

Is the Genetic Structure of Human Personality Universal? A Cross-Cultural Twin Study From North America, Europe, and Asia

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This study examined whether universality of the 5-factor model (FFM) of personality operationalized by the Revised NEO Personality Inventory is due to genetic influences that are invariant across diverse nations. Factor analyses were conducted on matrices of phenotypic, genetic, and environmental correlations estimated in a sample of 1,209 monozygotic and 701 dizygotic twin pairs from Canada, Germany, and Japan. Five genetic and environmental factors were extracted for each sample. High congruence coefficients were observed when phenotypic, genetic, and environmental factors were compared in each sample as well as when each factor was compared across samples. These results suggest that the FFM has a solid biological basis and may represent a common heritage of the human species.

Keywords: five-factor model, Revised NEO Personality Inventory, universality, behavioral genetics, twin study

One of the most significant advances made in personality psychology in the 20th century has been the development of a comprehensive taxonomy of personality traits. This has been made

possible by a psycholexical approach that uses a comprehensive set of personality-relevant terms selected from a dictionary (e.g., Goldberg, 1993) coupled with a traditional questionnaire approach that puts these descriptors into a set of sentences to define scales (e.g., Costa & McCrae, 1992). These two approaches have consistently converged to reveal a five-factor structure (for a review, see John & Srivastava, 1999), which has come to be called the “five-factor model” (FFM; e.g., Digman, 1990). The Revised NEO Personality Inventory (NEO-PI-R; Costa & McCrae, 1992) is a popular operationalization of the FFM. This labels the five factors or *domains* as Neuroticism (N), Extraversion (E), Openness to Experience (O), Agreeableness (A), and Conscientiousness (C). Each domain is indexed by the sum of responses on six subscales or *facets*. For example, the facets of C are Competence, Order, Dutifulness, Achievement Striving, Self-Discipline, and Deliberation.

The NEO-PI-R has become popular, especially for cross-cultural research because a large body of empirical research has demonstrated that the factorial structure and psychometric properties of the inventory are remarkably consistent across gender, age, and race and, when translated into different languages, across cultures as well (e.g., Costa, McCrae, & Dye, 1991; McCrae &

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Allik, 2002; McCrae, Terracciano, & Members of the Personality Profiles of Cultures Project, 2005). This stability has led many to consider the FFM to be the best universal description of personality worldwide (but for a different perspective, see also Ashton et al., 2004). What remains unexplained, however, is why the FFM is universal.

One possible explanation is that the FFM reflects a species-wide genetic basis. The behavioral genetic approach is of particular relevance here. Univariate genetic analysis, the most basic and well known method in behavioral genetics, decomposes the variance of a single variable (phenotypic variance) into the variance due to genetic differences between individuals and that due to the environment unique to each individual. This is done by comparing the similarity (e.g., measured by a correlation coefficient, r) of monozygotic (MZ) and dizygotic (DZ) twins on the measured variable. The rationale for this method is that the greater similarity of MZ compared with DZ twins reflects the influence of genetic factors because the greater similarity of MZ twins is attributable only to the twofold greater genetic similarity of MZ compared with DZ twins. Performed using this technique, the vast body of behavioral genetic research has shown that a substantial portion of the variance (about 45 to 50%) in various personality measures is attributable to genetic factors (for a review, see Bouchard & Loehlin, 2001). This has also been shown to be true of the FFM with different scales and methods and across different regions of the world (e.g., Jang, McCrae, Angleitner, Riemann, & Livesley, 1998; Loehlin, 1992; Riemann, Angleitner, & Strelau, 1997). This evidence led McCrae and Costa (1997, 1999) to suggest that the five domains are endogenous personality traits that reflect solely biological tendencies; more specifically, (a) the structure of the FFM reflects a genetic rather than environmental influence, and (b) the universality of the FFM is attributable to common biological and genetic mechanisms worldwide.

However, estimates of the genetic influence on *individual* trait scales do not provide any information on the *pattern of correlations* between trait scales that define each of the five factors; examination of this matter requires a multivariate approach. Similar to univariate analysis, multivariate genetic analysis presumes that the correlation (or covariation) between two variables is mediated by both genetic and environmental factors shared by the two variables. The extent to which the two variables share genetic (i.e., pleiotropy) and environmental influences is indexed by the genetic (r_G) and environmental (r_E) correlation coefficients, respectively. Estimation of r_G and r_E is accomplished by comparing cross-correlations (the correlation between one twin's score on one of the variables and the cotwin's score on the other variable) of MZ and DZ twins. In brief, the higher cross-correlation in MZ twins suggests shared genetic effects between the two variables because it is attributable only to the greater genetic similarity of MZ twins (see the Method section for detailed descriptions; for a review, see also Jang, 2005). Because r_G and r_E serve as indices of etiological homogeneity (i.e., the degree to which variables share a common etiological basis), they provide important information for addressing whether the phenotypic structure of the FFM reflects the underlying genetic structure.

Ando et al. (2004) actually demonstrated the differences between the phenotypic and genetic structures for the three dimensions of Cloninger's Temperament and Character Inventory (Cloninger, Svrakic, & Przybeck, 1993), that is, Novelty Seeking (NS),

Harm Avoidance (HA) and Reward Dependence (RD). Like most personality scales, each of these dimensions are composed of several subscales that were positively correlated with other subscales defining the same dimension, but were uncorrelated with subscales defining other dimensions. However, when the r_G values between subscales from these three dimensions were computed and factored, it was found that (a) only the RD scales emerged as a single genetically coherent factor, and (b) one of the NS subscales, Exploratory Excitability, was more influenced by a genetic factor underlying HA rather than NS. This result suggests that NS is not what Faraone, Tsuang, and Tsuang (1999) referred to as a "genetically crisp" measure, which reflects only the influence of a common set of genes. An implication of this work is that such genetic heterogeneity of the NS scale reduces the statistical power to detect and localize the actual genes responsible for the trait and may explain the inconsistent pattern of results reported for the association between NS and the dopamine receptor D_4 gene (e.g., Schinka, Letsch, & Crawford, 2002). One purpose of the present study was therefore to examine whether each of the five domains of the FFM is genetically homogeneous.

It is also unclear whether genetic influences on personality are universal (i.e., gene pools do not differ considerably across nations). Genotyping studies have revealed ethnic differences in the frequencies of alleles associated with human personality traits (e.g., Gelernter, Kranzler, Coccaro, Siever, & New, 1998). Considering the pleiotropic action of genes, this suggests that the reason why the FFM structure is universal is not because people in different regions of the world share common gene pools associated with personality, but because they share an environment or developmental context that influences personality. It also suggests that cultural differences across nations are not as divergent as is commonly assumed, at least in terms of their effect on the structure of personality. Alternatively, differences in gene pools may affect only the levels of personality, which was in fact phenotypically observed (Allik & McCrae, 2004), but not the structure of personality. Thus, multivariate genetic analysis that compares genetic and environmental structures across diverse national samples is necessary to determine whether genetic structure is universal.

Although far from conclusive, previous cross-national multivariate genetic research on the FFM as assessed by the NEO-PI-R suggests that the genetic structure of the inventory tends to be similar across nations, but may be different from the phenotypic FFM structure. For example, Jang, Livesley, Angleitner, Riemann, and Vernon (2002) examined the genetic and environmental covariance structures of facets defining each of the five NEO-PI-R domains individually. They needed two (not one) genetic and environmental factors to explain the matrices of r_G and r_E values, respectively, but the pattern of r_G and r_E values was similar across Canadian and German samples. Jang et al. (2001) examined the relationship between the facets defining two domains, N and A, and observed substantial negative r_G values between facets defining a different domain. Furthermore, these patterns were observed in diverse cross-national samples drawn from Canada, Germany, and Japan and were partly explained by a gene controlling the serotonin transporter (*5-HTTLPR*). However, analyses in the Jang et al. study were limited to patterns of r_G and r_E values within a single domain or between only the N and A domains; thus, the entire genetic structure of the FFM, as well as its universality, is unclear.

There has been only one study that examined the factorial structure of the genetic and environmental correlations among all 30 facets of the NEO-PI-R. Using combined twin samples from Germany and Canada, McCrae, Jang, Livesley, Riemann, and Angleitner (2001) extracted five genetic factors that were recognizable as N, E, O, A, and C, but they only broadly corresponded to the normative structure of the scale (Costa & McCrae, 1992). This general lack of correspondence may reflect the actual genetic architecture of the scale, but could also be due to a major methodological limitation of the study. Specifically, the method used to estimate r_G and r_E was to subtract MZ from DZ twin cross-correlations rather than the more precise structural equation modeling approach commonly used in behavioral genetics today (e.g., Neale, Boker, Xie, & Maes, 2004). This may have introduced a measurement error and underestimated the correspondence between the genetic and normative factors. Furthermore, comparisons of the genetic and environmental structures of the Canadian and German samples were not performed; thus, the similarity of these structures across nations is unclear.

With the limitations of the previous research in mind, in the present study, we performed multivariate genetic analyses on the facet-level data of the NEO-PI-R from the three diverse geographic regions: North America (Canada), Europe (Germany), and Asia (Japan). Specifically, the present research was designed to serve two purposes, the first of which was to assess to what degree the phenotypic structure of the FFM corresponds to genetic and environmental structures. This was accomplished by factor analyses on the matrices of phenotypic, genetic, and environmental correlations among all 30 NEO-PI-R facets separately for the three nations. Then, the levels of correspondence of phenotypic factor structure to genetic and environmental factor structures were examined within each nation. The second purpose was to assess the universality of each of the phenotypic, genetic, and environmental factor structures across the three nations. This was accomplished by comparing the levels of correspondence of the phenotypic, genetic, and environmental structures for one nation with those for other nations.

Method

Participants

Participants were 1,209 MZ and 701 DZ volunteer general-population twin pairs from Canada, Germany, and Japan. The Canadian twin sample consisted of 250 MZ and 203 DZ twin pairs recruited from Vancouver, Canada, by the University of British Columbia Twin Project (see Jang, Livesley, & Vernon, 2002). The German twin sample consisted of 531 MZ and 275 DZ twin pairs recruited from across Germany by the University of Bielefeld Twin Study (see Riemann et al., 1997). The Japanese twin sample consisted of 428 MZ and 223 DZ twin pairs from the Keio Twin Project in Tokyo (see Ando et al., 2004). The Canadian and German samples of twins were recruited using media appeals. The Japanese twin sample was recruited via invitations mailed to twins included on a population-based twin residential list for Tokyo and its neighboring cities.

Zygoty was determined by a questionnaire assessing the frequency of one twin being mistaken for another by different relatives across the life span. The well established questionnaires of Nichols and Bilbro (1966), Oniszczenko, Angleitner, Strelau, and Angert (1993), and Ooki, Yamada, Asaka, and Hayakawa (1990) were used in the Canadian, German, and Japanese samples, respectively, supplemented by the examination of color photographs by researchers experienced in working with twins. For the

Table 1
Twin Sample Characteristics

Zygoty	Pairs	Age		
		<i>M</i>	<i>SD</i>	Range
Canadian twins				
MZ male	89	35.75	15.59	16–86
MZ female	161	34.40	14.74	15–76
DZ male	52	31.56	12.40	16–66
DZ female	106	33.46	13.06	16–76
DZ female–male	45	30.60	10.03	16–49
German twins				
MZ male	105	32.21	13.03	15–67
MZ female	426	32.31	13.52	15–80
DZ male	38	30.76	13.77	15–66
DZ female	166	32.48	12.38	15–65
DZ female–male	71	29.54	9.45	14–57
Japanese twins				
MZ male	134	19.09	3.78	14–29
MZ female	292	20.60	3.91	15–30
DZ male	46	19.78	3.76	14–30
DZ female	96	20.51	3.74	14–30
DZ female–male	78	19.71	4.76	14–30

Note. MZ = monozygotic; DZ = dizygotic.

Japanese sample, zygoty diagnoses for 269 pairs were made on the basis of two gene polymorphisms (*DRD4* and *5-HTTLPR*); and for 19 pairs for which zygoty was unclear, genetic fingerprinting was also conducted to diagnose zygoty. Table 1 presents the characteristics of each sample.

Measures

The participants in the Canadian sample completed the English self-report version of Costa and McCrae's (1992) NEO-PI-R; the participants in the German sample completed Ostendorf and Angleitner's (2004) German self-report version; and the participants in the Japanese sample completed the Japanese self-report version developed by Yoshimura et al. (1998). All participants were instructed to complete the forms independently of their twins in nondistracting settings.

Statistical Analyses

A number of significant gender differences were detected by analysis of variance, and correlations with age were observed among some NEO-PI-R scores.¹ Because age and gender effects have been shown to bias behavioral genetic analyses (McGue & Bouchard, 1998), each facet score was adjusted for these effects by regressing each on age and gender and by utilizing the residual scale score in all subsequent analyses.

Previous analyses of these data sets (Jang et al., 1998; Ono, Ando, Onoda, Yoshimura, & Asai, 2000) have shown that additive genetic and nonshared environmental factors explain the observed phenotypic variance, and thus, we estimated additive genetic (r_G) and nonshared environmental (r_E) correlations among the NEO-PI-R facets. Additive genetic factors represent the effects of genotypes that "breed true" from parent to offspring. Nonshared environmental factors (see Hetherington, Reiss, & Plomin, 1994) include events that have differential effects on individual family members (e.g., pre- and postnatal traumas or differential parental treatment). Computation of r_G and r_E followed estimation of the genetic and

¹ The results of the age and gender analyses for each NEO-PI-R score in each sample are not shown here for the sake of brevity, but are available upon request.

environmental covariance matrices by subjecting the MZ and DZ within-pairs covariances to AE Cholesky decomposition (Neale & Cardon, 1992), that is, the decomposition into additive genetic (A) and nonshared environmental (E) covariance matrices. AE Cholesky decomposition transforms each of the A and E matrices into a moment of triangular matrix and its transposed one and serves as a necessary constraint for A and E covariance matrices to be reasonably estimated. As such, it provided us with the estimates for the genetic or environmental covariance between a facet i and a facet j (a_{ij}/e_{ij}) and for the genetic or environmental variance of i (a_{ii}/e_{ii}) or j (a_{jj}/e_{jj}) for any i and j . Using these estimates, the genetic correlation between i and j was computed as $r_G = a_{ij}/(a_{ii} \times a_{jj})^{1/2}$.

The environmental correlation was computed in the same way. Thus, the values of r_G and r_E are standardized so that they vary from -1.0 to $+1.0$ and reflect the degree to which two variables are influenced by the same genetic and environmental factors.

The matrix decomposition and subsequent computation of r_G and r_E were conducted using Mx (Neale et al., 2004). Because of the limited workspace of this program, the AE Cholesky decomposition of the entire 60×60 covariance matrix (i.e., the NEO-PI-R 30 facets for each twin sibling) was untenable. Therefore, calculations were performed by dividing the full covariance matrix in the following way: (a) To obtain r_G and r_E among facets within a domain, the Cholesky decomposition was applied to a 12×12 covariance matrix of the variables for each domain; and (b) to obtain r_G and r_E among facets across domains, the Cholesky decomposition was applied to a 24×24 covariance matrix of facets defining two domains for each of the possible combinations of the five domains.

Once the matrices of r_G and r_E were derived, we conducted Varimax-rotated principal factor analysis to reveal the genetic and environmental structures for each sample (Crawford & DeFries, 1978). To assess the comparability of each factor across matrices (phenotypic, genetic, and environmental) in each sample, for every possible pair of matrices, we first rotated one matrix by an orthogonal Procrustes rotation (Schonemann, 1966) with another matrix as a target (e.g., the phenotypic matrix in the Canadian sample was rotated to the genetic matrix in the same sample) and then computed congruence coefficients for each of the five factors across the two matrices (Haven & ten Berge, 1977; McCrae, Zonderman, Costa, Bond, & Paunonen, 1996; Wrigley & Neuhaus, 1955). The congruence coefficients were computed as the cross products of two column vectors of normalized factor loadings of interest, and conventional criteria with coefficients above .90 were taken as evidence of factor replication (Barrett, 1986). These analyses show the extent to which phenotypic structure is a reflection of genetic, environmental, or both structures in each sample. Furthermore, the same procedure was adopted to assess the comparability of each factor across samples (e.g., the phenotypic matrix in the Canadian sample was rotated to the phenotypic matrix in the German sample, and then congruence coefficients were computed for each of the five factors across the two matrices). These analyses show the extent to which phenotypic, genetic, and environmental structures are invariant across samples.

Results

To examine the phenotypic structure of the NEO-PI-R, principal factor analysis of the age- and gender-corrected phenotypic NEO-PI-R facet scales was conducted for each sample. In the Canadian and German samples, five factors with $\lambda > 1.0$ were extracted (Canadian eigenvalues (λ) = 6.60, 3.83, 3.02, 2.48, 1.69, 0.96, and 0.91; German λ = 6.06, 4.10, 3.05, 2.44, 1.62, 0.99, and 0.97). In the Japanese sample, six factors were extracted (λ = 6.79, 3.39, 3.08, 2.44, 1.73, 1.04, and 0.87); however, examination of the scree plot indicated that five factors should be retained. Table 2 shows the Varimax-rotated phenotypic factor loadings for a five-factor solution for each sample. The factors were clearly identifiable as the N, E, O, A, and C domains, and these structures were

highly similar across samples. The Varimax-rotated phenotypic factor loadings replicated cross-domain loadings, such that the N facet Angry Hostility loaded on A factors in all three samples, and indicated in general that facets of the N domain and facets of the C domain were moderately negatively correlated. However, some domains and facets did not correspond well to the normative pattern. For example, the O and A domains were somewhat weakly reproduced in the German and Japanese samples. On the O domain, the facets Actions and Values had loadings less than .40. In the Japanese sample, a facet of the A domain, Tender-Mindedness, did not contribute to any domains, and Modesty loaded on the N domain.

To examine the genetic structure of the NEO-PI-R, principal factor analysis of the 30×30 matrix of r_G values was conducted. Five factors were extracted for each sample.² The Canadian λ values were 8.74, 4.42, 3.05, 2.60, 1.43, 0.63, and 0.58; the German λ values were 6.94, 5.19, 3.63, 2.51, 1.57, 0.69, and 0.47; and the Japanese λ values were 8.98, 3.91, 3.26, 2.39, 2.07, 0.67, and 0.60. Table 3 shows the Varimax-rotated genetic factor loadings for a five-factor solution for each sample. In comparison with phenotypic factors, genetic factors were somewhat more clearly identifiable as the N, E, O, A, and C domains. Also, the genetic structures were highly similar across samples, including secondary loadings. Overlaps of domains seen in the phenotypic structure, such as Angry Hostility with A factors and negative cross-loading among facets of the N and C domains, were also present in the genetic structure. There were also a number of cross-loadings that were not apparent from the phenotypic structure, such that the E facet Activity loaded on C factors in all three samples.

To examine the environmental structure of the NEO-PI-R, principal factor analysis of a 30×30 matrix of r_E values was conducted. Using the $\lambda > 1.0$ criteria, five nonshared environmental factors were extracted in the Canadian sample (λ = 4.58, 2.86, 2.32, 1.46, 1.02, 0.46, and 0.38). In contrast, only four factors could be retained from the German (λ = 4.50, 2.65, 1.87, 1.71, 0.69, 0.59, and 0.40) and Japanese (λ = 5.06, 2.52, 2.36, 1.84, 0.81, 0.45, and 0.36) samples.³ However, we chose to extract five environmental factors for the two samples because this enabled us to directly assess how different environmental structure is from phenotypic five-factor structure. Table 4 shows the Varimax-rotated environmental factor loadings for a five-factor solution for each sample. In each sample, three of the five factors were clearly recognizable as N, O, and C domains (with the O domain explaining least variance). However, the remaining two factors were defined by facets from the E and A domains, although the E domain was somewhat clearer in the Japanese sample. These results suggest that environmental structure is less reflective of phenotypic structure than is genetic structure as far as the

² The full matrices of phenotypic, additive genetic, and nonshared environmental correlations for each sample are not reproduced here for the sake of brevity, but are available upon request.

³ In the four-factor solution, two of the factors were clearly recognizable as the N and C domains for both the German and Japanese samples. The other factors were defined by loadings from facets of the E and A domains and from facets of the E, O, and A domains for both samples. The four-factor solutions are not reproduced here for the sake of brevity, but are available upon request.

Table 2
Phenotypic Factor Structure of the Revised NEO Personality Inventory (NEO-PI-R) in Canadian, German, and Japanese Samples

NEO-PI-R facet	Varimax-rotated principal factors														
	N			E			O			A			C		
	Cnd	Grm	Jpn	Cnd	Grm	Jpn	Cnd	Grm	Jpn	Cnd	Grm	Jpn	Cnd	Grm	Jpn
N1: Anxiety	78	79	75	-09	-09	-15	01	03	06	01	01	00	-07	-05	-06
N2: Angry-Hostility	66	70	44	-10	08	-02	-04	00	-08	-46	-41	-66	-09	-05	-14
N3: Depression	78	82	79	-24	-18	-15	01	03	06	03	-01	-12	-26	-17	-18
N4: Self-Consciousness	67	66	73	-30	-22	-19	00	-08	03	07	07	-02	-19	-17	-03
N5: Impulsiveness	41	27	43	20	43	22	09	22	13	-22	-17	-27	-42	-26	-37
N6: Vulnerability	65	77	72	-22	-13	-13	-07	-03	-14	02	04	-01	-40	-33	-39
E1: Warmth	-19	-20	-13	70	62	72	17	23	21	32	42	33	12	13	13
E2: Gregariousness	-19	-18	-10	59	60	66	-03	01	-08	-01	15	16	-03	-04	05
E3: Assertiveness	-26	-34	-25	44	51	49	16	18	07	-38	-27	-31	31	28	22
E4: Activity	-07	-10	-17	47	52	55	14	12	07	-25	-15	-27	39	39	38
E5: Excitement Seeking	-05	-07	-09	43	44	54	12	08	17	-23	-21	-18	-18	-11	-06
E6: Positive Emotions	-23	-29	-17	67	58	71	29	34	22	12	14	09	11	08	-02
O1: Fantasy	08	06	05	08	17	04	57	57	57	-02	-07	-05	-25	-21	-20
O2: Aesthetics	10	07	08	06	03	15	06	72	71	06	12	06	10	07	02
O3: Feelings	31	17	08	29	23	33	59	69	59	02	09	05	14	08	23
O4: Actions	-19	-28	-18	20	27	22	48	37	16	01	-02	00	-14	-12	-08
O5: Ideas	-05	-14	-06	-05	04	-04	74	65	67	-09	-10	-12	13	16	22
O6: Values	-18	-11	-14	06	05	14	41	35	36	05	04	19	-12	-15	01
A1: Trust	-38	-28	-20	31	31	43	10	14	16	45	44	59	00	03	12
A2: Straightforwardness	-04	-01	05	-08	-29	-05	-06	-09	-08	65	49	58	23	03	10
A3: Altruism	-08	-09	-04	37	14	38	08	12	17	64	69	55	27	17	29
A4: Compliance	-16	-11	-02	-11	-12	-10	-01	-04	-02	68	68	71	02	-07	-07
A5: Modesty	15	24	41	-19	-23	-27	-15	-19	-16	53	49	30	-06	-11	-28
A6: Tender-Mindedness	04	18	22	12	17	33	23	27	21	46	48	37	-02	-02	-02
C1: Competence	-36	-39	-39	17	16	17	11	15	17	03	-03	-06	67	62	68
C2: Order	02	-05	02	00	-10	01	-10	-12	-01	01	-04	00	60	68	64
C3: Dutifulness	-09	-11	-16	02	-08	04	-08	-09	04	22	21	16	70	67	58
C4: Achievement Striving	-08	-02	-11	15	13	29	16	14	11	-13	-11	-10	73	74	70
C5: Self-Discipline	-27	-29	-30	12	-01	11	-09	-11	00	08	05	09	73	75	75
C6: Deliberation	-15	-44	05	-23	-44	-23	-11	-14	-07	20	16	16	61	42	61
% of variance explained	11.7	12.5	11.3	9.0	9.3	11.2	8.3	8.4	6.7	9.2	8.4	9.1	12.5	10.8	11.8

Note. Decimal points have been omitted; loadings over .40 in absolute magnitude are given in boldface. N = Neuroticism; E = Extraversion; O = Openness to Experience; A = Agreeableness; C = Conscientiousness; Cnd = Canadian factor loadings; Grm = German factor loadings; Jpn = Japanese factor loadings.

Table 3
Genetic Factor Structure of the Revised NEO Personality Inventory (NEO-PI-R) in Canadian, German, and Japanese Samples

NEO-PI-R facet	Varimax-rotated principal factors														
	N			E			O			A			C		
	Cnd	Grm	Jpn	Cnd	Grm	Jpn	Cnd	Grm	Jpn	Cnd	Grm	Jpn	Cnd	Grm	Jpn
N1: Anxiety	87	87	83	-15	-08	-18	00	04	03	-05	03	07	-06	-03	-14
N2: Angry-Hostility	86	76	56	-01	02	-15	-02	06	-11	-32	-41	-60	-19	01	-31
N3: Depression	82	90	83	-27	-17	-16	-01	05	04	12	05	-14	-27	-16	-25
N4: Self-Consciousness	76	75	82	-36	-21	-19	-04	-13	01	12	12	-08	-19	-27	-16
N5: Impulsiveness	45	37	51	35	46	21	08	29	15	-27	-20	-22	-53	-33	-52
N6: Vulnerability	76	85	71	-28	-13	-11	-08	03	-20	-07	05	08	-37	-34	-57
E1: Warmth	-39	-23	-16	70	67	76	22	23	19	13	45	24	21	13	19
E2: Gregariousness	-32	-18	-13	53	75	75	01	-05	-18	-23	11	28	-05	02	10
E3: Assertiveness	-43	-35	-19	55	55	50	23	25	11	-38	-26	-44	30	38	39
E4: Activity	-15	-10	-06	55	61	61	23	18	07	-18	-18	-30	48	53	54
E5: Excitement Seeking	-13	-01	-06	60	56	69	01	03	05	-13	-27	-23	-25	-16	-07
E6: Positive Emotions	-36	-31	-15	77	65	83	35	35	14	06	16	04	10	16	01
O1: Fantasy	06	10	-03	08	20	06	71	68	66	05	-13	-22	-17	-27	-20
O2: Aesthetics	04	11	20	10	-03	04	78	77	67	15	14	12	15	07	02
O3: Feelings	31	20	07	38	21	31	66	77	76	-01	07	-05	17	02	25
O4: Actions	-32	-29	-31	20	31	41	65	43	37	-04	00	07	-06	-18	-07
O5: Ideas	01	-13	-01	01	10	-07	81	71	79	-03	-12	-14	12	11	19
O6: Values	-25	-14	-26	-03	01	09	59	54	62	-05	-02	17	-11	-29	-02
A1: Trust	-59	-39	-29	34	39	48	19	14	16	49	51	60	-04	-02	12
A2: Straightforwardness	-08	-01	-05	-10	-33	-07	-01	-11	-13	78	65	70	27	01	10
A3: Altruism	-23	-14	02	39	21	49	11	08	24	57	82	44	47	12	46
A4: Compliance	-31	-08	-06	-31	-09	05	-01	-11	-02	65	82	81	03	-12	-03
A5: Modesty	24	32	41	-17	-25	-27	-22	-24	-22	58	65	45	00	-09	-42
A6: Tender-Mindedness	-02	31	33	06	17	37	36	28	29	65	62	45	03	-03	-07
C1: Competence	-48	-53	-38	22	15	09	14	12	22	05	-07	-09	69	70	82
C2: Order	05	-12	-03	-02	-08	09	-05	-23	00	04	-06	02	77	80	84
C3: Dutifulness	-13	-09	-30	-04	-10	05	-07	-20	05	17	17	12	81	79	68
C4: Achievement Striving	-11	01	-15	15	12	35	18	18	13	-03	-11	-09	81	81	80
C5: Self-Discipline	-27	-35	-26	19	-06	10	-10	-16	-02	22	03	04	73	78	91
C6: Deliberation	-16	-09	-02	-39	-53	-25	-05	-34	-19	02	16	26	74	45	83
% of variance explained	26.3	23.8	20.0	17.4	17.4	20.8	17.6	17.0	15.2	14.5	17.6	15.6	24.1	20.9	28.5

Note. Decimal points have been omitted; loadings over .40 in absolute magnitude are given in boldface. N = Neuroticism; E = Extraversion; O = Openness to Experience; A = Agreeableness; C = Conscientiousness; Cnd = Canadian factor loadings; Grm = German factor loadings; Jpn = Japanese factor loadings.

Table 4
Environmental Factor Structure of the Revised NEO Personality Inventory (NEO-PI-R) in Canadian, German, and Japanese Samples

Varimax-rotated principal factors

NEO-PI-R facet	N			E			O			A			C		
	Cnd	Grm	Jpn	Cnd	Grm	Jpn	Cnd	Grm	Jpn	Cnd	Grm	Jpn	Cnd	Grm	Jpn
N1: Anxiety	74	74	72	-05	-05	-14	05	04	09	05	-03	-06	-03	-01	05
N2: Angry-Hostility	49	56	40	37	34	40	-08	-01	-05	-39	-18	-50	-05	-12	-01
N3: Depression	75	74	77	-09	-06	-11	04	08	03	-17	-18	-11	-22	-16	-10
N4: Self-Consciousness	64	59	66	-17	-14	-22	06	00	06	-13	-17	-03	-13	-04	09
N5: Impulsiveness	42	19	43	16	40	32	07	13	14	00	25	-09	-35	-23	-29
N6: Vulnerability	57	73	71	-22	-12	-15	-03	-06	-10	-05	-05	-12	-36	-28	-25
E1: Warmth	-06	-17	-13	02	14	33	06	17	19	73	64	70	02	07	03
E2: Gregariousness	-10	-15	-06	22	19	49	-09	-01	-07	57	49	42	-06	-13	-01
E3: Assertiveness	-13	-34	-23	59	49	55	09	12	01	06	19	05	19	10	03
E4: Activity	-04	-13	-20	55	44	56	04	05	06	16	30	07	22	22	20
E5: Excitement Seeking	-01	-11	-08	37	37	44	25	10	27	07	15	12	-22	-06	-10
E6: Positive Emotions	-16	-30	-18	18	27	47	23	31	28	56	45	46	07	-03	-07
O1: Fantasy	08	04	14	09	12	-04	39	49	50	05	13	08	-40	-18	-20
O2: Aesthetics	11	03	-01	07	02	15	60	65	56	-02	22	23	-05	06	03
O3: Feelings	22	12	09	10	16	24	54	60	41	23	31	34	03	11	21
O4: Actions	-08	-26	-09	12	24	14	22	26	04	18	18	01	-26	-08	-10
O5: Ideas	-14	-10	-05	08	11	05	61	54	51	-12	02	-03	03	23	23
O6: Values	-14	-04	-08	-05	02	05	15	10	19	14	17	30	-17	04	04
A1: Trust	-22	-17	-18	-18	-10	03	-06	10	08	40	50	71	07	07	11
A2: Straightforwardness	-01	-01	06	-43	-47	-31	-14	-07	-15	29	09	44	28	06	12
A3: Altruism	-04	-04	-13	-31	-34	-06	06	14	05	62	50	70	17	18	17
A4: Compliance	-06	-12	-06	-56	-51	-55	05	02	-03	41	27	44	10	-01	-09
A5: Modesty	11	12	39	-51	-41	-37	-12	-10	-12	18	03	09	-02	-11	-13
A6: Tender-Mindedness	12	05	14	-13	-12	08	-01	27	11	43	41	50	-07	-04	-01
C1: Competence	-32	-27	-41	13	17	25	18	14	15	08	16	09	63	52	56
C2: Order	-02	03	09	11	-04	01	-15	01	-03	-02	-10	-03	51	60	57
C3: Dutifulness	-10	-12	-10	-05	-18	-05	-01	01	00	17	16	18	62	58	52
C4: Achievement Striving	-12	-04	-04	36	21	28	18	09	10	-01	07	06	55	67	61
C5: Self-Discipline	-30	-23	-33	16	-01	04	-05	-04	01	03	07	15	68	69	59
C6: Deliberation	-16	01	04	-27	-36	-22	-05	01	03	02	-17	-02	59	43	53
% of variance explained	21.0	23.3	23.9	17.8	17.2	19.8	11.9	13.8	10.4	19.8	17.7	24.3	23.1	20.0	18.1

Note. Decimal points have been omitted; loadings over .40 in absolute magnitude are given in boldface. N = Neuroticism; E = Extraversion; O = Openness to Experience; A = Agreeableness; C = Conscientiousness; Cnd = Canadian factor loadings; Grm = German factor loadings; Jpn = Japanese factor loadings.

Varimax-rotated factor structures were compared. However, it is unclear from the above analysis whether the lack of correspondence is due to a difference in the factor space itself or merely in the placement of axes. Therefore, the next step was to subject genetic and environmental structures to Procrustes rotation with phenotypic structure as a target for each sample and to compute congruence coefficients between them.

Congruence coefficients among the phenotypic, genetic, and environmental factors in each sample are presented in Table 5. Phenotypic, genetic and environmental factors were highly congruent, with congruence coefficients ranging from .83 to .99. These results suggest that differences between environmental and phenotypic structures are only in the placement of axes and that the phenotypic five-factor structure is reflective of not only genetic structure, but also environmental structure.

Finally, to examine the extent to which phenotypic, genetic, and environmental structures are universal, congruence coefficients that compared each type of factor across the three samples were computed (see Table 6). The phenotypic congruence coefficients ranged from .96 to .98, replicating universality in phenotypic structure of the scale. The genetic congruence coefficients were also high for most domains, ranging from .93 to .97, with the exception of the genetic congruence coefficient for the A domain between the Canadian and Japanese samples, which was .86. The environmental congruence coefficients were also high, ranging from .92 to .96. These results suggest that the environmental and genetic structures are highly comparable between these samples.⁴

Discussion

The purpose of this study was to examine whether the phenotypic structure of the FFM as assessed by the NEO-PI-R is reflective of an underlying genetic structure and whether the genetic structure is universal across populations from Canada, Germany, and Japan. The results were clear. Both genetic and environmental structures were highly congruent with phenotypic structure, and all

Table 5
Congruence Coefficients Among Phenotypic, Genetic, and Environmental Factors in Canadian, German, and Japanese Samples

Matrix	Factor				
	N	E	O	A	C
P-G					
Canada	.99	.98	.99	.95	.99
Germany	.99	.99	.99	.99	.99
Japan	.98	.99	.98	.98	.99
P-E					
Canada	.99	.97	.95	.97	.99
Germany	.99	.99	.97	.99	.99
Japan	.99	.99	.98	.99	.98
G-E					
Canada	.96	.92	.89	.83	.95
Germany	.97	.98	.94	.96	.94
Japan	.95	.94	.89	.96	.97

Note. P-G = phenotypic-genetic; P-E = phenotypic-environmental; G-E = genetic-environmental; N = Neuroticism; E = Extraversion; O = Openness to Experience; A = Agreeableness; C = Conscientiousness.

Table 6
Congruence Coefficients of Phenotypic, Genetic, and Environmental Factors Comparing Across Canadian, German, and Japanese Samples

Matrix	Factor				
	N	E	O	A	C
Phenotypic					
Canada-Germany	.98	.98	.98	.99	.99
Canada-Japan	.97	.98	.96	.97	.97
Germany-Japan	.97	.97	.97	.97	.97
Genetic					
Canada-Germany	.97	.95	.96	.92	.96
Canada-Japan	.96	.93	.96	.86	.96
Germany-Japan	.96	.96	.95	.94	.93
Environmental					
Canada-Germany	.96	.95	.93	.93	.94
Canada-Japan	.96	.95	.92	.94	.95
Germany-Japan	.96	.95	.93	.93	.94

Note. N = Neuroticism; E = Extraversion; O = Openness to Experience; A = Agreeableness; C = Conscientiousness.

three structures were highly congruent across samples. These results support McCrae and Costa's (1997, 1999) view that the FFM reflects a genetic structure that is universal and that the FFM is a reflection of environmental structure as well.

Genetic Basis of the FFM

An interesting finding of this study is that the classic five-factor structure is more apparent in genetic structure than in phenotypic structure. For example, in the phenotypic structure, the O and A domains were only generally reproduced in the German and Japanese samples, but these domains were clearly extracted from the matrix of genetic correlations. These results suggest that the five-factors are indeed "genetically crisp" (see Faraone et al., 1999) and reflect a homogenous set of genetic influences. The implication is that molecular genetic studies of personality seeking putative loci would clearly benefit from the use of the NEO-PI-R—an opinion also expressed in recent meta-analyses (Schinka, Busch, & Robichaux-Keene, 2004; Sen, Burmeister, & Ghosh, 2004).

At first glance, the present findings appear to be inconsistent with those of Jang, Livesley, Angleitner, et al. (2002), who discovered that two genetic factors were necessary to explain the genetic covariance of six facets defining the same domain, suggesting far more genetic heterogeneity within each domain than found in the present study. However, the present results are rather more consistent with the previous findings when the results are examined in detail. Specifically, the two genetic factors in Jang, Livesley, Angleitner, et al.'s study overlapped each other substantially: For each domain, one of the two factors influenced all six of the facets within the domain, whereas the other factor had its highest loadings for just a specific subset of these six facets, yet also influenced almost all of the other remaining facets.

⁴ Congruence coefficients among all of the phenotypic, genetic, and environmental facets extracted from the NEO-PI-R were similarly quite high. The results are available upon request.

The theme of within-domain genetic heterogeneity has also been suggested by other studies; Jang et al. (2001) found a substantial negative genetic correlation between facets of the N and A domains, and Ono et al. (2000) examined the covariation between five domain scores and found that at least one common genetic factor is necessary. However, their findings are rather consistent with the present findings in that we also observed some genetic overlap between domains. For example, a facet of the N domain, Angry Hostility, loaded on both the genetic N and A factors in the German and Japanese samples. In another example, although phenotypically indistinct, a facet of the E domain, Activity, cross-loaded on the C factor in each sample. Furthermore, phenotypic overlap among facets of the N and C domains, which have been reported by virtually all studies examining the structure of the NEO-PI-R (e.g., McCrae & Costa, 1997), also extended to genetic structure. The fact that these cross-loadings were observed for genetic structure, together with the findings of our previous studies (Jang et al., 2001; Ono et al., 2000), suggests the involvement of higher order genetic factors such as Digman's (1997) *alpha* (defined by the N, A, and C domains) and *beta* (defined by the E and O domains). In fact, the genetic cross-loadings highlighted in the present study are roughly commensurate with alpha and beta (see also Jang et al., in press).

With regard to the interpretation of such higher order factors, McCrae and Costa (1999) argued that higher order factors such as alpha and beta are merely the *evaluation* of one's personality. People evaluate themselves with two independent positive and negative dimensions (Waller, 1999), and high scores in the N domain but low scores in the A and C domains typically indicate negative evaluations, whereas high scores in the E and O domains indicate positive evaluations. As such, McCrae and Costa suggested that the higher order factors are no more than such evaluative artifacts and should not be confused with personality itself and that the five factors should remain at the highest level of generality.

However, some evidence suggests that such higher order factors may have a genetic and biological basis. For example, Jang et al. (2001) observed a substantial genetic correlation between the N and A domains, which was explained in part by variations in the serotonin transporter gene. Manuck et al. (1998) also showed that peak prolactin responses to fenfluramine, a measure of serotonergic responsivity, correlated with both the N and C domains. These findings suggest that the N, C, and A domains are all modulated by the serotonergic system and may form a higher order alpha factor. Thus, future research should examine whether there is a reliable relationship between the five factors and higher order factors at the genetic level, as was done at the phenotypic level (Markon, Krueger, & Watson, 2005). However, at the very least, the results of the present study support the claim that the FFM provides a genetically valid framework for understanding human personality at a high level of generality.

Environmental Structure of the FFM

Another finding in this study is that environmental factors are also congruent with phenotypic and genetic factors and that they remain invariant across samples. Why do genetic and environmental influences mirror each other? Various interpretations are possible. Environmental influences may not impact individuals inde-

pendently of genetic architecture and may instead act on an a priori genetic and hence biological basis. Alternatively, a more psychological explanation could be that environmental influence is mainly through social interaction and that other people's personality traits influence one's corresponding personality traits.

However, previous research suggested that environmental structure is less reliable due to a systematic error of measurement. It is not an ordinary error of measurement or unreliability; it is included in nonshared environmental variance, but is unlikely to be included in the covariance between multiple traits. Rather, what makes environmental structure less reliable is the implicit personality theory (IPT), a systematic bias in self-reported personality judgments (Borkenau, 1992). McCrae et al. (2001) showed that reproduction of the FFM structure from the matrix of r_E is due to the IPT and not to the differential influences of environmental and experiential influences on personality. When the IPT bias was removed from the matrix of r_E estimated among the 30 NEO-PI-R facets, only two factors, resembling the concepts in Freud's famous dictum of "love" and "work," could be extracted. As such, it is possible that the five environmental factors reported here reflect IPT bias that merely secondarily reflects the genetic relationships between traits.

Thus, when only self-reported measures are obtained and when the resultant genetic and environmental structures mirror each other, genetic structure provides more credible information on the "true" personality structure and thus is generally more useful. It is also directly relevant to biological and genetic research on personality. However, when IPT is properly handled, such as by multi-method design (Riemann et al., 1997), examination of environmental structure is also useful because it has a stronger power to detect cultural differences that are otherwise obscured by genetic universality. For example, cultural differences in structures of values (Schwartz, 1992) or more indigenous personality dimensions (e.g., Cheung et al., 2001) may be found when examining environmental structure rather than genetic and phenotypic structures.

Universality of the FFM

The high congruence coefficients of genetic factors across samples suggest that genetic structure is invariant across nations and contributes to universality in the phenotypic structure of the FFM shown in previous literature. In our previous studies (Jang, Livesley, Angleitner, et al., 2002), we observed a similar r_G pattern between facets within a single domain or between facets defining the N and A domains in the Canadian, German, and Japanese samples. The present study extended these findings by showing that such genetic similarity applies to the genetic covariance among the entire 30 facets of the NEO-PI-R. This finding provides support for the claim that the FFM is a human universal (McCrae & Costa, 1997, 1999).

However, another interpretation is that such genetic universality is not unique to the FFM, but is also true of other personality models such as the three-dimensional model of Tellegen (1982) and the seven-dimensional model of Cloninger et al. (1993). Especially the structure of the former has received support from multivariate behavioral genetic research (Krueger, 2000). These structures remain to be tested cross-culturally, but when the phenotypic, genetic, and environmental structures of the model were

found across cultures, the question was raised as to which model of personality represents the universal standard. One possibility could be that what is genetically universal is not the FFM, but the structure of personality in general or the hierarchical nature of personality (Markon et al., 2005). Alternatively, only the FFM, but not other personality models, may be shown to be genetically universal. In that case, the FFM can be taken as the “common heritage of the human species” (McCrae, 2004) that specifically captures the genetically universal component of personality variation, and evolutionary consideration of why all humans systematically vary in genetic predisposition in the continuum of the five dimensions is in order. Clearly, further cross-cultural multivariate behavioral genetic study on other personality measures is required. Also, although gene pools associated with personality may be quite different across the three nations examined in this study, it is necessary to sample other populations such as Africans and Hispanics.

Limitations of the Study

Finally, some limitations should be noted. First, this study should be supplemented with the emic approach (e.g., Ashton et al., 2004; Cheung et al., 2001). The aims of the emic approach are to describe and interpret behavior in terms that are meaningful to members of each culture and to discover the constructs specific to each culture. In contrast, the aims of the etic approach are to verify that the concept identified in a given culture can be found in another culture and to discover universal concepts across cultures (Berry, 1969). The weakness of the NEO-PI-R is its imposed etic nature; it can capture neither a culturally unique way of carving personality structure nor an indigenous personality dimension in a culture. In fact, from the emic perspective, Ashton et al. proposed a six-factor solution that was replicated in seven different lexicons and suggested that the FFM needs to be revised. Also, Cheung et al. (2001) reported that Interpersonal Relatedness, originally proposed as a construct unique to the Chinese culture, was not captured well by the FFM even in non-Chinese cultures. Thus, one direction for future behavioral genetic research is to incorporate the emic approach. For example, one of the bases of the six-factor solution proposed by Ashton et al. was the fact that the O domain or Intellect Imagination factor sometimes did not appear in the five-factor solution, but was rescued in a six-factor solution. In the present study, the O domain also did not explain the unique variance that was enough to form the fifth environmental factor in the German and Japanese samples. An interesting direction for future research will be to pursue whether or not such a weak replicability of the O domain can be reliably attributed to environmental structure. Also, whether or not an indigenous personality dimension appears in the genetic, environmental, or both structures is another question to be addressed in the future.

Second, our analyses specified that the genetic and environmental factors of importance were only additive and nonshared, respectively. We did not test the presence of nonadditive genetic or shared environmental factors. This may appear to be an unrealistic simplification, but we did this because additive genetic and nonshared environmental factors have been consistently shown to be the most important in explaining personality (Bouchard & Loehlin, 2001). In fact, previous analyses of these data sets have shown that additive genetic and nonshared environmental factors explain the

phenotypic variance (Jang et al., 1998; Ono et al., 2000). However, the reason why nonadditive genetic or shared environmental factors do not emerge may simply be that a larger sample size is required to detect them. Furthermore, classical twin design is limited in that it cannot simultaneously estimate additive and nonadditive genetic effects and shared and nonshared environmental effects and that it tends to overestimate additive genetic influences and to underestimate shared environmental influences if assortative mating is modest, as is the case with personality traits (Keller & Coventry, 2005). Thus, the present study should be supplemented with studies utilizing a larger sample size, an extended-twin-family design, or an adoption design. However, considering that MZ twins reared apart were as highly correlated as MZ twins reared together on scores of personality traits (e.g., Bouchard, McGue, Hur, & Horn, 1998), the validity of the present study will not be substantially minimized as far as shared environmental influences are concerned.

Finally, caution in the interpretation of r_G values should be taken. Although it is appealing to consider r_G values as a reflection of biological pleiotropy, two variables may be genetically independent not because they do not share any genes, but because they share more than one; whereas a set of genes causes two variables to be positively correlated (i.e., influence in the same direction), another set of genes may make them negatively correlated (i.e., influence in the opposite direction). Therefore, the genetic structure that we found in this study was, at best, a rough sketch of overall genetic influences, and thus, this study should be supplemented with a molecular genetic approach. Because the molecular genetic method is now becoming inexpensive, more such efforts will be made and will reveal the extent to which statistical pleiotropy, as computed in twin studies, in fact reflects biological pleiotropy (e.g., Jang et al., 2001).

Conclusions

The biological basis of the FFM has been estimated from circumstantial evidence that the five domains and their facets are substantially heritable. However, this evidence does not favor the FFM exclusively, as almost all human behavior can be shown to be heritable (Turkheimer, 1998). The present study had provided the first direct evidence that the FFM reflects underlying genetic structure. Our findings provide strong support for McCrae and Costa's (1999) claim that the five domains are endogenous traits that have a solid biological basis. Also, the present study is the first showing that the genetic structure of the FFM is universal, suggesting that the FFM may represent the common heritage of the human species. However, other personality models should also be tested for their genetic universality to determine which is universal: the FFM or personality structure in general.

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