
Genetic Similarity, Mate Choice, and Fecundity in Humans

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Increasing evidence suggests that both mating patterns and fecundity correlate with the genetic similarity of the interactants in plants, animals and humans. Direct evidence is reported here for this phenomenon in humans. Based on blood antigen analyses of nearly 1,000 cases of disputed paternity, it was found that the degree of genetic similarity within pairs predicts (1) whether the pair is sexually interacting or randomly generated, and (2) whether the pair produced a child together or not. Seven polymorphic marker systems (ABO, Rhesus (Rh), P, MNSs, Duffy (Fy), Kidd (Jk), and HLA) at ten loci across six chromosomes were examined. Sexually interacting couples were found to share about 50% of measured genetic markers, part way between mothers and their offspring who share 73% and randomly paired individuals from the same sample who share 43%. Moreover, in the cases of disputed paternity, degree of genetic similarity in the sexually interacting couple predicted male inclusion: males not excluded from paternity were 52% similar to their partners whereas those excluded were only 44% similar.

KEY WORDS: Assortative mating; Blood testing; Genetic similarity; Kin recognition; Human sociobiology.

Much previous research fits with the view that organisms optimize the degree of genetic compatibility in mates by selecting partners neither too similar nor too dissimilar. Evidence for this phenomenon comes from the study of plants (Willson and Burley 1983), non-human animals (Bateson 1983; Thiessen and Gregg 1980), and humans (Rushton and Nicholson, 1988; Rushton and Russell 1985; Russell, Wells and Rushton 1985; van den Berghe 1983). Although a pattern of positive assortment can arise for reasons other than homotypic preference, such as the consequences of competition for the most fit mates (Burley 1983), many investigators have hypothesized the adaptive advantage of an optimal degree of genetic similarity (Bateson 1983; Rushton, Russell and Wells 1984; Thiessen and Gregg 1980). Advantages thought to accrue to optimal genetic

Received September 23, 1987; final draft accepted October 29, 1987.

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Ethology and Sociobiology 9: 329-333 (1988)
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655 Avenue of the Americas, New York, NY 10010

0162-3095/88/\$03.50

similarity in mates include increased marital stability, greater fecundity, increased relatedness to offspring, and increased within-family altruism.

Preliminary evidence supports each of the hypothesized advantages. Several studies have shown that not only the occurrence but also the stability of relationships is predicted by the degree of matching on personality characteristics (see Rushton, Russell and Wells 1985, for review). Other studies have shown that the degree of assortative mating correlates with the number of children for anthropometric variables, intelligence test scores, educational attainment, and family size (see Thiessen and Gregg 1980, for review). In addition Bresler (1970) found that fetal loss increased with each additional country of birth among great-grandparents and with distance between the birthplaces of mates. With respect to within-family altruism, data shows that while similar children are preferred (Daly and Wilson 1982; Littlefield and Rushton 1986), step children are at risk for abuse (Daly and Wilson 1985).

The upper limit on the fitness-enhancing character of assortative mating occurs with incest. Too much genetic similarity between mates increases the chances that harmful recessive genes may combine, producing the negative effects of "inbreeding depression" which have been demonstrated in many species including humans (Thiessen and Gregg 1980; van den Berghe 1983). As a result it has been hypothesized that epigenetic rules have evolved to underlie the "incest taboo", possibly working through negative imprinting on intimate associates at an early age (Lumsden and Wilson 1981).

Optimal fitness, then, may consist in selecting a mate who is genetically similar but not actually a relative; van den Berghe (1983) speculates the ideal percentage to be about 12.5%, or the same as that between first cousins. One classic study was carried out with Japanese quail who, although promiscuous, proved particularly sophisticated, preferring first to third cousins, and both of these to either siblings or to unrelated birds thus avoiding the dangers of too little or too much inbreeding (Bateson 1983).

In the current study degrees of genetic similarity in humans are estimated by using blood antigen analyses for four categories of relationship.

METHOD

Overview

Blood antigen data from nearly 1,000 pairs of sexually interacting couples were examined. These analyses were made possible by records provided by Serological Services Limited, a company based in Toronto, Canada, offering blood testing and legal testimony in cases of disputed relationships such as paternity. Genetic similarity was calculated using blood antigens at ten loci for four relationship dyads: 1) mother-offspring, 2) sexually interacting couples with males not excluded from paternity, 3) sexually interacting couples

with males excluded from paternity, and 4) randomly generated male-female pairs.

Subjects and Procedures

Since blood groups are known to differentiate ethnic groups, the samples were limited to those of North European appearance. This was done prior to analysis by examining photographs maintained for purpose of legal identification. All analyses were conducted by officials of the company and confidentiality was maintained throughout. Each case of disputed paternity available in the records was examined, and the percentage of similarity between the male-female pairs across ten loci was calculated based on the proportion of concordant antigens both within and between genetic systems. These genetic markers derive from seven polymorphic systems (ABO, Rhesus (Rh), P, MNSs, Duffy (Fy), Kidd (Jk), and HLA) across six chromosomes, and in most cases of paternal dispute are sufficient to provide a 95.00% to 99.75% confidence rating of inclusion (Bryant 1980). They provide a less precise but still useful estimate of genetic distance among unrelated individuals. For comparison purposes the same metric was used to calculate the percentage of similarity for 100 mother-offspring pairs and 200 randomly paired male-female couples from the entire set of 986 pairs after excluding the possibility of an individual being re-paired with the same partner.

RESULTS

The percentage similarity for the four relationship categories are shown in Table 1. A one-way analysis of variance revealed a highly significant difference in degree of genetic similarity across the groups ($F(3,1282) = 161.37$, $p < 0.001$). A priori contrasts of adjoining categories were performed, also demonstrating significant differences (Groups 1,2: $t(1282) = 16.57$, $p <$

Table 1. Percentage of Genetic Similarity Based on 10 Blood Loci in Four Types of Human Relationship

Relationship	Number of pairs	Mean \pm SE	Standard deviation	Range	95% Confidence interval for mean
Mother-offspring	100	73.37 \pm 0.91	9.31	50-88	71.52-75.22
Sexually interacting adults in which male is not excluded from paternity	799	52.02 \pm 0.4	11.84	17-90	51.20-52.85
Sexually interacting adults in which male is excluded from paternity	187	44.42 \pm 0.9	12.13	15-74	42.67-46.17
Randomly paired individuals	200	43.10 \pm 1.0	14.40	11-81	41.09-45.11

0.001; groups 2,3: $t(1282) = 7.71, p < 0.001$; Groups 2,4: $t(1282) = 9.29, p < 0.001$). Sexually interacting couples who produced a child together are more genetically similar than either randomly paired individuals or sexually interacting couples in which the male is excluded from paternity. The two sexually interacting groups combined share about 50% of measured genetic markers, part way between the mothers and their offspring who share 73%, and the randomly generated dyads who share 43%. Thus these results demonstrate that successful human mating follows lines of genetic similarity.

DISCUSSION

Several mechanisms may be responsible for the observed relationships. Since blood groups are known to be differentiated across geographical areas and clines within these areas (including both those associated with socioeconomic status (Beardmore and Karimi-Booshehri 1983) and with personality and cognition (Eysenck 1982)), the blood antigen similarities result from assortment on related variables. These blood group differences are not an unimportant epiphenomenon because the results do demonstrate that *in effect*, successful human mating follows lines of genetic similarity. Moreover, pleiotropy may be involved. As mentioned, the postulated value of optimal homogamy includes the avoidance of inbreeding, greater fecundity, a strengthened mating bond, and increased parental care. Of interest in this respect is the finding of greater genetic similarity within couples who produce a child than within those who do not. Although this result may be due to differing degrees of casualness in the relationships, it is worth repeating that associations have been found between fecundity and similarity of spouses for anthropometric variables, intelligence test scores, educational attainment, and family size (Thiessen and Gregg 1980).

The hypothesis that human mate choice is influenced by genetic similarity is further supported by the observations of positive correlations between independent estimates of heritability and assortative mating for a range of anthropometric, cognitive, and social behavioral characteristics (Rushton and Nicholson, 1988; Rushton and Russell 1985; Russell et al. 1985). Put another way, it has been observed that humans assort on the basis of the more genetically influenced of a set of traits. These data were predicted by genetic similarity theory, a formulation that extends the idea of kin selection by postulating that organisms have a tendency to favor any individual of similar genotype, regardless of whether or not they are "kin" (Rushton et al. 1984).

Moreover recent data show that male friendships also appear to be mediated by genetic similarity as measured by blood tests and differential heritability estimates (Rushton and Chan 1987). More generally then, the evidence suggests that ontogeny in the domain of social preferences may depend on the activity of epigenetic rules biasing individuals in the direction

of genetic similarity, instead of alternatives (Rushton, Littlefield and Lumsden 1986). Irrespective of this wider issue the results from a range of studies, including the present one, are in accord with the view that humans, like other animals, select mates with an optimum degree of genetic similarity.

I am grateful to N. J. Bryant, P. K. F. Chan, I. R. Nicholson and Serological Services Ltd. of Toronto for comments and/or help with the data analysis. The work was supported by a grant from The Pioneer Fund.

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