The Five-Factor Model of Personality and Borderline Personality Disorder: A Genetic Analysis of Comorbidity

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Background: Recently, the nature of personality disorders and their relationship with normal personality traits has received extensive attention. The five-factor model (FFM) of personality, consisting of the personality traits neuroticism, extraversion, openness to experience, agreeableness, and conscientiousness, is one of the proposed models to conceptualize personality disorders as maladaptive variants of continuously distributed personality traits.

Methods: The present study examined the phenotypic and genetic association between borderline personality and FFM personality traits. Data were available for 4403 monozygotic twins, 4425 dizygotic twins, and 1661 siblings from 6140 Dutch, Belgian, and Australian families.

Results: Broad-sense heritability estimates for neuroticism, agreeableness, conscientiousness, extraversion, openness to experience, and borderline personality were 43%, 36%, 43%, 47%, 54%, and 45%, respectively. Phenotypic correlations between borderline personality and the FFM personality traits ranged from .06 for openness to experience to .68 for neuroticism. Multiple regression analyses showed that a combination of high neuroticism and low agreeableness best predicted borderline personality. Multivariate genetic analyses showed the genetic factors that influence individual differences in neuroticism, agreeableness, conscientiousness, and extraversion account for all genetic liability to borderline personality. Unique environmental effects on borderline personality, however, were not completely shared with those for the FFM traits (33% is unique to borderline personality).

Conclusions: Borderline personality shares all genetic variation with neuroticism, agreeableness, conscientiousness, and extraversion. The unique environmental influences specific to borderline personality may cause individuals with a specific pattern of personality traits to cross a threshold and develop borderline personality.

Key Words: Borderline personality disorder, five-factor model, genetics, personality, twin study

Researchers have proposed to conceptualize personality disorders as maladaptive variants of normal personality traits (1–4). This dimensional approach provides quantitative estimates of the degree to which relevant personality traits are present in each individual. This representation of personality disorders has several advantages. First, a dimensional representation can explain symptom heterogeneity and the lack of clear boundaries between different categorical diagnoses. Second, important information is retained about subthreshold traits and symptoms of clinical and empiric interest. Finally, dimensional models can integrate scientific findings concerning the distribution of personality traits and associated maladaptivity into a classification system (5).

Several dimensional models of personality and personality disorders have been suggested. Some are based on personality traits that underlie personality disorders; others are designed to measure normal personality. Within the first category falls Livesley's model (Dimensional Assessment of Personality Pathology) (6), which identifies four higher order dimensions underlying personality pathology, or Clark's model (Schedule for Nonadaptive and Adaptive Personality) (7), which specifies 12 dimensions of maladaptive personality function. The second category includes Cloninger's Seven-Factor Model (8), which distinguishes four dimensions of temperament and three dimensions of character, or the Five-Factor Model (FFM) (9) of personality, which distinguishes five domains of personality. The FFM of personality is the most popular and is often promoted for inclusion in the 5th edition of the *Diagnostic and Statistical Manual* (DSM) for mental disorders (10).

In this study we investigate the association between borderline personality disorder (BPD) features and FFM personality traits: neuroticism, extraversion, openness to experience, agreeableness, and conscientiousness. BPD is characterized by disturbances in emotional regulation, impulse control, interpersonal relationships, and identity. Until now, studies of the relationship between FFM personality traits and BPD focused on analyses at the phenotypic level. Widiger and Costa (11) reviewed 56 studies into the association between DSM-IV personality disorders and the FFM and showed that borderline patients (measured in 35 studies) tend to score high on neuroticism and low on agreeableness and conscientiousness. Two meta-analytic studies of FFM personality disorder research confirmed this association (12,13).

The heritability of the FFM personality traits has been studied intensively, showing broad-sense heritability estimates ranging from 33% to 65% (14–18). In studies with sufficient statistical power, the influence of both additive (9%–36%) and nonadditive genetic factors (4%–33%) are suggested for the neuroticism and extraversion scale of the Eysenck Personality Questionnaire (19–22). Genetic studies of BPD are scarce. Three large-scale studies of the genetic liability for BPD and BPD features report broad-sense heritability estimates around 40% (23–25). Applying

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a multigenerational design, Distel *et al.* (24) established that additive (21%) and nonadditive (24%) genetic factors explain familial resemblance in BPD features.

If an association between normal personality traits and BPD is also found at the genetic level, this provides further evidence in favor of a dimensional model of personality disorders. Multivariate genetic analysis can address this issue (26–29). In multivariate genetic analysis, the comorbidity or covariance between traits is decomposed into genetic and environmental parts. The genetic contribution to the covariance between traits is a function of the proportion of variance that two traits share because of genetic causes (genetic correlation) and the extent to which trait variance is explained by genetic factors. Likewise, the environmental contribution to the covariance between traits is a function of the proportion of variance that two traits share because of environmental causes (environmental correlation) and the extent to which trait variance is explained by environmental factors. The phenotypic, genetic, and environmental covariance structures among a set of variables is not necessarily the same: for example, the phenotypic correlation among traits can be low and the genetic correlation high, meaning that the overlap that is there is predominantly explained by an overlap in genes.

Here, we explore the genetic and environmental etiology of the relationship between borderline personality and the FFM personality traits. Data on borderline personality and FFM traits were available for 10,489 twins and siblings from Dutch, Belgian and Australian twin registries. We first investigate the genetic and environmental influences on individual differences in FFM personality traits and borderline personality. The large sample size and the inclusion of data from siblings in the analyses allows for the investigation of both additive and nonadditive genetic factors (30). Next, we explore the phenotypic association by examining how much variance in borderline personality can be explained by the FFM traits. Finally we apply multivariate genetic analysis to determine to what extent the phenotypic association is due to genetic and environmental associations among the traits.

Methods and Materials

Participants

Data were collected as part of a project on borderline personality in Dutch, Belgian, and Australian twin family cohorts. Twins and siblings were approached by mail and invited to participate in the study by completing a questionnaire. In total there were 10,489 twins and siblings registered with the Netherlands Twin Register (31), the East Flanders Prospective Twin Survey (32), and the Australian Twin Register (33) who completed the questionnaire. There were 1336 monozygotic male twins, 773 dizygotic male twins, 3067 monozygotic female twins, 1751 dizygotic female twins, 778 males from dizygotic opposite sex pairs, 1123 females from dizygotic opposite sex pairs, and 609 brothers and 1052 sisters from 6140 families. Mean age of the total sample was 33 years (SD = 9.97, range 18–90).

Zygosity of same-sex twins was determined from DNA polymorphisms or from self-report answers to validated survey questions on physical twin resemblance and confusion of the twins. Further details can be found elsewhere (23,34–36).

Measures

Borderline personality was assessed with the 24-item Personality Assessment Inventory–Borderline Features scale (PAI-BOR) (37,38). The PAI-BOR consists of 24 statements concerning, for example, stability of mood and affects, self-image, feelings of emptiness, intense and unstable relationships, impulsivity and self-harm, that are rated on a 4-point scale (0–3; false, slightly true, mainly true, very true). Several studies have supported the reliability and the validity of PAI-BOR scores (37,39,40). Receiver operating characteristic analyses showed that the PAI-BOR discriminates reasonably well between borderline patients and patients with major depressive disorder or dysthymia (area under curve = .78). At the best cutoff point of 42, the sensitivity was 71% and the specificity 69% (41). Multigroup confirmatory factor analysis showed that the PAI-BOR is measurement invariant across sex and age (42). The 6-month test-retest reliability and internal consistency (Cronbach's α) of the Dutch version of the PAI-BOR are .78 and .84, respectively (23). The PAI-BOR was scored according to the test manual (37).

FFM personality traits were measured by the NEO Five Factor Inventory (NEO-FFI), a shortened version of the Neo-PI-R (9). The NEO-FFI contains 60 items that are to be rated on a 5-point scale (1–5; totally disagree, disagree, neutral, agree, totally agree) and derives scores for the personality traits neuroticism, extraversion, openness to experience, agreeableness, and conscientiousness. A score was calculated if no more than nine items in total or three items per subscale were left unanswered. Missing and ambiguous answers were substituted with the neutral option.

Genetic Modeling

Twin family studies make use of the different degree of genetic relatedness of pairs of family members to estimate the relative contribution of genes and environment to the variance in a trait (43). Monozygotic (MZ) twins are genetically (nearly) identical, whereas dizygotic (DZ) twins share on average 50% of their segregating genes, like nontwin siblings. Quantitative genetic modeling is based on the fact that the phenotypic variance is a function of genetic (G), shared (C), and nonshared environmental (E) variance. Genetic variance can be additive (A), indicating that the effects of multiple alleles are additive, or nonadditive (dominance, D) meaning that alleles at a particular locus interact. Twin correlations provide a first impression of the relative contribution of A, C, D, and E. The more similar MZ twins are in their phenotypes compared with DZ twins and nontwin siblings, the more variance in a trait is caused by genetic effects. When the DZ correlation is less than half the MZ correlation, there is evidence for D. Differences within MZ twin pairs are due to E, which also include measurement error (26,43). In multivariate analyses, a significant cross-twin cross-trait correlation suggests that there is a familial influence on the etiology of the correlation between traits. If the MZ cross-twin cross-trait correlation exceeds the DZ cross-twin cross-trait correlation, this suggests that the familial influence on the correlation is at least partly genetic in origin. A twin–sibling design only provides information to model either an ACE model or an ADE model.

Statistical Analyses

All analyses were carried out using structural equation modeling in Mx (44). Because the PAI-BOR data showed a somewhat skewed distribution, a square root data transformation was performed for this variable. We first ran univariate saturated models for the FFM personality traits and borderline personality that estimate means, standard deviations, and covariances among family members. We tested for the significance of sex differences in standard deviations and the heterogeneity of correlations of males versus females and DZ twins versus nontwin siblings. We included effects of age, sex and country on the mean scores.

Table 1. Number of Twins (from Complete/Incomplete Twin Pairs) and Siblings and Sample Descriptives for the Dutch, Belgian, and Australian Samples

	Total Sample	The Netherlands	Belgium	Australia
Sample Configuration				
Monozygotic males	930/406	472/205	122/41	336/160
Dizygotic males	438/335	208/171	28/36	202/128
Monozygotic females	2,292/775	1,376/403	146/172	770/200
Dizygotic females	1,220/531	578/304	94/55	548/172
Dizygotic opposite sex	1,068/833	506/430	148/74	414/329
Brother	609	509	6	94
Sister	1,052	892	17	143
Total	10,489	6,054	939	3,496
Sample Descriptives				
Mean age (SD)	33.02 (9.97)	35.33 (11.81)	28.48 (6.92)	30.24 (4.61)
Age range	18–90	18–90	18–67	18–45
% Females	67%	68%	66%	65%

Next, in a multivariate saturated model phenotypic correlations (cross trait—within person) and cross-twin cross-trait correlations were estimated. These correlations show the association between BPD features and the FFM traits and the importance of genetic and environmental influences on this association. We tested whether the correlations differed for males and females and between the countries.

Comparison of different models was done by means of likelihood ratio tests, subtracting the negative log likelihood (−LL 2) for a more restricted model from the −2LL for a more general model. This yields a statistic that is distributed as chi-squared with degrees of freedom equal to the difference in the number of parameters in the two models. If the chi-squared test yields a p value $>.01$, the constrained model is deemed not significantly worse.

To determine which personality traits predict the PAI-BOR score best and contributed most to the variance, multiple regression analysis was conducted. The FFM traits were included in the model as predictors and the PAI-BOR as dependent variable. Age, sex, and country were also included in the model as predictors. Analyses were conducted using backward stepwise regression. First, all predictor variables were included in the regression equation: PAI-BOR = $\alpha + \beta_{neu}*$ Neu + $\beta_{agr}*$ Agr + $\beta_{con}*$ Con + $\beta_{ext}*$ Ext + $\beta_{open}*$ Open + $\beta_{age}*$ Age + $\beta_{sex}*$ Sex +

Table 2. Estimated Twin and Sibling Correlations for the Five-Factor Model Personality Traits and Borderline Personality, Intercepts (Mean Score at Age 18 for Males) and Beta Coefficients of the Regression Equation and Standard Deviations for Males and Females

	Neuroticism–Emotional Stability	Antagonism–Agreeableness	Irresponsibility–Conscientiousness	Introversion–Extraversion	Openness–Closedness To Experience	Borderline Personality
Full Mean Model						
Intercept	28.71	−42.36	−44.03	−43.35	37.06	4.0217.25
$\beta_{sex=female}$	3.05	−2.76	−.85	.19	.39	.171.32
β_{age}	−.05	−.04	−.03	.08	−.02	−.01−.12
$\beta_{Australia}$	.93	−1.34	−1.44	.39	1.86	.131.33
$\beta_{Belgium}$	2.65	.59	.036	.15	−.08	.282.24
SD males	7.59	5.18	5.89	6.04	6.06	1.068.63
SD females	8.03	4.89	5.63	6.13	5.82	1.079.03
Twin and Sibling Correlations						
MZ males	.48	.39	.49	.47	.53	.47
DZ males	.14	.14	.11	.29	.28	.26
MZ females	.43	.38	.43	.47	.55	.46
DZ females	.24	.18	.22	.16	.28	.22
DZ opposite sex	.18	.14	.16	.12	.25	.19
Brother–brother	.21	.13	.18	.06	.27	.19
Sister–sister	.21	.19	.18	.19	.28	.27
Brother–sister	.13	.11	.16	.16	.27	.14
All MZ	.45	.38	.45	.47	.54	.46
All DZ/sibling	.19	.15	.17	.16	.26	.21
Parameter Estimates Full Genetic Model						
A	.31 (.17–.45)	.2 (.22–.37)	.24 (.21–.39)	.17 (.02–.31)	.51 (.51–.55)	.36 (.21–.48)
D	.14 (.00–.29)	.16 (.01–.33)	.21 (.05–.37)	.31 (.15–.46)	.01 (.00–.18)	.10 (.00–.26)
E	.56 (.52–.59)	.62 (.58–.66)	.55 (.55–.59)	.53 (.49–.56)	.46 (.43–.49)	.54 (.50–.58)

For borderline personality, estimates of the mean model are given for the square root–transformed data and the untransformed data. The variables agreeableness, conscientiousness, and extraversion are recoded such that they reflect opposite traits which are positively associated with borderline personality features (hence the negative mean values).

A, proportion of variance explained by additive genetic factors; D, proportion of variance explained by dominant genetic factors; E, proportion of variance explained by unique environmental factors; MZ, monozygotic; DZ, dizygotic.

Table 3. Estimates of Phenotypic Correlations and Monozygotic (MZ) and Dizygotic/Sibling (DZ, Sib) Cross-Trait Correlations

	Phenotypic Correlation						MZ/DZ, Sib Cross-Twin Cross-Trait Correlation					
	N/E	A/A	I/C	I/E	O/C	B	N/E	A/A	I/C	I/E	O/C	B
Neuroticism/Emotional Stability	—						—					
Antagonism/Agreeableness	.32	—					.14/.08	—				
Irresponsibility/Conscientiousness	.40	.24	—				.23/.10	.12/.04	—			
Introversion/Extraversion	.50	.27	.35	—			.29/.11	.13/.05	.21/.08	—		
Openness/Closedness To Experience	.01	−.07	.04	−.10	—		.04/−.02	−.03/−.05	.06/.02	−.02/−.04	—	
Borderline Personality	.68	.41	.35	.31	.06	—	.36/.17	.22/.12	.21/.09	.19/.09	.04/−.01	—

Note: the variables agreeableness, conscientiousness, and extraversion are recoded such that they reflect opposite traits that are positively associated with borderline personality features.

$\beta_{country}$* Country + ε, where α and ε stand for intercept and residual, respectively. As in the saturated model, a dummy coding was used for the effects on the mean of country. After fitting the full regression model, the predictor explaining the least variance (as reflected in the squared product of the regression coefficient multiplied by the variance of the predictor, i.e., $\beta^{2*}Var_{pred}$) was dropped from the model. This procedure was repeated until all predictor variables were tested.

To determine to what extent borderline personality and the FFM traits share genetic liability, a multivariate triangular decomposition (Cholesky model) was fitted to the data in which a 5 × 5 phenotypic covariance matrix (openness was not included in this analysis; see results section) was decomposed into genetic and environmental covariance matrices (45). A Cholesky model is a factor model in which the first variable loads only on the first factor, the second variable loads on the first two factors, and so on, yielding a triangular factor loading matrix. In this way, the first variable (neuroticism) is assumed to be caused by a latent variable that also explains part of the variance of the four remaining variables in the model. The second variable (agreeableness) is assumed to be caused by a second latent variable that explains the variance of the three remaining variables, and so on. The last variable (borderline personality) is assumed to be caused by a fifth latent variable that can explain the remaining variance of borderline personality that was not yet explained by the previous variables.

Results

Descriptive statistics of the sample are provided in Table 1. The upper part of Table 2 describes the mean structure (full model) of the FFM personality traits and borderline personality. The description includes a mean value for each trait in 18-year-old men, and regression of these scores on sex (deviation for women), age (deviation per increasing age year), and country of origin. Extraversion, agreeableness, and conscientiousness are negatively associated with borderline personality. We therefore recoded the data of these variables by multiplying each score by minus one, such that the associations between BPD and all five personality traits were positive. Therefore, in the tables, we refer to introversion versus extraversion, antagonism versus agreeableness, and irresponsibility versus conscientiousness. Standard deviations were equal in male and female participants for extraversion ($\chi^2(1) = 1.08$, $p = .298$) but not for neuroticism, ($\chi^2(1) = 3.59$, $p < .001$), agreeableness ($\chi^2(1) = 15.76$, $p < .001$), conscientiousness ($\chi^2(1) = 8.60$, $p = .003$), and openness to experience ($\chi^2(1) = 7.23$, $p = .007$). The middle part of Table 2 shows the MZ and DZ twin and sibling correlations for males and females within each variable. Correlations were similar for DZ twins and siblings for all variables (all ps $> .01$). For all variables, the correlations were equal for DZ males and females and for MZ males and females (all ps $> .01$), suggesting that the heritability is the same for men and women. Additionally, the DZ and sibling same-sex correlations were equal to the DZ and sibling opposite-sex correlations (all ps $> .01$), indicating that the same genes influence the variables in men and women. All MZ twin correlations were more than twice as large as the correlations for DZ twins and siblings, indicating that the genetic effects that contribute to individual differences may be partly nonadditive; thus, in subsequent analyses, A, D, and E were modeled. On the basis of the results of the univariate model, variances for males and females were allowed to differ in all subsequent analyses for neuroticism, agreeableness and conscientiousness by including a fixed scalar in the variance covariance model. The variance components for males were constrained to be equal to a scalar multiple (k^2) of the female variance components. In this way, the standardized variance components were equal across sexes, but the unstandardized variance components were allowed to differ (45). Broad-sense heritability estimates ranged from 36% for agreeableness to 54% for extraversion. Table 2 lists estimates of A, D, and E of the full models.

Table 4. Regression Coefficients and the Proportions of Explained Variance in Borderline Personality

Predictor	β	$\beta^{2*}var._{pred}$
Neuroticism/Emotional Stability	.0832	.4518
Antagonism/Agreeableness	.0456	.0564
Irresponsibility/Conscientiousness	.0154	.0079
Introversion/Extraversion	−.0148	.0083
Openness/Closedness to Experience	.0099	.0035

Next, phenotypic correlations (cross-trait within-person) and cross-twin cross-trait correlations for MZ and DZ twin and sibling pairs were estimated, which are shown in Table 3. Phenotypic correlations between borderline personality features and the FFM personality traits ranged from .06 (openness to experience) to .68 (neuroticism). Consistent with the expectation that the same genetic factors contribute to personality and personality pathology, all cross-twin correlations between the FFM personality traits and borderline features were stronger in MZ than in DZ twins.

Because the FFM personality traits are correlated among each other and four out of five scales are correlated with the PAI-BOR, stepwise backward multivariate regression analysis was run with the PAI-BOR scores as dependent variables, to investigate whether variance in borderline personality can be explained by FFM personality traits above and beyond neuroticism. Even with a conservative p value of $p < .01$, all variables significantly predicted the PAI-BOR score. However, openness to experience explained less than 1% of the variance. In the regression model including all variables,

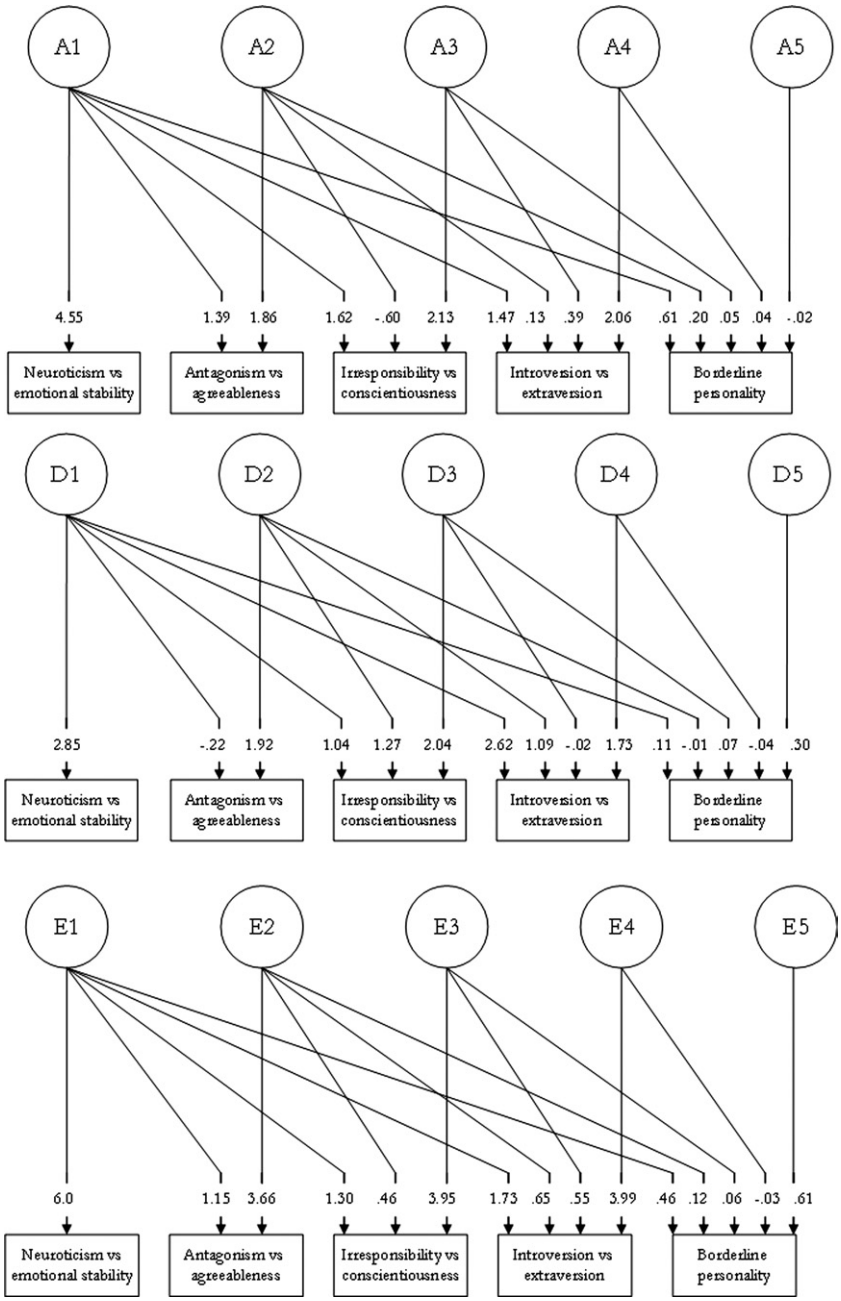

Figure 1. Unstandardized path coefficients of the Cholesky model for the Five-Factor Model personality traits and borderline personality. A1–A5 = additive genetic factors; D1–D5 = nonadditive genetic factors; E1–E5 = unique environmental factors. All latent A, D, and E factors have unit variance.

neuroticism best predicted the PAI-BOR score, explaining 45% of the variance in borderline personality. Conscientiousness and extraversion explained around 1% of the variance and agreeableness explained 6% of the variance. Regression coefficients and the proportions of explained variance in borderline personality are shown in Table 4.

To determine to what extent BPD and the FFM personality traits share genetic liability, a multivariate model was fitted to the data. Openness to experience was not included in these analyses because it does not correlate with borderline personality or the other FFM dimensions. A graphical representation of the model is depicted in Figure 1 (scalar not depicted). The path coefficients can be standardized and squared to calculate the proportion of variance accounted for by the latent predictor variables A, D, and E. For example, the total variance in neuroticism is 64.82 (4.55^2 + 2.85^2 + 6.0^2). The variance in neuroticism accounted for by the common genetic factor divided by the total variance gives the proportion of variance in neuroticism accounted for by the common genetic factor ($4.55^2/64.82 = .32$). Genetic and environmental correlations between the traits are shown in Table 5. Additive genetic correlations ranged from .18 to .95. The correlations between the environmental influences on the traits were moderate to high. Approximately 50% of the phenotypic correlation between borderline personality and the FFM traits can be explained by common genetic effects. The remaining variance can be explained by environmental effects common to borderline personality and the FFM traits. On the basis of the full model depicted in Figure 1, nearly all genetic variation is shared between the FFM traits and borderline personality and a substantial amount of environmental effects on borderline personality

Table 5. Genetic and Environmental Correlations (Left off Diagonal) Among the Neuroticism, Antagonism, Irresponsibility, Introversion, and Borderline Personality; Estimates of A, D, and E (Right Diagonal); and the Proportion of Phenotypic Correlation Accounted for by A, D, and E (Right off Diagonal)

	Additive Genetic Correlation					A and % of r_p Accounted for by A				
	N/E	A/A	I/C	I/E	B	N/E	A/A	I/C	I/E	B
Neuroticism/Emotional Stability	1					.32				
Antagonism/Agreeableness	.60	1				.50	.22			
Irresponsibility/Conscientiousness	.59	.18	1			.41	.17	.24		
Introversion/Extraversion	.57	.38	.45	1		.27	.28	.26	.18	
Borderline Personality	.95	.81	.56	.62	1	.47	.57	.47	.51	.37
	Dominant Genetic Correlation					D and % of r_p Accounted for by D				
Neuroticism/Emotional Stability	1					.13				
Antagonism/Agreeableness	−.12	1				−.05	.16			
Irresponsibility/Conscientiousness	.40	.44	1			.16	.34	.22		
Introversion/Extraversion	.79	.23	.47	1		.31	.18	.34	.30	
Borderline Personality	.34	−.07	.28	.18	1	.05	−.02	.11	.10	.10
	Unique Environmental Correlation					E and % of r_p Accounted for by E				
Neuroticism/Emotional Stability	1					.55				
Antagonism/Agreeableness	.30	1				.55	.62			
Irresponsibility/Conscientiousness	.31	.20	1			.43	.49	.55		
Introversion/Extraversion	.39	.26	.26	1		.42	.54	.40	.53	
Borderline Personality	.59	.32	.27	.22	1	.47	.45	.42	.39	.54

A, proportion of variance explained by additive genetic factors; D, proportion of variance explained by dominant genetic factors; E, proportion of variance explained by unique environmental factors; r_p, phenotypic correlation.

(33%) is specific to borderline personality. Testing the significance of the genetic factors (A + D) specific to borderline personality showed that these factors did not contribute significantly to variance ($\chi^2(2) = .12$, $p = .944$).

Discussion

All FFM personality traits significantly predict borderline personality scores. Neuroticism (45%) and agreeableness (6%) explained the largest part of the variance, conscientiousness and extraversion explained only 1%, and openness to experience less than 1% of the variance. These findings are in line with previous studies reporting the association between the FFM personality traits and BPD (12,13). One might argue that the high association between the PAI-BOR and the neuroticism scale is in part the result of semantic overlap in the items. However, removing systematically one of the 12 items of the neuroticism scale does not result in a large change in correlation with the PAI-BOR, thus the influence of semantic overlap on the association is unlikely to be large.

Also, in line with previous studies (14–18), genes contributed significantly to the variance in personality traits, with broad-sense heritability estimates ranging from 36% for agreeableness to 48% for extraversion. Broad-sense heritability for borderline personality was estimated at 45%. Multivariate genetic analyses showed that dominant genetic effects explain 10% (borderline personality) to 30% (extraversion) of the variance. The influence of nonadditive genetic effects is not an uncommon finding for personality traits. Eaves (19,46), Rettew *et al.* (21), and Keller *et al.* (22) found dominant genetic effects on extraversion and neuroticism in adults and adolescents.

Consistent with the idea that pathological personality traits are the extreme forms of normal personality traits, we found that 50% of the phenotypic association between borderline personality and the FFM traits can be explained by genetic effects. The genetic correlation was highest between neuroticism and borderline personality ($r_{ag} = .95$), but high genetic correlations of .81, .56, and .62 were also found between borderline and agreeableness, conscientiousness and extraversion, respectively.

The most important finding from our study is that all genetic variation for borderline personality disorder is shared with normal personality traits. In contrast, a significant proportion of the unique environmental effects (33%) on borderline personality is not shared with the FFM personality traits. We hypothesize that unique environmental factors specific to borderline personality may cause individuals with a specific pattern of personality traits to cross a threshold and develop borderline personality disorder. For example, it is often hypothesized that childhood neglect or traumatic life events are risk factors for the development of BPD (47). In the context of this study, these factors may serve as the environmental factor that leads to the development of BPD in individuals with a high (genetic) score on neuroticism and low scores on conscientiousness and agreeableness. Additionally, this structure of unique environmental factors might also explain why some individuals with borderline personality are not high on, for example, neuroticism. The effects of some unique environmental factors (e.g., a traumatic life event such as a sexual assault) might be so strong that even individuals with average neuroticism cross the threshold and develop BPD. Seventy-seven percent of the unique environmental effects on borderline personality is shared with neuroticism, extraversion, agreeableness, and conscientiousness. This finding is important because it indicates that unique environmental influences do not consist merely of measurement error. The trait-specific unique environmental influences on borderline personality do include measurement error, although the test–retest correlation of .78 suggests it is unlikely that all unique environmental influences reflect measurement error.

Our results show that all genetic variance in borderline personality is shared with FFM personality traits. This result is in line with, but more extreme than, findings for other psychiatric disorders (48–50). For example, Kendler *et al.* (49) reported that the association between neuroticism and major depression resulted largely from shared genetic risk factors, with a genetic correlation of .47, which is substantially lower than the genetic correlation between neuroticism and borderline personality found in our study ($r_{ag} = .95$).

Studies into the genetic architecture of normal personality traits may thus contribute to knowledge about the biological pathways leading to BPD. For many quantitative traits, disorders, and diseases, common genetic variants in the population are identified using Genome Wide Association (GWA) analyses (51–54). To date, two GWA studies for personality traits have been conducted, one on the Eysenck Neuroticism Scale (55) and the other on all five FFM personality traits (56). For neuroticism and agreeableness, the two personality traits that showed the highest genetic correlation with borderline personality, association with single nucleotide polymorphisms in candidate genes have been suggested. For neuroticism, some evidence exists for an association with the rs362584 polymorphism in the *SNAP25* gene (56), which is important in the regulation of neurotransmitter release, axonal growth, and synaptic plasticity (57). Abnormalities in the level of *SNAP25* gene have been linked to mood disorders and bipolar I disorder (58,59). Agreeableness may be associated with the *CLOCK* gene (56), which encodes proteins regulating circadian rhythm affecting both the persistence and length of the circadian cycle (60). The *CLOCK* gene has been associated with sleep and mood disorders among other disorders (61–63). Potential quantitative trait loci (QTL) for neuroticism also have been reported from genomewide linkage scans, although linkage signals often did not reach genomewide significance (64–69). Using a sample of twins extremely discordant and concordant for neuroticism Fullerton *et al.* (69) identified five loci (at 1q, 4q, 7p, 12q, and 13q) that exceeded the genomewide significance threshold. Of these loci, the region 12q has been reported in multiple studies. Wray *et al.* (67) found three chromosomal regions which exceeded empirically derived thresholds for suggestive linkage (10p five Kosambi centiMorgan, 14q 103 centiMorgan and 18q 117 centiMorgan), but only the 14q locus retained significance after correction for multiple testing. Linkage intervals for these regions all overlapped with regions identified in other studies of neuroticism or related traits and/or in studies of anxiety in mice. The genes reported in genomewide linkage and association studies on normal personality traits, especially those on neuroticism, are thus likely also involved in the biological pathways leading to borderline personality.

There are several implications for future research and clinical practice. First, the results support the usefulness of measures of normal personality in clinical practice, as recently proposed by many researchers (5,70), because a specific pattern of scores on the FFM dimensions represents a genetic vulnerability to develop BPD. Second, large sample sizes are needed to detect the effects of single genes influencing BPD because each effect is likely to be small, as is true for most complex disorders (71). Because borderline personality shares all genetic variance with normal personality traits, data from individuals with a specific pattern of normal personality traits may also be informative in the search for genes influencing BPD. In this way, large data sets of individuals at risk to develop BPD may be combined to increase the likelihood to detect genes involved in the development of BPD. In addition, future research should focus on identifying environmental factors that may cause individuals with many neuroticism characteristics and little characteristics associated with agreeableness to develop BPD. These studies will enable us to move toward a comprehensive model of the development of BPD in which biological and environmental influences on BPD are integrated.

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