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Further Evidence Against the Environmental Transmission of Individual Differences in Neuroticism from a Collaborative Study of 45,850 Twins and Relatives on Two Continents

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We examine the hypothesis that environmental transmission is a significant factor in individual differences for Neuroticism among 45,850 members of extended twin kinships from Australia (N = 20,945) and the United States (N = 24,905). To this large data set we fitted a model estimating genetic and environmental components of variance and gene–environmental covariance to examine the causes of individual differences in Neuroticism. For the combined sample we reject models including environmental transmission, shared environment, and a special twin environment in favor of more parsimonious genetic models. The best-fitting model involved only modest assortative mating, nonshared environment, and both additive and nonadditive genetic components. We conclude, first, that there is no evidence for environmental transmission as a contribution to individual differences in Neuroticism in these replicated samples, drawn from different continents, and, second, that a simple genetic structure underlies familial resemblance for the personality trait of Neuroticism. It is interesting that, despite the opportunity provided by the elaborate design and extensive power of our study, the picture revealed for the causes of individual differences in Neuroticism is little more complex than that found from earlier, simpler designs applied to smaller samples. However, this simplicity could not have been confirmed without using a highly informative design and a very large sample.

KEY WORDS: Neuroticism; personality; twins; environment; genes; assortative mating.

INTRODUCTION

Studies of identical and fraternal twin pairs reared together (e.g., Floderus-Myrhed *et al.*, 1980; Rose *et al.*, 1988; Eaves *et al.*, 1989a) and reared apart (e.g., Shields, 1962; Pedersen *et al.*, 1988; Tellegen *et al.*, 1988; Bouchard *et al.*, 1990), as well as studies of adoptees and their relatives (e.g., Loehlin *et al.*, 1981, 1985; Scarr *et al.*, 1981), have all produced findings consistent with an important genetic contribution to personality differences in adults. These findings, based on self-report questionnaire responses, are also supported by at least one twin study that use informant ratings of personality (Heath *et al.*, 1992).

Despite this consistency, however, important questions about the generalizability of findings from twin and adoption studies of personality differences remain (Loehlin, 1992). Analyzed separately, results from adoption studies generally have yielded lower estimates

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of the heritability of personality differences—the proportion of the total variance explained by additive and nonadditive genetic effects—than have twin studies. This may be a result of substantial nonadditive genetic effects—such as interactions between alleles at the same locus (dominance) or alleles at different loci (epistasis)—on personality differences (e.g., Eaves *et al.,* 1989a), which would contribute disproportionately to the resemblance of MZ twin pairs but might also be the result of greater sharing of environmental influences in twin pairs than in ordinary siblings (Loehlin, 1992). The reliance upon unusual relative types such as adoptees and twins also raises more general questions about the generalizability of findings from studies on the genetics of personality.

A weakness of twin and adoption studies is their poor ability to test for environmental transmission of behavior. In the traditional adoption or separated twin design, because adopted parents are screened and typically are older, a much narrower range of adversity is likely to be experienced by their offspring. In data on twin pairs reared together, insofar as shared environmental effects interact with genetic differences, these G × E effects are confounded with genetic estimates (Eaves *et al.,* 1977). These shortcomings can be overcome by extension of the traditional classical twin design to include assessment of the relatives of twin pairs—their parents, siblings, spouses, and children.

The extension of the twin design permits many of the assumptions implied in the traditional adoption and twin studies to be tested. The extended twin-family design includes a total of 80 unique relationships for which different correlations are predicted under different assumptions about gene action, parent–offspring and sibling environmental influences, assortative mating, and other factors (Truett *et al.,* 1994). While others have reported analyses of extended twin-family data (e.g., Finkel and McGue, 1997), surprisingly no attempt has been reported to use the full power of these designs to test environmental models for the transmission of personality differences. Here we present results of two parallel studies, conducted in Australia and the United States, each involving the assessment of more than 20,000 adult participants, which have examined the familial transmission of Neuroticism using an extended twin-family design.

Eysenck's original conception of Neuroticism was as a continuum from the "normal" to the "neurotic," where neurotic represented the clinical extreme. Our interest in Neuroticism derives in large part from its close relationship in the extremes to important psychiatric conditions of generalized anxiety disorder and major depression and, in particular, its close genetic relationship to these conditions (Jardine *et al.,* 1984; Kendler *et al.,* 1993a, b; Andrews, 1996). While psychiatric diagnoses are relatively expensive and time-consuming and contain little information for unaffected individuals, Neuroticism is easily measured on large population samples, and considerable power is gained from the continuous nature of the measure and the consequent ability to select extreme discordant sib pairs for linkage analysis (Eaves and Meyer, 1994; Risch and Zhang, 1995). Furthermore, Neuroticism is longitudinally stable and its heritability may be increased by judicious choice of multiple measurements (Boomsma, 1996). Neuroticism represents, therefore, an attractive target for association and linkage analysis to identify major genes underlying anxiety and depression.

METHOD

Participants

The data used in this study come from two samples: the Australian sample comprises 21,222 respondents who completed a self-report mailed questionnaire and the United States sample comprises 24,905 respondents. Both samples are based on twins and include their spouses and their first-degree relatives (i.e., parents, siblings, and offspring). Within the family structure in this study there are 80 relationships, if the relationships across three generations are discounted (in practice there are few of these) and relationships such as between twins and their parents and between twins and their offspring are both treated as a parent–offspring relationship.

The Australian sample was ascertained through two cohorts of twins. The first cohort was recruited in 1980–1982 from a sampling frame which comprised 5967 twin pairs aged 18 years or older (born 1893 to 1964) then enrolled on the Australian NHMRC Twin Registry (ATR). Responses were obtained from 3808 complete pairs [64% (Jardine *et al.,* 1984)] and these were followed up with a second mailed questionnaire in 1988–1990 with responses from 2708 complete pairs (Heath *et al.,* 1994) and 337 incomplete pairs (81% of those still contactable). In this follow-up questionnaire, twins were asked to provide the names of parents, siblings, spouses, and children who would be prepared to answer similar mailed questionnaires. The second cohort of twins, born 1964–1971, was recruited from the ATR in 1989 and was mailed similar questionnaires in

1989–1991, with responses from 3769 individuals of 4269 eligible pairs. This cohort was also asked to provide names of relatives who were prepared to fill in questionnaires. In total, names of 14,421 relatives were provided for Cohort 1, and 4999 names for Cohort 2. A suitably modified version of the questionnaire was prepared for parents, and another version for siblings, spouses, and children of twins. These were mailed out during the period 1989–1991, and 8601 (60%) and 2799 (56%) of relatives from Cohorts 1 and 2, respectively, returned questionnaires (response rates varied with type of relative, from 65% for mothers to 56% for siblings). There was vigorous follow-up of nonresponding twins (up to five phone calls) but somewhat less assiduous follow-up of relatives (up to two phone calls). In total there were 21,222 respondents in the Australian sample, of whom 20,945 had valid scores for EPQ Neuroticism.

The United States twins were ascertained from a population-based birth registry for the Commonwealth of Virginia and from a volunteer sample through the American Association of Retired Persons (AARP), described in detail by Truett *et al.* (1994). Their first-degree relatives and spouses were recruited in a similar fashion to the Australian sample, and in total there were 24,905 respondents (of 29,080) with valid scores for Neuroticism and for whom the zygosity of the proband twins could be determined. The response rates were 70% for twins and 45% for relatives.

The breakdown by type of relative for the two samples is shown in Table I. There are some differences in the breakdown between the two samples. The United States sample has proportionally fewer siblings and parents and more spouses and offspring than the Australian sample, probably reflecting the older age of the subsample from the AARP.

Table I. Breakdown of the Australian and United States Samples by Type of Relative

	Australia	United States
Female member of MZ twin pair	3,043	3,943
Male member of MZ twin pair	1,496	1,625
Female member of DZ twin pair	1,966	2,518
Male member of DZ twin pair	1,019	1,218
Member of DZ opposite-sex pair	2,280	2,792
Female sibling	2,066	1,647
Male sibling	1,566	1,073
Mother	2,021	1,240
Father	1,457	803
Wife	851	1,567
Husband	1,568	2,261
Female child	940	2,543
Male child	673	1,675
Total	20,945	24,905

Measures

Participants in both studies completed a mail-back questionnaire covering a range of health and lifestyle issues and including the short form of the revised Eysenck Personality Questionnaire [EPQ-R(S) (Eysenck *et al.*, 1985)]. The Neuroticism construct in the Eysenck personality system is in the same domain as Neuroticism in the five-factor models (Eysenck and Eysenck, 1985; Digman, 1994; Watson *et al.*, 1994) and the second-order factor of Negative Emotionality from the Multidimensional Personality Questionnaire (McCrae and John, 1992; Harkness *et al.*, 1995). The Neuroticism scale in the EPQ-R(S) has 12 yes/no items and the scale score is the number of "yes" responses. This scale is a subset of Eysenck's full 23-item Neuroticism scale. In a previous study (Martin and Jardine, 1986) we used the full scale, and the correlation between the short and the full scale is $r(7616) = 0.94$. Participants also gave their date of birth, from which their age could be calculated.

An angular transformation[6] of the raw Neuroticism scores was conducted to remove the marked effects of heteroscedasticity associated with scales comprising dichotomous items (Snedecor and Cochran, 1989). This leads to more robust estimates by minimizing departures from multivariate normality (to which the maximum-likelihood techniques we use are sensitive). Sex differences in means lower DZ twin and sibling correlations relative to MZ twin correlations (decreasing evidence for shared environment and increasing evidence for genetic nonadditivity), while uncorrected age regression effects increase differences between twin pairs (which would be interpreted in the model as a shared environmental effect) and decrease sibling correlations relative

[6] The Neuroticism score has a binomial distribution, since it comprises the sum of dichotomous items, and hence has a mean–variance relationship which is unsatisfactory for methods such as ML estimation that assume multivariate normality. The angular or arcsine transform is a variance stabilizing transformation that makes the binomial distribution more closely approximate a normal distribution and is $p_i' = \sin^{-1}\sqrt{p_i}$, where p_i is the proportion of successes or, in this case, the proportion of "yes" items. Snedecor and Cochran (1989) suggest a correction, due to Bartlett, for the tails of the distribution such that $p_i' = 1/4n$ when $p_i = 0$ and $p_i' = \left(n - \frac{1}{4}\right)/n$ when $p_i = 1$, where n is the number of items (12) in the scale.

to DZ twin pair correlations (potentially creating a false impression of a special twin environment). To avoid these erroneous effects on parameter estimates, transformed scores were corrected for regression on age, sex, age^2, age × sex, and age^2 × sex interactions.

Correlations Between Relatives

Although the models are fitted to the raw data, we find it useful also to examine the Pearson–product moment correlations for each data set for every pairing. Some of these correlations are replicates, for example, the parent–offspring correlation occurs between the twins and their parents and also between the twins and their offspring. The replicates of correlations were then pooled within data sets using Fisher's (1921) *z* transformation to give 80 unique correlations. Table II shows the 80 two-generation pairings of relatives grouped by type of relationship with the correlations and numbers in each pairing for both samples. The correlations are remarkably congruent, even to casual inspection. Comparing all 80 pairs of correlations simultaneously (using a chi-square test) showed there was no significant difference between the Australian and the U.S. sets of correlations [$\chi^2(79) = 63.22$, $p = 0.90$]. At an individual pair level, only 2 of the 80 pairs of correlations had a significant heterogeneity chi-square value ($\alpha = 0.05$), and this is fewer than expected at the 5% significance level.

Statistical Methods

The path model we use to describe family resemblance in twin pedigrees is shown in Fig. 1 and described in detail elsewhere (Truett *et al.*, 1994; Maes *et al.*, 1997). The phenotypes, P, have subscripts M and F for male and female, respectively, as have the path coefficients. The latent variables represent genetic and environmental components of variance.

The latent variables, *A* and *A′*, are additive genetic effects, where *A* is a sex-common factor and *A′* is a male-specific factor (we also could have modeled this as a female-specific factor). The correlation between sex-common and male-specific genetic factors is $r_{AA'|M}$ and $r_{AA'|F}$. The latent variable, *D,* represents nonadditive genetic effects. The correlation between the additive genetic factors for the parents and offspring is 0.5, reflecting the principles of Mendelian inheritance. The nonadditive genetic factors are uncorrelated between parents and offspring and have a correlation of r_{DD} between siblings. r_{DD} is fixed at 0.25 for same-sex siblings but is allowed to vary between −0.25 and +0.25 for opposite-sex siblings.

There are three environmental components of variance: a shared sibling environment, *C;* a shared twin environment, *T;* and a residual shared family environment, *E.* Parent-to-offspring vertical cultural transmission is shown by the paths b_{FF}, b_{FM}, b_{MF}, and b_{MM}. The correlation, r_{CC}, between sibling shared environment is 1 for same-sex siblings and can vary between −1 and +1 for opposite-sex siblings. Similarly, the correlation, r_{TT}, between shared twin environment is 1 for same-sex twins and can vary for opposite-sex twins.

Other components in the model are the phenotypic correlation between parents modeled as primary phenotypic assortment (*i*) and the correlation between genotype and environment ($r_{AE|M}$, $r_{A'E|M}$, $r_{AE|F}$, and $r_{A'E|F}$). Other models of phenotypic assortment and cultural transmission have also been developed and may yield outcomes slightly different from those obtained under this specification.

Model Fitting

The above model is fitted by maximum-likelihood estimation to the raw data using the statistical package Mx (Neale, 1997). The full model is fitted first, followed by a set of submodels in which sets of parameters are deleted or equated across sexes. The log-likelihood difference test is used to assess the change in fit between models—and so the fit statistic reported is −2 times the log-likelihood (−2*LL)—and Akaike's (1987) information criterion (AIC) is used to select the final model. We also compute likelihood-based confidence intervals (Neale and Miller, 1997) for the selected model.

RESULTS

The results of model fitting are shown in Table III, and the fitting proceeded in two stages. In the first stage we examined the heterogeneity of the two data sets by fitting models to each data set and to a combined data set. The test for heterogeneity is the difference between the log-likelihood for the combined data set and the sum of the log-likelihoods for the separate data sets. This difference is not significant [$\Delta\chi^2(19) = 26.625$, $p = 0.114$], and since there is no evidence of heterogeneity between the two data sets, subsequent models are fitted simultaneously to both data sets. A purely environmental model for family resemblance (Model 4) includes only parameters for phenotypic assortment (*i*), nonparental shared sibling and twin environmental factors (c_F, c_M, r_{CC}, t_F, t_M, r_{TT}), environmental transmis-

Table II. Correlations and Number of Relative Pairs for the 80 Pairings in the Australian and United States Data Sets by Category of Relationship; Also Shown is the $\chi^2(1)$ Contribution of Each Pairing to the Total Heterogeneity Chi-Square Value for the 80 Correlations on the Two Continents

			Australia		United States		
Number	Category[a]	Relationship	*r*	*N*	*r*	*N*	χ^2
1	N	Spouses	0.074	3618	0.092	4815	0.64
2	N	Mother–daughter	0.152	4460	0.157	4542	0.07
3	N	Mother–son	0.114	3076	0.148	3034	1.87
4	N	Father–son	0.151	2322	0.134	2218	0.34
5	N	Father–daughter	0.143	3121	0.127	3033	0.39
6	N	Sibling, female	0.143	3438	0.172	3551	1.57
7	N	Sibling, male	0.127	1637	0.109	1514	0.26
8	N	Sibling, opposite sex	0.113	4693	0.137	4304	1.38
9	N	DZ female twin	0.171	857	0.224	1141	1.47
10	N	DZ male twin	0.125	400	0.178	556	0.68
11	N	DZ opposite-sex twin	0.126	919	0.097	1295	0.46
12	N	MZ female twin	0.424	1405	0.410	1799	0.21
13	N	MZ male twin	0.359	658	0.353	766	0.02
14	S	MZ female twin with cotwin's husband	0.013	812	0.066	1132	1.32
15	S	DZ female twin with cotwin's husband	–0.016	413	–0.002	594	0.05
16	S	DZ female twin with male cotwin's wife	0.042	200	–0.017	450	0.47
17	S	Female sibling with female twin's husband	0.023	969	0.056	732	0.46
18	S	Female sibling with male twin's wife	0.056	460	0.047	463	0.02
19	S	MZ male twin with cotwin's wife	0.029	359	0.064	602	0.27
20	S	DZ male twin with cotwin's wife	0.169	200	–0.039	405	5.81
21	S	DZ male twin with female cotwin's husband	0.027	224	–0.062	361	1.07
22	S	Male sibling with male twin's wife	0.002	394	0.070	350	0.87
23	S	Male sibling with female twin's husband	–0.039	723	0.092	431	4.59
24	S	Spouses of MZ female twins	0.017	189	0.018	296	0.00
25	S	Spouses of DZ female twins	0.057	69	0.098	124	0.08
26	S	Spouses of MZ male twins	0.039	84	–0.045	180	0.40
27	S	Spouses of DZ male twins	0.175	36	0.005	101	0.73
28	S	Spouses of DZ opposite-sex twins	–0.235	71	–0.022	169	2.29
29	S	Mother with son's wife	0.034	423	0.053	302	0.06
30	S	Mother with daughter's husband	0.014	769	–0.047	348	0.89
31	S	Father with son's wife	0.086	331	0.085	215	0.00
32	S	Father with daughter's husband	–0.009	550	0.002	210	0.02
33	CA	Aunt (MZ female cotwin)–niece	0.123	345	0.118	1006	0.01
34	CA	Aunt (MZ female cotwin)–nephew	0.176	300	0.190	645	0.04
35	CA	Aunt (DZ female cotwin)–niece	0.133	198	0.183	511	0.37
36	CA	Aunt (DZ female, cotwin)–nephew	0.135	108	0.107	331	0.06
37	CA	Uncle (MZ male cotwin)–niece	0.085	113	0.034	327	0.22
38	CA	Uncle (MZ male cotwin)–nephew	–0.041	93	–0.016	216	0.04
39	CA	Uncle (DZ male cotwin)–niece	0.209	43	0.094	140	0.43
40	CA	Uncle (DZ male cotwin)–nephew	0.350	23	0.118	104	1.02
41	CA	Uncle (male cotwin of female parent)–niece	0.190	94	0.042	199	1.40

(continued)

Table II. (Continued)

Number	Category[a]	Relationship	Australia		United States		
			r	*N*	*r*	*N*	χ^2
42	CA	Uncle (male cotwin of female parent)–nephew	–0.007	48	0.141	152	0.77
43	CA	Aunt (female cotwin of male parent)–niece	0.056	51	0.089	180	0.04
44	CA	Aunt (female cotwin of male parent)–nephew	–0.031	32	–0.012	114	0.01
45	CA	Aunt (female sibling of female parent)–niece	–0.023	296	0.032	537	0.57
46	CA	Aunt (female sibling of female parent)–nephew	0.146	237	0.145	388	0.00
47	CA	Uncle (male sibling of male parent)–niece	0.191	77	–0.028	156	2.44
48	CA	Uncle (male sibling of male parent)–nephew	0.205	60	0.062	94	0.75
49	CA	Uncle (male sibling of female parent)–niece	0.036	243	–0.005	291	0.22
50	CA	Uncle (male sibling of female parent)–nephew	0.066	204	0.098	234	0.16
51	CA	Aunt (female sibling of male parent)–niece	0.040	118	0.188	192	1.62
52	CA	Aunt (female sibling of male parent)–nephew	0.236	72	0.081	130	1.13
53	AA	Uncle (husband of MZ female cotwin)–niece	–0.078	151	0.009	501	0.87
54	AA	Uncle (husband of MZ female cotwin)–nephew	0.157	141	0.051	340	1.14
55	AA	Uncle (husband of DZ female cotwin)–niece	0.025	57	0.213	172	1.49
56	AA	Uncle (husband of DZ female cotwin)–nephew	0.000	32	0.084	124	0.17
57	AA	Aunt (wife of MZ male cotwin)–niece	0.078	64	0.105	212	0.04
58	AA	Aunt (wife of MZ male cotwin)–nephew	0.057	52	–0.146	129	1.47
59	AA	Aunt (wife of DZ male cotwin)–niece	0.376	10	–0.075	77	1.42
60	AA	Aunt (wife of DZ male cotwin)–nephew	0.000	5	–0.076	55	0.01
61	AA	Aunt (wife of DZ male opposite-sex twin) niece	0.045	23	0.033	67	0.09
62	AA	Aunt (wife of DZ male opposite-sex twin)–nephew	0.248	7	–0.147	35	0.04
63	AA	Uncle (husband of DZ female opposite-sex twin)–niece	0.141	36	0.128	95	1.78
64	AA	Uncle (husband of DZ female opposite-sex twin)–nephew	0.196	20	0.304	69	3.55
65	C	Female cousins (through MZ female parents)	0.041	35	0.096	341	0.09
66	C	Male–female cousins (through MZ female parents)	–0.039	81	0.044	453	0.46
67	C	Male cousins (through MZ female parents)	0.187	33	0.097	153	0.21
68	C	Female cousins (through DZ female parents)	–0.235	6	0.243	139	0.70
69	C	Male–female cousins (through DZ female parents)	0.000	4	0.189	158	0.04
70	C	Male cousins (through DZ female parents)	—[b]	3	0.068	52	0.00
71	C	Female cousins (through MZ male parents)	0.172	93	0.102	93	0.23
72	C	Male–female cousins (through MZ male parents)	0.082	177	0.114	103	0.07
73	C	Male cousins (through MZ male parents)	0.256	82	0.027	41	2.14
74	C	Female cousins (through DZ male parents)	0.197	39	0.046	40	1.10
75	C	Male–female cousins (through DZ male parents)	0.217	52	0.042	49	0.76
76	C	Male cousins (through DZ male parents)	–0.237	11	–0.197	17	0.01
77	C	Female cousins (through DZ opposite-sex parents)	–0.006	42	0.238	72	1.53
78	C	Male–female cousins (through DZ male–female parents)	–0.037	22	0.330	50	1.96
79	C	Female–male cousins (through DZ male–female parents)	–0.174	26	0.154	70	1.87
80	C	Male cousins through (DZ opposite-sex parents)	0.301	10	0.250	38	0.02

[a] N, nuclear family; S, spousal relationship; CA, consanguineous avuncular; AA, affine avuncular; C, cousins.
[b] Correlation not calculated due to low *n*.

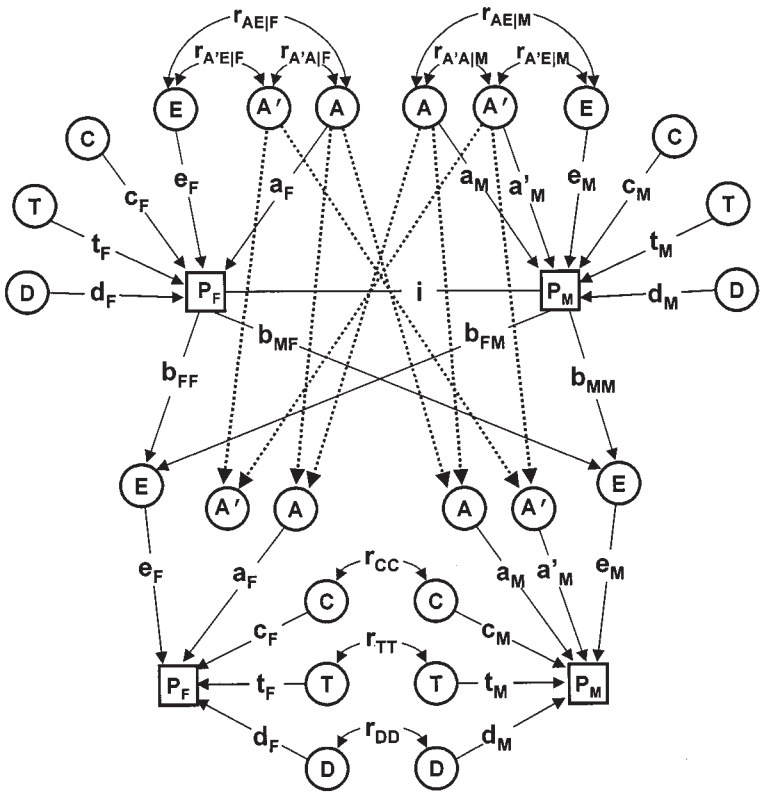

Fig. 1. Path diagram of the relationships between parents and offspring. See text for explanation of symbols and diagram. The coefficients of the dotted paths are fixed at 0.5 *ex hypothesi* and the variances of all latent variables are fixed at unity.

sion from parent to offspring (b_{MM}, b_{FM}, b_{MF}, b_{FF}), and person-specific environmental factors (e_F, e_M). This model is significantly worse in fit than the full model [$\Delta\chi^2(6) = 168.98$, $p < 0.001$].

A model in which only genetic factors account for family resemblance (Model 5) includes parameters for phenotypic assortment (i), sex-common and male-specific additive genetic factors (a_F, a_M, a'_M), nonadditive genetic factors (d_F, d_M, r_{DD}), and a person-specific residual term (e_F, e_M). This model is not significantly worse in fit than the full model [$\Delta\chi^2(10) = 5.43$, $p = 0.86$].

We now test submodels of the genetic model. The person-specific environmental factor is retained since it contains the residuals for the model. We can drop the male-specific additive genetic factor (a'_M; Model 6) and the nonadditive genetic correlation between opposite-sex siblings (r_{DD}; Model 10) without significantly affecting the fit of the model. We cannot drop the nonadditive genetic factors (d_F, d_M; Model 7) or the phenotypic assortment parameter (i; Model 8). We also cannot equate the male and female genetic parameters (Model 9). Further submodels (Models 11 to 14) involve combinations of these submodels, and of these, only Model 11 and Model 12 are not significantly different in fit from the full model. We prefer Model 12 since it has the lower AIC (−1.43 vs. 0.566).

The final model (Model 12) is not significantly different in fit from the full model [Model 3, $\Delta\chi^2(12) = 8.00$, $p = 0.79$] and includes only sex-common additive and nonadditive genetic factors, a nonshared environment factor, and the assortative mating parameter. The path diagram showing path coefficients for this model is shown in Fig. 2 and the estimates for the genetic and environmental variance components and spousal correlation with confidence intervals are shown in Table IV.

DISCUSSION

To our knowledge, the combined Australian and U.S. samples comprising 45,850 adult individuals from 80 distinct biological and social relationships constitutes the largest and most informative study of

Table III. Summary Statistics of the Fit of the Genetic–Environmental Models to the Combined Australian and U.S. Data[a]

Model No.	Model	Model fit, −2*LL	Model comparison			
			Comparison	Change χ^2	df	*p*
	Full model					
1	Australian data	8,583.840	—			
2	U.S. data	10,899.278	—			
3	Combined data	19,509.743	3–(1+2)	26.625	19	0.114
	Submodels (based on combined data)					
4	Environmental	19,678.726	4–3	168.983	6	<0.001
5	Genetic	19,515.174	5–3	5.431	10	0.861
6	Genetic: drop male-specific additive genetic factor (a'_M)	19,515.911	6–5	0.737	1	0.391
7	Genetic: drop nonadditive genetic factors (d_M, d_F, r_{DD})	19,555.581	7–5	40.407	3	<0.001
8	Genetic: drop assortment parameter (i)	19,565.147	8–5	49.973	1	<0.001
9	Genetic: equate male and female genetic parameters ($a_F = a_M$, $d_F = d_M$)	19,521.740	9–5	6.566	2	0.038
10	Genetic: fix nonadditive genetic correlation between opposite-sex siblings ($r_{DD} = 0.25$)	19,517.451	10–5	2.367	1	0.124
11	Genetic: drop male-specific additive genetic factor (a'_M and equate male and female genetic parameters ($a_F = a_M$, $d_F = d_M$)	19,521.740	11–5	6.566	3	0.087
12	**Genetic: drop male-specific additive genetic factor (a'_M) and fix nonadditive genetic correlation between opposite-sex siblings ($r_{DD} = 0.25$)**	**19,517.741**	**12–5**	**2.567**	**2**	**0.277**
13	Genetic equate male and female genetic parameters ($a_F = a_M$, $d_F = d_M$) and fix nonadditive genetic correlation between opposite-sex siblings ($r_{DD} = 0.25$)	19,544.540	13–5	29.366	3	<0.001
14	Genetic: drop male-specific additive factor (a'_M); fix nonadditive genetic correlation between opposite-sex siblings ($r_{DD} = 0$); equate male and female genetic parameters ($a_F = a_M$, $d_F = d_M$)	19,544.540	14–5	29.366	5	<0.001

[a] The preferred model is boldfaced.

the inheritance of personality to date. Our results add considerable weight to previous findings that environmental transmission and shared environmental effects contribute little to family resemblance in Neuroticism. The overall contribution of genetic factors to individual differences is somewhat greater for females (broad heritability, 41%) than males (35%), consistent with previous large twin and family studies (Floderus-Myrhed *et al.,* 1980; Eaves *et al.,* 1989a; Loehlin, 1992; Viken *et al.,* 1994; Finkel and McGue, 1997). However, in contrast with these previous studies, we have explicitly modeled the effects of assortative mating and environmental transmission.

Critics may argue that we have found nothing new in this study. We would argue that previous studies have arrived at simple conclusions because their designs would not permit the detection of anything more complex. Our study, in contrast, has both the design and the power to detect more complex patterns of causation if they exist (Eaves *et al.,* 1977, 1989b; Martin *et al.,* 1978; Heath and Eaves, 1985; Heath *et al.,* 1985). The fact that we have not detected any great complexity gives us confidence that the causes of variation in Neuroticism really are simple, and not just a consequence of the shortcomings of our design.

The evidence for nonadditive genetic effects, inconsistent in previous studies, is quite unambiguous in the present data, implying that there are interactions between alleles at the same locus or indeed at different loci which influence an individual's Neuroticism score. However, at least some of it may reflect the expression of different genes at different ages (Eaves *et al.,* 1978). While the correlation between spouses (0.09) is statistically significant and agrees closely with earlier estimates (Eaves *et al.,* 1989a), it is too small to have a substantial effect on the amount of genetic variation or on the correlation between relatives. The correlation between the squared spousal difference for Neuroticism and the duration of the marriage in years was extremely small [$r(3602) = 0.025$, $p = 0.14$] and

suggests that spousal interaction is not responsible for the small observed correlation between mates.

Our data confirm the widespread finding of previous studies that the shared family environment including the environmental effect of parents on their children plays no significant role in family resemblance for Neuroticism (Plomin and Daniels, 1987; Eaves *et al.*, 1989a; Loehlin, 1992). We also modeled environmental influences shared only by twins but found that these were not significant. The only significant environmental effects were the substantial effects of nonshared environment, although it must be recognized that our estimate includes error variance which for the angular transformation of a scale of *n* equivalent items is 1/4*n*, that is, 0.021 for *n* = 12. The total variance under the angular transformation is 0.0962 for males and 0.0906 for females. Thus about 22% (0.021 divided by the weighted sex-averaged variance) of the total phenotypic variance can be attributed to measurement error, reducing estimates of stable nonshared environment to 37% in females and 43% in males. A limitation of our study is that, whereas most previous studies have employed the full Neuroticism scale of 23 items, both our studies employed the short scale of 12 items, with a concomitant increase in the variance due to measurement error and reduction in the proportion of variance due to genetic factors; the heritabilities expressed as a proportion of the stable variance are 45% in males and 53% in females.

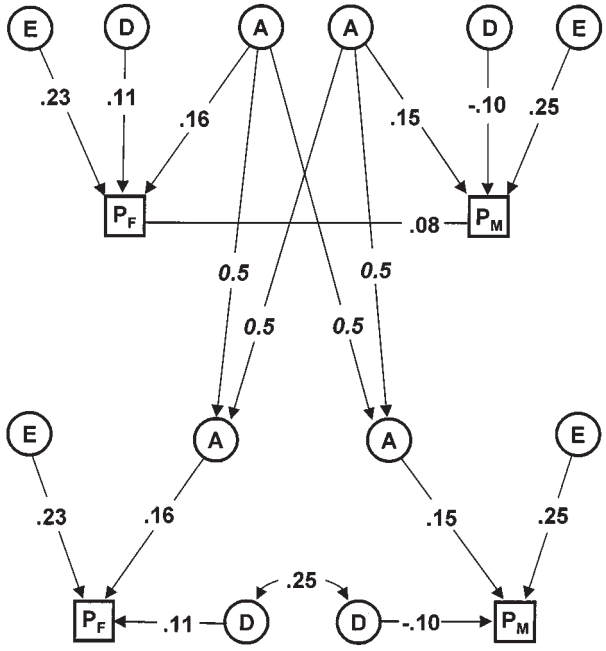

Fig. 2. Path diagram showing the estimated path coefficients for the most parsimonious model for the combined data sets (coefficients in italics are fixed *ex hypothesi*).

Another limitation of our study is the reliance on a volunteer sample and the attendant possibility of response bias. This possibility is hard to check, especially when our samples are larger than any "standardization" samples. Response bias is a concern principally if missingness is related to the response variable (Little and Rubin, 1987), and with relatives we are in the fortunate situation that we have information about nonresponding relatives through the relatives who did respond (Neale and Eaves, 1993). If there is a correlation between Neuroticism and cooperation, and Neuroticism is partly heritable, then we would expect scores for single twins where the cotwin has not responded to be biased in the direction of the nonresponsive phenotype. The bias will be more marked for single MZ than for single DZ twins; the same will apply to all the other relative pairs in our sample. The fortunate consequence of maximum-likelihood estimation with single relatives

Table IV. Variance Components for the Final Model by Sex for the Combined Australian and U.S. Data Sets

	Sex			
	Female		Male	
Variance components (%)	Raw[a]	Adjusted[b]	Raw[a]	Adjusted[b]
Additive genetic	28 (24–31)	36	25 (21–29)	32
Additive genetic via assortment[c]	*6 (4–8)*	*8*	*6 (4–8)*	*8*
Nonadditive genetic	13 (9–18)	17	10 (4–15)	13
Nonshared environment	58 (56–61)	46	65 (61–69)	55

[a] The 95% confidence intervals are shown in parentheses.
[b] The adjusted values reflect the estimated 22% measurement error (see text).
[c] The part of additive genetic variance due to phenotypic assortative mating.

jointly with complete pairs is to correct the bias in mean and variance of the former toward their true population values (Little and Rubin, 1987; Muthén *et al.*, 1987). A further empirical point is that none of the mean scores for the different relative types was significantly different from the mean for the total sample, after correction for age and sex. This argues strongly against bias arising from differential response rates in different relative types.

Our data show that a very simple genetic model is sufficient to account for the causes of variation and family resemblance in Neuroticism in two very large samples spanning an exceptionally wide range of biological and social relationships. There is no need to invoke any nongenetic causes of family resemblance. Furthermore, whereas most previous studies have depended entirely on twin data or small samples of other relatives, our studies contain more nontwin relatives than twins, and the results of model fitting are much the same if the twin relationships themselves are excluded.

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