

The Genetic Structure of the Traditional Moral Values Triad

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Abstract

Personality and social attitudes researchers have frequently noted high correlations, typically between .5 and .7, between measures of religiousness, conservatism, and right-wing authoritarianism. Koenig and Bouchard (2006) proposed that this pattern of correlations indicated the presence of a single latent factor of traditionalism. The three components of this factor, known as the Traditional Moral Values Triad (TMVT), were hypothesized to share a common genetic basis. The present study tested this hypothesis using data from the Minnesota Study of Twins Reared Apart (MISTRA), a sample of twins who were raised in different homes. The best-fitting model identified the three TMVT measures as different manifestations of a single latent and significantly heritable factor. Further, the genetic basis for this factor was found to overlap heavily with that for the Multidimensional Personality Questionnaire Traditionalism factor, supporting our conception of traditionalism as the latent factor represented by the TMVT scales.

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Introduction

The events of World War II elevated the question of the development and nature of social attitudes to one of the central themes of personality and social psychology. This research, especially in its earliest manifestations, has focused most heavily on attitudes taken to be comparable to those held by both the leaders and populace of wartime Germany and Italy. Understanding the psychological roots and concomitants of dispositions such as Fascism and Authoritarianism was understood as central to identifying the individuals and the contexts likely to bear such deadly fruits.

In more recent years several investigators have attempted to identify a latent factor structure behind political, philosophical and social attitudes. In a study of college student attitudes towards 266 “isms,” from Fascism to Hedonism to Pacifism, Saucier (2000) found three underlying factors, roughly characterized as orthodox traditionalism, self-interestedness, and spiritual liberalism. Each of these factors had a wide scope: Saucier’s traditionalism factor, for example, represented attitudes towards ideas as seemingly divergent as Creationism, Legalism and Humanitarianism.

While Saucier used responses on a single instrument to construct these factors, others have suggested that factor analyses of multiple distinct instruments will produce very similar results. Altemeyer’s Right-Wing Authoritarianism scale, Wilson-Patterson’s Conservatism scale, and various measures of religiousness have been found by multiple investigators to correlate substantially with each other, generally between .50 and .70 (Bouchard et al., 2003; Altemeyer, 1988; using Lorr’s Conservatism scale, Tarr & Lorr, 1991). Koenig and Bouchard (2006) have suggested that the substantial correlations among these measures indicate that these three traits (labeled by Bouchard as the Traditional Moral Values Triad, or TMVT) can be interpreted as representing a single factor of Traditionalism. Each of these factors has been shown to be substantially influenced by genetic factors (Bouchard et al., 2003), leading to the further hypothesis that this common factor behind the TMVT is itself heritable. A comparable idea was suggested by D’Onofrio et al.’s (1999) demonstration of a possible common genetic basis for a portion of the phenotypic correlation between religiousness (as measured by church

attendance) and sexual conservatism, shown using cross-trait cross-twin correlations in the Virginia 30,000 sample.

Bouchard has also hypothesized (Bouchard, in press) that any factor common to the TMVT would likely covary highly with other measures of traditionalism (such as the MPQ Traditionalism scale), and that both the TMVT and these alternative measures would share a common genetic basis. Phenotypic covariance between MPQ Traditionalism and the TMVT factor represents a cross-instrumental test of our hypothesis for the unity of the TMVT components. Meanwhile, a common biometric basis for MPQ Traditionalism and the TMVT factor would suggest that any findings for biometric commonality behind the TMVT scales were not the result of instrumental artifact.

Recent efforts to identify “bottom-up” origins for social attitudes are also relevant to the question of a common genetic basis behind these seemingly distinct social attitudes. Jost et al. (2003) identified psychological attributes associated with political conservatism, such as anxiety regarding death and loss, close-mindedness, and intolerance of ambiguity and uncertainty. These observed correlations between these traits and political orientation were argued to reflect a causal relationship, with political attitudes resulting from needs to manage uncertainty and threat. The attributes postulated by Jost et al. (2003) are not examined here, as the relevant assessments were never performed on the subject pool being analyzed. Nevertheless, the present analysis addressed the question of whether a common latent trait is responsible for much of Conservatism, Right Wing Authoritarianism, Religious Fundamentalism, and the phenotypic covariance typically found with these traits. Specifically, each of these attitudes appears to us to represent a disposition towards obedience to authority, though the source of that authority is different for each of the three constructs.

The Wilson-Patterson Conservatism measure uses the “catch-phrase” method to measure attitudes on political and social questions on a conservative versus liberal dimension. Our analysis involves the 28-item version of the measure, shown in earlier studies to have strong convergent and discriminant validity (e.g. Bouchard et al., 2003). The items in the Wilson-Patterson measure include several which are out-dated for

contemporary subjects (e.g. Segregation, Busing), but our sample was assessed as adults in the 1980s and early 1990s, and was thus an appropriate audience.

Altemeyer's Right Wing Authoritarianism (RWA) measure largely concerns moral questions on the organization of the family and society. Respondents rate their agreement or disagreement with value statements like "There is nothing wrong with premarital intercourse" on a nine-point Likert scale, with every question addressing the traditional versus progressive perspective.

Finally, the Wiggins Religious Fundamentalism scale from the MMPI assesses the extent of Judeo-Christian religious belief in the respondents. In analyses not presented here, it was shown that these items discriminated effectively between those with a "spiritual" religious orientation, as measured by Hood's Special Experiences measure of mysticism (Hood, 1975), and those with a conventional Judeo-Christian orientation.

Each of these measures explicitly addresses markedly different topics, but as noted above they are highly correlated at the phenotypic level. This study examines our hypothesis that these correlations are due to a common and heritable trait underlying these phenotypes, representing a tendency towards traditionalism and obedience to authority. While each scale has a different focus and explicit content, we posited that the primary difference between them is the source of authority represented in each measure, whether social traditions, political structures, family dynamics, or obedience to spiritual beings and earthly authorities.

We further hypothesized that the common genetic basis behind these features would also be shared with any comparable measures, such as the Traditionalism scale of the Multidimensional Personality Questionnaire (MPQ) (Tellegen and Waller, 2008). High scorers on this measure are described as having a strict moral standards and child-rearing practices, valuing convention propriety and reputation, opposing rebelliousness and selfish disregard of others, and valuing religious institutions and practices. In our view, this measure represents a broader assessment of the tendency towards to obedience which is common to each of the three TMVT scales.

Methods

The data used in this analysis was from the Minnesota Study of Twins Reared Apart. This sample consists of over 100 pairs of twins, both monozygotic (MZ) and dizygotic (DZ), who were separated in infancy and reunited later as adults. Details of their recruitment and assessment are provided elsewhere (Bouchard et al., 1990). MISTRA evolved over time to include additional instruments not administered to some early participants. While many of these pairs then completed these instruments at a follow-up visit or by mail, the staggered addition of instruments into the study led to different sample sizes for some of the measures used here. Our measure of Religious Fundamentalism was comprised of 12 items from the Minnesota Multiphasic Personality Inventory (MMPI; Butcher et al, 1989). As both the MMPI and MPQ were completed by nearly all participants, data were available for nearly all members of the MISTRA sample for both Religious Fundamentalism and MPQ Traditionalism (Religious Fundamentalism: MZ=66 pairs, DZ=36 pairs; Traditionalism: MZ=66 pairs, DZ=37 pairs). Altemeyer's Right-Wing Authoritarianism (RWA) measure and the Wilson-Patterson Conservatism scale were added to the MISTRA assessment battery after some of the sample had already participated, and so had somewhat less data available (RWA: MZ=55 pairs, DZ=33 pairs; Conservatism: MZ=53 pairs, DZ=33 pairs). Some MISTRA participants returned for a follow-up assessment, leading to multiple data points for some scales. For these individuals, scores were taken from whichever assessment was the most complete from the perspective of the four scales being analyzed. The validities and properties of these instruments have been discussed elsewhere (Tellegen & Waller, 2008; Bouchard et al. 2004; Wiggins, 1966).

Because the constructs analyzed in this study have significant associations with age, sex, and IQ (Waller et al. 1990; Koenig and Bouchard, 2006), the raw scores of participants on RWA, Conservatism, Religiousness and Traditionalism were transformed by regressing out the effect of these variables and transforming the raw score into a z-score, using SPSS. It was these z-scores which were then used for analysis (McGue & Bouchard, 1984).

We evaluated four alternative models of the fit of the various TMVT scales. Each model was in turn evaluated under three different assumed biometric variance structures, with fit statistics provided by Mx. The first biometric structure tested was the traditional ACE model, in which one assumes that the total phenotypic variance for a given scale (P) could be decomposed into additive genetic (A), shared environmental (C), and nonshared environmental (E) components. Additive genetic factors represent the contributions to the phenotype made by genes in a manner that was not affected by the presence or absence of other genes. Shared environment refers to the aspects of the environment that have similar effects on the phenotype of interest in each twin, regardless of zygosity. Nonshared environment refers to environmental variables that cause phenotypic differences between the two members of a twin pair. The second model fit was an AE model, in which the variance attributable to C is constrained to 0. The total phenotypic variance is thus forced into the A and E parameters. The third model fit was an ADE model, in which the genetic effects are represented under both additive (A) and dominant (D) parameters. Dominant genetic effects represent any contributions of genetic factors that are due to the configuration between multiple genetic loci. The mechanics of biometric modeling are such that all variance attributable to measurement error is included in the nonshared parameter estimate in each of the three biometric structures.

Because MZ twins share 100% of additive genetic effects whereas DZ twins share only 50%, and because shared environmental effects are assumed to contribute equally to the similarity of the two types of twins, three biometric variance components (of A, C, D and E) can be estimated at one time from the observed variances and covariances for the two types of twins. The rationale and empirical support for the assumptions that underlie application of the standard biometric model to twin data have been extensively discussed and justified elsewhere (Johnson, Krueger, Bouchard, & McGue, 2002; Kendler, Myers, Prescott, & Neale, 2001; Plomin, DeFries, McClearn, & Rutter, 1997). Nonetheless, we recognize that because we cannot directly establish the validity of these assumptions in the present application, the estimates of the variance components we report should be considered approximate. In particular, the standard assumption of twin models that the parents of the twins were paired independent of the phenotype of interest is tenuous.

Investigators have noted assortative mating in other samples for the traits in the Traditional Moral Values Triad (Watson et al. 2004). The consequences of a violation of the independent mating assumption for biometric estimates are discussed below. Further, because this sample consists entirely of twins who were raised in different households, we hypothesized little to no variance attributable to C, any of which would presumably result from the very small selective placement found for related traits (Bouchard & McGue 1992).

We evaluated each of the three biometric structures under four different models, each of which presents a different picture of the inter-relatedness of the TMVT scales. One of these models (the Base) represented a particular poor fit, but the remaining three (the Cholesky, Independent Pathways and Common Pathway) are represented pictorially in Figures 1, 2 and 3.

The Base model provides estimates for the biometric parameters for each of the phenotypes without using any information beyond the twin correlations for the phenotype in question. In contrast, the other models allow for any correlations between the phenotypes to influence the parameter estimates (A, C, D and E) provided by the model. The Base model thus represents the hypothesis that biometric parameters can be most parsimoniously estimated (without significant loss of fit) by treating each of the TMVT phenotypes as biometrically independent of each other. That is, it entails the assumption there is no significant common genetic or environmental basis behind the TMVT traits, which represents the primary null hypothesis for our study.

The Cholesky model relies on the assumption that biometric estimates for each phenotype will be largely independent of each other, but allows for phenotypic correlations between the three TMVT phenotypes to influence the biometric estimates for each. Like the Base and Cholesky models, the Independent Pathways model employs the assumption that the phenotypes are distinct. Unlike those models, however, it will fit best if these phenotypes have significant biometric overlap. In contrast, the Common Pathways model will show superior fit if each phenotype is best represented as a manifestation of a single, underlying phenotype which has its own biometric

presentation. In both the Independent and Common Pathways models, residual biometric components specific to the original phenotypes are also estimated.

Figure 1

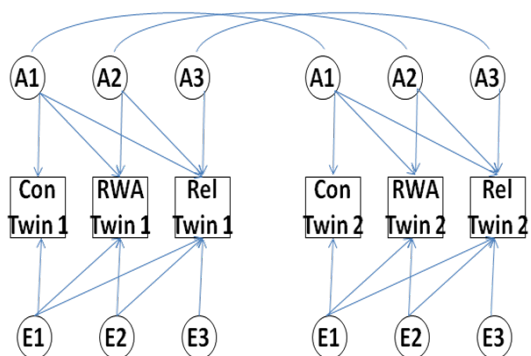
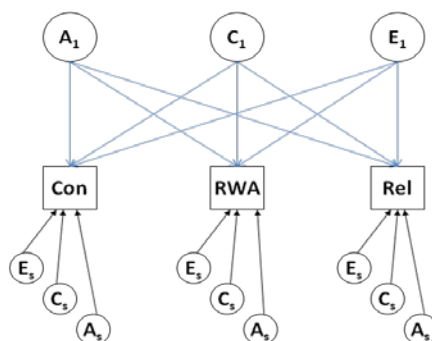


Figure 2



Figures 1 and 2. Figure 1 is the Cholesky AE model, chosen for ease of presentation. In a Cholesky ACE model, shared environmental influences (C_1 , C_2 , and C_3) are also drawn in following the same pattern as genetic influences (A_1 , A_2 , A_3), with connections between each component (C_1 , C_2 , C_3) for Twin 1 and Twin 2. Figure 2 is the independent pathways model, which allows for biometric overlap between the TMVT, but is most consistent with each assessment being phenotypically distinct. Like the common pathways model, residual biometric estimates are provided for each measure.

Figure 3

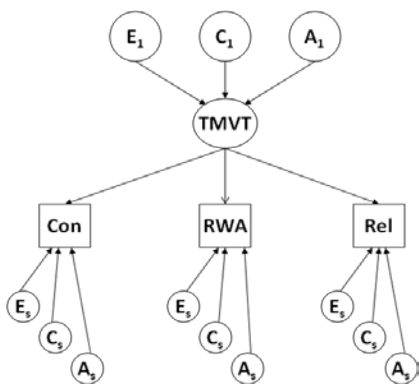
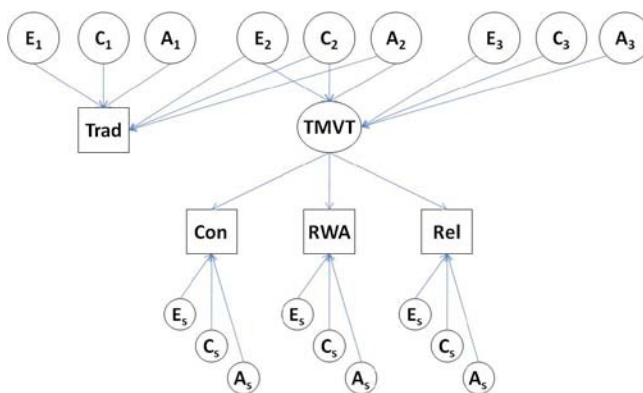


Figure 4



Figures 3 and 4. The common pathway model (Figure 3) fits best when the traits being measured are best represented as different faces of a latent trait with its own biometric presentation. The Cholesky Factor model (Figure 4) estimates the biometric commonalities between the latent TMVT factor and MPQ Traditionalism.

For our secondary analysis, we analyzed the possible overlap between a common TMVT factor and the MPQ Traditionalism scale using a Cholesky factor model. This model involves decomposing the primary biometric variance components into three separate groups. One group provides the estimates for the MPQ Traditionalism scale's biometric components that are not shared with the TMVT factor. Another provides estimates for those that are shared with the TMVT factor. The third provides estimates for the biometric components that are unique to the TMVT factor. Residual biometric variance components for the TMVT traits are also estimated. This model is represented pictorially in Figure 4.

Results

Correlations

Early behavior genetic work relied on Falconer's formulas (cf. Falconer, 1960) for estimates of biometric parameters, relying exclusively on twin correlations to provide the estimates. While more sophisticated modeling techniques have now replaced this method, a brief look at the twin correlations will help highlight some important patterns. Table 1 provides the correlations of MZ and DZ twins on RWA, Conservatism, Religiousness and MPQ Traditionalism. High correlations were observed across all scales in the MZ twins. In contrast, only the Conservatism measure showed a significant correlation for DZ twins. The magnitude of the difference between the MZ and DZ correlations was, excepting Conservatism, extremely high: Falconer estimates for the heritability of these features range from .38 (for Conservatism) to 1.00 (for Religiousness). Further, the negligible DZ correlations indicated that emergent effects could be present (Lykken et al., 1992). When genetic influence on traits is purely additive, the trait should exhibit DZ correlations of at least half the size of MZ correlations; however, only Conservatism meets this criteria in the present analysis, while the other scales quite starkly do not. This indicates that some genetic influence on this trait may derive from the configuration of multiple genetic factors, and it is from this configuration that the trait "emerges."

Table 2 provides the observed phenotypic correlations between these scales, after the effects of age, sex and IQ were regressed out. The high correlations (.46-.71) suggest the possibility that these scales represent a common factor.

Table 1. Twin correlations

	Authoritarianism	Conservatism	Religiousness	MPQ Traditionalism
Monozygotic	.48	.48	.51	.50
Dizygotic	.07	.29	-.04	.06

The correlations between monozygotic and dizygotic twins on the three TMVT scales (Authoritarianism, Conservatism and Religiousness) and the MPQ Traditionalism scale. Correlations are produced from scores that were transformed from the raw participant scores by regressing out the important covariates of these scales including age, sex, and IQ.

Table 2. Phenotypic correlations

	Conservatism	Religiousness	RWA
Conservatism			
Religiousness	.53**		
RWA	.71**	.48**	
MPQ Traditionalism	.56**	.46**	.70**

The observed phenotypic correlations between the three TMVT scales and the MPQ Traditionalism scale. Correlations are produced from scores that were transformed from the raw participant scores by regressing out the important covariates of these scales including age, sex, and IQ.

Biometric Modeling

The Common Pathway model provided the best fit for the data. (Fit statistics for each of the three models run under each of the three biometric assumptions are presented in Table 3.) While the AIC value indicated that an ADE model provided the best fit, a superior fit of the AE model was suggested by both BIC and the significant Chi-Square value ($X^2=4.58$, $df=1$, $p<.05$) found when comparing the AE against the ADE. The significance of this disagreement will be discussed below, but by all metrics there is clear support for the TMVT as a single higher-order factor. The ADE Common Pathways

model component estimates were .30 for additive genetic factors, .11 for dominant genetic factors, and .59 for nonshared environmental factors. For the AE Common Pathways model, the A and D parameters were simply combined, leading to estimates of .41 for genetic factors and .59 for non-shared environmental factors.

Cholesky factor models were then used to examine the relationship between this TMVT factor and MPQ Traditionalism. Results from the ADE model indicated a significant overlap in the biometric components behind Traditionalism and the TMVT factor. One hundred percent of both additive and dominant genetic components were shared, as was 65% of the nonshared environmental component. An AE model suggested that 88% of the additive genetic component and 66% of the nonshared environment component were shared.

Table 3. Fit statistics

	Cholesky Model			Common Pathways Model			Independent Pathways Model		
	ACE	AE	ADE	ACE	AE	ADE	ACE	AE	ADE
-2xLL	1331.65	1331.93	1328.10	1350.02	1350.02	1345.44	1348.21	1348.45	1344.05
df	537	543	537	550	551	550	546	549	546
AIC	257.65	245.93	254.10	250.02	248.02	245.44	256.21	250.446	252.05
BIC	-598.68	-612.67	-600.46	-620.11	-622.46	-622.40	-611.60	-618.543	-613.68

-2xLL = -2 times log-likelihood; df = Degrees of Freedom. Fit statistics for each model with the three biometric alternatives considered. Comparison of the -2 times log-likelihood and degrees of freedom shows that both the Common and Independent Pathways models provide significant Chi-Square values when compared to the Cholesky, indicating that each model represents significant information above that provided by the Cholesky. The AIC and BIC are measures of fit which emphasize different aspects of the model, where a lower score on each fit statistic is more desirable. The lowest AIC and BIC values are found in the Common Pathways model, indicating that it is the best fitting model for this data, though the two fit measures disagree on the preferred biometric presentation (ADE or AE).

Discussion

Based on the analyses performed, Religiousness, Conservatism and Right-Wing Authoritarianism appeared to be different measures representing a common, heritable factor. With 41% of the variance accounted for by genetic factors, the heritability of this feature is near that of most social attitude measures in adult populations. Interpretation of the sizeable nonshared environmental coefficient (representing the remaining 59% of the variance) is tempered, as always, by the recognition that this coefficient also includes all variance due to measurement error.

As indicated by the second analyses performed in this study, it also appears that the common factor behind the TMVT is highly similar to what is measured by instruments like the MPQ Traditionalism scale. Genetic factors responsible for each construct were, depending on the model used, entirely (100% for the ADE model) or nearly entirely (88% for the AE model) shared with the other. Further, even the non-shared environmental factors were largely common between the two phenotypes: 65% for the ADE model, 66% for the AE model. We interpret this high level of biometric overlap between a construct derived from three distinct instruments (Altemeyer's RWA scale, Wilson-Patterson's Conservatism scale, and Wiggins' Religious Fundamentalism scale) and an independent fourth scale (MPQ Traditionalism) as highly supportive of our hypothesis of a latent trait that heavily influences each of these measures. However, while the extremely high correlation between the genetic factors involved in the TMVT factor and in MPQ Traditionalism was expected on the grounds that this scale appeared to us to be the purest measure of the latent TMVT factor, analyses not presented here were not consistent with this view of MPQ Traditionalism: in a Common Factor model using the three TMVT scales and MPQ Traditionalism, Right Wing Authoritarianism shows the highest loading (.91), followed by Religious Fundamentalism (.82), MPQ Traditionalism (.77) and Wilson-Patterson Conservatism (.52).

Perhaps even more impressive than the genetic correlations between MPQ Traditionalism and the TMVT factor is the high correlation between nonshared environmental factors: with alphas for each instrument typically ranging between .80 and .90, the upper limit on the possible correlation between these two factors for this

parameter approximates the observed correlation, indicating that the entirety of the biometric contributions to the TMVT factor are extraordinarily close to those for MPQ Traditionalism.

Finally, our substantive interpretation of the nature of the common core values behind the TMVT traits as indicative of obedience to authority was supported by analyses to be presented in future work showing that each of the TMVT scales (as well as MPQ Traditionalism) correlated between .2 and .5 with a cluster of values labeled “Restrictive Conformity” by Schwartz (1987).

Connections

The present research draws together several bodies of existing work on social attitudes. An increasingly well-established literature has demonstrated the heritability of these attitudes, as surveyed by Bouchard and McGue (2003). This literature begins with Eaves and Eysenck (1974) and was extended in reared-apart twin samples like the one discussed in the present study by Martin et al. (1986), until finally crossing into the political science literature with Alford et al.’s (2005) investigation.

Less attention has been directed to connecting this literature with efforts like those of Saucier’s (2000) study to identify potential latent factor structures behind seemingly diverse attitudes. While D’Onofrio et al. (1999) made an important step in this direction with the identification of cross-trait cross-twin correlations between religiousness and personal sexual conservatism, to our knowledge the present study is the first concerted effort to address these issues.

We also anticipate that further investigations will connect the present work with research regarding the bottom-up origins of attitudes (Jost et al, 2009). The prospect of such a unification requires some attention to the appropriate interpretation of the results presented in the current study. In particular, the nature of the latent trait responsible for the TMVT will be of particular interest. In their survey of the literature, Jost et al (2003) identify a host of processes potentially involved in the formation of political attitudes, from death anxiety to intolerance of ambiguity to openness to experience. On the surface, this approach may appear at odds with the present results: instead of identifying

a range of processes responsible for political orientation, our results suggest that a seemingly diverse range of expressions of social and political attitudes result from a common psychological basis with its own biometric presentation. However, our analysis is unable to identify whether this is a single, unitary process, or instead a collection of processes that have comparable influences on the various TMVT facets. Thus, it may be that death anxiety and intolerance of ambiguity, for example, individually contribute to a tendency towards a tendency of obedience to authority. The present study indicates only that such a contribution is not independent to a characteristic such as political conservatism, but also has effects on right-wing authoritarianism and conventional religiousness.

Assortative Mating and the ADE Model

Perhaps the most surprising result from our study concerned the superiority of an ADE model. The success of this model is unexpected not merely because of the complexity of the phenotype in question (and the according lack of appeal of the concept of dominating epistatic contributions) but also because the phenotype appears highly subject to true assortative mating.

For most phenotypes, assortative mating effects are largely small or absent, or explicable by alternative phenomena suggesting that partners are not actively selecting their partners based on similarity for the phenotype. For example, the apparent assortative mating for IQ (for which spouses correlated approximately .35) appears largely due to social homogamy or propinquity (Tambs et al, 1993). That is, your IQ significantly predicts who you associate with – professionally, socially, or even as a neighbor – and the correlation between partners appears significantly due to one's choosing of a partner from the groups to which one is exposed. For social attitudes and religiousness, however, it appears that more active selection is taking place. Watson et al. (2004), in a study of newly-weds, found that while corrections for education and age decreased the correlation for IQ (indicating social homogamy), these corrections did not weaken the correlation for religiousness or political conservatism. Further, the comparably high spousal correlations for social attitudes in couples both new and old

(Bouchard, 2009) indicates that induction (in which one member of a pair influences the other) is insufficient to explain this phenomenon.

To see why assortative mating makes an ADE model fit perplexing requires understanding how the parameters are computed, and how assortative mating can affect these parameters. Dominance (D) is suggested whenever the correlation between monozygotic (MZ) twins exceeds the correlation of dizygotic (DZ) twins multiplied by two. This is because DZ twins are (under normal conditions) half as similar, genetically, as MZ twins. When doubling the phenotypic correlation between DZ twins still leads to estimates lower than the MZ phenotypic correlation, it suggests that the genetic factors are not acting purely additively. Most frequently, this is interpreted as indicating that the phenotype is produced by an interaction between genes that go beyond their independent contribution to the phenotype.

However, assortative mating for a phenotype should, in principle, act to disguise the role of any non-additive genetic factors. This is because it can create DZ twins which, for the genes involved in the phenotype under assortative mating, are more than half as similar as MZ twins. This occurs because the assortatively-mating parents are likely to be genetically similar for those genes involved in producing the phenotype. This situation has no effect on MZ twins as they are already genetically identical; DZ twins, however, will systematically share more than the standard 50% of varying genes for the phenotype, as they may inherit the same genes even when receiving them from different parents.

The general implausibility of ADE inheritance for complex phenotypes, and the particular challenges for this phenotype in particular, are daunting. While they do not change the results found in our study, they do indicate the importance of considering our data within the broader literature. It is also worth noting that it is only for the Common Pathways model that an ADE presentation provided the best fit – for both the Cholesky and the Independent Pathways models, the more biologically-plausible AE model provided a better fit than their respective ADE models.

Nevertheless, an emergent inheritance pattern (Lykken et al., 1992) for the TMVT may yet find further support. For example, further bottom-up research regarding

the processes potentially responsible for the development of social attitudes may support an interactional model involving multiple heritable processes. There is one model of note with these characteristics: the dual process model of Duckitt et al (2002) concerns the interaction of Right-Wing Authoritarianism and Social Dominance Orientation to explain political conservatism. However, we believe the TMVT factor is most appropriately seen as a representative of only the first of these two processes, rather than as the result of the two of them, leaving the curious heritability pattern a mystery to be explained by future work.

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