canadian sample consisted of 183 MZ twins (75 brother and 108 sister pairs) and 175 DZ twins (48 brother, 84 sister, and 43 brother-sister pairs). The mean age of the MZ pairs is 31.92 years, SD = 12.75 years, range 16–71 years. The mean age of the DZ pairs is 31.51 years, SD = 11.19 years, range 16–68 years. Twin pairs were recruited from Vancouver, Canada, by the University of British Columbia Twin Project, an ongoing study of psychiatric disorder and personality (see also Jang, Livesley, Vernon, & Jackson 1996). To reduce sampling bias, twins were paid to participate (Lykken, Tellegen, & DeRubis, 1978), yielding approximately equal numbers of MZ and DZ twins.

German twins. The German sample consisted of 526 MZ (103 brother and 423 sister pairs) and 269 DZ (38 brother, 163 sister, and 68 brother-sister) twin pairs recruited from across Germany by the University of Bielefeld Twin Study (see Riemann, Angleitner, & Strelau, 1997). Twins were recruited through newspaper advertisements and media stories. Although MZ twins were overrepresented relative to DZ twins, the fact that German and Canadian samples showed similar genetic structures (Jang et al., 1998) suggests that bias in the German study is minimal. The mean age of the MZ pairs is 32.34 years, SD = 13.44 years, range 15–80 years. The mean age of the DZ pairs is 31.23 years, SD = 11.93 years, range 14–66 years.

Zygosity was diagnosed in the Canadian sample by a questionnaire designed by Nichols and Bilbro (1966) and in the German sample by a questionnaire designed by Oniszczenko, Angleitner, Strelau, and Angert (1993). Both questionnaires have been shown to predict zygosity as determined by red blood cell polymorphism analysis with at least 94% accuracy (e.g., Kasriel & Eaves, 1976).

Self/Spouse samples. Self/spouse correlations were obtained from two samples that were pooled to provide a stable estimate of **Rss**. Sample A consisted of 47 couples who each rated themselves and their spouses. Participants were members of the Baltimore Longitudinal Study of Aging (BLSA; Shock et al., 1984), ranging in age from 26 to 85. BLSA participants in general are healthy, well-educated, community-dwelling volunteers. For details on this sample, see McCrae, Stone, Fagan, and Costa (1998). Sample B included 59 women and 46 men, aged 23 to 68, who were private practice psychotherapy patients and who volunteered to provide self-reports and spouse ratings of personality. As a

group they scored in the high range on Neuroticism but in the average range on the other factors.

Recent research (Livesley, Jang, & Vernon, 1998; Yang et al., 1999) has shown that the structure of personality is essentially the same in normal and clinical samples, and preliminary factor analysis of **Rss** matrices from Samples A and B separately showed similar structures. There are, however, mean level differences between volunteer and clinical samples. To control for these differences, correlations were calculated within sample and averaged across the two samples.

Measure and Procedures

Personality was assessed by the Revised NEO Personality Inventory (NEO-PI-R; Costa & McCrae, 1992), a questionnaire measure of the FFM. The NEO-PI-R consists of 30 eight-item facet scales, six for each of the five factors. Evidence on the reliability, stability, and validity of the instrument is summarized in the manual.

The NEO-PI-R was originally developed in English but has subsequently been translated into several other languages; the American factor structure has been consistently replicated in these translations (McCrae & Costa, 1997). The German version of the NEO-PI-R (Ostendorf & Angleitner, 1994) was used in the German twin study.

In addition to the usual first-person, self-report version, the NEO-PI-R has a third-person version designed for observer ratings of personality; evidence of reliability and validity are presented in the manual. In the present study, self-reports and spouse ratings were gathered independently, although respondents were aware that the two would be compared. Self/spouse agreement on the five factors ranged from .46 to .74 in Sample A and from .55 to .73 in Sample B, all p < .001.

Analyses

The matrices of chief interest in this study are estimated rather than observed, and, as Loehlin (1987) pointed out, are "not necessarily proper correlation or covariance matrices" (p. 140). In particular, the diagonal values of the residual matrices are problematic; although all of them ought in principle to be non-negative, in fact, a small number of negative values were found, complicating the process of factoring.

Two strategies were considered. Because it has been used in most studies of the FFM, principal components (PC) analysis (with 1s substituted for the diagonal values) appeared to be a straightforward way to describe structure, giving unit weight to each variable. A theoretically quite different approach is offered by minimum residual (MINRES) factor extraction. MINRES is an iterative process that seeks to minimize the off-diagonal residuals, without regard to the diagonal. MINRES factors best account for the observed or estimated cross-correlations that are the focus of the present paper and thus might be regarded as the factor method of choice.

Preliminary analyses were conducted for three matrices: **Rmz**, **Rdz**, and **Cns'**. For each, five PC factors and five MINRES factors were extracted, and both sets were subjected to Varimax rotation. Factor congruence coefficients were calculated between corresponding factors. Although factor loadings were somewhat lower in the MINRES analyses, congruences for the five factors across the three analyses ranged from .96 to 1.00 (median = .99), demonstrating identical patterns. This analysis suggests that the method of factor analysis is largely irrelevant, probably because the sheer number of off-diagonal elements (870) outweighs the diagonal elements (cf. Velicer & Jackson, 1990).

Because it is both more familiar and computationally simpler, PC was adopted for subsequent analyses. In the first phase, five varimax-rotated factors were examined, and congruence coefficients were calculated to compare them to the phenotypic FFM structure in published norms (Costa & McCrae, 1992). Coefficients above .90 are conventionally required as evidence of factor replication, although Haven & ten Berge (1977) have shown that values as low as .85 correspond to expert human judgments of a match.

When hypothesized factor structures fail to show high congruence, it may in some cases be attributable to arbitrary differences in rotation. In such cases, a targeted rotation serves as a more appropriate test of factor matching because it evaluates the best possible alignment between two factor matrices (McCrae et al., 1996). Targeted rotations were examined in those cases in which varimax factors did not replicate the FFM.

Whenever targeted rotations failed to reproduce the FFM, exploratory analyses were conducted to ascertain whether there was some other replicable structure in the data. For these analyses, Canadian and German twin samples were randomly divided into halves, and two sets of covariance matrices were computed, each combining data from half the Canadian and half the German samples. The first unrotated factor and Varimax rotations of two through eight factors were compared across the two subsamples; the solution in which all factors could be matched determined the correct number of factors to extract. This method is particularly useful in the analysis of covariance matrices, in which the usual rules for number of factors in a correlation matrix may not apply.

RESULTS

Table 2 reports congruence coefficients, comparing factors from covariance matrices in the present study with the published factor structure of the NEO-PI-R (Costa & McCrae, 1992). (The basic correlation and factor loading matrices are available from the first author.) The phenotypic structure of personality as assessed by Canadian and German twins' self-reports (\mathbf{R}) is a near-perfect replication of the original American factor structure. A replication almost as good is provided by factoring the cross-observer correlations from the self/spouse sample (\mathbf{Rss}), despite the fact that this second, heteromethod matrix is presumably free of IPT bias.

Conventional behavior genetics analyses have typically shown minimal contribution of shared environment to the variance of individual traits (Loehlin, 1992). Previous analyses of the present data (Jang et al., 1998) showed that the best fitting models for most NEO-PI-R facets excluded any shared environmental effect. The third row of Table 2 suggests that shared environmental effects (**Cs**) appear to contribute little to the phenotypic FFM structure. Congruences were poor even after Procrustes rotation, with congruence coefficients ranging from .39 for Agreeableness to .74 for Extraversion.

Analyses of the genetic covariance matrix, **Cg**, yield at best a fair match, with only two factors—Openness and Agreeableness—showing conventionally acceptable levels of factor replication. In this case, Procrustes rotation improves congruences, yielding values of .87, .81, .94, .91, and .75 for N, E, O, A, and C factors, respectively. In evaluating these

Matrix	Ν	Е	0	Α	С
Phenotype					
Twins' Self-reports (R)	.99	.97	.97	.99	.99
Self/Spouse Ratings (Rss)	.96	.93	.91	.98	.98
Shared Environment (Cs)	.68	.68	.12	.30	.68
Genetic/Familial					
Genetic (Cg)	.83	.72	.92	.88	.70
Familial (Rmz)	.98	.95	.97	.98	.97
Familial (Rdz)	.93	.92	.85	.86	.88
Nonshared Environment					
With IPT Bias (Cns)	.96	.93	.90	.93	.97
IPT Bias (Cipt)	.81	.45	.81	.89	.85
Without IPT Bias (Cns')	.53	.68	.27	.61	.80

 Table 2

 Congruence Coefficients Between Varimax-rotated Factors in the Present Study and the Normative NEO-PI-R Factors

values, it must be recalled that the **Cg** matrix is composed of differences between two other matrices and that difference scores are notoriously unreliable. Alternative estimates of genetic covariance that avoid difference scores are given by **Rmz** and **Rdz**. In theory, those matrices include both shared environmental and genetic covariances, but if one assumes shared environmental effects are trivial in size (Jang et al., 1998), **Rmz** and **Rdz** can be used directly as more reliable bases for assessing the structure of genetic covariance. Because genetic influences are twice as large in **Rmz** as in **Rdz**, the former may show a clearer FFM structure.

As Table 2 shows, the FFM structure is clearly replicated in these analyses, especially the MZ data. As Rowe (1982) argued, these results effectively refute the hypothesis that the factor structure of traits is attributable solely to IPT.

The last three rows of Table 2 examine the structure of the nonshared environmental covariance. As in previous research (e.g., Loehlin, 1987), when calculated as the residual from the monomethod matrix **R**, **Cns** faithfully reproduces the phenotypic structure. These data are consistent with a large literature (Plomin et al., 1990) showing parallels between genetic and nonshared environmental structures. But this covariance matrix can itself be decomposed into two others, one representing IPT bias, the other, true nonshared environmental effects uncontaminated by IPT bias.

Both **R** and **Rss** estimate the covariance of phenotypic traits in individual targets, but the monomethod **R** matrix includes method bias that the heteromethod **Rss** matrix lacks. When the difference, **Cipt**, is factored, the results show considerable resemblance to the FFM, except for the E factor. After Procrustes rotation, the observed congruences are .85, .73, .79, .91, and .91. N, A, and C factors are replicated in IPT, and the remaining factors show some resemblance to E and O.

Factors from the final matrix, representing IPT-free nonshared environmental covariance, show low congruences with the FFM. Even after Procrustes rotation (see Table 3), congruence coefficients for N, E, O, A, and C are only .71, .75, .57, .75, and .79, respectively. Although these values are technically higher than chance, as shown in Monte Carlo simulations (McCrae et al., 1996), they would be judged *terrible* to *poor* matches by Tucker's criteria (MacCallum, Widaman, Zhang, & Hong, 1999). Variable congruence coefficients show that only 9 of the 30 facets show a better-than-chance similarity to the target structure.

NEO-PI-R			Variable			
Facet	Ν	Ε	0	Α	С	Congruence
Neuroticism						
Anxiety	.48	10	15	.11	.04	.89*
Angry Hostility	.32	.06	.05	43	.20	.85
Depression	.48	13	11	.12	04	.90*
Self-Consciousness	.19	.05	31	.22	.05	.47
Impulsiveness	.09	08	.22	.03	39	.41
Vulnerability	.35	.15	.06	14	.15	.43
Extraversion						
Warmth	.25	.36	.17	.38	.00	.79
Gregariousness	.23	.49	.23	.33	.08	.68
Assertiveness	.07	.03	.39	17	.32	.59
Activity	.03	.31	42	13	.17	.48
Excitement Seeking	37	.27	.22	15	.26	.53
Positive Emotions	17	.52	.01	05	20	.81
Openness to Experience						
Fantasy	05	.23	.24	23	32	.81
Aesthetics	08	.35	.30	13	20	.42
Feelings	.36	.29	.25	.09	.01	.93*
Actions	37	.47	10	05	.08	.29
Ideas	15	42	.37	09	04	.66
Values	04	11	.53	.33	.03	.67
Agreeableness						
Trust	20	.21	09	.33	.08	.89*
Straightforwardness	04	06	05	.11	.25	.70
Altruism	.01	.29	.06	.34	.10	.97**
Compliance	23	.06	02	.47	.07	.93*
Modesty	03	19	22	.22	06	.77
Tender-Mindedness	13	.19	.34	.30	03	.78
Conscientiousness						
Competence	11	16	.05	.17	.38	.75
Order	.08	.11	08	07	.47	.95**
Dutifulness	.06	.02	.05	02	.49	.83
Achievement Striving	21	.08	23	16	.40	.74
Self-Discipline	16	.11	04	.06	.51	.99**
Deliberation	31	18	06	.33	.29	.89*
Factor Congruence	.71**	* .75**	.57*	.75**	.79**	

 Table 3

 Factor Loadings From the IPT-Free Nonshared Environmental Covariance Matrix After Procrustes Rotation

Note. Loadings greater than .30 in absolute magnitude are given in boldface. *Congruence higher than that of 95% of rotations from random data. **Congruence higher than that of 99% of rotations from random data.

A comparison of corresponding factor congruence coefficients following Procrustes rotation shows that each of these values is substantially lower in the analysis of **Cns'** than in the analysis of **Cipt**. Thus, when the conventional estimates of nonshared environmental covariances are decomposed into IPT bias and true nonshared effects, most of the resemblance to the FFM appears to be attributable to the IPT bias.

Two matrices of interest—**Cs** and **Cns'**—do not conform to the FFM, but it is possible they have some other replicable structure. Table 4 reports the results of parallel factor analyses conducted on two random subsamples of twins. We calculated congruence coefficients for the unrotated first factor, and for Varimax-rotated two-, three-, four-, five-, six-, seven-, and eight-factor solutions. Factors were matched by identifying the highest congruence coefficient, then the highest coefficient among the remaining factors, and so on. In such analyses, congruence coefficients

		Factor Congruence Coefficient						
Factors Rotated	1st	2nd	3rd	4th	5th	6th	7th	8th
Shared Environment (Cs)								
8	.49	.39	.39	.36	.30	.23	.19	.08
7	.56	.56	.37	.36	.26	.21	.08	
6	.51	.49	.42	.26	.25	.12		
5	.62	.50	.25	.25	.06			
4	.64	.34	.23	.00				
3	.64	.29	.22					
2	.72	.31						
1	.54							
Nonshared Environment W	ithout IPT	Bias (Cns')					
8	.87	.81	.78	.75	.63	.49	.44	.23
7	.79	.74	.71	.66	.57	.37	.11	
6	.82	.78	.75	.68	.62	.60		
5	.88	.80	.67	.56	.46			
4	.80	.80	.69	.68				
3	.78	.68	.01					
2	.82	.80						
1	.29							

 Table 4

 Factor Congruences for Varimax-Rotated Principal Components in Two Random Subsamples

are evaluated as a set (Everett, 1983)—that is, one seeks the solution in which all congruences exceed .90 (or perhaps, .85). It is clear that none of the solutions meets this criterion; no solution is replicable over random halves of the present sample.

It is, however, perhaps worthwhile to relax the usual criteria. None of the solutions for **Cs** even approaches replication, as would be expected given the negligible influence shared environmental factors have repeatedly been shown to have on personality variables. However, the two-factor solution for **Cns'** merits some attention. As shown in Table 5, Factor I has loadings over .30 in both samples for Activity, Order, Dutifulness, Achievement Striving, Self-Discipline, and (low) Impulsiveness, and thus resembles a broad form of Conscientiousness. Factor II includes Warmth, Gregariousness, Positive Emotions, Openness to Feelings, Altruism, and Tender-Mindedness. That combination of traits from Extraversion and Agreeableness domains produces a factor that resembles the Love axis of the Interpersonal Circumplex (Wiggins, 1979). The other interpersonal axis—Dominance—does not appear to be influenced by the nonshared environment: Note that Assertiveness loads on neither factor.

DISCUSSION

Behavior genetic covariance analyses are designed to reveal the underlying causal sources of structure in trait associations. In addition to the usual separation of genetic, shared environmental, and nonshared environmental effects, the present study decomposed the nonshared environmental influences into method covariance and true environmental effects.

Results showed that the familiar five-factor structure of personality can be found not only in the phenotype but also in the genotype, particularly as estimated by cross-correlations from MZ twins. These data provide no basis for a distinction between the hypothesized genetically determined temperament factors (Neuroticism and Extraversion) and the putatively environmentally determined character factors (Openness, Agreeableness, and Conscientiousness); the structure of all five factors is genetically based. Ironically, as the congruence coefficients in Table 2 attest, the clearest factor replication in these analyses of genetic covariance is for Openness to Experience, a dimension sometimes held to be "unnecessarily ambiguous and complex" (Carroll, in press, p. 35; cf. Glisky, Tartaryn, Tobias, Kihlstrom, & McConkey, 1991). The present

NEO-PI-R	Fac	tor I	Factor II		
Facet	Subsample 1	Subsample 2	Subsample 1	Subsample 2	
Neuroticism					
Anxiety	27	.11	.04	24	
Angry Hostility	.01	.00	.01	20	
Depression	29	.01	.06	32	
Self-Consciousness	.01	.19	.07	14	
Impulsiveness	51	33	.14	.04	
Vulnerability	10	.11	.25	14	
Extraversion					
Warmth	11	.07	.48	.45	
Gregariousness	03	.17	.59	.54	
Assertiveness	.18	.03	.17	.01	
Activity	.36	.34	.07	05	
Excitement Seeking	.28	.31	.17	.37	
Positive Emotions	.01	.02	.42	.43	
Openness to Experience	e				
Fantasy	21	38	.28	.23	
Aesthetics	08	29	.43	.39	
Feelings	18	07	.31	.37	
Actions	.44	.18	.28	.41	
Ideas	10	27	23	16	
Values	01	24	.27	.30	
Agreeableness					
Trust	.14	.38	.19	.25	
Straightforwardness	.23	.20	04	01	
Altruism	.15	.13	.31	.43	
Compliance	.12	.29	.11	.29	
Modesty	.00	.01	19	11	
Tender-Mindedness	.03	05	.41	.40	
Conscientiousness					
Competence	.38	.22	15	.04	
Order	.36	.45	.11	06	
Dutifulness	.40	.32	08	.05	
Achievement Striving	g .54	.40	10	12	
Self-Discipline	.55	.52	.16	.02	
Deliberation	.43	.25	10	.00	

 Table 5

 Factor Loadings From the IPT-Free Nonshared Environmental Covariance Matrix: Two Factor Solution

Note. These are varimax-rotated principal components. Loadings greater than .30 in absolute magnitude are given in boldface.

analyses show that imagination, aesthetic sensitivity, emotional depth, need for variety, intellectual curiosity, and liberal thinking share a common set of genetic influences that unite them in a single factor.

As in most studies of trait heritability, shared environmental influences appeared to have no systematic effect on personality structure. However, past research (e.g., Loehlin, 1987) had suggested that nonshared environmental influences would be important and would yield a structure that paralleled that found for genetic influences. That expectation was confirmed when conventional methods were used to estimate nonshared influences, but further analyses suggested that the resemblance was primarily due to artifacts of method variance. Clear N, A, and C factors were found—along with two other factors with some resemblance to E and O—in analyses of **Cipt**, a matrix from which true trait variance had been systematically removed. As years of research on implicit personality theory had suggested, the remaining method variance in personality ratings resembled the structure of personality itself.

By contrast, analyses of nonshared environmental influences free from method artifacts showed only a weak resemblance to the FFM, even after targeted rotation. From these data, it would appear that the FFM personality structure is almost entirely the result of genetic influences, and that personality assessments reflect both the true, geneticallydetermined patterns of covariance and the systematic biases that mimic them. The surprising parallelism between genetic and nonshared environmental influences appears to have been artifactual.

Although the full FFM was not found in analyses of the unbiased nonshared influences, exploratory analyses suggested that two factors might prove replicable—one related to Love, the other to Conscientiousness, or work. Love and work, in turn, have been related to well-being, not only in Freud's famous dictum, but also in empirical research (McCrae & Costa, 1991). If there are indeed nonshared environmental influences on these factors, and if they can be identified, they might permit environmental interventions that could enhance psychological well-being.

The present study illustrates the possible confounding effects of implicit personality theory, but it does not provide definitive proof of it. The self/spouse correlation matrix used to provide an unbiased estimate of the phenotypic covariation of traits was based on a different sample than the MZ twins from whom the familial covariation was derived. It might be argued that the difference between these two matrices thus provides only a rough estimate of the unbiased, nonshared environmental effects, potentially distorted by sample differences. However, both twin and self/spouse samples showed the same five-factor structure in the pheno-type, so any sample differences must have been relatively subtle.

A somewhat different problem is raised by the possibility that spouse ratings are not fully independent of self-reports. Spouses may, to some extent, have adopted the biased perceptions of the target; **Rss** would then be at least somewhat contaminated by IPT bias. The effect of such a shared bias would be to reduce the artifactual variance in **Cipt** and increase it in **Cns'**. Thus, Table 4 appears to give conservative estimates of how well method variance mimics the FFM and how poorly true nonshared environmental effects do.

It might also be objected that the present design was less than optimal because the data came not only from different observers but also from different kinds of observers. Self-reports and spouse ratings represent internal and external perspectives on personality, respectively, and it is possible that IPT takes a somewhat different form when applied to self-and other assessments. A cleaner design would rely on two (or more) peer raters for each member of a sample of MZ twins. **R** would then be derived from single peer ratings, **Rss** (here, **Rpp**) from peer/peer cross-correlations, and **Rmz** from cross-twin correlations based on single peer ratings. A comparison of the structures in **Cns**, **Cipt**, and **Cns'** derived from these matrices would provide a clear test of the relative importance of bias and true nonshared environmental influences. Such data are currently being collected.

Finally, it should be recalled that the present design involved factor analysis of estimated covariation matrices that may not have preserved some of the mathematical properties of true covariance matrices. The fact that generally sensible results were obtained, however, suggests that any distortions introduced were probably minor.

The problem of unreliability in conventional behavior genetic analyses has frequently been addressed; failures to take it into account can lead to an underestimation of the effects of genetic and shared environmental effects. But less attention has been paid to systematic bias, which can be particularly misleading in genetic covariance analyses. The present analyses suggest that the role of nonshared environmental effects has been misunderstood, with important consequences. The search for mechanisms by which such influences affect personality should take a different direction if their effects are limited to Love and Conscientiousness than if, as previously believed (Plomin et al., 1990), they duplicate the full range of genetic effects.

CONCLUSION

Turkheimer (1998) has argued that almost all human behavior can be shown to be heritable and, thus, that evidence on heritability is not informative: "the very ubiquity of these findings makes them a poor basis for reformulating scientists' conceptions of human behavior" (p. 782). It is certainly the case that the mere identification of a genetic influence does not automatically point to specific genes or to neuropsychological structures or processes that explain the trait or behavior. But the analyses presented here have important implications for research on the determinants of personality. Shared environmental influences (which have preoccupied personality theorists and researchers until recently; Scarr, 1987) are apparently unimportant; the role of nonshared environmental influences also appears to have been misunderstood. However difficult the search for specific genes may prove to be, there is at least reason to think that it is on the right track.

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