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THE GENERALIZABILITY OF GENETIC ESTIMATES

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Summary—Evidence for both the differential and generalizable nature of estimates of genetic influence has recently been found across distinct ethnic and national groups. Estimates of genetic influence on cognitive tasks calculated from Korean parent–offspring regressions significantly correlate with similar estimates from Japanese-American and European-American samples, and together they predict similarities between spouses in still other samples. Heritabilities calculated for personality in Australian twins significantly correlate with those calculated in British twins and, together with heritabilities for social attitudes calculated in Australian twins, they predict similarities between Canadian friends. Inbreeding depression scores calculated in Japan on the WISC subtests in the 1950s predict black–white difference scores on the WISC—R in the 1970s. These findings cannot be attributed to the confounding effects of measurement error for the relationships remain after controlling for reliability. The resuls suggest that estimates of genetic influence on various traits may be more robust across populations, languages, time periods and measurement specifics than has been considered to date.

INTRODUCTION

It is usual to consider estimates of genetic influence to be properties of particular populations and not to be highly generalizable (Falconer, 1981). Moreover, the question of whether personal attributes are differentially heritable is not considered to be conclusively answered (Loehlin, 1986; Loehlin and Nichols, 1976; Loehlin, Willerman and Horn, 1988). In a series of recent studies, however, differing estimates of genetic influence have been used to test predictions from sociobiological theorizing concerning the role of the genes in mediating similarity between marriage partners and same sex friendships, and in mediating racial-group differences in cognitive abilities. The positive results emanating from these studies cannot be attributed to the confounding effects of unreliability of measurement for, as we will see, the relationships remain even after controlling for reliability.

EPIGENETIC RULES IN SOCIAL PREFERENCES

The topic of differential and generalizable heritabilities arose in the context of testing genetic similarity theory (Rushton, Russell and Wells, 1984), an extension of the kin-selection theory of altruism, which postulates that people detect genetic similarity in others (nonkin as well as kin) in order to proffer preferential treatment to those most similar. This suggests a new theory of attraction and friendship. One prediction is that since social assortment in humans is genetically mediated it should occur on the basis of traits of high rather than low heritability because the more genetically influenced traits better reflect the underlying genotype and provide a more accurate cue for matching. In order to control for the operation of other variables it is best to test this hypothesis using sets of homogeneous traits (e.g. anthropometric vs attitudinal variables). Using a within-subjects design, Russell, Wells and Rushton (1985) examined data from three studies reporting independent estimates of genetic influence and assortative mating and found positive correlations between the two sets of measures ($r = 0.36$, $P < 0.05$, for 36 anthropometric variables; $r = 0.73$, $P < 0.10$, for 5 perceptual judgement variables; and $r = 0.44$, $P < 0.01$, for 11 personality variables). In the case of the personality measures, test–retest reliabilities over a 3 yr period were available and were found not to influence the results.

Another test of the hypothesis was made by Rushton and Russell (1985) using data on 54 personality traits where similarity between spouses was found to be predicted $r = 0.44$ ($P < 0.001$) by the parent–offspring regression, and $r = 0.46$ ($P < 0.001$) by the doubled sib–sib intraclass coefficient. Moreover the two estimates of genetic influence were found to correlate with each other at $r = 0.38$ ($P < 0.001$), and a simple arithmetic composite of the two raised the relationship with assortative mating to $r = 0.55$ ($P < 0.001$), a figure not altered when controlling for test reliability, assessed in this study by α coefficients. Rushton and Russell (1985) also reviewed other reports of similar correlations, including Kamin's (1978) calculation of $r = 0.79$ ($P < 0.001$) for 15 cognitive tests and DeFries, Ashton, Johnson, Kuse, McClearn, Mi, Rashad, Vandenberg and Wilson's (1978) calculation of $r = 0.62$ ($P < 0.001$) for 13 anthropometric variables. Differential test reliability is unlikely to have been the cause of the findings with the anthropometric variables reported by DeFries *et al.* (1978) nor those reported above by Russell *et al.* (1985), for Rushton (1989a) found that these particular anthropometric measures can be made with high degrees of precision (e.g. inter-rater reliability > 0.90).

Subsequently, these analyses were extended to include a between-subjects design and the phenomenon was found to be robust. Thus Rushton and Nicholson (1988) analyzed data from studies using 15 subtests from the Hawaii Family Study of Cognition (HFSC) and 11 subtests from the Wechsler Adult Intelligence Scale (WAIS); positive correlations were calculated within and between samples. For example, with the HFSC, parent–offspring regressions (corrected for reliability) from Americans of European Ancestry (AEA) in Hawaii, Americans of Japanese Ancestry (AJA) in Hawaii, and Koreans in Korea intercorrelated positively (mean $r = 0.54$, $P < 0.01$). Spousal similarity scores were taken from five samples including, in addition to the three aforementioned, Americans of Mixed Ancestry (AMA) in California, and a group in Colorado. The estimates of genetic influence calculated on one sample often predicted the degree of spousal similarity in the others, e.g. AJA $r = 0.60$ with AEA and $r = 0.63$ with AMA, with an overall mean $r = 0.38$ for the 15 tasks. Aggregating across the estimates to form the most reliable composite resulted in a substantially higher prediction of mate similarity from the estimate of genetic influence ($r = 0.74$, $P < 0.001$). Similar results were found with the WAIS. Three estimates of genetic influence intercorrelated with a mean $r = 0.82$ and predicted an aggregate of spousal similarity scores $r = 0.52$ ($P < 0.05$).

Parenthetically, it is worth noting that partialling out *g* in both the HFSC and WAIS analyses led to substantially lower relationships between estimates of genetic influence and assortative mating, thus offering support for the view that marital assortment on intelligence occurs primarily on the *g* factor (Cattell, 1982; Eaves, Heath and Martin, 1984; Nagoshi and Johnson, 1986). The *g* factor tends to be the most heritable part of cognitive performance measures (Vernon, 1989a), as well as being highly generalizable across measures and samples (Vernon, 1989b).

Close friends are also found to be most similar on the more genetically influenced sets of attitudinal, personality and anthropometric characteristics. Rushton (1989a) recruited 76 non-related long term male Caucasian friendship pairs ranging in age from 18 to 57, from the general community. Many variables were explicitly measured because calculations had been made of the degree of genetic influence on the components or items. Thus with respect to 50 social attitude items, 36 heritabilities were available from 3810 Australian twin pairs (Martin, Eaves, Heath, Jardine, Feingold and Eysenck, 1986). For 90 items from the Eysenck Personality Questionnaire, two independent sets of heritability estimates were available for a total of 81 of the items, one set from 3810 Australian twin pairs (Jardine, 1985), and the other set from 627 British twin pairs (Neale, Rushton and Fulker, 1986). These intercorrelated $r = 0.44$ ($P < 0.001$) and were aggregated to form a more reliable composite. For 13 anthropometric measures, estimates of genetic influence were available based on mid-parent offspring regressions from 125 families in Belgium (Susanne, 1977). In addition, test–retest data were available from the two questionnaire measures, and pilot work showed that the anthropometric measures could be made with very high levels of precision.

Examples of the varying heritabilities include: 51% for attitude to the death penalty vs 25% for attitude to the truth of the bible (Martin *et al.*, 1986), 41% for having a preference for reading vs 20% for having a preference for many different hobbies (Neale *et al.*, 1986), and 80% for midfinger length vs 50% for upper arm circumference (Susanne, 1977). Unlike the estimates of genetic influence calculated for relationships between spouses based on parent–offspring regressions, in the current study the heritabilities are based on the comparison of monozygotic and dizygotic twins. In evaluating these results it should be kept in mind that the heritabilities are being generalized from one sample (e.g. Australian twins) to another (Canadian friends).

Like marriage partners, similarity among the friends was most marked on the more genetically influenced of the characteristics. For the 36 conservatism items, the correlation between the heritabilities and the friendship similarities was 0.40 ($P < 0.05$), a relationship not altered when correcting for test–retest reliability. For the 81 personality items, the correlation was $r = 0.20$ ($P < 0.05$), also not altered when correcting for test–retest reliability. For the 13 anthropometric variables, however, the correlation was a non-significant $r = 0.15$. It may also be worth noting that the genetic basis of relationships has been confirmed by blood antigen analyses, for both male friendship dyads (Rushton, 1989a) and for sexually interacting couples (Rushton, 1988a).

That social assortment occurs most on the more genetically influenced of traits has been confirmed on over 20 separate tests, some of which were quite stringent as when estimates of genetic influence calculated on Koreans and Australians were used to predict similarity in marriages and friendships in Americans and Canadians. These results imply that estimates of genetic influence are both differential and generalizable.

PREDICTING POPULATION DIFFERENCES IN COGNITIVE ABILITY

Inter- and intra-national average differences exist on measures of intelligence and educational attainment with Mongoloids > Caucasoids > Negroids (Jensen, 1985; Lynn, 1987). While the causes of the differences remain debated (Rushton, 1988b,c; Zuckerman and Brody, 1988), data suggest that some of the between-group variance may be genetic in origin. Black–white differences are greatest, for example, on the more *g* loaded subtests (Jensen, 1985) which are the ones found to be most genetically influenced (Jensen, 1987; Vernon, 1989a) as well as to be the most generalizable (Vernon, 1989b). Thus Jensen (1987) reported rank order correlations of +0.55 and +0.62 between estimates of genetic influence from two twin studies and the *g* loading of the 11 WAIS subtests. Vernon (1989a) found a correlation of +0.60 between the heritabilities of a variety of speed of reaction time tasks and their relationship with the *g* loadings from a psychometric test of general intelligence. Assuming these results are not due to the operation of differential reliabilities, they too provide evidence for the generalizable (predictable) nature of different heritabilities.

To more directly test the hypothesis that the group differences in intelligence are in part mediated by genetic factors, Rushton (1989b) correlated estimates of genetic influence based on inbreeding depression scores from 7 to 10 yr old Japanese children (Jensen, 1983) with black–white difference scores on a revised version of the same tests from U.S. children twenty years later (Jensen, 1985). The Japanese children were tested in the 1950s on 11 Wechsler Intelligence Scale for Children (WISC) subtests and the American children were tested in the 1970s on the same subtests from the WISC—R. Also reported by Jensen (1985) were the reliabilities of the subtests. Spearman and Pearson correlations between the estimates of genetic variance and the magnitude of the black–white differences were then computed both before and after correcting for reliability (by dividing the black–white difference scores by the square root of the test's reliability, and also through partial correlation). These data are shown in Table 1.

Table 1. Inbreeding depression scores on WISC from Japan, and black–white difference scores and test reliabilities on WISC—R from the United States

			Black–white standardized differences				
WISC Subset	Inbreeding depression (N = 1854)	Reliability	Sample 1 (N = 2173)	Sample 2 (N = 570)	Sample 3 (N = 646)	Sample 4 (N = 1237)	Sample 5 (N = 172)
Information	8.30	85	81	69	93	101	54
Similarities	9.95	81	79	53	84	82	67
Arithmetic	5.05	77	61	48	63	68	43
Vocabulary	11.45	86	88	67	78	90	53
Comprehension	6.05	77	94	80	65	65	47
Picture completion	5.90	77	79	61	63	65	41
Picture arrangement	9.40	73	77	65	76	79	38
Block design	5.35	85	93	73	96	89	80
Object assembly	6.05	70	82	64	81	82	66
Coding	4.45	72	47	39	50	46	07
Mazes	5.35	72	69	59	83	81	—

Taking a weighted average of these correlations and testing their significance using Fisher's test for combining probabilities (Winer, 1962), the Spearman ρ between inbreeding depression and the black–white average difference before correction is 0.48 ($P < 0.05$; Pearson's $r = 0.42$, $P < 0.05$) and after correction is 0.40 ($P < 0.05$; Pearson's $r = 0.32$, $P < 0.10$). Partialling out reliability rather than correcting for it reduced the average Pearson correlation to 0.23. (Reliability correlated $r = 0.50$ with both the inbreeding depression and the difference scores, as well as with the g loadings from the Japanese sample. The merits of different correction procedures have been discussed by Jensen, 1985, and commentators, and the partial correlation represents a very conservative procedure, even to the point of making a gross over-correction; Rushton, 1989b.)

CONCLUSION

The main methodological difference between our studies finding differential and generalizable heritabilities and previous studies apparently failing to do so (Loehlin, 1986; Loehlin and Nichols, 1976) seems to be our use of correlational statistics (rather than χ^2) which serve to capture more variability. Otherwise the sensitivity of the design should have favoured the earlier studies since they used a within-subjects procedure to predict the same measures whereas we often used a between-subjects procedure to predict disparate measures. It would be of interest to see the earlier data re-analyzed using correlations. In any case, from the data reported here, estimates of genetic influence appear to have a greater robustness across populations, languages, time periods and measurement specifics than has been considered to date.

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