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Transmission of social attitudes

(attitudes/cultural inheritance/twins/assortative mating/behavior genetics)

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ABSTRACT **Data gathered in Australia and England on the social attitudes of spouses and twins are largely consistent with a genetic model for family resemblance in social attitudes. There is substantial assortative mating and little evidence of vertical cultural inheritance.**

The facility with which humans learn and their great investment in mate selection, parental care, and education make the human species a model system for the study of cultural inheritance. Until comparatively recently, however, genetic models for family resemblance such as those devised by Fisher (1) were superior to cultural models because the former were quantitative and led naturally to statistical estimation and hypothesis testing. The emphasis of theoretical analysis has changed over the last 10 years, with the formulation of many quantitative models for the contribution of cultural inheritance to individual differences and family resemblance (2–8). Such models have explored vertical transmission between parent and child, horizontal transmission between siblings, and one-to-many oblique transmission between teacher and students.

This seminal theoretical work on cultural inheritance has not been matched by the collection of informative data. For example, Cavalli-Sforza *et al.* (8) illustrate their models of vertical transmission with data on interests and attitudes from a small sample of nuclear families ($n = 203$) and pairs of friends ($n = 98$) ascertained from Stanford University undergraduates. The authors themselves admit that the nuclear family design, comprising only parents and children, may illustrate models of vertical transmission but is incapable of resolving biological and cultural inheritance. Thus, while their study focused on measures in which the *a priori* likelihood of cultural inheritance was greatest, the power of their analysis was constrained by their experimental design and small sample size.

Over the last 15 years, data on very large samples of monozygotic and dizygotic twins and spouses have been collected in the attempt to provide more powerful resolution of the basic elements of cultural and biological inheritance. In the case of personality measures, mate selection is virtually random and the resemblance between relatives is almost entirely genetic in origin (9–12). There is little evidence that cultural inheritance contributes to individual differences in personality in the populations studied so far.

Social attitudes present a marked contrast to personality measures. They too show substantial family resemblance (8, 13, 14), but the similarity between mates for social attitudes is also considerable (14, 15). Secular changes in attitudes are so rapid (16) that frequent revision of test instruments is necessary. On the face of it, such findings lend support to a purely cultural model for family resemblance. However, studies of attitudes so far have not tested the assumption that vertical transmission is cultural. They have not addressed the alternative hypothesis that individuals are influenced by their genotypes in their acquisition of particular opinions from the range current in a given society (17). Insofar as latent genetic factors influence the individual's preference for particular attitudes, vertical transmission will have a genetic component and purely cultural models will be inappropriate.

The Samples

In two separate studies, social attitudes questionnaires were mailed to twins enrolled on the Australian National Health and Medical Research Council Twin Registry and on the Institute of Psychiatry Twin Register, London, England. Both registries comprise volunteers and there is a marked excess of female monozygotic twins in both studies. Zygosity was determined by querying similarity in childhood and confusion of one twin for the other by parents, friends, and teachers, and it has been validated by blood-typing in subsets of both samples (18, 19). The Australian sample (Table 1) obtained responses from 3810 of 5967 pairs (64%) to whom questionnaires were originally mailed. The British sample (Table 2) generated 825 complete pairs, a pairwise response rate of ≈50%. The Australian twin sample was supplemented by 103 pairs of spouses studied by Feather (13), and the British twin sample was supplemented by 562 spouse pairs ascertained from the London area.

Test Instruments

The Australian study employed a 50-item version of the Wilson–Patterson conservatism scale (refs. 20 and 21; Table 1), which comprises a series of one-word items (e.g., "censorship") to which the subjects rate their agreement by circling "Yes," "?," or "No." The test yields a "conservatism" score by weighting odd-numbered items "+1" and even-numbered items "−1." A subsample completed the scale twice at an average interval of 3 months and test–retest reliability was 0.86 in 64 females and 0.92 in 32 males.

The British study of twins and spouses employed a Public Opinion Inventory comprising 40 frequently encountered statements relating to such issues as religion, sex, treatment of criminals, and nationalism (22). Respondents rate their agreement with each item on a 5-point scale. The instrument was scored for two factors: (*i*) radicalism, which describes the "left vs. right" dimension in British politics, and (*ii*) toughmindedness, exemplified by approval of capital and corporal punishment. In the entire British sample ($n = 2774$), the correlation between these two factors was 0.17.

Data Summary

For the more numerous Australian data, we present analyses of both the individual item responses and the composite

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Table 1. Polychoric correlations (×100) and results of item analysis for Australian sample

Item	Key	MZ		DZ			*C*	*H*	Heterogeneity
		M	F	M	F	U			
1 Death penalty	+	52	51	31	24	22	0	51	
2 Evolution theory	−	50	53	44	44	30			*
3 School uniforms	+	48	53	38	49	24			*
4 Striptease shows	−	61	51	48	37	34			*
5 Sabbath observance	+	50	54	33	36	36	18	35	
6 Hippies	−	51	55	36	45	37	26	27	
7 Patriotism	+	56	41	28	33	24			*
8 Modern art	−	38	48	18	37	24			*
9 Self-denial	+	29	37	25	20	19	6	28	
10 Working mothers	−	37	48	26	32	23	9	36	
11 Horoscopes	+	37	50	22	34	23			*
12 Birth control	−	46	66	51	56	27			*
13 Military drill	+	52	50	36	29	31	11	40	
14 Coeducation	−	35	42	42	42	31	34	7	
15 Divine law	+	51	46	44	38	33	26	22	
16 Socialism	−	42	48	40	36	29	21	26	
17 White superiority	+	49	49	32	30	20	9	40	
18 Cousin marriage	−	39	39	17	25	22	4	35	
19 Moral training	+	44	51	31	41	30	19	29	
20 Suicide	−	48	48	4	40	39			*
21 Chaperones	+	30	44	24	25	16			*
22 Legalized abortion	−	60	67	55	46	49	33	32	
23 Empire building	+	28	40	19	18	10			*
24 Student pranks	−	54	47	43	35	30	19	30	
25 Licensing laws	+	31	12	22	19	4			*
26 Computer music	−	32	27	38	8	11	0	26	
27 Chastity	+	41	48	32	43	17			*
28 Fluoridation	−	43	44	23	28	28	10	34	
29 Royalty	+	53	59	42	36	32	14	44	
30 Women judges	−	31	50	41	20	22	14	27	
31 Conventional clothes	+	36	37	9	22	5	0	35	
32 Teenage drivers	−	39	37	28	23	24	11	26	
33 Apartheid	+	53	46	31	27	24	5	43	
34 Nudist camps	−	60	60	52	42	47	32	28	
35 Church authority	+	47	51	39	38	31	20	29	
36 Disarmament	−	35	40	22	16	21	0	38	
37 Censorship	+	41	45	26	21	23	3	41	
38 White lies	−	38	41	26	23	22	5	35	
39 Caning	+	36	39	27	19	34	17	21	
40 Mixed marriage	−	37	49	19	33	29	12	33	
41 Strict rules	+	34	41	27	24	21	8	31	
42 Jazz	−	41	50	27	27	21	2	45	
43 Straitjackets	+	16	25	24	16	16	13	9	
44 Casual living	−	52	47	34	40	26	19	29	
45 Learning Latin	+	30	33	13	20	20	6	26	
46 Divorce	−	47	54	39	32	29	12	40	
47 Inborn conscience	+	26	40	5	23	16			*
48 Nonwhite immigration	−	44	43	47	33	19			*
49 Bible truth	+	57	59	50	51	41	34	25	
50 Pyjama parties	−	49	53	42	51	48	44	8	
Number of pairs		565	1232	351	750	905			
Conservatism: Mean		45.3	49.5	45.1	49.2	46.2			
SD		13.2	12.2	13.9	12.3	12.6			
r (age-corrected)		0.60	0.64	0.47	0.46	0.41			

C and *H* are contributions to variation of common environmental and genetic influences. Asterisk indicates heterogeneity between men and women in causes of variation. Direction of contribution of each item to the conservatism factor score is indicated as + or −. The distribution of conservatism scores and the correlation for each twin group is at the bottom of the table. MZ, monozygotic; DZ, dizygotic; M, male; F, female; U, unlike sex.

conservatism score; for the British data, only analyses of the two factor scores are shown. Analysis of the individual items reflects any idiosyncrasies in the transmission of particular attitudes and is the approach adopted by Cavalli-Sforza *et al.* (8). The composite scores include information on the covariation between the items and will be especially informative when, as is the case for social attitudes, responses to individual items reflect consistent patterns of individual differences in underlying social and biological variables whose effects are generalized over many specific items. The twin data on the individual items were summarized in the form of contingency tables. Separate tables were computed for the five twin groups (monozygotic males, monozygotic females, dizygotic males, dizygotic females, unlike-sex dizygotic).

Twin and spouse resemblance for composite scores was summarized by computation of partial correlations between scores of pair members after correction for age (Tables 1 and 2). Since the ages of twins are perfectly correlated, the correlation between twins is adjusted for only one variable. The ages of spouses, however, only correlate 0.78 in the British sample, so the adjustment involves the ages of both spouses of a pair. Age adjustment was conducted separately for each twin and spouse group except for the Australian spouses where the unadjusted correlation (0.675 based on 103 pairs of spouses) given by Feather (13) was used. Although the age effects are significant, the adjustments are uniformly small.

Analysis of Cultural and Biological Inheritance

Item Analysis. The method of maximum likelihood was used to estimate polychoric correlations for all types of twins from the contingency tables for each item in the Australian study (Table 1) and to test alternative hypotheses about the genetic and social determinants of twin resemblance for these items (23, 24). The model assumes that observed response categories are arbitrary divisions on a normally distributed continuum of liability. Likelihood ratio tests were used to compare the following hypotheses about familial similarity, which might explain the relative values of the polychoric correlations in the five groups of twins for each item: shared environment with no genetic effects, additive gene action with no shared environment, shared environment with additive gene action, additive gene action with sex-limited gene expression, additive gene action and shared environmental influences both with sex-dependent expression. The models have been described fully elsewhere (9–12). Random mating was assumed in the analysis of individual items. Positive assortative mating results in inflated estimates of the shared environmental effect in twin data. For the case in which genetic and environmental effects do not depend on sex, we let H be the proportion of variance in liability due to additive genetic effects and C be the proportion due to the effects of the family environment and genotype–environment covariance. The remainder, $E = 1 - H - C$, is the proportion of variance attributable to unique environmental effects within the family.

Maximum likelihood estimates of H and C, from the model in which both were estimated, are given in Table 1. Both estimates were constrained to be non-negative and both are tabled, even if one of them (most often C) was not significantly different from zero as assessed by the change in likelihood associated with its removal from the model. In several items, different values of H and C were required in males and females and this fact is noted in the table where appropriate.

Fourteen of the 50 items in the Australian study (nos. 5, 6, 15, 16, 19, 22, 24, 29, 34, 35, 39, 40, 44, and 49) showed significant evidence of both genetic and social components of twin resemblance—i.e., both H and C were judged significant by likelihood ratio tests. In four of these items (nos. 15, 22, 34, and 49) the contribution of C exceeded that of H. In all cases, random environmental effects including errors of measurement accounted for at least 35% of variation in liability underlying the attitude items. Fourteen items gave strong indication of sex differences in genetic and environmental effects. If different genetic and social effects operate in the two sexes, then the correlation between unlike-sex twins will be less than that between like-sex pairs. Models that ignore this type of sex-dependent effect may yield inflated estimates of H. The effects of sex interaction were especially marked for attitudes to birth control, chastity, and nonwhite immigration, but in view of the large number of items analyzed it is difficult to know how seriously such specific differences can be interpreted. Nineteen items show marked support for a genetic component of transmission, but no significant support for C (nos. 1, 9, 10, 13, 17, 18, 26, 28, 30, 31, 32, 33, 36, 37, 38, 41, 42, 45, and 46). These include attitudes to issues as important as the death penalty, disarmament, and race as well as comparatively trivial items such as computer music and conventional clothes. Only three items showed significant cultural transmission but no genetic transmission (nos. 14, 43, and 50).

Analysis of Composite Measures

Preliminary examination of the twin correlations shows that the conservatism scores of monozygotic twins are more highly correlated than those of dizygotic twins in the Australian data but that the dizygotic correlation exceeds half the monozygotic correlation (Table 1). These results suggest that both H and C will be needed to explain the familial aggregation of conservatism. A similar trend is seen for radicalism and toughmindedness in the British sample (Table 2), but there are indications of heterogeneity between sexes in the correlations, suggesting different contributions of cultural and genetic influences in males and females.

Both the samples show remarkably high correlations between spouses. Indeed, the resemblance between spouses is comparable to that between twins. The spousal correlations exceed those reported for other psychometric variables, including measures of intelligence. If such correlations reflect association between cultural and genetic determinants of

Table 2. Distribution and correlations for attitudes factor scores in British twin and spouse sample

	MZ		DZ			
	M	F	M	F	U	Spouses
Number of pairs	120	325	59	194	127	562
Radicalism						
Mean	−0.08	−2.97	2.23	−1.61	1.32	−4.05
SD	9.67	9.06	10.23	9.98	10.47	7.88
r (age-corrected)	0.75	0.60	0.52	0.51	0.48	0.51
Tough-mindedness						
Mean	−21.5	−28.0	−22.8	−28.7	−26.3	−17.8
SD	13.3	14.0	12.8	12.9	14.5	14.1
r (age-corrected)	0.49	0.69	0.18	0.41	0.28	0.55

MZ, monozygotic; DZ, dizygotic; M, male; F, female; U, unlike sex.

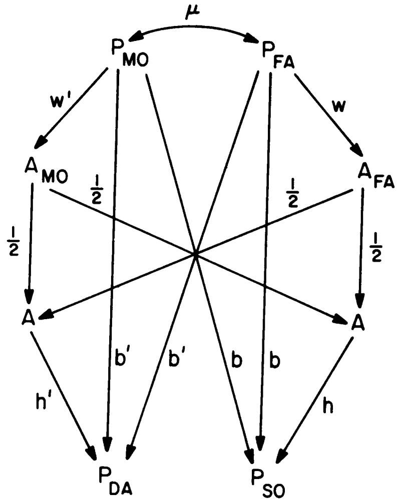

FIG. 1. Path model for vertical transmission in nuclear families. P, phenotypic deviation; A, additive genetic deviation; MO, mother; FA, father; DA, daughter; SO, son; see text for definition of parameters.

attitudes rather than convergence in the opinions of spouses after marriage, they will generate parental and sibling correlations in excess of those predicted under random mating. The effect of assortative mating, therefore, is to simulate the effects of cultural resemblance between relatives even when vertical transmission is purely genetic. As Cavalli-Sforza *et al.* have suggested (8), a longitudinal study of spouses is desirable to analyze spousal interaction. However, in a sample of 301 spouse pairs in Virginia with a 42-year range in duration of marriage, we found correlations between duration of marriage and absolute spouse differences for the radicalism and toughmindedness factors of −0.11 and 0.08, respectively. In the same sample, correlations of absolute spousal differences with ages of husband and wife were all smaller than these values. In the British sample of spouses, duration of marriage was not obtained but correlations of absolute spousal differences with ages of husband and wife ranged from −0.06 to 0.15.

The path model in Fig. 1 represents genetic and cultural components of vertical transmission in nuclear families in the presence of phenotypic assortative mating. The model assumes transmission of additive genetic differences (A) and a direct cultural effect of parental phenotype (P) on the phenotype of offspring. The regression of phenotype on genotype is h in males and h' in females; the partial regression of offspring phenotype on parental phenotype is b in males and b' in females. The parameter b, therefore, embodies vertical cultural inheritance in the model. The phenotypic correlation between mates is μ. The paths from phenotype of parent to additive genetic effect (w and w') can be expressed as functions of h, h', b, and b' at equilibrium under cultural transmission and assortative mating. The rules of path analysis permit the expected correlations of twins and spouses to be derived as follows:

Relationship	Expected correlation
Spouses	μ
Monozygotic twins	$h^2 + 2b^2(1+\mu) + 2bhw(1+\mu)$
Dizygotic twins	$\frac{1}{2}h^2(1+\mu w^2) + 2b^2(1+\mu) + 2bhw(1+\mu)$,

where $w = h + bw(1 + \mu)$. For simplicity, the expectations are given on the assumption that $h = h'$ and $b = b'$ and, hence, $w = w'$.

The method of nonlinear weighted least squares was applied to the z transforms of the observed correlations to recover estimates of the parameters that correspond closely to maximum-likelihood values (23, 24). Since the z's are normally distributed and independent, the sum of weighted residuals is approximately distributed as χ^2 for $n - p$ degrees of freedom, where n is the number of observed correlations and p is the number of free parameters in the model. The residual χ^2 may be used as a guide to the goodness-of-fit of the model and χ^2 values for certain alternative hypotheses may be compared to justify reducing the general model to a more parsimonious form.

The results of the model fitting are given for the Australian data in Table 3 and for the British data in Table 4. Models in which h is set to zero in both sexes give a very poor fit to the data in both studies (see models 1 and 2) since the associated residual χ^2 values are large. On the other hand, models that leave out cultural inheritance ($b = b' = 0$) give an extremely good fit when allowance is made for assortative mating (models 3 and 4). The Australian sample gives no evidence of heterogeneity over sexes in the contribution of genetic and environmental factors since models 4 and 6 fit no better than models 3 and 5. Because the spousal correlation $\mu = 0.675$ used in this analysis is from another study (13), is based on relatively small numbers ($n = 103$), and has not been age-corrected, we repeated the analysis specifying a value of $\mu = 0.40$. Even with this conservative estimate of the spousal correlation, the conclusions of model fitting were unaltered and the estimate of $b = 0.07$ was trivial and nonsignificant.

For the two factors scored in the British study, the best fit is obtained when different genetic contributions to variance are allowed in males and females (model 4). A greater proportion of variance is genetic in males than in females for radicalism and in females than in males for toughmindedness.

Discussion

We are aware of the many criticisms of the twin method and of the responses others have made to these (25). For example, it is alleged that monozygotic twins see each other more frequently than dizygotic twins and that this greater frequency of contact is reflected in greater monozygotic similarity in attitudes. Since the correlation between reported frequency of contact and absolute intrapair difference in conservatism

Table 3. Results of fitting phenotype-to-phenotype transmission models to Australian twin and spouse correlations for conservatism scores

Model	h	h'	b	b'	μ	df	χ^2	P
1. $b\mu$			0.40		0.67	4	73.38	<0.001
2. $bb'\mu$			0.38	0.41	0.67	3	68.68	<0.001
3. $h\mu$	0.79				0.67	4	4.61	0.33
4. $hh'\mu$	0.78	0.80			0.67	3	2.84	0.42
5. $hb\mu$	0.81		−0.02		0.67	3	4.46	0.22
6. $hh'bb'\mu$	0.75	0.83	0.02	−0.02	0.67	1	2.70	0.10

df, Degrees of freedom.

Table 4. Results of fitting phenotype-to-phenotype transmission models to English twin and spouse data for radicalism and toughmindedness factor scores

Model	h	h'	b	b'	μ	df	χ^2	P
				Radicalism				
1. $b\mu$			0.44		0.51	4	15.05	0.005
2. $bb'\mu$			0.47	0.43	0.51	3	11.46	0.009
3. $h\mu$	0.81				0.52	4	9.55	0.049
4. $hh'\mu$	0.87	0.79			0.52	3	3.39	0.34
5. $hb\mu$	0.63		0.13		0.51	3	6.73	0.08
6. $hh'bb'\mu$	0.85	0.49	0.01	0.20	0.51	1	0.05	0.83
				Toughmindedness				
1. $b\mu$			0.41		0.55	4	47.22	<0.001
2. $bb'\mu$			0.32	0.44	0.55	3	30.32	<0.001
3. $h\mu$	0.79				0.54	4	16.21	0.003
4. $hh'\mu$	0.65	0.83			0.54	3	2.25	0.52
5. $hb\mu$	0.96		−0.15		0.55	3	12.43	0.006
6. $hh'bb'\mu$	0.87	0.89	−0.21	−0.05	0.55	1	0.07	0.79

df, Degrees of freedom.

scores is −0.08 in female and −0.14 in male twin pairs in the Australian sample, any such effect must be trivial, even if the cause of such covariation is in the direction asserted.

The problem with many "social" explanations of our data is that they do not lead to predictions about other kinds of relationship unless social interaction is based ultimately on genetic differences (e.g., see ref. 8). Our model can be used to predict the results of other studies. For example, we predict a zero correlation between foster parent and adult foster child for all our attitude scales. Our model (Table 3, model 3) predicts a parent–offspring correlation of $\frac{1}{2}h^2(1 + \mu) = 0.52$ for conservatism. We predict correlations of $\frac{1}{4}h^2(1 + h^2\mu)^2 = 0.31$ for the offspring of monozygotic twins and $h^2 = 0.62$ for separated monozygotic twins. If our model of mate selection is right, we predict that the spouses of siblings should show a correlation of $\frac{1}{2}h^2\mu^2(1 + h^2\mu) = 0.20$. The correlation between the spouse of one monozygotic twin and the co-twin is expected not to differ significantly from $h^2\mu = 0.42$. All these data are obtainable and can yield further tests of our model.

If our model withstands the further tests we propose, it will have radical implications for our understanding of cultural inheritance in humans and undermine the naive assumption that the resemblance of family members can be interpreted in purely social terms. We began with psychometric instruments, which might have been expected to maximize our chances of detecting nongenetic transmission. We fitted a model that specifies both social and genetic components of vertical transmission and we have obtained estimates of the cultural parameter that do not differ significantly from zero in many cases. One interpretation of our finding is that our method and model are fundamentally wrong. If this is the case, then our predictions will be falsified by the data still to be gathered. The alternative possibility is that geneticists and social scientists have misconceived the role of cultural inheritance and that individuals acquire little from their social environment that is incompatible with their genotype. In no way does our model minimize the role of learning and social interaction in behavioral development. Rather, it sees humans as exploring organisms whose innate abilities and predispositions help them select what is relevant and adaptive from the range of opportunities and stimuli presented by the environment. The effects of mobility and learning, therefore, augment rather than eradicate the effects of the genotype on behavior.

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