
Genetic Similarity Theory, Intelligence, and Human Mate Choice

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When we tested predictions from genetic similarity theory, we found that spouses assort on the basis of the more genetically influenced of cognitive tests. From our analysis of data from several studies employing 15 subtests from the Hawaii Family Study of Cognition and 11 subtests from the Wechsler Adult Intelligence Scale, we calculated positive correlations between assortative mating coefficients and estimates of genetic influence both between and within samples. Thus, estimates of genetic influence calculated on Koreans and Canadians predicted assortative mating in European Americans in Hawaii and California. These observations were weaker when the *g* loadings of the tests, on which the spouses assorted most, were partialled out. They confirm the robust nature of the phenomenon and suggest that epigenetic rules may incline people to detect and prefer genetically similar others as marriage partners.

KEY WORDS: Altruism; Assortative mating; Behavior genetics; Epigenetic rules; Similarity; Kin recognition; Sociobiology.

GENETIC SIMILARITY THEORY

Resemblance has long been considered important for marriage, attraction, friendship, altruism, prejudice, and group functioning. Most explanations of the role of similitude in human behavior focus on proximate causation suggesting, for example, its reinforcement value (Byrne 1971). Recent analyses, however, suggest that genetic influences may also be operative (Rushton et al. 1984). Genetic likeness may exert subtle effects on a variety of relationships and have implications for the study of social behavior in small groups and even large collectives both within and between nations. In this paper we present this perspective within the context of spouse selection and provide novel data in support. To anticipate and summarize, it is proposed that people have a tendency to choose as marriage partners those who are genetically similar.

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Choosing genetically similar others to marry can be viewed as part of a more general pattern of altruistic preference. Kinship was the basis of seminal work by Hamilton (1964) and Maynard Smith (1964) that provided a solution to the question of how altruism could evolve. The answer proposed was that individuals behave so as to maximize their inclusive fitness, rather than only their individual fitness by increasing the production of offspring by both themselves and their relatives, a process now known as kin selection. This formulation provided a conceptual breakthrough, redirecting the unit of analysis from the individual organism to his or her genes, for it is these which survive and are passed on.

While the idea of kin selection is not new (Hamilton 1964; Maynard Smith 1964) and is considered central to sociobiological theorizing (Dawkins 1976; Wilson 1975), only recently has it been applied to human relationships (Alexander 1979; Glassman et al. 1986; Reynolds et al. 1987; Rushton 1980, 1984; van den Berghe 1981; Wilson 1978). This delay may be due in part to the theory's focus on altruism between relatives, an emphasis of limited applicability to humans where altruism is frequently directed to non-kin and is often explained by empathy, reciprocity, social rules, and other proximate mechanisms (Rushton 1980), although twin studies have shown that human altruism is also heritable (Rushton et al. 1986a).

Adopting the mechanistic viewpoint of the selfish gene, however, Rushton et al. (1984) provided an extension of kin selection theory to the human case by arguing that if a gene can better ensure its own survival by acting so as to bring about the reproduction of family members with whom it shares copies, then it can also do so by benefiting *any* organism in which copies of itself are to be found. Thus kin recognition would be but one form of genetic similarity detection. Several data sets were ordered under the rubric "genetic similarity theory" including (a) kin recognition studies in animals raised apart, (b) mate selection, (c) intrafamilial relations, (d) human friendship, and (e) ethnic nepotism.

In order to pursue the strategy of benefiting kin and genetically similar others, an organism must, in effect, be able to detect copies of its genes in others. Several procedures have been suggested whereby this may occur, including (a) innate feature detectors, (b) phenotypic matching, (c) familiarity or association, and (d) location and selective placement (Holmes and Sherman, 1983). We can at present only speculate on the extent to which these differing processes operate in humans. It should be noted that they are not mutually exclusive. If there are evolutionary advantages to be gained from the ability to detect genetic similarity, several mechanisms may be operative. To the degree to which the "stronger" versions (innate feature detectors, phenotype matching) are correct, it should be possible to demonstrate that interpersonal relationships are mediated by genetic similarity in the absence of learning through familiarity or placement. In support of this thesis, studies have shown that animals alter their behavior depending upon the degree of genetic similarity in conspecific animals not previously encountered (Holmes

and Sherman, 1983), and that 2-to-3 month old human infants prefer to look at those human faces independently judged to be "attractive" (Langlois et al. 1987).

Preliminary evidence for the genetic similarity theory formulation is available. Through the use of computer simulations and mathematical modeling techniques, several authors have found that positive selection exists under a variety of conditions for genetic mutations inclining organisms to favor other organisms that share copies of genes, but who are not necessarily kin (Samuelson 1983; Glassman et al. 1986; Russell 1987). Using Monte Carlo procedures, for example, Russell (1987) showed that if the benefit to the recipient is one-and-a-half times as great as the cost to the donor, a gene for directing altruism toward siblings disappears, but a gene for like-gene detection evolves.

When the genetic similarity theory extension to kin-selection is contrasted with precursors, alternative expectations are highlighted. For example, because sociobiological theorizing has emphasized relatives "identical by descent" where all siblings have a .5 coefficient of relationship (Mealey 1985; Trivers 1985), family favoritism as a topic of research has been overlooked. However, because of assortative mating in which parents resemble each other, if a father provides 50 percent of his genes, 10 percent of which overlap with the mother's contribution, and a mother provides 50 percent of hers, 20 percent of which overlap with the father's, the child would be 60 percent similar to the mother and 70 percent similar to the father, and family members can be expected to favor those most similar. Support for this prediction was found in a study of bereavement following the death of a child: Both mothers and fathers, irrespective of the sex of the child, grieved most for children they perceived as resembling their side of the family (Littlefield and Rushton 1986). Among siblings perceived similarity is correlated with genetic similarity measured by blood tests (Scarr and Grajeck 1982).

Differential predictions can also be made with respect to ethnic relations. Some sociobiologists have argued that inclusive fitness theory has no direct implications for ethnic or national preferences (Dawkins 1981; Trivers 1985). Thus, Dawkins (1981) states: "The equating of 'kin-ship' in the sense of kin-selection with 'ties of race' appears to result from an interesting variant of what I have called the fifth misunderstanding of kin-selection" (p. 528). The genetic similarity formulation, on the other hand, provides an explicit biological basis for what van den Berghe (1981) has characterized as "ethnic nepotism." To date several analyses favor the genetic similarity theory perspective (Rushton 1986; Russell 1987).

ASSORTATIVE MATING AND INTELLIGENCE

If humans do detect and prefer those who are genetically similar, it should be possible to demonstrate this within interpersonal relationships. With re-

spect to marriage it is widely accepted that partners resemble each other in such characteristics as age, ethnic background, socioeconomic status, physical attractiveness, religion, level of education, and intelligence (Buss 1985; Epstein and Guttman 1984; Thiessen and Gregg 1980). The median assortative mating coefficient for standardized IQ (intelligence quotient) measures, for example, averaged over 16 studies involving 3,817 pairings, is 0.37 (Bouchard and McGue 1981). Correlations between spouses tend to be higher for opinions, attitudes, and values (0.40–0.70) and lower for personality traits and personal habits (0.02–0.30). Less well known is the fact that spouses also resemble each other on socially undesirable characteristics, including criminality, alcoholism, and psychiatric disorders, as well as on a variety of physical features. For example, Rushton et al. (1985) aggregated anthropometric data from a wide range of studies and reported low but positive correlations on over 60 different measures, including height (.21), weight (.25), hair color (.28), eye color (.21), chest breadth (.20), wrist circumference (.55), and interpupillary breadth (.20). Since heritabilities have been found for most of these characteristics, it follows that spouses are genetically more similar to each other than to random members of the population. This conclusion has recently been confirmed with nearly 1000 pairs of sexually interacting couples using blood antigen analyses at 10 loci across six chromosomes (Rushton in press).

While a degree of assortment occurs through simple propinquity, as well as through competitive and selective placement (Burley 1983; Mealey 1985), other data suggest a more finely tuned genetic detection system may also be operating. Holding type of trait constant (since sequential filtering may be involved in relationship formation) spouse resemblance is observed to be highest on those most genetically influenced. Positive correlations between estimates of heritability and similarity have been found on several anthropometric, cognitive, and social-behavioral characteristics (Rushton and Russell 1985; Russell et al. 1985). That assortment continues within groups already selected on the basis of propinquity and placement is compatible with the stronger versions of kin-recognition and a view that epigenetic rules incline individuals to *choose* spouses on the basis of their genetic similarity (Rushton et al. 1986b). Epigenetic rules may also place an upper limit on assortative mating by producing the negative sexual imprinting that occurs between people raised together (usually kin) and the avoidance of incest (Lumsden and Wilson 1981; van den Berghe, 1983). Too much genetic similarity between mates increases the chances that harmful recessive genes may combine.

Cognitive ability is a particularly salient dimension on which spouses assort, and it has important evolutionary implications. As mentioned, reviews of the world literature indicate a spousal correlation of between .37 (Bouchard and McGue 1981) and .41 (Jensen 1978) for standardized IQ measures. While it will not necessarily change the population mean of the at-

tribute in question (unless there is directional dominance involved), positive assortment will increase variability and influence the genetic structure of the population. For example, given a mean IQ of 100 and a standard deviation of 15, Jensen (1978) estimated that if the present level of assortative mating for intelligence had existed for several generations, it may account for half the present frequency of persons with IQs above 130 and 80 percent of those with IQs over 145 and would show that there are approximately 20 times as many persons above an IQ of 160 as would be expected from random mating. Consequently, IQ-based stratification systems may emerge and society become more differentiated (Gottfredson 1986; Hunter and Hunter, 1984).

The effects of assortative mating for intelligence may be stronger than Jensen's (1978) analysis envisaged for intelligence appears to be both dominant in the Darwinian sense of fitness (as shown by inbreeding depression studies, Jensen 1983) thereby altering population means upwards, and to have higher assortative mating coefficients than the reviews of the world literature indicate. Both Cattell (1982) and Eaves et al. (1984) have suggested that assortative mating for intelligence may be higher on the more *g*-loaded components of the tests (*g* being the label given to the general factor of intelligence that emerges when factor analysis is carried out on different measures of complex mental ability). Nagoshi and Johnson (1986) provided evidence for this perspective, finding that assortative mating coefficients correlated .63 with the *g* loadings from 15 tasks. Moreover, since highly *g* loaded items typically have higher heritability than less *g* loaded items, it is implied that spouses assort on the basis of the more genetically influenced parts of intelligence, in accord with our own predictions.

In the present paper, we extend the evidential basis for the genetic similarity theory perspective on spouse selection where marriage partners are predicted to choose each other on the basis of the more heritable of traits. In previous studies on this topic (Rushton and Russell 1985; Russell et al. 1985), estimates of genetic influence and of assortative mating were calculated on the same sample. Given that the two measures are mathematically independent (DeFries et al. 1979), such a within-subjects design is maximally sensitive for testing predictions, since heritabilities can vary with circumstance. Generally, removing environmental impediments increases heritability, as when intergenerational increases in educational opportunity and health care lead to higher heritabilities for educational attainment and health (Heath et al. 1985; Scriver 1984). Indeed, it is usual to consider heritabilities to be properties of particular populations and not to be highly generalizable (Falconer 1981; Russell et al. 1985). On the other hand, it is virtually unknown how extrapolatable most estimates are. Those for intelligence in North American and European populations, for example, have been robust for many years across diverse samples and procedures, typically being $> .50$ (Bouchard and McGue 1981).

METHODS AND RESULTS

Overview

In this paper we use a between-subjects design to examine whether estimates of genetic influence calculated in one sample predict assortative mating coefficients calculated in others. To the extent that they do, we can conclude that the phenomenon is robust. We chose as our data base studies of cognitive functioning that used either the 15 subtests from the Hawaii Family Study of Cognition for a description of this study, see Wilson et al. (1975) or the 11 subtests from the Wechsler Adult Intelligence Scale (Matarazzo 1972). Our choices were determined by the necessity of finding psychometrically established instruments used on a variety of samples on a dimension of individual differences of some significance, and on which both estimates of genetic influence and assortative mating could be derived.

It should be noted, however, that one of the estimates of genetic influence that we use, the midparent-offspring regression calculated from within intact families, actually combines both genetic and shared-family environmental influences. As far as we can determine, this latter source of variance is surprisingly small (Plomin and Daniels, 1987) and serves primarily to add error to our predictions. Nonetheless, it should be borne in mind that we have frequently defined genetic influence in this way.

Hawaii Family Study of Cognition

A survey of the IQ literature uncovered seven publications reporting either estimates of genetic influence or assortative mating coefficients with the 15 tests from the Hawaii Family Study of Cognition. Two of these (DeFries et al. 1976; Johnson et al. 1976a) reported information later incorporated into a subsequent publication (DeFries et al. 1979), and in another instance the zero-order assortative mating coefficients were reported in one publication (Johnson et al. 1976b) with corrections for age listed in another (Zonderman et al. 1977). We chose between overlapping studies, preferring those in which (a) the estimates of genetic influence had been corrected for test unreliability, (b) the assortative mating coefficients had been adjusted for age, and (c) the sample was the largest and most complete. We selected five samples.

1. *Koreans*. Johnson et al. (1976b) reported the assortative mating coefficients for 209 families in the Republic of Korea. Park et al. (1978) subsequently reported the midparent-offspring regression for these tasks from the same families.
2. *Americans of European ancestry (AEA) in Hawaii*. DeFries et al. (1979) reported both the assortative mating coefficient and midparent-offspring regression from 871 American families of European ancestry living in Hawaii.

3. *Americans of Japanese ancestry (AJA) in Hawaii*. DeFries et al. (1979) similarly reported the assortative mating coefficient and midparent-offspring regression from 311 American families of Japanese ancestry (AJA) living in Hawaii.
4. *Americans of mixed ancestry (AMA) in California*. Watkins and Meredith (1981) reported assortative mating coefficients based on 215 newlywed couples from a variety of ethnic backgrounds (82 percent European, 8 percent black, 5 percent Hispanic, 3 percent Asian, 2 percent Native American Indian) who had been married in California.
5. *Americans of European ancestry (AEA) living in Colorado*. Zonderman et al. (1977) reported the assortative mating coefficients for 123 American families of European ancestry living in Colorado.

The 15 cognitive tasks were the same across these five samples except that one task was not included in the Korean analyses. As a preliminary, we calculated the Pearson product-moment correlations among the estimates of genetic influence and assortative mating. The three genetic influence correlations were positive, with a mean $r = .54$, $p < 0.01$ (Koreans with AEA, .37; Koreans with AJA, .47; AEA with AJA, .78). It could be argued that these effects are primarily a function of the general intelligence factor g underlying these tests. Since the g loadings have been calculated for the AJA and AEA samples (Nagoshi et al. 1984) and for the Colorado sample (Zonderman et al. 1977), we re-correlated the data partialling g out. The two g loadings correlated $r = 0.92$ ($p < 0.001$) so we aggregated them, partialled them out, and found that all the correlations remained positive with a mean $r = .55$, $p < 0.05$. The correlations among the ten assortative mating coefficients also demonstrated generalizability with 9/10 being in the predicted direction and 4/10 being significant (mean $r = .28$). However, removing g reduced the degree of intercorrelation to an average $r = .07$, thus offering support for the views of Cattell (1982), Eaves et al. (1984), and Nagoshi and Johnson (1986) that marital assortment on intelligence occurs primarily on the g factor.

To test the genetic similarity theory hypothesis that spouses assort most on the more genetically influenced components, we calculated the correlations between the three estimates of genetic influence and the five of assortative mating. These are displayed in Table 1. As can be seen, estimates of genetic influence calculated on one sample (e.g., AJA) predict the degree of assortative mating in other samples (e.g., the AEA and Californian), with an overall mean $r = 0.38$ for the 15 tasks. Aggregating across the numerous estimates to form the most reliable composite (Rushton et al. 1983) resulted in a substantially higher prediction of mate similarity from the estimates of genetic influence ($r = 0.74$, $p < 0.001$), although it should be noted that this is somewhat inflated by inclusion of the within-sample prediction. Even after partialling out g , the genetic influence estimates remain predictive of assortative mating with six of the 15 correlations being at least marginally

Table 1. Correlations Between the Estimates of Genetic Influence in Three Samples With Those of Assortative Mating in Five Samples.^a

Assortative Mating	Estimates of Genetic Influence		
	Americans of European Ancestry (AEA) in Hawaii	Americans of Japanese Ancestry (AJA) in Hawaii	Koreans
Americans of European Ancestry (AEA) in Hawaii	.71 ^b (.51 ^c)	.60 ^b (.50 ^c)	.55 ^b (.46 ^d)
Americans of Japanese Ancestry (AJA) in Hawaii	.14 (.12)	.13 (.13)	-0.9 (-0.15)
Koreans	.33 (-.33)	.38 ^d (.01)	.53 ^c (.40 ^d)
Americans of European Ancestry (AEA) in Colorado	.58 ^c (.60 ^c)	.25 (.14)	.14 (-.02)
Americans of Mixed Ancestry (AMA) in California	.62 ^b (.17)	.63 ^b (.38 ^d)	.13 (-.23)

^a Corrected for age and reliability, on subtests of the Hawaii Family Study of Cognition Battery (the correlations in brackets are the result of partialling out *g*).

^b $p < 0.01$.

^c $p < 0.05$.

^d $p < 0.10$.

significant at $p < 0.10$, although with an overall mean $r = 0.18$ for the 15 tasks. Finally, we note that it is the AEA Hawaii sample that is the most predictive. It is also the largest, and these two variables are presumably not unrelated.

Wechsler Adult Intelligence Scale

A survey of the literature on the Wechsler Adult Intelligence Scale (WAIS) discovered four samples in which husband–wife similarities and estimates of genetic influence had been calculated for various of the 11 subtests and total scores:

1. *Kentucky Americans*. Block (1968) calculated heritability estimates for all 11 subtests on 120 pairs of adolescent twins in Louisville, Kentucky, using Holsinger's H formula.
2. *Canadians*. Williams (1975) reported both husband–wife correlations and midparent–offspring regressions from a study of 55 families in Alberta, Canada.
3. *Minnesota Americans*. Scarr and Weinberg (1978) reported both husband–wife and midparent–offspring correlations for 120 families in Minnesota for four of the subtests as well as for the total score. We calculated the heritability from these statistics using the formula $h^2 = 2r_{po}/(1 + r_{pp})$, where r_{po} is the parent–offspring correlation and r_{pp} is the correlation between the parents.
4. *California Americans*. Lewak et al. (1985) reported assortative mating coefficients for 81 married couples in California. The couples were as-

Table 2. Correlations Between the Estimates of Genetic Influence and Those of Assortative Mating on Subtests of the Wechsler Adult Intelligence Scale^a

	Estimates of Genetic Influence			Assortative Mating		
	Kentucky Americans	Canadians	Minnesota Americans	Canadians	Minnesota Americans	California Americans
Genetic Influence						
Kentucky Americans	—	.68 ^b	.91 ^b	.68 ^b	.82 ^b	.55 ^b
Canadians	.74 ^c	—	.86 ^b	.23	.86 ^b	.34
Minnesota Americans	.94 ^b	.92 ^b	—	.45	.68	.83 ^b
Assortative mating						
Canadians	.26	.11	.36	—	.71 ^d	.50 ^d
Minnesota Americans	.94 ^b	.91 ^b	.99 ^e	.40	—	.93 ^c
California Americans	.56 ^d	.77 ^b	.95 ^b	-.04	.96 ^b	—

^a Above diagonal, *g* factor left in; below diagonal, *g* factor partialled out.

^b $p < 0.05$.

^c $p < 0.01$.

^d $p < 0.10$.

^e $p < 0.001$.

sessed on the revised, rather than the original WAIS scales (WAIS-R; Wechsler 1981).

As shown in Table 2, many of the correlations between and among the measures of genetic influence and assortative mating are significant. All three genetic influence estimates intercorrelate significantly, despite the Minnesota sample being limited to only four subtests plus total score (mean $r = 0.82$; with *g* out, $r = 0.87$). Of the three correlations of assortative mating, all are positive, one significant at $p < 0.05$ and the two remaining at $p < 0.10$ (mean $r = 0.72$; with *g* out, $r = 0.44$). Moreover, the estimates of genetic influence often predict assortative mating, with 5/9 of the correlations being significant (mean $r = .60$; with *g* out, $r = 0.65$). The *g* estimate for the WAIS and WAIS-R subtests were taken from Cohen (1957) and Silverstein (1982), respectively. Finally, the different estimates of genetic influence were aggregated, as were those of assortative mating and found to be intercorrelated both with *g* left in ($r = 0.52$, $p < 0.05$) and with *g* partialled out ($r = 0.35$, ns).

DISCUSSION

The evidence presented here is compatible with the conclusion that spouses select each other on the basis of genetic similarity. That spouse selection occurs for social class and IQ is well established (Thiessen and Gregg 1980). That assortment on subtests of intelligence is higher the more genetically influenced the test suggests that mate choice may be particularly fine-tuned. This evidence, derived from a between-subjects methodology, joins data already assembled from a within-subjects procedure in which positive cor-

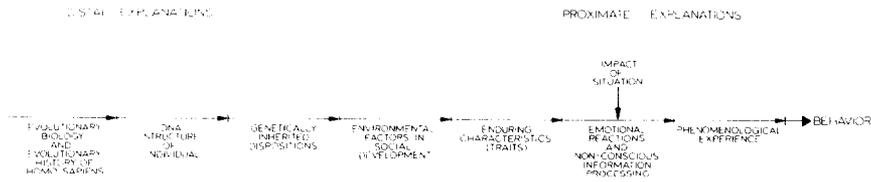


FIGURE 1. The distal-proximal dimension and levels of explanation in social behavior.

relations were observed between measures of assortative mating and genetic influence for a variety of anthropometric, cognitive, and social behavior traits (Rushton and Russell 1985; Russell et al. 1985). As such, increasing confidence can be placed in the robustness of the phenomenon.

The evaluation processes underlying human mate choice presumably build on those already in existence for assortative mating is known to occur in other species from insects through birds to primates, in laboratory as well as in natural settings (Bateson 1983; Thiessen and Gregg 1980). Among humans it also occurs cross-culturally, for, in addition to the data cited in our study, assortment for height in Pakistani arranged marriages has been found to be at least as high as it is in Europe and North America, even when controlling for such variables as social class (Ahmad et al. 1985). In all cases, the selectors obviously rely on phenotypic attributes. Advantages thought to accrue to choosing optimal genetic similarity in mates include increased marital stability, greater fecundity, increased relatedness to offspring, and increased within-family altruism. For example, Bresler (1970) found that fetal loss increased with each additional country of birth among great-grandparents, as well as with distance between birthplaces of mates.

One reviewer queried how information from genetic and environmental sources combines to assemble phenotypic behavior. Some clarification may result from Figure 1, which provides a time dimension of explanations (Rushton 1984). As can be seen, there is no necessary conflict between different levels. Evolutionary biologists do not find the heritability of traits problematic, trait theorists accept that dispositions are modified by later learning, and learning theorists believe that the products of early experiences interact with subsequent situations to produce emotional arousal and cognition.

Another reviewer questioned how variance in cognitive measures can legitimately be apportioned into estimates of genetic and environmental influence. Such doubts are common in both the evolutionary and social sciences. Increasingly powerful behavioral genetic techniques are available, however, with which to test evolutionary hypotheses about development (Eaves et al. 1978; Plomin 1986). For example, while small fluctuations in one or two molecules might affect ontogeny, studies show that siblings raised apart for many years in complex environments grow to be significantly similar to each other on a variety of traits and that their degree of similarity is predicted by the number of genes they share (Bouchard 1984). Another dis-

covery is that the environmental factors influencing development are unique to each sibling rather than common, even for traits such as altruism and aggression which parents are expected to socialize heavily (Plomin and Daniels 1987; Rushton et al. 1986a). These data imply the presence of genetically based stabilizing systems that channel development such that, within the constraints allowed by the total spectrum of cultural alternatives, people create environments maximally compatible with their genotypes (Lumsden and Wilson 1981; Rushton et al. 1986b). The epigenetic rules biasing spouses to choose each other on the basis of similarity would seem to be particularly fine-tuned. If social forces are canalized by inherent preferences, then epigenetic rules may be of considerable theoretical use in ordering the levels in Figure 1, for the distal "purpose" of the genes must necessarily be mediated by proximal mechanisms.

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