

Religion and Education as Mediators of Attitudes: A Multivariate Analysis

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The transmission of social attitudes has been investigated as a possible model of cultural inheritance in a sample of 3810 twin pairs from the Australian National Health and Medical Research Twin Registry. Six social attitude factors were identified and univariate genetic models fitted to scores on each factor. A joint multivariate genetic analysis of the six attitude factors, church attendance, and education indicated that the attitudes were correlated—the same genes and shared environments influenced more than one attitude factor. A current controversy regarding social attitudes is whether the significant loadings on this shared environmental component represent true cultural influences or are actually the genetic consequences of phenotypic assortative mating for church attendance and educational attainment (Martin et al., 1986). In our data, church attendance is almost entirely due to the impact of the shared environment. The large shared environmental component on church attendance also accounts for a substantial part of the family resemblance in social attitudes, suggesting that not all of the apparent cultural effects found in earlier studies can be ascribed to the genetic effects of assortative mating. However, church attendance and education do not completely account for the cultural component. Therefore, effects in addition to church attendance, education, and assortative mating for church attendance and education must be involved in the cultural component of the inheritance of attitudes.

KEY WORDS: religion; education; attitudes; genes; family environment; assortative mating; multivariate genetic analysis; LISREL.

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INTRODUCTION

It is commonly supposed that social attitudes present a paradigm of cultural inheritance (Cavalli-Sforza *et al.*, 1981, 1982). Insofar as differences in social attitudes could be attributable to human interaction, adaptability, and capacity for learning, familial resemblance in social attitudes should be explained entirely by common family environment. However, twin studies of social attitudes have given as much support for genetic factors as they have for cultural factors as determinants of social attitudes (e.g., Martin *et al.*, 1986; Eaves *et al.*, 1989).

Unlike personality measures for which shared environment has not been found to be significant (Tellegen *et al.*, 1988; Pedersen *et al.*, 1988; Bouchard *et al.*, 1990; Eaves, *et al.*, 1989), studies of the inheritance of individual social attitudes items in twin population samples from London (Feingold, 1984) and Australia (Jardine, 1985) [see Eaves *et al.*, (1989) for a detailed review of both studies] have consistently supported the involvement of additive genetic effects and family environment. Approximately one-third of the phenotypic variance in attitudes was attributable to individual-specific environmental effects, one-third to additive genetic effects, and one-third to shared environmental effects. Significant sex differences were observed in the thresholds between response categories, but the genetic and environmental influences were remarkably consistent across the sexes.

A problem with studies of twins reared together is the fact that the genetic consequences of assortative mating are completely confounded with the shared environmental effects (Eaves *et al.*, 1989). A more recent analysis by Martin *et al.* (1986), which supplemented data on twins reared together with data on spouses, suggested that the inclusion of the genetic consequences of assortative mating into the model for twin resemblance could account for virtually all of the apparent shared environmental effects in twin studies. Consequently, the magnitude of the genetic contribution to family resemblance claimed for social attitudes by Martin *et al.* is much greater than in previous studies. However, their analyses assumed that spousal similarity arises because of direct phenotypic assortment for social attitudes. Alternative assumptions about the causes of spousal resemblance for attitudes (e.g., Heath and Eaves, 1985; Heath, 1987) would lead to different conclusions, as noted by Eaves *et al.* (1989).

Separate analysis of individual attitude items such as those reported by Cavalli-Sforza and in part by Martin *et al.* does not provide a fully satisfactory treatment of the data. Item responses are interdependent, so common genetic and environmental effects may act upon many items.

The assumption of a single common factor is probably an oversimplification of the data since factor analyses of social attitude data have found evidence for at least two phenotypic dimensions (e.g., Eysenck, 1975). Feingold (1984) analyzed five dimensions of social attitudes in the London twin sample (authoritarianism, religious conservatism, socialism, prejudice, and permissiveness). Another feature of previous studies is heterogeneity between the sexes. This was observed for religious conservatism and prejudice in the London data with a very low opposite-sex dizygotic twin correlation for religious conservatism, indicating that the factors responsible for variation in religious attitudes may be different in men and women.

By conducting a joint multivariate genetic analysis of multiple social attitude factors together with measures of educational attainment and church attendance, we attempted to discriminate further between the genetic effects of assortative mating in the model proposed by Martin *et al.* (1986) and the effects on familial correlations in attitudes caused by the impact of a correlated, culturally transmissible variable such as religiosity which may be the primary source of spousal similarity.

The specific hypotheses to be tested fall into two groups:

1. The first group concerns the general genetic and environmental components of individual differences.
 - a. The simple model, which assumes additive genetic effects, and within- and between-family environment, is sufficient to account for the variation in church attendance, educational attainment, and attitudes considered jointly without any explicit parsimonious model for the latent factor structure among the multiple variables.
 - b. The effects of genes and environment differ in magnitude across the sexes.
2. The second group concerns hypotheses which bear on the specific issue of the resolution of the effects of family environment from the genetic consequences of assortative mating.
 - a. The apparent cultural correlation among religion, education, and attitudes is actually the genetic consequence of assortative mating for religion and education. The variable loadings on shared environmental factors involving religion and education are constant multiples of their loadings on genetic factors resulting in identical structure for genetic and shared environmental effects of these factors.
 - b. At least some of the variation attributed by Martin *et al.* to genetic consequences of assortative mating may actually be

due to purely cultural impact of religion and/or education. Such a conclusion would be favored if there were no genetic variation in either religion or education, yet these two covariates showed significant between family covariation with the attitude dimensions.

METHODS

Samples and Items

The Australian National Health and Medical Research Twin Registry is comprised of a large, volunteer sample of adult twins. Between November 1980 and March 1982, questionnaires were mailed to all adult pairs then registered (5967 pairs aged 18–88 years). Demographic, health, and behavioral data were obtained from the 3810 twin pairs who returned the questionnaire. Details regarding the sample and phenotypic measurements are provided elsewhere (Jardine, 1985; Martin and Jardine, 1986). Zygosity was determined from questions concerning childhood similarity and recognition confusion; this method has been validated against blood-typing in a number of studies (Nichols and Bilbro, 1966; Martin and Martin, 1975; Kasriel and Eaves, 1976). Zygosity results were as follows: 1233 monozygotic female, 567 monozygotic male, 751 dizygotic female, 352 dizygotic male, and 907 unlike-sex pairs. Data from unlike-sex pairs were used in univariate, but not multivariate, analyses.

A 50-item version of the Wilson–Patterson conservatism scale (Wilson and Patterson, 1968; Feather, 1975) surveyed social attitudes by presentation of key-word items to which participants circled “Y” (agree), “?” (uncertain), or “N” (disagree). Educational attainment was self reported and scored on a 7-point scale: less than 7 years = 1; 8–10 years = 2; 11–12 years = 3; apprenticeship, etc. = 4; technical or teacher’s college = 5; university first degree = 6; university postgraduate training = 7. Self-reported church attendance was scored on a 5-point scale: more than once a week = 1; once a week = 2; every month or so = 3; once or twice a year = 4; rarely = 5.

Factor Analysis

For the total sample ($N = 7620$ individuals), polychoric and polyserial correlations between the 50-attitude item responses and age were estimated by maximum likelihood using LISREL7 (Jöreskog and Sörbom, 1985). The FACTOR procedure (SAS Institute, Inc., 1985) was then used to perform factor analysis using the partial correlation matrix,

controlling for age. Using the joint criteria of scree plot and interpretability, six factors were retained. The first six eigenvalues of the original phenotypic correlation matrix were 7.26, 3.19, 2.91, 1.58, 1.01, and 0.78. After rotation to oblique simple structure, the six dimensions of social attitudes were identified as religious conservatism, political conservatism, racial prejudice, general conservatism, sexual conservatism, and traditional values. Factor loadings for each item are presented in Table I. Interfactor correlations for the six factors were relatively low, ranging from 0.04 to 0.50, with only 4 of the 15 exceeding 0.20. The largest correlation was between sexual and religious conservatism (0.50) and the smallest (0.04) was between sexual conservatism and traditional values. There is no simple economical computational strategy for estimating scores of subjects on the several latent dimensions derived from the polychoric correlations. We, therefore, derived scores on the six dimensions by applying the scoring coefficients from the factor analysis of the polychoric correlations to the raw responses of subjects to the items. For each zygosity group, a 16×16 covariance matrix was computed including six factors, educational attainment, and church attendance for the first and second members of twin pairs. Twins were designated first and second on the basis of birth order, or randomly when birth order was uncertain. For ease of inspection, Table II presents the phenotypic correlation matrices for like-sex pairs by zygosity group, although covariance matrices were used for model fitting. Table III presents the variances associated with the diagonals of the correlation matrices. The cross-twin within-trait correlations have been highlighted, as have any cross-trait correlations that exceed 0.40. Univariate models were fitted to covariance matrices from all five zygosity groups. Multivariate genetic models were fitted to the four like-sex groups.

Univariate Analysis

Figure 1 illustrates the univariate genetic model (Heath *et al.*, 1989) which allows for additive genetic effects, shared environmental effects, and unique environmental effects. All parameters were constrained to be equal within twin pairs and between same-sex monozygotic and dizygotic twins. A sex limitation model was used to parameterize the DZ opposite sex twin covariances, in which the same genes and common environment effects were assumed to be expressed in both sexes but the magnitude of each effect was allowed to differ. LISREL7 (Jöreskog and Sörbom, 1985) was used to fit univariate models separately for each factor by the method of maximum likelihood. LISREL7 yields a chi-square goodness-of-fit statistic which was used to assess the overall goodness-of-fit of a

Table I. Factor Loadings ($\times 100$) Under a Six-Factor Oblique Solution^a

	Religion (RC)	Political conservatism (PC)	Racial prejudice (RP)	General conservatism (GC)	Sexual conservatism (SC)	Tradition values (TV)
49. Bible truth	74
35. Church authority	69
15. Divine law	63
5. Sabbath observance	61
27. Chastity	33
20. Suicide	-41
2. Evolution	-51
46. Divorce	-60
12. Birth control	-63	36
22. Legalized abortion	-77
19. Moral training	.	55
3. School uniforms	.	54
7. Patriotism	.	53
37. Censorship	.	49
13. Military Drill	.	49	35	.	.	.
29. Royalty	.	47
25. Licensing laws	.	46
30. Women judges	.	42	.	-31	.	.
47. Inborn conscience	.	36	-30	.	.	.
31. Conventional clothes	.	32
1. Death penalty	.	31
16. Socialism	.	-37	.	-36	.	.
17. White superiority	.	.	70	.	.	.
33. Apartheid	.	.	67	.	.	.
23. Empire building	.	.	43	.	.	.
11. Horoscopes	.	.	35	-30	.	.
36. Disarmament	.	.	-31	.	.	.
40. Mixed marriages	.	.	-42	.	.	.
48. Colored immigration	.	.	-50	.	.	.

8. Modern art	.	.	.	-60	.	.
45. Learning Latin	.	.	.	-50	.	.
42. Jazz	.	.	.	-45	.	.
6. Hippies	.	.	.	-38	-35	.
10. Working mothers	.	.	.	-32	.	.
26. Computer music	.	.	.	-32	.	.
4. Striptease shows	-72	.
34. Nudist camps	-67	.
50. Pajama parties	-54	.
44. Casual living	-42	.
24. Student pranks	-32	.
39. Caning	44
43. Strait-jackets	38
41. Strict rules	.	32	.	.	.	32
21. Chaperones	31

^a In the factor pattern, factors whose loading were less than .3 (absolute value) are not shown. Six items (fluoridation, cousin marriages, coeducation, teenage drivers, self denial, and white lies) did not have any factor loading greater than .3. The number preceding each item refers to the item number on the survey completed by the twins.

Table II. Twin Correlations ($\times 100$; MZ, Lower Triangle; DZ, Upper Triangle) for Social Attitude Dimensions, Educational Attainment (ED), and Church Attendance (CH)^a

Male twins																	
Twin 1									Twin 2								
RC	PC	RP	GC	SC	TV	ED	CH		RC	PC	RP	GC	SC	TV	ED	CH	
Dizygotic twins ($N = 352$)																	
RC		45	17	21	61	16-16	66	60	33	11	14	44	13-18	50			
PC	42		33	10	30	37-04	33	27	41	17	12	25	21-15	25			
RP	12	39		56	17	25-30	-05	09	19	46	19	10	12-22	-02			
GC	08	07	49		39	08-27	06	15	02	20	25	16	00-14	10			
SC	54	26	11	27		13-09	46	42	15	00	09	45	04-06	37			
TV	19	34	24	06	12	-08	11	15	15	19	15	19	18 -08	07			
ED	-14	-13	-30	-26	-09	02		04	-16	-09	-27	-16	-09	-04	43	-02	
CH	68	26	-06	02	46	13	02		54	28	-10	01	34	01	02	68	
RC	62	33	11	15	41	09-15	49		47	13	09	59	19-17	70			
PC	29	53	23	15	20	15-08	18	47		26	-01	27	38-13	31			
RP	14	28	52	31	09	10-25	-02	14	35		46	13	32-32	-08			
GC	09	12	27	40	13	07-24	-03	04	01	41		31	02-29	01			
SC	40	27	12	19	58	05-07	35	55	27	13	22		13-11	44			
TV	21	27	15	06	06	27-05	11	31	41	27	04	14	-02	05			
ED	-11	-12	-24	-25	-08	07	65	06	-21	-16	-34	-28	-10	-06		03	
CH	52	24	-04	04	37	11	04	66	61	25	-08	-06	43	15	09		
Monozygotic twins ($N = 567$)																	
Female twins																	
Twin 1									Twin 2								
RC	PC	RP	GC	SC	TV	ED	CH		RC	PC	RP	GC	SC	TV	ED	CH	
Dizygotic Twins ($N = 751$)																	
RC		40	07	14	58	22-14	65	56	26	04	15	39	18-15	49			
PC	40		37	08	23	32-22	21	30	45	20	15	24	14-10	22			
RP	09	41		35	19	19-36	-18	10	22	37	22	18	07-26	-09			
GC	12	08	36		44	-06-25	00	14	16	18	30	23	07-21	02			
SC	56	27	22	42		09-16	38	39	19	10	21	44	18-17	33			
TV	21	27	12	02	08	-08	16	16	15	08	08	13	22 -02	06			
ED	-13	-16	-35	-26	-21	-02		10	-13	-10	-21	-21	-15	00	48	02	
CH	66	19	-12	02	35	13	07		43	13	-10	06	24	08	06	57	
RC	71	30	08	15	45	15-15	54		40	09	14	58	26-20	64			
PC	34	58	33	17	25	18-19	17	43		41	10	26	25-13	22			
RP	07	28	64	23	18	08-35	-13	07	42		33	20	11-34	-13			
GC	15	13	25	45	30	06-18	00	13	10	27		44	00-26	02			
SC	47	26	15	26	60	12-20	32	58	28	17	43		13-17	34			
TV	16	22	13	11	12	39 -07	10	20	30	20	07	13	-03	17			
ED	-11	-16	-34	-19	-19	-03	69	09	-13	-19	-39	-22	-17	-05		05	
CH	54	16	-10	03	31	11	05	67	65	21	-17	-03	36	11	09		
Monozygotic twins ($N = 1233$)																	

^a Cross-twin within-trait correlations and cross-trait correlations greater than .40 are in bold-face.

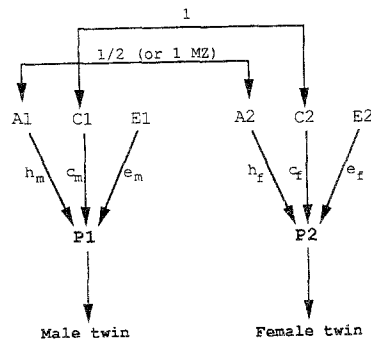


Fig. 1. Univariate genetic model. P1, E1, A1, and C1 denote the phenotype, unique environmental factor, additive genetics factors, and shared environmental factors for the first twin; P2, E2, A2, and C2 denote the corresponding variables for the second twin.

model. Likelihood-ratio chi-square tests, comparing the full genetic model to simpler sub models, were used to determine which, if any, of a number of submodels did not give a significantly worse fit than the full model. Three hypotheses were tested independently for each attitude dimension. The hypothesis that the same additive genetic influences and the same common environment influences affect males and females similarly was tested by comparing a general model which permitted sex differences to a model that constrained parameters to be equal across the sexes. The chi-square goodness of fit for submodels lacking additive genetic effects or common environment was compared with the full model to determine the significance of these parameters.

Multivariate Analysis

Multivariate models were fitted to the twins' covariance matrices of the six attitude factors, church attendance, and education by maximum likelihood. A convenient parameterization of each of the genetic and environmental covariance matrices is the so-called Cholesky or triangular decomposition (Martin *et al.*, 1982; Cantor *et al.*, 1982; Fulker *et al.*, 1983), which has the advantage of yielding positive definite estimates of the component covariance matrices. The number of unique genetic, common environment, and unique environmental factors in the Cholesky decomposition equals the number of phenotypes. In our particular application, the first genetic factor loads on all six attitude dimensions, education, and church attendance. The second genetic factor loads on the six attitude dimensions and education. Each subsequent factor loads

on one less dimension (see Fig. 2). The specific form of triangle chosen in our case has the added advantage that any genetic effects on church attendance must be absorbed by the first factor. This means that the first genetic factor, if significant, is essentially a church attendance factor; likewise the second genetic factor absorbs all effects of education. Subsequent factors reflect genetic and environmental effects on attitudes that are independent of religion and education.

The full model was specified in LISREL7. Unweighted least-squares estimates were obtained and used as starting values for maximum-likelihood estimates. After the full model was fitted, factors whose loadings approached zero were removed from the genetic and common environmental matrices. The full unique environmental matrix was retained because we were not interested in testing hypotheses regarding the structure of this matrix. The Cholesky model was fitted constraining the genetic and shared environmental covariance matrices to be equal for both sexes and then estimates were obtained for males and females separately in order to test for heterogeneity between the sexes. Heterogeneity was expected because the univariate analysis results were sex dependent.

In assessing the relative value of different submodels, we exploit Akaike's information criterion (AIC; Akaike, 1970):

$$\text{AIC} = \chi^2 - 2(\text{df}),$$

where χ^2 is the goodness-of-fit likelihood-ratio chi-square based on degrees of freedom. AIC quantifies the information content of a model in terms of the joint criterion of fit and parsimony. Minimization of AIC

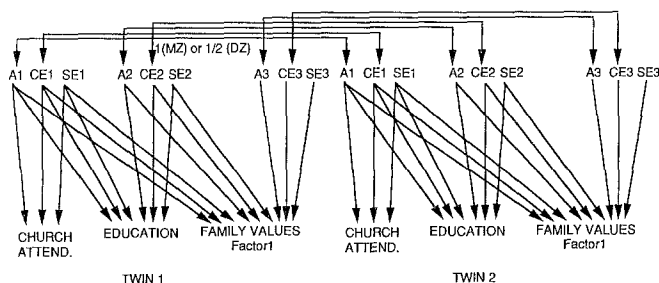


Fig. 2. Cholesky decomposition model for three phenotypes. Model is shown for three phenotypes for illustrative purposes only. The model which was fitted contained eight phenotypes (the three shown plus the five other attitude factors). Each gene or environmental factor (A, CE, or SE) loads on every subsequent phenotypic dimension. Thus the full model contains A1–A8, CE1–CE8, and SE1–SE8 for each twin. All genetic and common environmental factors are correlated as diagrammed for A1 and CE1.

yields a model which has a relatively good fit to the data (low residual chi-square) and relatively few free parameters (large residual degrees of freedom).

It was postulated by Martin *et al.* that the apparent cultural effects on attitudes may result from genetic effects of assortative mating. If this were true, at least some of the cultural factors should have the same structure as the corresponding genetic factor, i.e., the loadings on the common environmental factors should be some scalar multiple of the genetic factor loadings. To test this, scalar multipliers were estimated between the common environment and genetic effects for church attendance and education (see Appendix for additional details). Each factor was also scaled independently to determine whether the loadings on each factor were constant multiples of the shared environmental loadings. If such scaling is possible for factor loadings on religion and education, social attitudes could, indeed, be explained, as Martin *et al.* proposed, as the result of the genetic influences from the parents, and not familial environmental effects.

If the cultural component is real, then the common environment may be mediated by religion and education. This would be most clearly the case if there were no genetic component to religion and education and some of the common environmental effects on attitudes also influenced religion and education. This model would imply that the attitudes have genetic components and a common environmental component which is the result of the influence of religion and education on attitudes.

Univariate analysis in the Australian twin sample yields estimates of 21 and 0% for the genetic contribution in females' and males' church attendance (multivariate analysis: 18.1% in females and 4.9% in males). Since church attendance is mainly environmental, any significant common environmental effect of church attendance on the attitude factors (loadings of the first factor on the attitudes) is most probably a true cultural component. Complete removal of the genetic effects of church attendance would mean that any effects of church attendance must be environmental and would thus show that at least part of the inheritance of social attitudes is truly environmental.

RESULTS

Univariate Analysis

Table IV presents the best-fitting, univariate models for each attitude factor, church attendance, and educational attainment. The standardized components of variance are presented along with the chi-square goodness

Table IV. Standardized Components of Variance Under the Best-Fitting Univariate Genetic Models for Social Attitude Dimensions, Church Attendance, and Education^a

Phenotype	Parameter estimate ($\times 100$)						χ^2	df	<i>p</i> value
	h_f^2	c_f^2	e_f^2	h_m^2	c_m^2	e_m^2			
Religious conservatism	37	34	29	16	47	37	11.68	9	.238
Political conservatism	28	30	42	30	21	48	9.92	9	.357
Racial prejudice	49	14	37	11	40	49	7.59	9	.575
General conservatism	36	10	54	42	—	58	8.34	10	.595
Sexual conservatism	33	27	41	(33)	(27)	(41)	5.60	12	.935
Traditional values	25	13	62	14	14	72	11.79	9	.226
Church attendance	21	46	33	—	66	34	3.50	10	.967
Education attainment	38	30	32	59	06	35	9.25	9	.415

^a A single set of parameter estimates is displayed for sexual permissiveness because the univariate model with sex differences yielded no significant improvement of fit to the data. For general permissiveness and church attendance in males, the submodels which had a better fit than the full model are presented.

of fit for the covariances. For religious conservatism, political conservatism, racial prejudice, traditional values, and educational attainment, the full model with sex differences fitted the data best. For males, common environmental effects on general conservatism and genetic effects on church attendance were insignificant. Allowing for heterogeneity of genetic and environmental effects across the sexes did not improve the fit to sexual conservatism, so sex-independent estimates are presented. The actual proportion of variance explained by genetic and shared environmental factors differed considerably among the variables. This raises the possibility that analysis of the single common conservatism factor obscures etiological heterogeneity, which can be revealed only by a more fine-grained resolution analysis of multiple factors. Such heterogeneity needs to be resolved before we can be absolutely confident of the relative impact of cultural transmission and assortative mating on family resemblance for social attitudes.

Because familial inheritance is of particular interest in the multivariate models to be tested, it is informative to determine the contribution of the familial factors in the inheritance of each attitude factor in these univariate analyses. For females and males, respectively, familial factors

(additive genes and shared environment) accounted for 71 and 63% of the phenotypic variance of religious conservatism, 58 and 51% of political conservatism, 63 and 51% of racial prejudice, 46 and 42% of general conservatism, 50% of sexual conservatism, and 38 and 42% of traditional values. Thus, although the estimated contributions of genetic and shared environmental effects varied between the two sexes, the magnitude of familial resemblance was comparable.

Multivariate Analysis

The full Cholesky model with no sex differences produced a chi-square of 880.47 with $df = 449$ ($p = .00$). When we allowed for sex differences in the parameters of the full Cholesky model, the chi-square dropped very significantly, to 342.87, with 328 degrees of freedom ($p = .275$). For this reason, all other models were fit independently to both sexes. Statistics for all models fitted are presented in Table V.

The full models allowing for sex differences (model 1) contained superfluous factors. Reduction of the model to five genetic and three shared environmental factors in males did not make the fit appreciably worse (chi-square change = 3.53, for 21 df ; model 2, males). For female data, seven genetic factors and four common environmental factors were retained (chi-square = 0.29, for 12 df ; model 2, females). The resulting factors were unrotated because our principal hypothesis requires the first

Table V. Results from Multivariate Model Fitting

Model	Males				Females			
	χ^2	df	AIC	<i>p</i> value	χ^2	df	AIC	<i>p</i> value
1. Full cholesky (8A, 8CE, 8SE) ^a	180.32	164	-147.68	.182	162.55	164	-165.45	.517
2. Reduced Cholesky	183.85	185	-186.15	.510	162.84	176	-189.16	.753
3. Constrained; $A_i = kCE_i$ ($i = 1, 2$)	381.41	200	-18.90	.000	209.46	191	-172.54	.171
4. Constrained $A_1 = kCE_1$	220.50	192	-163.50	.078	170.73	183	-195.27	.733
5. Constrained $A_2 = kCE_2$	218.51	191	-163.49	.084	174.86	182	-189.14	.635
6. All CE = church and education	255.00	200	-145.00	.005	304.24	200	-95.76	.000
7. No "church attendance" genes	220.92	193	-165.08	.082	196.65	184	-171.35	.248

^a A, genes; CE, common environment; SE, separate environment.

and second factor to be defined by church attendance and educational attainment respectively.

The variance components from model 2 (Table VI) indicate common environmental and genetic factors that influence several attitude dimensions and also influence church attendance and education, confirming the interdependence of these items in both males and females. Although the full within-family environmental matrix was retained in the model fitting, the resulting matrix was nearly diagonal, so a single component is presented in Table VI for each variable. This component is the sum over all eight factors of the unique environmental effects on each attitude. In both sexes, environment is more important than genes for determining church attendance, while both genes and environment (or the genetic consequences of assortative mating) contribute approximately equally to educational attainment.

The first two factors of the Cholesky model are chosen to exhaust all the contribution of religion and education to the variation and covariation in the attitude factors. If all the apparent shared environmental effects on attitudes were due to the genetic consequences of assortative mating for religion and education, the shared environmental loadings on these two factors are expected to be multiples of their loadings on the corresponding genetic factor. When the two common environmental factors were scaled relative to the first two genetic factors [chi-square change (males) = 197.56 for 15 df and (females) 46.62 for 15 df; model 3], the fit was significantly worsened. Scaling each factor separately also resulted in models that were significantly worse than the unscaled model in males (models 4 and 5; chi-square changes = 36.65 for 7 df and 34.66 for 6 df). The fit was not significantly worse for females (7.89 for 7 df and 12.02 for 6 df). Pooling these chi-squares over sexes, the total chi-square changes of 44.54 (14 df) and 46.68 (12 df) are both significant, confirming the overall conclusion that the common environment parameters can not be scaled as simple multiples of the genetic parameters. It thus appears that the apparent cultural effects on the general conservatism factor reported by Martin *et al.* cannot be explained entirely as the genetic consequences of assortment for a single correlated variable such as religion or education.

The model which constrained common environment to be the result of church attendance and education (model 6) also fit poorly [chi-square change (males) = 41.15 for 15 df and (females) 141 for 24 df], indicating that the apparent effects of common environment on attitudes cannot be entirely explained by church attendance and education alone. When the genetic component of church attendance was fixed to zero (model 7), the model was significantly worsened [chi-square change (males) = 37.07

Table VI. Contribution of Genetic and Environmental Factors to Variance in Social Attitudes, Educational Attainment, and Church Attendance^a

Parameter estimate ($\times 1000$)										
Males	A1	A2	A3	A4	A5	C1	C2	C3	E	
Religion	52	-4	-7	1	77*	-353**	-97**	56*	350**	
Politics	-4	70*	5	105*	70	-95**	-153**	-21	477**	
Racism	89*	-23	35	21	7	14*	-299**	-45	468**	
Gc. conserv.	19	-143*	122	56	55	0	-31*	0	575**	
Sc. conserv.	55	-17	-6	252**		159**	-21	-95*	385**	
Trad. values	0	63	108*			10	-74*	-16	729**	
Education	112	294**				-2	238**		354**	
Church	49*					631**			321**	

Parameter estimates ($\times 1000$)												
Females	A1	A2	A3	A4	A5	A6	A7	C1	C2	C3	C4	E
Religion	149**	-24*	-30*	0	48	0	48	288**	-39**	79**	4	291**
Politics	0	-39*	18	7	-19	22	139*	56**	-12	81**	184**	422**
Racism	-24	-77**	4	19	18	337**		-6	-71**	38*	38*	367**
Gc. conserv.	-2	0	32	172**	90*			4	-129**	9	17	545**
Sc. conserv.	42*	-12	-38	198**				109**	-74**	122**		405**
Trad. values	54*	-22*	150**					1	0	150**		623**
Education	12	360**						1	309**			319**
Church	182**							486**				332**

^a After removal of factors approaching zero, the covariance matrixes were standardized and the results are shown above. Although the table gives components of variance, the signs of the factor loadings have been retained to indicate the direction of the relationship between variables. The unique environmental component presented is the sum of the loadings over all eight factors. See text for more details.

* Significant at $p = .05$.

** Significant at $p = .001$.

for 8 df and (females) 33.81 for 8 df]. This indicates that environmental effects may explain most of the familial effects on the cross correlation of church attendance and attitudes, but common genetic effects are significant.

DISCUSSION

The social attitude dimensions identified in the Australian sample were strikingly similar to the dimensions described by Feingold (1984) in the London test (825 twin pairs), even though a different questionnaire was used to assess attitudes. Feingold allowed for sex differences in a univariate transmission model for religious conservatism and prejudice. The overall variance explained by familial factors (additive genes and shared environment, estimated in the univariate analyses) was comparable in the British (BR) and Australian (AU) samples for religion (BR, 64% in females and 60% in males; AU, 71% in females and 61% in males) and prejudice (BR, 62% in females and 46% in males; AU, 64% in females and 54% in males). However, the magnitude of the contribution of the additive genetic effects and shared environment varied notably. For the Australian sample, 16% of the variance in religious conservatism was attributable to additive genetic effects in males compared with 26% for the London sample. Additive genetic effects also accounted for less of the phenotypic variance in prejudice in the Australian data (11%) than in the London twin population (32%). The London sample is considerably smaller, however, so these differences may not be significant. Finally, estimates of the shared environmental effect on prejudice were reversed between the sexes in the Australian sample (14% in females, 40% in males) and the London data (34% in females, 14% in males). Waller (1990) examined the effects of gene and environment on religious attitudes in MZ and DZ twins reared apart and found genes to have greater effects than we found in our study (range, .42–.52). Some of these differences, if not due to sampling or population differences, may reflect the assumptions about mate selection in the studies of twins reared together.

Unique, within-family environmental effects account for approximately one-third of the variation in both sexes. The first striking finding of the multivariate analysis is that the within-family environmental covariances are very small compared with the between-family environmental variances. That is, the covariation between church attendance, education, and attitudes is almost entirely explained by the effects of genes and the shared environment. Insofar as the unique environment of individuals is concerned, effects are virtually all trait specific. Males and females also

show obvious differences in the inheritance of attitudes and the covariance of church attendance and educational attainment as shown in Tables IV and V.

The fact that the shared environmental loadings on the "religion" and "education" factors cannot be scaled relative to the loadings on the corresponding genetic factors may argue against a simple interpretation of all apparent cultural effects in terms of the genetic consequences of assortative mating for church attendance and educational attainment. The data also suggest that the correlations between church attendance and attitudes cannot be entirely explained by environment, although the genetic contribution is admittedly small.

The case for not regarding all apparent shared environmental effects as due to the genetic consequences of assortative mating is strengthened by the fact that any genetic contribution to church attendance and its correlation with attitudes is very small. The effects of assortment would have to be very large indeed to explain the large genetic effects between families relative to those within families, but this possibility cannot be entirely excluded for a population in which there is extreme social stratification with respect to religious affiliation and practices. Additionally, the possibility that assortative mating is occurring for factors other than church attendance or educational attainment has not been examined.

The multivariate analysis of attitudes, incorporating religion and education as covariates, adds weight to the interpretation of part of the family resemblance in attitudes in cultural rather than genetic terms. However, this issue cannot be regarded as fully resolved until comparable data become available on large samples involving relationships in addition to twins reared together (Heath and Eaves, 1985; Heath *et al.*, 1985), which will permit a more complete resolution of hypothesis concerning cultural transmission and assortative mating.

APPENDIX

Phenotypic assortment from nonrandom mating can increase the similarity between sibling's genotype (that is, produce a genetic correlation greater than 0.5 between siblings). When modeling in LISREL, the genetic correlation between siblings (and DZ twins) is fixed at 0.5. Any additional similarity is assumed to result from common family environment (C). If assortative mating is occurring, then the apparent effects of C may actually be genetic effects (A). In this paper, we have tested the most extreme situation, that all the apparent common environment is actually excess genetic similarity resulting from nonrandom mating. If this were the case, C could be expressed as $C = xA$, where x is

a scalar multiplier. Parameterization is accomplished by equating the path “from C to phenotype” and the path “from A to phenotype” and freeing the variance [x (ϕ in LISREL)] of C . Thus, the total within-twin variance,

$$a^2 + c^2 + e^2,$$

can be rewritten as $a^2 + xa^2 + e^2$, and the covariance between DZ twins,

$$1/2a^2 + c^2,$$

can be rewritten as $1/2a^2 + xa^2$. The LISREL code and model are shown in Figs. A1 and A2.

```

**MZ: Cholesky decomp with C1 scaled to A1
DA NG=2 NG=2 NI=4 NO=1232 MA=CM
LA
  FACTOR1A FACTOR2A FACTOR1B FACTOR2B
CM FU FO
*PUT 4X4 MZ COVARIANCE MATRIX HERE*
MO NY=4 NE=12 NK=12 GA=FU,FR LY=FU,FI PH=FI PS=ZE TE=ZE BE=ZE
LK
  A11 A21 C11 C21 E11 E21
  A12 A22 C12 C22 E12 E22
PA GA
1 1 0 0 0 0 0 0 0 0 0 0
1 0 0 0 0 0 0 0 0 0 0 0
0 0 1 1 0 0 0 0 0 0 0 0
0 0 1 0 0 0 0 0 0 0 0 0
0 0 0 0 1 1 0 0 0 0 0 0
0 0 0 0 1 0 0 0 0 0 0 0
0 0 0 0 0 1 1 0 0 0 0 0
0 0 0 0 0 1 0 0 0 0 0 0
0 0 0 0 0 0 1 1 0 0 0 0
0 0 0 0 0 0 1 0 0 0 0 0
0 0 0 0 0 0 0 1 1 0 0 0
0 0 0 0 0 0 0 0 1 0 0 0
0 0 0 0 0 0 0 0 0 1 1
0 0 0 0 0 0 0 0 0 0 1 0
EQ GA(1,1) GA(7,7) GA(3,3) GA(9,9)
EQ GA(2,1) GA(8,7) GA(4,3) GA(10,9)
EQ GA(1,2) GA(7,8)
EQ GA(3,4) GA(9,10)
ST 1. PH(1,1) PH(2,2) PH(3,3) PH(4,4) PH(5,5) PH(6,6) PH(7,7)
ST 1. PH(8,8) PH(9,9) PH(10,10) PH(11,11) PH(12,12)
ST 1. PH(1,7) PH(2,8) PH(3,9) PH(4,10) PH(5,11)
ST 1. PH(6,12)
FR PH(3,3) PH(9,9) PH(3,9)
EQ PH(3,3) PH(9,9) PH(3,9)
MA LY
1 0 0 1 0 0 0 0 0 0 0 0
0 1 0 0 1 0 0 0 0 0 0 0
0 0 1 0 0 1 0 0 0 0 0 0
0 0 0 0 0 1 0 0 1 0 0
0 0 0 0 0 0 1 0 0 1 0
0 0 0 0 0 0 0 1 0 0 1
OU TM=3000 ND=5
**DZ: Cholesky decomp with C1 scaled to A1**
DA NG=2 NI=4 NO=751 MA=CM
LA
  FACTOR1A FACTOR2A FACTOR1B FACTOR2B
CM FU FO
*PUT 4X4 DZ COVARIANCE MATRIX HERE*
MO NY=4 NE=12 NK=12 GA=IN LY=IN PH=FI PS=ZE TE=ZE BE=ZE
LK
  A11 A21 C11 C21 E11 E21
  A12 A22 C12 C22 E12 E22
ST 1. PH(1,1) PH(2,2) PH(3,3) PH(4,4) PH(5,5) PH(6,6) PH(7,7)
ST 1. PH(8,8) PH(9,9) PH(10,10) PH(11,11) PH(12,12)
ST 5. PH(1,7) PH(2,8)
ST 1. PH(3,9) PH(4,10) PH(5,11) PH(6,12)
FR PH(3,3) PH(9,9) PH(3,9)
EQ PH(1,3,3) PH(9,9) PH(3,9)
OU TM=3000 ND=5

```

Fig. A1. LISREL7 coding for the scalar modeling.

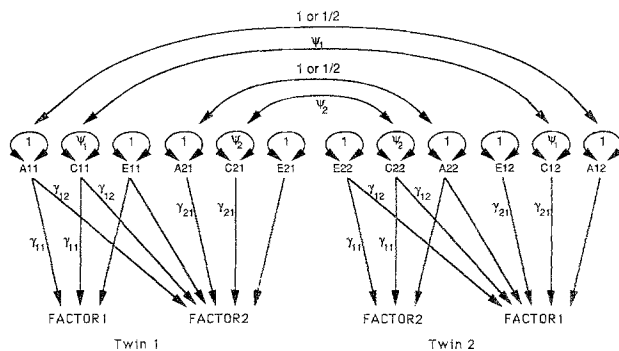


Fig. A2. The variable names here correspond to the variable names used in the LISREL code.

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