Hum. Genet. 39, 69—86 (1977)

Human Genetics

Absence of a Relationship between Degree of White Ancestry and Intellectual Skills within a Black Population

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Introduction

Genetic differences have been offered as an hypothesis to explain the average IQ difference usually found between US black and white populations (Jensen, 1973; Shockley, 1972). While most behavioral scientists would choose to ignore the hypothesis as distasteful, there is little direct evidence against it (Scarr and Weinberg, 1976). Those who prefer an environmental hypothesis to account for the average difference between black and white groups on intellectual tests have not succeeded in accounting for the magnitude of the effect, nor have those who hold a genetic hypothesis been able to refute an environmental stance. No direct comparisons of black and white samples will settle the issue of possible genetic differences, because obvious environmental differences are confounded with any genetic differences between the populations that are socially classified as black and white (Scarr-Salapatek, 1971a, 1971b, 1972, 1973, 1974; Scarr and Weinberg, 1976).

The fact that US blacks are a hybrid population[1] makes the study of admixture a potential method to evaluate the effects of racial genetic differences. Those environmental differences between the races that affect *all* blacks equally, but no whites, will not contaminate the possible relationship between genetic racial differences and intellectual performance within the hybrid group. Thus, if genetic, racial differences do contribute to average intellectual differences between blacks and whites, then those blacks with higher degrees of white ancestry should perform better on intellectual tests than those with lesser degrees of admixture (Jensen, 1973; Shuey, 1966).

Even within the hybrid group, the effects of environmental differences cannot be ignored. The amount of racial discrimination may be related to the degree of

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[1] In the United States, any person with visible signs of African ancestry is socially classified as black. This social classification of race provides the basis for Reed's (1969a; 1969b; 1973) report that blacks in the Oakland, California area have about 22% European ancestry, whereas socially classified whites in the same area have less than 0.1% African ancestry

African ancestry (Klineberg, 1963). Invisible markers for ancestry, such as blood group loci, are likely to be correlated with visible markers for discrimination, such as skin color, nose and lip width, hair texture, and the like. Great care must be taken to separate the effects of correlated genetic and environmental variables on intellectual performance.

This study will evaluate the hypothesized effects of genetic racial differences, estimated from blood group and serum protein loci, on intellectual performance in a sample of black twins. Social, environmental effects will be considered apart from genetic differences between the racial groups. The construct validity of two measures of ancestry will be examined.

Admixture Estimates for US Blacks. Estimates of the degree to which contemporary black gene frequencies derive from ancestral African and Caucasian populations vary, depending upon the region of the country, the gene loci used to estimate admixture, and the sampling procedures (Adams and Ward, 1973; Class and Li, 1953; Pollitzer, 1972; Reed, 1969a, 1969b, 1973). There is general agreement, however, that the Duffy (Fy) locus offers the best estimates of about 22% of Caucasian admixture in Northern urban populations.

Population admixture estimates are an *average* of the individuals in the hybrid population. Individual ancestry can vary from near zero to near one when the admixture has continued over ten generations. Independent assortment and mating that is random with respect to admixture serve to distribute Caucasian genes throughout the hybrid population; assortative mating with respect to admixture tends to restrict gene flow within the population. Because there are no accurate pedigrees over ten generations and because the population parameters that affect the distribution of admixture cannot be measured historically, it is very difficult to estimate the distribution of Caucasian genes among individuals in the contemporary black population. Recently, MacLean and his colleagues (1974) estimated the distribution of admixture in a large black sample from upstate New York. The individual Caucasian admixture values ranged from less than 10% to more than 60%, with a mean around 20%. The standard error of estimate for their admixture value (θ), based on nine blood group systems, is so large (± 2 SE.2 ± 0.16) that point estimates of admixture were not really achieved. They did find, however, a significant relationship between θ and hypertension in the black group.

Correlates of Ancestry and Intellectual Skills. Any positive or negative relationship between blood group estimates of ancestry and intellectual skills will be confounded with correlates of the two variables. For example, blood group estimates of ancestry are likely to be correlated with skin color, another set of genetic markers. If skin color depends upon a few gene loci (Stern, 1970), then a large set of independent blood group markers drawn from the same ancestral population should be correlated with skin color. The magnitude of the correlation will depend upon the degree of reassortment and the dispersion of admixture in the black population. But skin color is also a visible marker for racial discrimination and has in the past been associated with socioeconomic status within the US black population. The darker one is, the lower one's social status (Klineberg, 1963). Socioeconomic status is usually positively correlated with intellectual achieve-

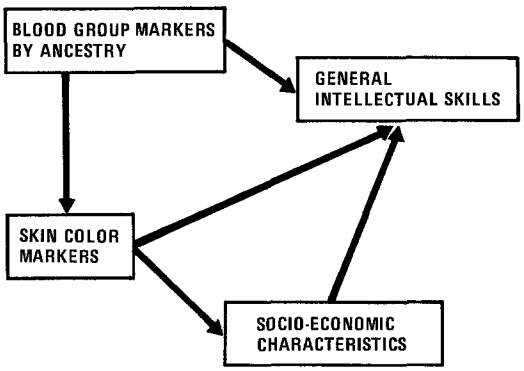

Fig. 1. A model for the effects of ancestry and socioeconomic status on the intellectual skills of US blacks

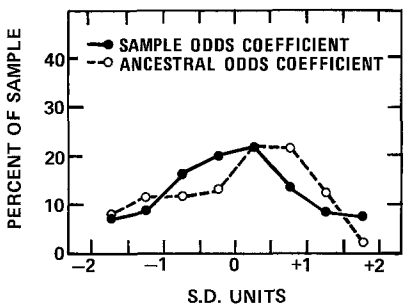

Fig. 2. The distribution of ancestral and sample odds coefficients in the sample of Philadelphia blacks

ments. Thus, skin color and socioeconomic characteristics must be considered as correlates of any estimate of ancestry and intellectual skills in the black population.

The path model shown in Figure 1 specifics the genetic and environmental contributions of ancestry (blood groups and skin color) and life chances (socioeconomic status and skin color) to intellectual skills.

Blood Group Markers. Blood group loci, including red cell antigens and serum proteins, are the most reliable markers of population differences. While 90% of the variance in blood group phenotypes occurs within populations, some 10% occurs between populations (Nei and Roychoudhury, 1972). At some loci, such as Duffy and Gm, alternate alleles are found in some populations and not others; for most loci, however, only allelic frequencies vary among populations.

Known blood group loci are a very small sample of the total genome, which is estimated to contain from 15 000 to 100 000 loci. It is possible that blood group markers do not sample those segments of the genome associated with cognitive abilities (Loehlin et al., 1973). If independent assortment has occurred repeatedly over many generations, one might not expect any association among genes from the same ancestral population, except those that are closely linked.

On the other hand, if reassortment is limited by low crossover rates and by assortative mating with respect to admixture, genetic markers from an ancestral population will not be totally dissociated in the hybrid group, even after ten generations. Evidence on the nonindependence of population markers can be found in the correlations among blood groups and between blood groups and other genetic markers, such as skin color. If unlinked genetic markers are still associated, then there is some reason to believe that other genes (those associated with cognitive skills) from the same ancestral population are still associated with the blood group markers.

It should be clear nonetheless that even without assortative mating for admixture to maintain a high degree of association of Caucasian genes, the use of genetic loci to index the proportion of Caucasian ancestry—contrary to what some authors seem to suggest (Loehlin et al., 1973)—is not invalidated. From a sampling perspective, if 40% of an individual's genome derives from the white population, then an adequate, random sample of genetic markers discriminating ancestral origin of the alleles should *on the average* reflect that actual percentage. This in turn should also be the best estimate of the proportion of genes influencing cognitive phenotypes that derive from one or other ancestral group.

An even greater problem in producing reliable estimates of individual admixture is the high degree of overlap in gene frequencies among contemporary human populations. MacLean and Workman (1973) proposed a method by which individual admixture estimates in a hybrid population can be calculated. Reed (1973) noted, however, that at least 18 loci that discriminate perfectly between the two ancestral populations would be required to obtain point estimates of individual admixture with acceptable standard errors. There are only two nearly perfect loci and many which yield far less information about ancestry. Given the paucity of blood group loci that discriminate African from Caucasian populations, we reject the possibility of *point* estimates of admixture at the present time.

We propose instead an *odds coefficient*[2] that establishes a rank order of individuals depending upon their resemblance at several blood group loci to one of two populations. By using phenotype[3] frequency estimates for populations A and B, the odds that an individual's phenotype came from population A can be estimated with the following formula:

$$O_A = \log \left[\frac{A_1 A_2 A_3 \ldots A_n}{B_1 B_2 B_3 \ldots B_n} \right]$$

[2] Other coefficients were assessed for their efficiency in discriminating individual differences in ancestry within the black population. An additive model $\left[\frac{A_1 - B_1}{A_1 + B_1} + \frac{A_2 - B_2}{A_2 + B_2} + \ldots + \frac{A_n - B_n}{A_n + B_n}\right]$, a model that weighted the loci by the combined phenotypic frequencies for populations A and B $\left[\log \left(\frac{A_1 A_2 \ldots A_n}{A_1 A_2 \ldots A_n + B_{12} \ldots B_n}\right)\right]$, and several others were tried. The coefficients were all highly correlated (> 0.9) unless their distributions were very poor. We chose the simplest odds coefficient with a good distribution

[3] Phenotype frequencies were chosen instead of genotypes because, for many loci, estimating individual genotypes is another tentative step away from the data. For loci without codominant alleles, particularly complex ones such as Rhesus, estimating individual genotypes seemed unnecessarily combersome. The use of individual phenotypes and phenotypic frequencies avioded this problem

where A_1 is the frequency of the individual's phenotype at locus 1 in population A, B_1 is the frequency of his phenotype at locus 1 in population B, etc.

The odds coefficient is not an admixture estimate; it is merely an expression of the combined probabilities across n loci that an individual's blood group alleles come from population A, given the frequency to those alleles in populations A and B. The size of the odds coefficient, when considering only one marker locus, depends on how dissimilar the phenotype frequencies are in the presumed ancestral populations. Thus, perfect discrimination occurs when a gene exists in one ancestral population but not the other. The more similar the frequencies are, the less reliably the origin of the genetic marker can be predicted and consequently the smaller the odds. The formula can be used to express the relative odds that an individual comes from either one of two populations with contrasting phenotype frequencies.

African and Caucasian Populations: The Putative Parents. Many African groups contributed to the US black gene pool over several centuries. The estimation of an historical ancestral population from contemporary African populations is fraught with pitfalls. There is considerable heterogeneity in gene frequencies among contemporary African ethnic groups; no one knows the exact proportions of slaves that were brought to the USA from these varied groups, or even if the contemporary groups are the same ones that inhabited the regions from which slaves were brought. Further, no one knows if the slaves were an random sample of the African populations, or if survival and reproductive rates were equal across the African groups that became slaves. Possible selection trends and genetic drift complicate the estimation problem still more. Thus, the gene frequencies for any putative African 'parent' population for contemporary US blacks makes many tenuous assumptions (Adams and Ward, 1973).

Estimates of gene frequencies for European populations that contributed to the US black population pose similar problems, but there is less heterogeneity in gene frequencies among the Northern European groups that are thought to have contributed the majority of genes to the hybrid blacks. This putative parent population is probably more accurately estimated than the former.

Given the severe reservations that any reasonable person would have about our ability to estimate 'parent' populations for contemporary US blacks, we attempted to develop construct validity for two odds coefficients: one based on estimated ancestral frequencies and one based on contemporary samples of blacks and whites. The odds coefficients were then tested for relationships with measures of intellectual skills.

Material and Methods

Subjects. The subjects of this report are same-sex twins who were sampled from black and white populations in Philadelphia, Pennsylvania, for the study of genetic variability in physical, mental, and personality development from 10 to 16 years of age. The fact that the subjects are twins is not directly relevant to the study of ancestry or admixture. The black twins were drawn from 181 different families, each of whom is represented by two offspring. About 59% of the black pairs are dizygotic (DZ), and the remaining 41% monozygotic (MZ).

Table 1. Twin pairs by race, sex, and zygosity

Zygosity	Black		White		Total pairs
	Male	Female	Male	Female	
Monozygotic	34	43	67	63	209
Dizygotic	44	60[a]	52	42	196
Total	78	103[a]	119	105	405

[a] includes 2 sets of triplets

The major effect of using twin pairs in the study of ancestry is to confuse the issue of how many degrees of freedom ought to be allowed in the statistical analyses (Elston, personal communication 1974). In the case of monozygotic pairs, they have the same ancestry, as estimated by genetic markers, but they seldom have exactly the same mental test scores. Dizygotic twins have neither the same ancestry nor the same test scores. We would have used only one twin from each family and thereby eliminated the confusion about degrees of freedom, but the analyses would have lost some information in the reduced sample. We could have averaged the test scores of the co-twins, but it was not clear that this was an equally appropriate procedure for both MZ and DZ pairs. Therefore, after discussions with several statisticians, we decided to use both members of the twin pair but to reduce the degrees of freedom to a range between the number of independently sampled families and the number of individuals. In the tables, however, the number of families and twin pairs are both given.

The samples of black and white twins are described in Table 1. Of the black twin pairs, 157 come from the city public schools, the remainder from the city parochial schools. Socio-economic characteristics of their neighborhoods were taken from census tracts. The median income of the tracts in which black twins reside is $ 7910, and the median adult educational level is 10.2 years. Both figures are very close to the average 1970 census figures for urban black families. The subjects ranged in age from 10 years to 15 years, 11 months.

The actual sample sizes available for the several analyses to be reported in this paper varied from about 300 individuals from 160 twin pairs to 288 individuals in 144 pairs on whom we had complete blood group data on the 12 systems used for estimation of ancestry and nearly complete mental test data. The largest reduction in sample size occurred for the paired-associate learning task, because the established instructions were not sufficiently understood by the inner-city black children, resulting in the elimination of many of their results. The other mental test results have more valid pairs, as indicated in the tables.

Procedures. The children were each paid $ 10 to participate, and they received a free dental check up, physical growth assessment, and refreshments. They were brought after lunch by chartered bus from the elementary school nearest their homes and returned to the school after approximately 5 h at the Dental School, University of Pennsylvania.

Co-twins were separated into different small groups, each with an adult leader who explained the procedures, answered questions, and gave assistance. An average of 28 children, divided into four small groups, were tested each weekday afternoon from early July to early August, 1972.

For the psychologic assessments the small groups were assembled in a large auditorium. Seating was arranged in alternate seats and rows. Test materials were presented by 35 mm slides on a large screen. Instructions and test items were presented by audio tape and coordinated automatically with the slide presentations. No reading skills were required. All of the materials had been pretested with 30 black, inner-city children who were paid a consultant fee to criticize the procedures and tests. Based on the pretest, all test instructions were made more redundant than standard instructions to help the disadvantaged black children to understand the nature of tasks. Group leaders monitored the children's use of the simplified answer sheets for the tests.

Blood samples were drawn at the end of the day, just before the payments were given out. Although some children were reluctant to have blood drawn, peer pressure at the promise of ten dollars produced excellent cooperation and minimal distress.

Intellectual Skills. Five measures of intellectual skills were administered as parts of two 1¼ h psychologic assessments that also included personality and self-esteem measures. The two sessions were separated by approximately 1 h, in which dental, taste, dermatoglyphic, radiologic, physical growth, and other assessments were made. Refreshments were served during a break between sessions.

The Raven Standard Progressive Matrices, Sets A, B, C, and D were included to measure abstract reasoning skills. Seventy items from the Peabody Picture Vocabulary Test were used to measure knowledge of standard English vocabulary. Thirty items from the Columbia Test of Mental Maturity were used to assess conceptual skills. The Revised Figural Memory Test was included to test conceptual memory for designs. Finally, a paired-associate task was included to test rote, associative learning skills.[4]

The matrices, vocabulary, and conceptual skills tests were all found to have high internal consistencies, ranging from 0.82 to 0.95 in the black sample (Kuder-Richardson, Formula 20). The figural Memory Test and the paired-associate task are not suited to consistency analysis, but their expected correlations with the other cognitive measures (~0.5 and 0.3 respectively) were observed. Factor analysis of the first four cognitive tests showed similar high loadings (0.75 to 0.79) on a first principal component, accounting for half of the variance in separate analyses on the black and white samples. There is every reason to believe that the first four tests are valid, reliable measures of intellectual skills in a black sample. The paired-associate test is less related to the others, both theoretically and empirically. The scores used in this paper were standardized by 1-year age intervals to eliminate age variance.

Socioeconomic Status. Two measures of socioeconomic status were obtained. The Home Index (Gough, 1949), a 24-item measure of family SES, was administered as part of the first test battery. It was found to be unreliable for black children because co-twins often disagreed about information on their families (Carter-Saltzman et al., 1975). A revised scale of the ten most reliable items was included in this study. Census tract median values for educational level and income were obtained on all census tracts in which black twins lived. The census tract in an urban area is fairly homogeneous with respect to socioeconomic characteristics, but it is an imperfect measure of individual SES. It is a good measure of some neighborhood and school characteristics that are related to children's intellectual development.

Skin Color Reflectance. Both black and white twins were measured on skin reflectance. Three filters (red, blue, green) and three locations (forehead, medial aspect of the lower arm, and inside of the upper arm) combined to produce nine measures of skin color reflectance. The reflectance values were so highly intercorrelated ($r > 0.8$) that only one, red filter-forehead, will be reported here. The reliability of the skin color measures is reflected in the very high heritabilities, between 0.85 and 0.98.

Blood Group Markers. Two 10-cm^3 blood samples were obtained from each child, one in EDC solution, one in a clot tube. Blood samples were shipped daily by air in refrigerated cartons to the Minneapolis War Memorial Blood Bank for typing. The following marker loci were assessed: ABO (A_1, A_2, B, 0) MNSs, Kidd (Jk^a, Jk^b), Kell (K, k), Rhesus (r, r′, R^0, R^1, R^2), Ceruloplasmin (Cp^a, Cp^b, Cp^c), Group Specific (Gc^1, Gc^2), Transferrin (Tf^C, Tf^D), Duffy (Fy^a, Fy^b), Hemoglobin (Hb^A, Hb^S, Hb^C), Haptoglobin (Hp^1, Hp^2) , Adenylate kinase (AK^1, AK^2) Gm (a, x, b, c), and Inv(1). The distribution of the blood group phenotypes and the intellectual test scores are available from the American Documentation Service.

[4] J. C. Raven, *Standard Progressive Matrices:* Sets A, B, C, D, and E (H. K. Lewis and Co., London, 1958); L. M. Dunn, Peabody picture vocabulary test (American Guidance Service, Inc., Circle Pines, Minnesota, 1959); Columbia Test of Mental Maturity (Harcourt, Brace, and Winston, New York, 1959); A. L. Benton, The revised visual retention test, Form C (William C. Brown Co., Inc., Dubuque, Iowa, 1963); H. W. Stevenson, G. A. Hale, R. E. Klein, and L. K. Miller, Monographs of the society for research in child development, **33**, Whole No. 123 (1968)

Twin zygosity was established by comparing co-twin's blood groups at each of the loci. If dizygosity was determined by only one blood group difference, the tests for that locus were redone to affirm the diagnosis.

Ancestral Phenotype Frequencies. To calculate the ancestral African frequencies different weighting schemes were applied to the available data from different regions of sub-Saharan Africa. Curtin's (1969) speculative estimates of the proportion of slaves originating from eight arbitrary African regions is reproduced in row a of Table 2. Curtin based his calculations on records from colonial Virginia and South Carolina as well as the total British slave trade. Two other weighting schemes were used in this study. That shown in row b of Table 2 gives equal weighting to each region while row c is a modification of Curtin's estimates to give greater weight to regions VI, VII, and VIII.

Gene frequency estimates for each region were obtained from an extensive review of the published literature on African gene frequencies. Unlike earlier estimates, greater weight was given where possible to groups within 200 miles of the coast than to inland groups, who probably contributed less to the slave trade. The phenotype frequency estimates for the eight regions are given in Table 3.[5] While these data represents information on many thousands of individuals, the many empty cells emphasize the fragmentary nature of our knowledge of modern African populations, especially for those genetic loci of greatest value for the present study.

The three weights were combined with the eight regional phenotype frequency estimates to produce three possible ancestral populations.

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[5] The ancestral Caucasian and African gene frequencies used are found in the following sources. The same references were used as are found in footnote 18 of J. Adams and R. H. Ward, Science, **180**, 1137 (1973) plus these additional sources where they do not overlap: R. E. G. Armattoe, Am. J. Phys. Anthrop., n.s. **9**, 371 (1950); R. E. G. Armattoe, E. W. Ikin, and A. E. Mourant, W. Afr. Med. J. **2**, 89 (1953); S. H. Boyer and E. J. Watson-Williams, Nature (Lond.) **190**, 456 (1961); J. Buettner-Janusch, R. Reisman, D. Coppenhaver, G. A. Mason, and V. Buettner-Janusch, Am. J. Phys. Anthrop. **38**, 661 (1973); L. L. Cavalli-Sforza and W. F. Bodmer, The genetics of human populations (Freeman and Co., San Francisco, 1971), pp. 267—268; H. Cleve and A. G. Bearn, in Progr. Med. Genet., Vol. 2, A. G. Steinberg and A. G. Bearn, eds. (1962); G. M. Edington, A. Afr. Med. J. **5**, 71 (1956); A. Eyquem, L. Podliachouk, and J. Presles, Vox Sang. (Basel) **6**, 120 (1961); I. Faye, H. Ruscher, M. P. Tsala, and G. Bloc, Bull. Soc. Med. Afr. Noire lang. franç. **16**, 551 (1971); E. R. Giblett, in Progr. Med. Genet., Vol. 2, A. G. Steinberg and A. G. Bearn, eds. (1962); E. R. Giblett, Genetic markers in human blood (F. A. Davis Co., Philadelphia, 1969); G. Holmgren and K. G. Gotestam, Hum. Hered. **20**, 433 (1970); T. Jenkins, A. Zoutendyk, and A. G. Steinberg, Am. J. Phys. Antrop. **32**, 197 (1970); G. Kellermann and H. Walter, Humangenetik **15**, 84 (1972); F. D. Kitchin and A. G. Bearn, Nature (Lond.) **202**, 827 (1964); J. Lambotte-Legrand and C. Lambotte-Legrand, Ann. Soc. belg. méd. trop. **30**, 547 (1950); V. T. Matznetter and W. Spielmann, Z. Morph. Anthrop. **61**, 57 (1969); J. Moullec, J. M. Fine, C. Henry, and C. Silverie, Proc. 7th Cong. Internatl. Soc. Bl. Transf. (Rome, September 3—6, 1958), pp. 881—883, P. Moureau and J. Brocteur, Bull. Acad. roy. Méd. Belg. 7 (No. 2), 147 (1962; W. C. Parker and A. G. Bearn, Ann. hum. Genet. **25**, 227 (1961); R. R. Race and R. Sanger, Blood Groups in Man, 5th edition (Blackwell, Oxford, 1968); L. Reys, C. Manso, G. Stamatoyannopoules, and E. Giblett, Humangenetik **16**, 227 (1972); L. Rivat, M. Blanc, C. Rivat, C. Ropartz, and J. Ruffie, Humangenetik **13**, 108 (1971); H. Sagnet, J. Thomas, L. Vovan, C. Jesserand, A. Marie-Nelly, and A. Orsini, Pediatrie **26**, 611 (1971); M. H. K. Shokeir and D. C. Shreffler, Biochem. Genet. **4**, 517 (1970); A. G. A. Simbeye, Hum. Hered. **22**, 286 (1972); W. Spielmann, H. Ruppin, L. Schilling, and D. Teixidor, Dtsch. Z. ges. gerichtl. Med. **64**, 186 (1968); A. G. Steinberg, Am. J. hum. Genet. **18**, (1), 109 (1966); D. Tills, J. L. Van den Branden, V. R. Clements, and A. E. Mourant, Hum. Hered. **20**, 517 (1970) and Hum. Hered. **21**, 302 (1971); P. V. Tobias, in The biology of human adaptability, P. T. Baker and J. S. Weiner, eds. (1966); R. M. Winston, W. Afr. Med. J. **3**, 17 (1954). Although a small amount of American Indian admixture has been found in some local black populations (B. Glass, Am. J. hum. Genet. **7**, 368 (1955), the contribution is small enough to be safely ignored when so many other sources of error are more obvious

Table 2. Weighting schemes used to obtain the ancestral African frequencies

	I	II	III	IV	V	VI	VII	VIII
a	0.13	0.06	0.11	0.16	0.04	0.23	0.25	0.02
b	0.125	0.125	0.125	0.125	0.125	0.125	0.125	0.125
c	0.05	0.05	0.05	0.10	0.15	0.30	0.20	0.10

Caucasian phenotype frequencies for England, Ireland, Scotland, and Wales were used for the Caucasian ancestral population. While we recognize that other European groups also contributed to the contemporary US black population, no weighting scheme exists for the white ancestral populations comparable to the one Curtin provides for African groups. Besides, most of the US black population resided in the southeastern states during the time that hybrid group was forming and in that region the white population derived predominantly from British Isles' settlers. Table 3 also gives the Caucasian phenotype frequencies used as the second ancestral population.

Phenotype frequencies from the three estimated African ancestral populations and the Caucasian ancestral populations were inserted in Formula (1) to calculate the three *ancestral odds coefficients.* High values indicate closer resemblance to African phenotype frequencies.

Sample Frequencies. Since we were not concerned with an individual admixture estimate but with a rank order coefficient, the phenotype frequencies actually obtained in the black and white samples in Philadelphia could be used to rank order socially classified blacks according to their degree of resemblance to the white sample. Those individual phenotypes that closely resemble the black sample values, especially at those loci with large differences in phenotype frequencies between the black and white samples, will receive higher rank order values than those phenotypes that closely resemble the white sample frequencies. Using Formula (1), we calculated a *sample odds coefficient.*

Construct Validation of the Odds Coefficient. If these odds coefficients are valid measures of racial genetic variability, then they should meet two criteria. First, they should correlate with skin color, which also reflects racial genetic variability. Second, the correlation for the odds coefficients between dizygotic twins should be around 0.5 or a little higher if there is assortative mating for characteristics such as skin color that are related to admixture. DZ twins share half of their genes on the average.

Results

Ancestral Odds. The three putative African ancestral populations produced indistinguishable ancestral odds coefficients. Although the phenotype frequencies varied somewhat, the rank orders of black children were essentially the same. Thus, we chose to use Curtin's (1969) weighted values as the final measure.

Validity of the Odds Coefficients. The DZ twin correlations for ancestral and sample odds were 0.55 and 0.61 respectively (SE = 0.11). These intraclass correlations are in the expected range for a valid coefficient based on genetic variability. Plots of the co-twin values for the odds indicated that variability between co-twins was equally distributed across the range of the sample odds coefficient. Variability in ancestral odds was greater for low values that represent less African ancestry. Thus, a greater number of individuals with higher degrees of Caucasian ancestry are discriminated than there are in the range of the

Table 3. Phenotype frequencies used in computing ancestral and sample odds coefficients

Phenotypes		Regions[b] of Africa								Composite[a] ancestral African	Black sample	White sample	Ancestral Caucasian
		I	II	III	IV	V	VI	VII	VIII				
AB0	0	0.50	0.47	0.50	0.50	0.54	0.52	0.50	0.56	0.51	0.46	0.46	0.47
	A	0.24	0.24	0.22	0.21	0.21	0.25	0.27	0.22	0.24	0.25	0.35	0.42
	B	0.21	0.24	0.24	0.24	0.22	0.18	0.19	0.18	0.21	0.25	0.12	0.09
	AB	0.04	0.05	0.04	0.09	0.04	0.04	0.04	0.03	0.04	0.04	0.07	0.03
Adenylate kinase	1				1.00	1.00			0.99	1.0	0.98	0.96	0.91
	1–2				0.00	0.00			0.01	0.00	0.02	0.04	0.09
Ceruloplasmin	B						0.70	0.87	0.78	0.74	0.90	0.98	0.98
	BA						0.25	0.10	0.10	0.21	0.10	0.01	0.02
	BC						0.01	0.01	0.00	0.01	0.00	0.00	0.00
Duffy	A			0.01				0.07	0.00	0.04	0.13	0.23	0.20
	AB							0.01	0.00	0.00	0.03	0.40	0.46
	B							0.02	0.01	0.02	0.17	0.36	0.33
	A–B–							0.90	0.99	0.94	0.66	0.01	0.00
Group specific	1					0.89		0.82	0.90	0.88	0.76	0.51	0.51
	1–1					0.10		0.17	0.10	0.12	0.22	0.43	0.41
	2					0.00		0.01	0.00	0.00	0.02	0.06	0.08
Haptoglobin	1	0.40	0.44	0.51		0.52	0.38	0.36	0.25	0.42	0.32	0.15	0.16
	1–2	0.47	0.45	0.41		0.40	0.47	0.48	0.50	0.45	0.44	0.50	0.48
Inv(1)	(1+)	0.57						0.58	0.59	0.57	0.51	0.19	0.18
	(1–)	0.43						0.42	0.41	0.43	0.49	0.81	0.82
Kell	K			0.05	0.01	0.01	0.01			0.02	0.01	0.05	0.09
	k			0.94	0.98	0.98	0.98			0.97	0.99	0.95	0.91
MN	M	0.13	0.21	0.21	0.30	0.23	0.18	0.24	0.25	0.22	0.24	0.26	0.28
	MN	0.45	0.49	0.50	0.49	0.50	0.49	0.50	0.50	0.49	0.44	0.55	0.50
	N	0.39	0.30	0.29	0.20	0.27	0.33	0.26	0.25	0.29	0.32	0.20	0.22

Rhesus	rh	0.07	0.07	0.06	0.10	0.05	0.06	0.06	0.02	0.07	0.04	0.12	0.15
	rh'rh				0.03	0.01	0.01	0.00	0.01	0.02	0.00	0.00	0.01
	Rh_0	0.74	0.64	0.67	0.53	0.52	0.60	0.67	0.71	0.64	0.49	0.03	0.02
	Rh_1rh	0.09	0.10	0.13	0.18	0.22	0.04	0.11	0.03	0.11	0.28	0.34	0.35
	Rh_1Rh_1	0.00	0.00	0.01	0.01	0.01	0.00	0.01	0.00	0.00	0.01	0.20	0.19
	Rh_2rh	0.07	0.17	0.11	0.07	0.11	0.22	0.14	0.11	0.13	0.12	0.12	0.12
	Rh_2Rh_2	0.00	0.01	0.00	0.00	0.01	0.02	0.01	0.00	0.01	0.02	0.02	0.02
	Rh_zRh_0	0.00	0.01	0.01	0.01	0.02	0.01	0.01	0.01	0.01	0.04	0.16	0.13
Transferrin	C	0.96	0.94	0.92		0.88	0.86	0.94	0.92	0.91	0.93	0.99	0.99
	CD	0.04	0.05	0.07		0.11	0.12	0.05	0.08	0.08	0.07	0.01	0.00
	D	0.00	0.00	0.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Gm	a−, x−, b^1+, c^3−									0.00	0.02	0.50	0.53
	a+, x−, b^1+, c^3−									0.41	0.65	0.35	0.21
	a+, x+, b^1+, c^3−									0.07	0.03	0.08	0.18
	a+, x−, b^1+, c^3+									0.49	0.25	0.00	0.00
	a+, x−, b^1−, c^3−									0.00	0.03	0.03	0.02
	a+, x+, b^1−, c^3−									0.00	0.01	0.03	0.06
	a+, x+, b^1+, c^3+									0.03	0.01	0.00	0.00

Note: All zero frequencies were made equal to 0.0001 since the log of zero is undefined

[a] Using 'a' weights of Table 2, Curtin's (1969) speculative estimates

[b] The regional phenotype frequencies are pooled estimates and not simple averages

African nations corresponding to eight regions:

I Senegal, Gambia
II Sierra Leone, Guinea (Bissau), Guinea
III Liberia, Ivory Coast
IV Ghana
V Dahomey, Western Nigeria, Togo
VI Cameroons, Eastern Nigeria
VII Angola, Equatorial Guinea, Gabon, Congo, Zaire
VIII Malagasy, Mozambique

Table 4. Correlations among skin color, ancestral and sample odds coefficients, based on three and nine marker loci

	SC	AO(3)	AO(9)	SO(3)	SO(9)
Skin color reflectance	X				
Ancestral odds (3)	0.16	X			
Ancestral odds (9)	0.11	0.11	X		
Sample odds (3)	0.22	(0.58)	0.11	X	
Sample odds (9)	0.18	0.09	(0.76)	0.10	X

$n \cong 300$ individuals from ~ 160 twin pairs; If $n = 160$ and $r \geq 0.15$, $P \leq 0.05$

distribution reflecting higher degrees of African ancestry when the ancestral odds coefficient is used.

Both the ancestral and sample odds coefficients were found to be significantly correlated with the skin color measure, 0.21 and 0.27 respectively ($P < 0.01$). Although we were unable to make a point prediction for the correlations (because little is known about the distribution of admixture in the black population) we anticipated a low positive relationship that is consonant with the power of the genetic marker loci used to index degree of ancestry.

There is another hypothesis, however, to explain the correlation between skin color and blood group markers: that one skin color locus is closely linked to Gm and/or Fy (Gershowitz and Reed, 1972; Cavalli-Sforza, personal communication 1974). Indeed, skin color was found to be more highly correlated with Gm than any other single locus ($r = 0.20$), followed by Duffy, Transferrin ($r = 0.13$ for each) and AB0 ($r = 0.11$). These loci are good markers for ancestry, however, and could be correlated with skin color for that reason.

Skin color variation probably depends upon a few good markers of ancestry. If skin color phenotypes correlate with ancestral odds, because ancestral genes have not been dispersed throughout the black population, then any three good blood group markers ought to correlate positively with other markers from the same ancestral population. If, instead, the relationship between skin color and ancestry depends upon the close linkage between a skin color locus and Fy/Gm, then three blood group markers should not correlate positively with the rest, and skin color should not correlate with any set of blood groups lacking the linked marker.

To test the competing hypotheses we selected three good blood group markers (gm, Fy, AB0) to correlate with the remaining nine and to compare with the correlation of skin color to odds coefficients calculated on the set of three and the set of nine. The correlations are given in Table 4.

All of the correlations among skin color and the odds coefficients were in a positive direction. Three of the eight were statistically significant, including the correlations between skin color and the sample odds, with and without Gm and Duffy ($r = 0.22$ and 0.18 respectively). The correlations between the sets of three and nine blood group markers were not statistically significant. While no firm conclusions can be drawn, the relationship between skin color and the blood

Table 5. The distributions of ancestral and sample odds coefficients calculated separately for co-twins 1 and 2

	Co-twin 1	Co-twin 2
Ancestral odds		
Mean	4.13	4.22
SD	3.00	2.96
SE	0.26	0.24
Skewness	−0.93	−0.94
Kurtosis	1.67	1.46
Range	−8.3 to 10.1	−8.3 to 9.9
Sample odds		
Mean	2.96	2.98
SD	2.15	2.07
SE	0.19	0.17
Skewness	0.09	0.14
Kurtosis	0.18	−0.07
Range	−3.0 to 8.7	−3.0 to 8.4

group markers does not depend solely upon a hypothesized linkage with Gm. The data are consistent with a hypothesis of partial nondispersion of ancestry.

As a further test of the validity of the odds coefficients, the ancestral and sample frequencies were used to calculate 'admixture' for the white sample. Since African populations are not significant progenitors of the contemporary US white group, we did not expect the odds coefficients to correlate with skin color within the white sample. Although both skin color reflectance and the odds coefficients were sufficiently variable and reliable to produce the expected DZ twin coefficients of about 0.5 (red filter-forehead $r_{DZ} = 0.51$; ancestral odds $r_{DZ} = 0.48$; sample odds $r_{DZ} = 0.54$), the genetic variability in skin color and blood group markers were unrelated to African ancestry within the white sample (skin color, ancestral odds $r = 0.04$; sample odds $r = 0.05$).

In the black sample the distributions of the ancestral and sample odds coefficients were calculated separately for co-twins, randomly designated 1 and 2. The statistical characteristics of the four odds coefficients are given in Table 5.

Co-twins, separated into two samples, do not constitute a traditional replication study, but they do provide two related samples on which to test the distributional qualities of the proposed statistic. The odds coefficients for co-twins 1 and 2 are very similarly distributed. As shown in Figure 2, the ancestral and sample odds coefficients differed in the shapes of their distributions. The sample odds coefficient produced more individuals with low degrees of estimated African ancestry, and the ancestral odds produced a greater number of individuals in the high ranges of estimated African ancestry.

Relationships of Odds Coefficients to Social Variables. There were negligible correlations between the two measures of socioeconomic status and the odds coefficients. The census tract data correlate negatively with increasing resemblance to the black or African groups. (The higher SES, the less the resemblance to black or

Table 6. Correlations of the odds coefficients and SES

SES	Ancestral odds	Sample odds
Census	−0.10	−0.12
Individual	+0.09	+0.07

Table 7. Correlations of ancestral and sample odds coefficients with intellectual skills

	Ancestral odds	Sample odds
Raven standard progressive matrices	−0.08	−0.13
Peabod picture vocabulary test	−0.06	0.00
Columbia test of mental maturity	0.02	−0.04
Revised test of figural memory	−0.12	−0.10
Paired-associate test	0.15	0.12
First principal component	−0.03	−0.05

$n \cong 144$ pairs; $r \leq -0.14$, one-tailed test, $P \leq 0.05$; SE = 0.083

African groups.) The individual SES measure correlates positively with the odds coefficients. None of the coefficients is statistically different from zero, but they are given in Table 6.

Skin color is only slightly related to SES characteristics, in the same directions as the odds coefficients. The darker children tend to live in lower SES neighborhoods ($r = 0.15$) but do not tend to have lower SES families ($r = 0.03$). There are no significant correlations between skin color and SES.

The Odds Coefficients and Intellectual Skills. None of the correlations between the ancestral or sample odds and the five intellectual skills was significantly different from zero. There was no association between our estimates of ancestry and intellectual performance within the sample of black twins. The first principal component from the four cognitive tests, which most psychologists would call g, is the set of intellectual skills that is general to intellectual measures. The first principal component was significantly related to socioeconomic status ($r = -0.20$; $P < 0.05$) and tended to be related to skin color ($r = 0.155$), but general intellectual skills were not correlated with ancestry. Table 7 gives the results before social variables were partialled out of the correlations. A scatter plot of one of the correlations, that of sample odds and the first principal component, is given in Figure 3. It is clear that no statistically significant relationship exists.

Allthough the social correlates of the odds coefficients account for very little of the variance in intellectual performance, we computed the correlations between the odds coefficients and the intellectual skills holding skin color and SES (census tracts) constant. Since social discrimination can be based on visible markers of ancestry, it seemed advisable to partial out the social effects. Table 8 gives the results.

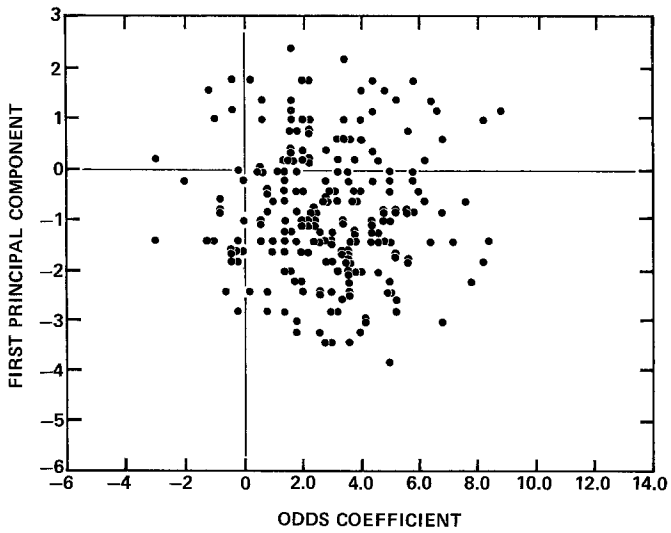

Fig. 3. A scatterplot of scores on the first principal component of four cognitive tests and the sample odds coefficient of ancestry within a sample of Philadelphia blacks

Table 8. Correlations of ancestral and sample odds with intellectual skills: SES (census tracts) and skin color partialled out

	Ancestral odds	Sample odds
Raven standard progressive matrices	−0.09	−0.10
Peabody picture vocabulary test	−0.03	0.04
Columbia test of mental maturity	0.03	−0.02
Revised test of figural memory	−0.10	−0.06
Paired-associate test	0.14	0.10
First principal component	−0.01	−0.02

$n \cong 144$ pairs; $r \leq -0.14$, one-tailed test, $P \leq 0.05$; SE = 0.083

To test further the relationships between the odds coefficients and intellectual performance, extreme groups were contrasted. The distributions of ancestral and sample odds coefficients were divided into thirds. The test scores of the group with the highest odds for African ancestry were compared to those of the group with the lowest. Skin color and social class differences are confounded in these contrasts, and the sample sizes are overestimated. Despite the confounding of social variables, in only one case out of 12 did extreme group contrasts achieve statistical significance with a sample size inflated to the number of individuals instead of the number of families independently sampled. These results are given in Table 9.

On the Revised Test of Figural Memory, the third of the sample with the least African ancestry had higher scores than the third with the most, but this result was not replicated with the sample odds coefficient. Most importantly, the

Table 9. Contrasts between extreme thirds of the ancestral and sample odds distributions on intellectual test scores (least black minus most black in standard deviation units)

	Sample odds				Ancestral odds			
	m diff.	SE[a]	*t*	*P*	*m*diff.	SE[a]	*t*	*P*
Raven standard progressive matrices	0.21	0.13	1.60	0.11	0.16	0.13		
Columbia test of mental maturity	0.09	0.13			0.06	0.13		
Peabody picture vocabulary test	−0.08	0.13			0.08	0.13		
Revised test of figural memory	0.07	0.12			0.31	0.12	2.31	0.02
Paired-associate test	−0.06	0.15			−0.23	0.15	1.63	0.11
First principal component	0.11	0.21			0.13	0.22		

[a] Assumes that individuals are independently sampled and $n \cong 280$. In fact, n is best considered between 280 individuals and 140 independent families

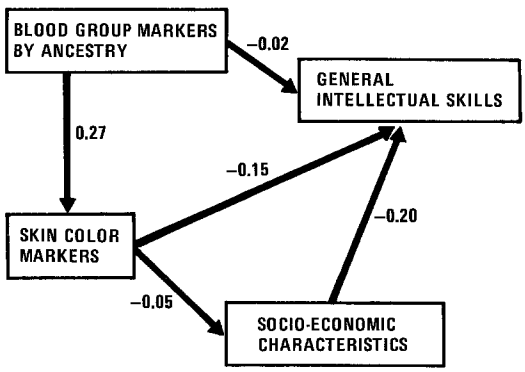

Fig. 4. Path coefficients of the effects of ancestry and socioeconomic status on the intellectual skills of a sample of Philadelphia blacks

general factor of the intellectual tests was not related to ancestry. Although intellectual skills were not consistently related to estimated ancestry in the extreme thirds, skin color was. The group with the highest estimated African ancestry was significantly darker than the group with the lowest (ancestral odds, $t = 2.05$, $P < 0.05$; sample odds, $t = 3.25$, $P < 0.001$).

To summarize the results, Figure 4 presents a path analysis of the model underlying this research, presented earlier as Figure 1. The path coefficients of ancestry (skin color and blood group markers) and life chances (skin color and socioeconomic status) with general intellectual skills support the stronger effects of life chances than ancestry on intellectual performance.

Discussion

The test of a relationship between degree of African ancestry, estimated with the odds coefficients, and intellectual skills failed to provide evidence for genetic racial differences in intelligence. Jensen (1973) predicted the correlation between the degree of Caucasian admixture and intellectual ability as around 0.50, under

the assumptions of his proposal that half to three-quarters of the IQ difference between races is due to genetic differences (Jensen, 1973). In the correlational analyses presented in this paper, no evidence at all can be found for a correlation of that magnitude (Tables 7 and 8). In fact, none of the correlations was reliably different from zero in the expected direction, given the sample size involved (a correlation of about -0.14 would be different from zero at $P \leqq 0.05$, one-tailed test). Even if the correlations between ancestry and intellectual skills could not exceed those between skin color and ancestry, because of less than perfect reliabilities, they would have been detected by this study.

Now, if we look as well at the differences between the averages of the upper and lower thirds of the black group on the various intellectual measures rather than rely solely on a correlational analysis, no consistent support for Jensen's hypothesis emerges either. The average difference between blacks and whites in this study on intellectual measures is around 0.9 standard deviations (SD). If we assume that the most extreme third of the black group averages 35% Caucasian ancestry, while the least admixed third averages 15% (based on data of MacLean et al., 1974), the average difference between extreme thirds should be about one-fourth of a standard deviation on the intellectual dimension.[6]

The sample size in this study is sufficient to detect a mean difference in intellectual skills of 0.26 between the extreme thirds of the distribution arrayed by estimated degree of ancestry, with a standard error of 0.13, when $P = 0.05$. If we let $P = 0.10$, an average difference of 0.22 achieves statistical significance. With a relaxed alpha value, one of the twelve mean differences between extreme thirds was statistically significant, and two others approached statistical significance—one in the direction of high to low degree of black ancestry and the other in the direction of low to high degree of black ancestry (see Table 9). An extrapolation from the contrast between extremes within the hybrid group to the average difference between the races predicts that not more than one-third of the observed difference between the races could be due to genetic differences. In view of the negligible correlations between estimated ancestry and intellectual skills, even this seems unlikely.

We suggest that stronger tests of the hypothesis of genetic racial differences can be provided by increased sample sizes, improved estimates of the ancestral population gene frequencies, and a larger number of polymorphisms that discriminate ancestral origin. Other approaches to the problem, such as the study of transracial adoption, have shown that black and interracial children reared by middle-class white families achieve IQ scores well above the average of white children in the US (Scarr and Weinberg, 1976). Neither the study of transracial adoption nor the present study provide any support for a strong hypothesis of genetic racial differences in intelligence.

[6] The rough calculation for the estimate of the difference between upper and lower thirds of the black group proceeds as follows. If the resultant difference in standard deviations is 0.9 between the races when the mean difference in degree of Caucasian ancestry is about $(0.99 - 0.22 = 0.77$, then the difference between upper and lower thirds of the black group alone should be about 0.23 SD when the difference in Caucasian ancestry is about $(0.35 - 0.15) = 0.20$. Furthermore, if three-fourths of that mean difference is due to racial genetic differences alone the smallest expected difference is $(0.75 \times 0.23) = 0.18$. So, about one-fifth to one-fourth of a SD would be the expected mean difference between upper an lower thirds of the black group

Acknowledgements. Our deepest appreciation to the many people who assisted in this research: to Dr. Herbert Polesky, Director of the Minneapolis War Memorial Blood Bank, for all of the blood analyses; to William Thompson, who helped to fomulate the odds coefficients, wrote the computer programs, and analyzed the data; to Louise Carter-Saltzman, who edited the psychologic test protocols; to Valerie Lindstrom, who supervised much of the data collection; to Professors Julian Adams, V. Elving Anderson, Luigi Cavalli-Sforza, T. E. Reed, and Peter Workman for consultation on the design and analysis of the study. None of them is responsible in any way for the conclusions drawn from the research by the authors. The research was supported by the Grant Foundation and by NICHHD (HD-08016) and in part by Mental Health Training Grant (MH 10679).

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Received November 11, 1976 / April 12, 1977