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# Genetics and the Human Race

## Definition of race on the basis of gene frequencies supplements definition from morphological characters.

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In considering racial classification it is necessary to understand how races are formed. Racial differentiation is the end result of the action of natural selection on the raw material provided by random mutations in a population sufficiently isolated genetically. In order to compare two races, especially to compare them quantitatively, one will choose to study characters with a known mode of inheritance. Only in this way can one decide how the frequency of a given gene in a given population compares with the frequency of that gene in another population.

The use of genetically analyzed characters in racial classification offers a number of other advantages over the use of characters such as morphology which have not been so analyzed. Only if genetic analysis has been effected can one be sure that the characteristic $X$ which has such and such a frequency in population I is genetically the same as the characteristic $X$ found in population II. Moreover, gene frequencies can be more readily tabulated and studied than crude phenotypic frequencies.

The exact mechanism of inheritance has been worked out for a few characters. They generally do not affect the individual's appearance, so far as we know, but have to do mainly with biochemical processes which are not ordinarily observed outside of the laboratory. Some genes of this category produce characteristic chemical substances, such as the blood-group antigens, which are easily detected by the appropriate reagents, such as the blood-group agglutinins, and this fact enormously simplifies the genetic analysis. The one-to-one correspondence between gene and effect makes it possible in many cases to identify *genotypes* merely by laboratory test, and even in cases where this is not possible, the precise genetic mechanism of the character can generally be worked out, so that from the frequency of phenotypes in a population the frequency of the genes and genotypes can be estimated. Genetic differences of this kind include the ability to taste phenylthiocarbamide, the excretion of various substances in the urine, and the formation of various kinds of abnormal hemoglobin. But the most useful characters in this class, at the present time, are the blood groups.

### Action of Selection on Blood Groups

Unless the blood groups are adaptive, they are not going to be very useful in racial classification. Are they adaptive? At first glance, it doesn't look as if it made any difference what blood group one belongs to. Healthy and successful people have belonged to each and every one of them, and even though it is easy to see how selection, through the agency of erythroblastosis fetalis, is changing gene frequencies in the Rh system, it is not easy to see how selection is acting in the other blood-group systems. (Actually, ABO incompatibility between mother and fetus causes the loss of more fertilized ova than does Rh incompatibility. The event usually takes place earlier in pregnancy, and is often not identified as an abortion.)

In most cases we have not yet found what the major selective agencies are for most of the blood-group systems, but we do have evidence that selection is acting to change some of their gene frequencies, although at a very slow rate. Evidence has been accumulating that disease may be affecting the frequencies of genes which have no obvious influence on the production of hereditary disease or resistance to infection. The pioneers in this field were Aird and his co-workers (*1*), who observed in patients with peptic ulcer and cancer of the stomach significant departures from the ABO blood group frequencies of the general population (Table 1). At the same time, the blood-group distribution of patients with other malignancies was found to be normal. The results of Aird and his associates suggested that, if their series were typical, persons of blood group O were about 35 percent more likely to develop peptic ulcer requiring hospital treatment than were persons of other blood groups. It subsequently has been found that the association of blood group O with peptic ulcer is more marked for duodenal than for gastric ulcer. Later workers found similar associations between the ABO blood groups and certain other diseases, but most diseases showed no such association. The subject has been reviewed by Roberts (*2*). Until recently, no disease was found to be associated with any blood-group system other than the ABO system, but in my laboratory we have recently observed an apparent cor-

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Table 1. Association between blood groups and disease. Blood-group frequencies are shown as percentages. [From Aird *et al.* (*1*)]

| Blood group | Peptic ulcer | | Cancer of stomach | | Cancer of colon and rectum | |
|---|---|---|---|---|---|---|
| | Control | Disease* | Control | Disease† | Control | Disease‡ |
| O | 47.00 | 55.40 | 46.78 | 42.95 | 46.07 | 44.79 |
| A | 40.99 | 34.67 | 41.38 | 46.19 | 41.78 | 43.63 |
| B | 8.98 | 7.44 | 8.79 | 7.76 | 8.94 | 8.66 |
| AB | 3.03 | 2.49 | 3.05 | 3.10 | 3.21 | 2.92 |

*3011 cases. †2745 cases. ‡2599 cases.

relation between the Rh blood-group system and ulcerative colitis. Buckwalter and Tweed (*3*) have found correlations of duodenal and gastric ulceration with the Rh blood groups; in fact, they believe the correlation of these conditions with the Rh system to be stronger than the correlation with the ABO system. They found less significant evidence of a correlation of Rh with gastric carcinoma and rheumatic fever. They also found a statistically significant increased likelihood that persons of the NN genotype will develop rheumatic fever.

The correlation between duodenal ulcer and blood group O has been confirmed by workers in other countries and among other types of populations. This seems to dispose of the argument that the correlation may be fictitious because of racial stratification within the population tested. If in England, for example, there were a stratum of the population which is more susceptible to duodenal ulcer and has more blood group O than the English population in general, this could give rise to the observed correlation in the absence of any genetic connection between blood group O and susceptibility to duodenal ulcer. But it is asking too much to suppose that the same stratification should be present in the ethnically quite different American Negroes, Italians, Poles, Norwegians, Swiss, Japanese, Chinese, and Bantu, where the same correlation has been found. Therefore there is little reason to question the significance of the correlation, although we do not as yet know the reason for it.

Another objection to these correlations has been based on the fact that the normal controls with which the diseased groups were compared were either hospital or Red Cross voluntary blood donors, or hospital patients suffering from some other disease. Such individuals are of course to some degree selected, as compared with the general population. Careful study of the whole problem of control populations, however, does not suggest that the use of such groups as controls has led to any spurious correlation. However, to make sure that we are detecting an actual effect of the blood-group genes, it would be desirable to make use of controls closely related to the affected group and thus similar with regard to their environment and to the other genes they possess. Such controls are provided by brothers and sisters of the diseased patients, and Clarke (*4*) has studied a number of these. In these studies, Clarke did not find a significant correlation between blood groups and duodenal ulceration, but Levene (*5*) points out that this may be because there are as yet insufficient data. To obtain a significant result, large numbers of relatives would have to be examined—on the order of 1500. Levene points out that the sib study of Clarke is *compatible* with an even greater association than that suggested by the population studies.

Hardin (*6*) has pointed out that the adaptive nature of the blood-group genes could have been deduced from Gause's principle.

Selection can also act against genes which, so far as we know, are not directly disadvantageous to their possessors. An example of this in our population is provided by the Rh negative gene (cde). When an Rh negative woman (cde/cde) becomes pregnant with a fetus which inherits from the father one of the Rh positive antigens C, D, or E, there occurs, in about one case in 20, a sequence of events as follows. Rh positive blood cells get into the mother's circulation from the blood of the fetus and stimulate the mother's immunological apparatus to produce anti-Rh antibodies. Of the three antigens mentioned, D is the most antigenic, so anti-D is the antibody most frequently observed. The mother's antibody diffuses back through the placenta into the fetal circulation and causes red-cell destruction, jaundice, edema, and the other symptoms of the disease erythroblastosis fetalis. The fetus may be aborted or stillborn, or it may die soon after birth, especially in the absence of treatment.

It can be shown by simple mathematics that this process, in a population such as ours which contains more Rh positive than Rh negative genes, constitutes a selective force tending to reduce the frequency of the Rh negative genes.

The question now arises: If selection is acting on genes, and nearly all genes are either advantageous or disadvantageous in a given environment, why do polymorphisms still exist? In other words, why haven't all gene frequencies in each population gone to either 1 or 0? There are probably a number of very good reasons. One is that even in the case of diseases where there is reason to think the observed mortality does suggest a significant selective action, we must remember that deleterious genes can be continually recruited by mutation. For example, although there is no reason to doubt that the gene for hemophilia is being eliminated from human populations by the great disadvantage it confers on the males who carry it, there is reason to think that the gene is continually being produced again. The evidence from the study of the European royal families seems to indicate that such a mutation occurred in the person of Queen Victoria and was transmitted by her descendants to the male members of various families, notably the Spanish and Russian royal houses.

If a gene is continually being eliminated by selection and continually being produced by mutation, an equilibrium between these two opposing forces will result. Sewall Wright (*7*) derived a simple formula for this:

$$q = \sqrt{(\mu/k)}$$

where $\mu$ is the mutation frequency, $q$ is the frequency of the mutated gene, and $k$ is the selection coefficient. The frequency of the gene which can be maintained by mutation is higher than might be supposed. For example, if the mutation frequency is $3 \times 10^{-5}$ (this is not at all unusual) and the selection coefficient is 0.001 (this used to be taken, at any rate, as a very reasonable selective coefficient), you have $q$, the frequency of the deleterious gene, equal to 0.17, or not far from 20 percent.

Another reason why polymorphism exists is that what may be a disadvantageous trait in one environment can prove advantageous in another. This is ex-

emplified by the relation between hemoglobin S and malaria. Hemoglobin S differs from normal hemoglobin in that, in the protein part of the molecule, a single one of the amino acids is different. The effect is astonishing. When the red cells of a person who has this abnormal hemoglobin are deprived of oxygen, instead of maintaining their biconcave disk shape, as normal red cells do, they become distorted and assume weird shapes, sometimes reminiscent of sickles (hence the name sickle-cell hemoglobin).

The abnormal hemoglobin results from possession by the individual of a gene called the sickle-cell gene or sickle-cell trait. The gene can, of course, be present in single or double dose. Regardless of whether a person has the gene in one dose or in two, his cells will "sickle" when deprived of oxygen. There is no great difference in the appearance of the cells in the two cases. But there is a very great difference in the fate of the individuals. The heterozygotes seem perfectly normal and get along well. The homozygotes develop a profound anemia and usually die before puberty. The gene is thus effectively a *lethal* when present in double doses. One might well ask, why hasn't natural selection wiped out such a deleterious gene. In most of the world it has. The sickle-cell trait, aside from a slight incidence in Greece and a few other places, is unknown in all parts of the world except Africa, and is found only in certain parts of Africa at that. So the question becomes, why hasn't natural selection wiped out the gene in these parts of Africa?

There is a reason. Possession of the sickle-cell gene in single dose greatly increases resistance to falciparum malaria, one of the great killers in the parts of Africa where the gene is frequent. The protection afforded the heterozygote more than offsets the elimination, each generation, of the homozygote, and in a malarious environment the gene becomes an asset. This is a good illustration of the relativity of the terms *advantageous* and *disadvantageous* as applied to genes, and a good illustration of the way in which populations that live in different environments may become different.

The process in this case seems to be a very rapid one, for there is reason to think that much of it has taken place in historical times. In fact (*8*), the gene seems still to be spreading to some of the most primitive tribes of West Africa.

The picture seems to be this. Some 2000 years ago the gene was probably practically unknown in West Africa. Then it either arose as a mutation or was introduced from other parts of Africa by cross breeding with members of outside tribes. Once introduced into a tribe, even in small amounts, the frequency promptly increased greatly, because in the malarious regions this is a very advantageous gene. Eventually it spread to neighboring tribes, and if they too inhabited a malarious region, the frequency of the gene increased. This process is still going on.

The sickle-cell trait thus is a splendid example of evolution in action, and an example of how natural selection acts to form races. At the same time, the sickle-cell trait is not of much interest to anthropologists in other ways, for two reasons. (i) Since the process is still going on, equilibrium has not yet been attained. Therefore, differences between tribes that we see today may disappear in the course of a few hundred or a few thousand years. (ii) Since the process has been so rapid, finding identical or similar frequencies of the trait in two populations tells us little or nothing about the possibility of common ancestry. This illustrates the fact that we want to use not the most labile genetic characters in our classifications but the most stable, in so far as we can identify them, and that we cannot depend on the frequencies of the genes at a single locus.

## Blood-Group Systems

*The ABO system.* The ABO blood-group system (*9*) has been known the longest and is consequently the best studied. In 1939 I summarized the data which had been published up to the middle of 1938 (*10*), and Mourant has summarized new data which had not been published at the time his book (*11*) was written. Mourant has also collected all the ABO data, including the con-

Table 2. Frequencies of blood groups O, A, B, and AB and of genes *A*, *B*, and *O* in typical populations; *p*, *q*, and *r*, frequencies of genes *A*, *B*, and *O*, respectively. Blood-group frequencies are given as percentages. [From Boyd (*10*)]

| Population | Place | Number tested | Blood-group frequency | | | | Gene frequency | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | O | A | B | AB | *p* | *q* | *r* |
| | | *Low A, virtually no B* | | | | | | | |
| American Indians: | | | | | | | | | |
| Toba | Argentina | 194 | 98.5 | 1.5 | 0.0 | 0.0 | 0.008 | 0.0 | 0.992 |
| Sioux | S. Dakota | 100 | 91.0 | 7.0 | 2.0 | .0 | .031 | .010 | .959 |
| | | *Moderate A, virtually no B* | | | | | | | |
| Navaho | New Mexico | 359 | 77.7 | 22.5 | 0.0 | .0 | .124 | .0 | .876 |
| Pueblo | New Mexico, Jemez, etc. | 310 | 78.4 | 20.0 | 1.6 | .0 | .106 | .008 | .885 |
| | | *High A, little B* | | | | | | | |
| Bloods | Montana | 69 | 17.4 | 81.2 | 0.0 | 1.4 | .583 | .0 | .417 |
| Eskimo | Baffin Land | 146 | 55.5 | 43.8 | .0 | 0.7 | .254 | .003 | .742 |
| Australian aborigines | S. Australia | 54 | 42.6 | 57.4 | .0 | .0 | .346 | .0 | .654 |
| Basques | San Sebastián | 91 | 57.2 | 41.7 | 1.1 | .0 | .239 | .008 | .753 |
| American Indians: | | | | | | | | | |
| Shoshone | Wyoming | 60 | 51.6 | 45.0 | 1.6 | 1.6 | .265 | .011 | .724 |
| Polynesians | Hawaii | 413 | 36.5 | 60.8 | 2.2 | 0.5 | .381 | .018 | .601 |
| | | *Fairly high A, some B* | | | | | | | |
| West Georgians | Tiflis | 707 | 59.1 | 34.4 | 6.1 | .4 | .198 | .038 | .764 |
| English | London | 422 | 47.9 | 42.4 | 8.3 | 1.4 | .251 | .050 | .699 |
| Icelanders | Iceland | 800 | 55.7 | 32.1 | 9.6 | 2.6 | .190 | .062 | .748 |
| French | Paris | 1,265 | 39.8 | 42.3 | 11.8 | 6.1 | .277 | .088 | .635 |
| Armenians | From Turkey | 330 | 27.3 | 53.9 | 12.7 | 6.1 | .377 | .109 | .514 |
| Lapps | Finland | 94 | 33.0 | 52.1 | 12.8 | 2.1 | .327 | .079 | .594 |
| Melanesians | New Guinea | 500 | 37.6 | 44.4 | 13.2 | 4.8 | .292 | .099 | .609 |
| Germans | Berlin | 39,174 | 36.5 | 42.5 | 14.5 | 6.5 | .285 | .110 | .605 |
| | | *High A and high B* | | | | | | | |
| East Georgians | Tiflis | 1,274 | 36.8 | 42.3 | 15.0 | 5.9 | .283 | .113 | .605 |
| Welsh | North Towns | 192 | 47.9 | 32.8 | 16.2 | 3.1 | .205 | .108 | .687 |
| Italians | Sicily | 540 | 45.9 | 33.4 | 17.3 | 3.4 | .212 | .117 | .671 |
| Siamese | Bangkok | 213 | 37.1 | 17.8 | 35.2 | 9.9 | .148 | .257 | .595 |
| Finns | Häme | 972 | 34.0 | 42.4 | 17.1 | 6.5 | .286 | .126 | .588 |
| Germans | Danzig | 1,888 | 33.1 | 41.6 | 18.0 | 7.3 | .288 | .139 | .573 |
| Ukrainians | Kharkov | 310 | 36.4 | 38.4 | 21.6 | 3.6 | .258 | .156 | .586 |
| Japanese | Tokyo | 29,799 | 30.1 | 38.4 | 21.9 | 9.7 | .279 | .172 | .549 |
| Russians | Near Moscow | 489 | 31.9 | 34.4 | 24.9 | 8.8 | .249 | .189 | .562 |
| Egyptians | Cairo | 502 | 27.3 | 38.5 | 25.5 | 8.8 | .286 | .202 | .512 |
| Egyptians | Assiut | 419 | 24.6 | 34.4 | 31.0 | 10.0 | .275 | .252 | .473 |
| Chinese | Peking | 1,000 | 30.7 | 25.1 | 34.2 | 10.0 | .193 | .250 | .556 |
| Buriats | Near Irkutsk | 1,320 | 32.4 | 20.2 | 39.2 | 8.2 | .156 | .277 | .568 |
| Asiatic Indians | Bengal | 160 | 32.5 | 20.0 | 39.4 | 8.1 | .154 | .278 | .569 |

Table 3. MN blood group frequencies in some typical populations; *m* and *n*, frequencies of genes *M* and *N*, respectively. Blood-group frequencies are given as percentages. [Data from Boyd (*37*) and Mourant (*11*)]

| Population | Place | Number tested | Blood-group frequency | | | Gene frequency | |
|---|---|---|---|---|---|---|---|
| | | | M | MN | N | *m* | *n* |
| American Indians (Navaho) | New Mexico | 361 | 84.5 | 14.4 | 1.1 | 0.917 | 0.083 |
| Germans | Berlin | 8144 | 29.7 | 50.7 | 19.6 | .550 | .449 |
| Australian aborigines | Queensland | 372 | 2.4 | 30.4 | 67.2 | .176 | .824 |
| Papuans | New Guinea | 355 | 1.1 | 15.5 | 83.4 | .089 | .911 |

siderable amount of material published between 1938 and 1954 (*12*). Thousands of populations have now been tested.

The ABO system is not the most useful anthropologically, but the availability of much more extensive data than for any other blood group system partially compensates for this, and even before such extensive information was available, preliminary racial classifications based on the ABO system alone had been proposed. None of these classifications, however, are of more than historical interest. ABO group frequencies, and the gene frequencies calculated from these, for some typical populations, are shown in Table 2.

Since these data are supposed to be representative, we should be able to draw the same sort of conclusions from them that we draw from the more extensive compilations of Boyd (*10*) and Mourant (*11*). We see that the only populations having no gene *A* and no gene *B* are certain tribes of American Indians, but some American Indians have a moderate-to-high frequency of *A*. The Australian aborigines resemble the latter in having a high frequency of *A*. Nowhere else is the frequency of *A* so high. But hardly anywhere is it zero. The populations of the rest of the world differ mainly in frequency of gene *B*; the frequencies range from 0.04 to 0.05 in Western Europe and the Caucasus to nearly 0.30 in parts of Asia. The Basques, long thought to be an isolated remnant of a very early European people, have virtually no *B*.

The ABO data alone do not enable us to separate the peoples of the world into clear-cut races which make much sense geographically; they would, for example, force us to put some of the American Indians, the Australian aborigines, and the Baffin Land Eskimos into the same racial category (*13*).

However, in view of the processes by which races are formed, we should not expect to be able to make a satisfactory classification on the basis of any one series of genes. Also, the clines between existing human populations are gradual, and populations distant from each other seem in some cases to have altered in the same direction.

The fact that blood antigen A can be divided into two main sorts, $A_1$ and $A_2$, probably determined by two corresponding genes, greatly increases the anthropological value of the ABO system. For it turns out that the $A_2$ gene is unknown in Eastern Asia, in the Pacific, and among the American aborigines, being found only in the peoples of Europe, the Middle East, and Africa. The proportion of $A_2$ to $A_1$ is higher in Africa than in Europe; the Middle East is in this respect, as in others, a transition area between Europe and Eastern Asia.

*The MN system.* The frequencies of genes *M* and *N* (*14*) show less geographical variation than do those of the ABO group, but two of the world's populations do differ sharply from the rest of the world (and from each other) in this respect. These are the American Indians and the Australian aborigines and Melanesians. This is shown in Table 3, which presents a sampling of the considerable mass of data that has been accumulated.

High frequencies of *N*, and consequently low frequencies of *M*, are found throughout the Pacific area, with the highest frequency of *N* in New Guinea.

The anthropological value of the MN system has been greatly increased by the discovery of a pair of antigens, S and s (not to be confused with the secretor gene) (*15*), which are closely associated with it. As a result we now postulate that four genes (or chromosomes)—*M*s, *M*S, *N*s, and *N*S—are involved instead of merely two, and if both anti-S and anti-s serums are available, nine phenotypes can be distinguished instead of three. Use of anti-S serum enables us to distinguish sharply between the natives of New Guinea and the Australian aborigines (see Table 3), for antigen S is present in New Guinea and absent in Australia (*16*). In many of the Asiatic and Pacific populations in which S is present, it is less common than in European populations and tends to be attached predominantly to the *N* gene. In the Punjab it is attached about equally to the *M* and *N* genes and is not much less common than in Europe. In Europe, where about 30 percent of the *M* and *N* genes have S attached, it is attached mainly to the *M* gene ($MS/MS = \sim 0.9$, $NS/Ns = \sim 0.2$).

Other antigens which form part of the MNS system are called Hunter and Henshaw antigens; these are much more common in Africa than elsewhere (*11*), although not really common anywhere.

*The Rh system.* The Rh system (*17*) is anthropologically the most useful blood-group system, although, so far, fewer data are available for it than for ABO or MN. The phenotypes distinguishable with the usual serums depend upon the action of at least eight genes (*18*) or chromosomes (*19*), and these genes, as I shall call them, vary significantly in frequency in different parts of the world. Wiener's gene symbols are *r*, *r'*, $R^0$, *r''*, $R^1$, $r^y$, $R^2$, and $R^z$; the corresponding Fisher-Race chromosome symbols are cde, Cde, cDe, cdE, CDe, CdE, cDE, and CDE. Wiener's notation has the advantage of brevity; the British notation has the advantage that the symbols tell at a glance what the serological reactions will be. The various combinations of eight genes make up 36 different genotypes, and if all six of the theoretically possible antiserums (anti-C, anti-D, anti-E, anti-c, anti-d, and anti-e) were available, 27 phenotypes could be distinguished. Actually, anti-d, predicted by Fisher (*20*), has probably not been found, and anti-e is available to few workers, so most anthropological work is carried out with the first four of the serums listed (plus certain special serums for detecting variants of the antigens). The use of four serums makes it possible to distinguish 12 phenotypes. In Table 4 are shown the frequencies of these phenotypes in seven representative populations.

In Table 5 are given the gene frequencies, calculated from the phenotype frequencies in Table 4. Comparison of Tables 4 and 5 illustrates the point made earlier—that the gene frequencies of a population provide a much clearer and more concise summary of information about it than the phenotype frequencies. The compari-

Table 4. Rh phenotypes in seven representative populations. The phenotypes are symbolized by a brief summary of their serological reactions with the four common sera. C, D, and E before the solidus signify positive reactions with anti-C, anti-D, and anti-E; c and e before the solidus indicate negative reactions with anti-C and anti-E and positive reactions with anti-c and anti-e. C after the solidus indicates a negative reaction with anti-c and a c-a positive reaction. [Data from Mourant (*11*)]

| Population | Number tested | Phenotype | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | cde | cdE | cDe | cDE | Cde/c | CdE/c | CDe/c | CDE/c | Cde/C | CDe/C | CDE/C |
| Germans | 2472 | 14.4 | 0.8 | 2.0 | 13.0 | 0.5 | 0.0 | 35.6 | 14.0 | 0.0 | 20.0 | 0.4 |
| Basques | 383 | 27.4 | .3 | 0.5 | 7.6 | 1.6 | .0 | 42.0 | 6.8 | .0 | 13.8 | .0 |
| South Chinese | 250 | 0.0 | .0 | .8 | 5.2 | .0 | .0 | 5.6 | 29.6 | .0 | 58.0 | .8 |
| American Indians (Chippewa) | 161 | .0 | .006 | .0 | 39.1 | .0 | .0 | 7.5 | 41.6 | .0 | 9.9 | 1.3 |
| Gilbertese | 159 | .0 | .0 | .0 | 8.8 | .0 | .0 | 10.7 | 32.7 | .0 | 47.8 | 0.0 |
| Australian aborigines | 234 | .0 | .0 | 1.3 | 8.6 | .0 | .0 | 10.3 | 27.4 | 1.7 | 47.9 | 3.0 |
| Bantu | 600 | 4.7 | .0 | 62.2 | 12.5 | 2.5 | .0 | 14.0 | 3.8 | .0 | 0.3 | 0.0 |

son also illustrates the great variation in the frequency of occurrence of the Rh gene. Note the high frequency of *r* (the Rh negative gene) in the Basques; the absence of this gene in Asiatics, American Indians, and Pacific populations; and the intermediate values for the black Africans. Striking also are the lower values in Africa. Finally, the very high frequencies of $R^o$ in black Africans and the very low frequencies of $R^o$ in the other populations (it seems to be altogether lacking in American Indians) make it practically an African gene.

*Other blood-group systems.* In addition to these three systems, other systems have now been well studied, and some of them have been found useful anthropologically. These newer systems include the P, Lutheran, Duffy, Kidd, Kell, Sutter, and Diego groups.

The P blood groups (*14*) have not been as well studied as many other systems, but P-positive individuals are known to be more common among Negroes than among whites, and less common among Chinese (*21*).

The Kell blood groups depend, as a first approximation, on two genes, *K* and *k*. The frequency of *K* seems to be zero in Pacific populations, Chinese, and some American Indians. It is low in Negroes and highest (about 0.1) in some Europeans.

The Lutheran blood groups (*22*) may be considered to depend on two genes $Lu^a$ and $Lu^b$. $Lu^a$ is absent in the populations lacking *K* and is not very frequent anywhere. The highest frequency of $Lu^a$ (+) individuals reported was in a sample of 73 Brazilian Indians (see *23*) and may not be typical.

The Duffy blood groups (*24*) promise to be among the most interesting of the newly studied blood groups. In Europeans, two genes, $Fy^a$ and $Fy^b$ are involved; in England the frequency of $Fy^a$ is about 0.40. The frequency is much higher than this in Lapland and Asia. In Africans there is another gene (*25*) which has been designated merely *Fy*, in accordance with Ford's (*26*) suggestion that until the antigen supposedly produced by a gene has been recognized by an antibody it should be represented merely by the systemic symbol without suffix. This gene, unknown in Europeans save in rare individuals, is actually the most frequent at this locus in Negroes, having a frequency of over 0.8. *Fy*, therefore, is another "African" gene.

The Kidd blood groups (*27*) promise to be of use in anthropology, for the frequency of the gene $Jk^a$ is 0.38 in American Indians, 0.52 in English and white Americans, 0.78 in Africans, and 1.00 in Sea Dyaks from Borneo (*11*). The frequency seems to be about 0.33 in Chinese.

*V*, a gene connected to the Rh system in a way not yet entirely clear (*28*), is rare in white people but common in Negroes, the frequency of the gene being 0.0025 in the English, 0.14 in New York Negroes, and 0.23 in West Africans. *V* is therefore a third example of an "African" gene.

Aside from $R^o$, *Fy*, and *V*, blood-group genes that are virtually restricted to one race are conspicuous by their absence, as would be expected from the way in which races originate.

*The Sutter blood group.* In 1958 Giblett (*29*) discovered an antigen, $Js^a$, which defines a new blood-group system (Sutter). It may prove to be of considerable anthropological value, since it seems to be another "African" gene. That still others may exist is suggested by the recent discovery of a blood antigen called "Diego" (*30*).

*Diego blood groups.* The Diego blood groups (named for the woman in whose serum the antibody was first found) was discovered by Levine and his co-workers in 1954. The worker who has done the most to use the Diego group anthropologically is Layrisse. The Diego factor is apparently inherited as a simple dominant, Di, with a recessive allele di. It is of considerable interest, since it is practically confined to the Mongoloids, and is not found in all of them. The Eskimo, for example, do not have Di. It is found in the Chinese and the Japanese but is much more common in certain South American Indians.

Layrisse and Wilbert (*31*) have suggested that the first migrations to the New World consisted of groups who did not possess the Diego factor, and that the Diego-positive tribes came later. The Eskimo, who also lack the Diego factor, seem to represent a still later migration.

## Other Genetic Data

*Secretor gene.* Another genetically analyzed character is related to the blood groups but is not itself a blood-grouping gene. It determines whether a person's characteristic blood-group substance appears in water-soluble form

Table 5. Rh gene frequencies in representative populations.

| Population | Frequency of gene | | | | | | |
|---|---|---|---|---|---|---|---|
| | *r* | *r''* | $R^o$ | $R^2$ | *r'* | $R^1$ | $R^z$ |
| Germans | 0.378 | 0.010 | 0.026 | 0.137 | 0.006 | 0.439 | 0.004 |
| Basques | .481 | .013 | .013 | .049 | .026 | .419 | .0 |
| Bantu | .214 | .0 | .596 | .085 | .058 | .047 | .021 |
| South Chinese | .0 | .0 | .041 | .195 | .0 | .759 | .005 |
| American Indians | .0 | .079 | .0 | .587 | .0 | .315 | .019 |
| Gilbertese | .0 | .0 | .070 | .235 | .0 | .695 | .0 |
| Australians | .0 | .0 | .085 | .201 | .129 | .564 | .014 |

Table 6. Three types of haptoglobin patterns, each probably determined by a pair of autosomal, incompletely dominant, genes.

| Phenotype | Genotype |
|---|---|
| Haptoglobin 1–1 | $Hp^1Hp^1$ |
| Haptoglobin 2–1 | $Hp^2Hp^1$ |
| Haptoglobin 2–2 | $Hp^2Hp^2$ |

in his saliva, gastric juice, and other body fluids. There are two genes, *Se* and *se,* the former being dominant. The secretor system is related in a rather complicated way to the Lewis blood-group system.

*Hemoglobins.* In the last decade or so it has been discovered that human hemoglobins are not all alike. By and large, of course, they are, and the great majority of human beings have the same molecule in their red cells. But there are at least 20 kinds of abnormal hemoglobins that differ from the normal in some detail of the protein part of the molecule. The difference is usually slight, by chemical standards, but it sometimes has a profound effect on the physiological behavior of the red cells containing the abnormal molecule, as in the case of hemoglobin S.

Scott *et al.* (*32*) failed to find any abnormal hemoglobins in Alaskan Eskimo, Indians, and Aleuts.

When the causes of the variation in the frequency of a given gene are not known, we tend to assume that these variations reflect adaptation of the two populations to different environments and that other gene frequencies have been modified at the same time. Probably in most cases this assumption is correct, and a case such as sickle-cell anemia is exceptional. It illustrates, however, the desirability of testing any such assumptions whenever possible.

*Haptoglobins.* Haptoglobins are plasma-protein $\alpha$-2-globulins that have the property of combining firmly with hemoglobin. It is generally supposed that their function in the body is to combine with any hemoglobin liberated into the circulation by hemolysis and thus prevent the loss from the body of hard-to-replace iron. If this is the principal function, the amount of haptoglobin present seems rather inadequate to deal with the amounts of hemoglobin that might sometimes be released.

Three types of haptoglobin patterns have been found, each probably determined by a pair of autosomal, incompletely dominant genes, as shown by the scheme in Table 6.

Some individuals apparently have no haptoglobin at all, but it is not yet known how this fits into the scheme of inheritance.

Some idea of the racial distribution of the various haptoglobin patterns can be gained from Table 7. A more extensive table appears in a paper by Sutton, Matson, Robinson, and Koucky (*33*). It may be seen that the Caucasoid populations are characterized by a comparatively low frequency of the 1-1 pattern and a high frequency of 2-2 pattern, whereas the Negroes have a high frequency of 1-1 and a low frequency of 2-2. The Australian aborigines also have a low frequency of the 2-2 pattern, but not nearly as low as the Negroes.

*Transferrins.* Transferrins are proteins that have the very important physiological function of transporting iron to the iron stores of the body and to the bone marrow where red cells are manufactured (*34*). They seem to be usually $\beta$-globulins. The different transferrins that have been identified (by electrophoresis) are designated by letter—*B, C, D,* and so on. Some racial variation in their incidence and in the combinations in which they occur have been observed.

*Gamma-globulin groups.* The gamma-globulin groups are determined in a complicated way, but there seems no doubt that the tests reveal a new human genetic locus.

The serum of most patients with rheumatic arthritis contains a gamma-globulin, called rheumatoid factor, of high molecular weight, which will agglutinate particulate bodies coated with specially prepared serum gamma-globulin. To detect this rheumatoid factor Grubb utilized, as particles, human Rh+ red cells coated with "incomplete" (that is, nonagglutinating) anti-Rh antibody. These cells were agglutinated by the rheumatoid serum. Grubb found that the serum of some, but not all, normal individuals could inhibit this agglutination (*35*). He also found that the possession of the inhibiting protein was determined by a single gene, $Gm^a$, which has a recessive allele $Gm^b$. Several other phenotypes have been discovered by using different combinations of Rh+ cells and rheumatoid arthritis serum. There is a striking difference in the distribution of these genes between certain populations: 100 percent of many non-European populations have the gamma-globulin type $Gm^a$, whereas only about 50 percent of white U.S. populations have it.

There is certainly no reason to suppose that heredity affects only the blood. But that is where emphasis has been placed, perhaps because of the fact that, up to the present, it is the easy tasks which have been undertaken. It does not take much acquaintance with work with native populations to make one realize that it is much easier to take a few milliliters of blood from the arm, or a few drops from the finger,

Table 7. Haptoglobin groups in various populations. [From Montagu (*23*)]

| Population | Place | Number tested | Group | | | |
|---|---|---|---|---|---|---|
| | | | 0–0 (%) | 1–1 (%) | 2–1 (%) | 2–2 (%) |
| English | Oxford | 218 | 2.7 | 10.1 | 55.5 | 31.7 |
| American whites | Chicago | 54 | | 11.1 | 53.7 | 35.2 |
| Australian aborigines | N. Queensland | 123 | | 12 | 68 | 20 |
| Norwegian | Norway | 1000 | | 13.2 | 46.2 | 40.6 |
| Basque | Spain | 107 | 0.9 | 14.0 | 45.7 | 39.3 |
| Australian whites | Queensland | 100 | | 14 | 58 | 28 |
| Finnish | Helsinki | 891 | .2 | 14.5 | 43.3 | 42.0 |
| Swedish | Sweden | 46 | | 15 | 50 | 35 |
| French | Paris | 406 | | 15.3 | 49.7 | 35.0 |
| Danish | Denmark | 2050 | .2 | 16.0 | 47.2 | 36.6 |
| Swedish | Sweden | 220 | | 18.6 | 50.0 | 31.4 |
| Canadian whites | Toronto | 49 | | 21.1 | 50.5 | 28.4 |
| Swedish | Sweden | 160 | | 21 | 41 | 38 |
| American Negroes | Seattle | 406 | 4.2 | 26.4 | 48.0 | 21.4 |
| Negro-white hybrids | Venezuela | 208 | | 27.4 | 54.8 | 17.8 |
| Australian aborigines | Central Australia | 100 | | 40 | 47 | 13 |
| Negroes | Liberia, Ivory Coast | 142 | | 48.6 | 42.2 | 9.2 |
| Negroes | W. Nigeria | 99 | 32.3 | 53.5 | 11.1 | 3.0 |
| Bushmen | Bechuanaland | 113 | 1.8 | 1.6 | 35.4 | 52.2 |
| Hottentots | Namaqualand | 59 | | 30.5 | 42.4 | 27.1 |
| Cape Coloured | Springbok | 88 | | 19.3 | 55.7 | 25.0 |
| Zulus | Johannesburg | 116 | 2.6 | 31.0 | 41.4 | 25.0 |
| Italians | Berra, N. Italy | 119 | | 16.8 | 48.0 | 35.2 |
| Italians | Naples | 93 | | 10.7 | 47.3 | 42.0 |
| Sardinians | Illorai | 147 | | 12.2 | 50.8 | 37.4 |
| Sicilians | Catania | 107 | | 15.0 | 49.5 | 35.5 |
| English | London | 114 | | 17.6 | 48.2 | 34.2 |

of an unenthusiastic native than it is to get him to collect all his urine for a whole 24 hours. There is the further fact that many of the blood-group genes produce their own antigens; this makes genetic analysis extremely simple when the right serums are available. Be that as it may, so much more effort is being put into blood-group research than into any other aspect of human genetics that the present situation is likely to persist for some time. It does not imply in any way that blood-group genes are better tools for anthropologists than other genes would be if we knew what they were and had some information about their frequency in various populations.

## Racial Classification

Let us now consider a racial classification based on blood groups. Wiener (*36*) proposed a classification of mankind on the basis of blood groups into three races, later increased to six (*18*), and I later proposed a slightly different classification into six races (*37*), as follows: Early European (hypothetical), European (Caucasoid), African (Negroid), Asiatic (Mongoloid), American Indian, and Australoid. After a trip to Pakistan and an investigation of the blood groups in Pakistan and India (*38*), I proposed distinguishing a seventh race, the Indo-Dravidian race, intermediate between the European and Asiatic, but closer to the European. In view of the data now available I propose (*39*) distinguishing 13 races, which fall into seven main groups.

### European Group

Populations of the European group possess the highest incidence of the Rh negative gene (cde) and a relatively high incidence of $R^1$ (CDe). Genes $A_1$ and $A_2$ are present in fairly high frequency, the latter generally higher than anywhere else. The *M* and *N* gene frequencies are "normal"—that is, $M = 0.5$ or more, $N = 0.5$ or less. S is present and attached mostly to *M*. No *Fy* (the African Duffy gene), *V*, or "Diego" are present. This group may be subdivided into five categories as follows.

1) *Early European* (hypothetical). This race possesses the highest incidence (nearly 0.5) of the Rh negative gene in the world, no *B*, and a relatively high incidence of $R^1$ and $A_2$. It is represented today by its descendants the Basques, and possibly the Berbers of North Africa.

2) *The Lapps.* This small but distinctive population has the highest frequency of *N* in Europe, a high value of $Fy^a$, and very low *B*, and its frequencies of $A_2$ are three times those found anywhere else in the world. The Rh negative gene is relatively infrequent, $R^1$ is somewhat above the usual European values, and $R^2$ is high.

3) *Northwest Europeans.* This race is characterized by fairly high *A* and by low *B* (less than 0.1), and by "normal" *MN* frequencies. Next to the Lapps, this is the population with the highest $A_2$ frequency. Except for the Basques, it is the race with the highest frequency of the Rh negative gene [in some areas (*40*) the frequency is actually higher than among the Basques].

4) *Eastern and Central Europeans.* In these populations the frequency of *B* is higher than 0.1, that of *M* is slightly higher than in the Northwest Europeans, and that of the Rh negative gene is somewhat less.

5) *Mediterraneans.* In these populations, which reside in southern Europe, the Middle East, and much of North Africa, the frequencies of *B* are higher than in Northwest Europeans, the frequency of the Rh negative gene is somewhat less, and the amount of $R^o$ (cDe) is greater, suggesting some relationship with Africans. In parts of this area the frequency of *M* is higher than "normal."

### African Groups

The populations of Africa can be broadly divided into (i) North Africans and Egyptians, both classified by me as predominantly European, and (ii) *"Afrique noire."* The latter populations, in spite of considerable diversity, have so many features in common that they may be collected into a race, as follows.

6) *African race.* This race is characterized by three distinguishing features: a very high frequency of $R^o$ (0.5-0.9), frequencies of *Fy* above 0.8, and a high frequency of "*V*." The frequency of $R^1$ is low. In addition, the frequency of the P factor is the highest known, $A_2$ is the highest anywhere except in Europeans, *B* is high (although not as high as in Asia), and some populations have high frequencies of the sickle-cell gene. Intermediate *A* genes, designated $A_{1,2}$ by Wiener (*41*) are more common than in Europeans.

7) *Asian race.* This race is characterized by high frequencies of $A_1$ and *B*, with little if any $A_2$. The frequency of the Rh negative gene is very low, although it may be present. Frequencies of *M* are "normal" (in northern Asia) to high (in southern Asia). S is relatively rare. $R^1$ is the predominant Rh gene. The frequencies of $Fy^a$ are higher than in Europe, and *K* (Kell) is low or absent.

8) *Indo-Dravidian race.* The population of the great Indian-Pakistan subcontinent is very varied, but until more is known about the blood groups of these peoples they may be classified into a single race, intermediate in many respects between Europeans and Asiatics. The Rh negative gene is present but less frequent than in Europe (about 0.2), $r'$ is present, and the frequency of $R^o$ is about the same as in Europe. $A_2$ is present, but accounts for somewhat less of the *A* than in the European group, and *B* approaches the highest frequencies found anywhere in the world. *M* is more frequent than in Europe (about 0.6); S is present, tending to accompany the *M* gene, as in Europe, although in some areas it is attached about equally to *M* and *N*.

### American Group

Some features of the data for American Indians suggest that it may eventually be possible to distinguish South and North American Indians serologically. However, until many more South and Central American and Mexican tribes have been tested, it may be best to continue to put all American aborigines into a single category, as follows.

9) *American Indian race.* This race possesses varying frequencies of $A_1$, sometimes very high (nearly 0.6) sometimes zero. $A_2$ and *B* are absent. The frequency of *M* is very high (0.8–0.9). S is present and tends to be attached more to *M* than to *N*. The frequency of $R^2$ is higher than anywhere else in the world, and the Rh negative gene is completely absent. $R^o$ is low. A striking characteristic of some American Indians is the presence of substantial amounts of the "Diego" factor ($Di^a$ as high as 0.4), which is nearly or completely absent in Europeans (*30*). I include the Eskimo in this race, although there are some differences. For example, some Eskimos definitely possess *B* which does not come from European mixture.

### Pacific Group

The vast Pacific area should be investigated further, despite the exten-

sive studies of Simmons and Graydon and their associates (*42, 43*) and of Birdsell (*32*). It may be too soon to set up any definitive classification, but it is tempting to tentatively classify the main Pacific populations (with the exception of Australia) into three races, as follows.

10) *Indonesian race.* In these populations, frequencies of *A* and *B* are in general fairly high (they are rather low in Sumatra), and $A_2$ is absent. The frequency of *M* varies from about 0.6 to 0.4. S is present. Only four Rh genes seem to be present—$R^1$, $R^2$, $R^o$, and $R^z$, with $R^1$ greatly predominating.

11) *Melanesian race.* In the Melanesians, frequencies of *A* and *B*, especially the latter, tend to be somewhat higher than in Indonesians. $A_2$ is absent. The frequency of *M* varies, but is generally low (about 0.1 in Papuans). S is present but much less common than in India, for example. In some parts of Melanesia the four Rh genes present in the Indonesians are found, but in natives of New Guinea, Fiji, and the Admiralty Islands only three Rh genes—$R^1$, $R^2$, and $R^o$—are present; $R^1$ predominates, and the frequency of $R^o$ is low. The frequency of $Jk^a$ is high. The sickle-cell gene is not present. *K* and $Lu^a$ are lacking. Findings for the Micronesians in general seem similar to those for the Melanesians.

12) *Polynesian race.* In the Polynesians in general the frequency of $A_1$ is high and *B* is almost negligible. But, possibly due to mixture, the frequency of *B* is nearly 0.04 in the Cook Islanders (*44*). *M* is somewhat higher than "normal" (nearly 0.6); S is present, but attached mostly to the *N*. Only three Rh genes are present—$R^1$, $R^2$, and $R^0$—with $R^1$ and $R^2$ about equally frequent and $R^0$ low. The frequency of *P* is fairly high (0.04) (*45*). In Polynesians (*44*) the frequency of $Fy^a$ seems to be between 0.5 and 0.7, whereas in the other Pacific races it is approximately 1.0. *K* and $Lu^a$ are lacking.

13) *Australian (aboriginal) race.* The Australians are characterized by high frequencies of $A_1$ and a total absence of *B*. The frequency of *M* is low (0.05–0.4) (*43*). S is almost completely lacking—a fact which sharply distinguishes the Australians from the Pacific group. Five Rh genes—$R^1$, $R^2$, $R^o$, $R^z$, and $r'$—are present; $R^1$ predominates, but its frequency is much less than in the Pacific group. The $R^z$ gene, never frequent anywhere and absent in parts of the Pacific area, has its highest frequency (about 0.07) in Australia. The Rh negative gene is absent. The $Lu^a$ antigen is completely absent. The frequency of *P* is not high. The gene *K* and the sickle-cell gene seem to be absent.

The races, as defined here on the basis of gene frequencies, do not differ in any startling way from races as defined on the basis of morphological characteristics. The question may well be asked, Have genetic methods added anything that was not already known from morphological studies? I believe we can answer this in the affirmative. Let me give two examples.

Confirmation of the Indian origin of the Gypsies was the earliest achievement of the genetical method. The Gypsies claimed an Indian origin, and George Borrow and others had established the fact that their language was a debased and diluted form of a modern derivative of Sanscrit. But though the Gypsies maintain that they never mix with the surrounding peoples, some Gypsy groups, particularly in Britain, are so like the people they live among that some authorities doubted their Indian origin. In 1921 Verzár and Weszeczky (*46*) removed all such doubts by determining the blood groups of some Hungarian Gypsies. The results showed that the blood groups agreed quite well with those of Indian soldiers tested at Salonika and differed significantly from the blood groups of Hungarians.

Or take the Lapps, whose exact position among the peoples of Europe has been a matter of controversy. For a long time they were classified with the Mongoloids. Haddon (*47*), Deniker (*48*), Coon (*49*), and others who wrote on the problem all recognized that the Lapps were a highly specialized group—a view that is confirmed by genetical methods. Almost all the isogene maps in Mourant's book (*11*) show that the Lapps have characteristically different frequencies of nearly all of the blood-group genes. On nearly all the maps there is a little area, like a "high" or "low" on a weather map, of which one can say, "There are the Lapps." But the earlier writers were wrong in thinking there was anything Mongoloid about the Lapps. All the blood-group evidence indicates that the Lapps evolved into their very distinctive race *in situ*. They are Europeans. Some physical anthropologists were coming to this conclusion on the basis of morphology, but it seems likely that without genetical evidence there would have remained many a doubt.

These are two among a number of possible examples. The genetic method has, in short, made contributions to anthropology that morphological methods could hardly have made, and is providing a new and fundamental basis for the study of race.

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