VIII   A Biological View of Race

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Most of the problems clouding the study and description of human variation can be traced to the taxonomic premise that *Homo sapiens* is divided into a series of races which are significant biological entities. We shall attempt to deal with this premise in the context of current biological thinking about the taxonomic structure of nature.

The historical development of taxonomy follows closely the changing prejudices and philosophies of other sciences and of the humanities and arts as well. At any period taxonomy more or less reflects the prevailing world view of a somewhat earlier historical period. Thus it is understandable that the first formal taxonomy should have been an outgrowth of herbals and bestiaries. The Linnaean system developed in the 18th century along with the pervasive compulsion to order nature into mechanically logical systems. The taxonomic framework of the recent past is the result of the 19th century's propelling need to think in terms of linear progression. Today, however, in many areas of creative activity, there is a growing interest in problems of portrayal, description, and quantification of complex nonlinear relationships. It is not surprising that the impact of these approaches and of the devices necessary to sustain them is now beginning to be felt in taxonomy.

The New Systematics

In recent years, following the lead of the physical sciences and mathematicians, biologists have begun to examine some of and basic tenets and assumptions of their discipline. Taxonomy, often thought of as the least dynamic of the biological sciences, has assumed a position of leadership in this reevaluation of methods and principles. Taxonomy has experienced what might be regarded as two revolutions (see Kuhn, 1962) in the last 25 years. The first led to the establishment of the "new systematics" and derived primarily from the introduction of ideas from genetics and cytology into a largely museum-oriented field. Awareness of the principles of Mendelian genetics and the analysis of large population samples of organisms resulted in a greater interest in infraspecific categories. Thus the concepts of subspecies and geographic races, championed by Rensch, Mayr, Dobzhansky, and others, increased in importance. The commonly acccepted definition of subspecies was well-expressed by Mayr (1942, p. 106):

The subspecies, or geographic race, is a geographically localized subdivision of the species, which differs genetically and taxonomically from other subdivisions of the species.

The new systematics shifted interest away from static species concepts, established by Linnaeus and reinforced, in a sense, by Darwin's emphasis on the term species. Differentiation of populations became the new point of focus and greater understanding was gained of the cytogenetic processes involved. However the problem of the taxonomic expression of the complex interrelationships discovered was largely ignored or attempts were made to solve the problem with the existing taxonomic framework. The new systematics, in introducing

dynamics into taxonomy, laid the groundwork for its own replacement. Extensive investigations of organisms in nature and of forms with widely divergent genetic systems (inbreeding, haplodiploidy, asexual reproduction, etc.), together with studies of multivariate patterns of geographic variation, made it apparent that the classical species-subspecies taxonomic structure (partially retained by the "new systematics") was inadequate for the expression of evolutionary relationships.

Perhaps the first signs of aging of the new systematics came in the early 1950's with the wide realization that the entities placed in the category "subspecies" were not necessarily evolutionary units. The subjective nature of the category had long been recognized (Mayr 1942). The dangers of its use were made clear by the controversy following a paper by Wilson and Brown (1953), who pointed out the arbitrary nature of the category and recommended that it no longer be used.

These problems were not unique to the subspecies category. Intensive studies of species, particularly in plants, have shown that the species itself is not necessarily a self-contained evolutionary unit (Epling and Catlin 1950). Attempts to create a rigorous and objective definition of species based on genetic criteria have failed because it is not possible to make them operational. A return to the original definition of species as "kind" has been recommended (Ehrlich and Holm 1962).

The major triumph of the "new systematics" was to introduce evolutionary thinking into taxonomy, and this led to the inevitable failure of the new systematics at the descriptive level. The inclusion of evolutionary hypotheses and assumptions into the word-symbols of taxonomy greatly reduces their usefulness for objective descriptions of patterns of relationships among organisms. If the process of evolution is to be inferred from the classifications of taxonomists, then the classifications cannot be based upon evolutionary hypotheses.

Numerical Taxonomy

The second post-Linnaean revolution in taxonomy began in the late 1950's and its effects are just beginning to be felt by the practicing taxonomist. The proximal cause of this revolution was the growing access to high-speed data-processing equipment. Although for many years taxonomists had recognized the usefulness of taxonomic systems based on multiple character comparisons (see, for instance, Anderson 1949), systems using large numbers of characters could not easily be analysed without the aid of digital computers. As availability of such equipment increased, people in many parts of the world began investigating phenetic relationships (relationships defined as degree of over-all similarity) among organisms. Developments in this field are largely outside the scope of this discussion; they are discussed concisely by Sneath and Sokal (1962) and in detail by Sokal and Sneath (1963). The broader implications of this approach, which perhaps are more concealed than revealed by the commonly used name, numerical taxonomy, are considered by Ehrlich and Holm (1962).

In brief, numerical taxonomy consists of the quantifying of large numbers of characteristics (usually 75 or more) which vary in the group of organisms to be studied. This is followed by the computation of some kind of coefficient of similarity among the units studied, based upon these characteristics. These coefficients may then be used as the basis for a taxonomic system by clustering the most similar entities. A simplified example is given in Figure 1.

The table (upper left) lists three entities, *A, B, C.* These entities may be individuals, species, genera, or any other units which are to be compared. In this example, only seven characters are evaluated for *A, B,* and *C.* A character, in the idiom
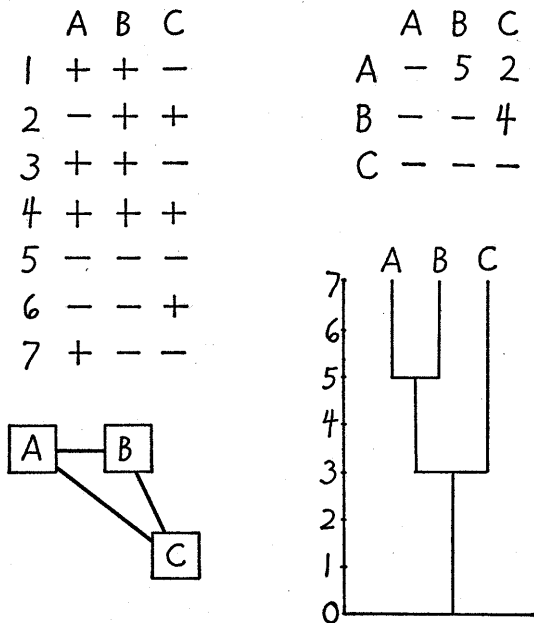
Figure 1. An example of numerical taxonomy. (Explanation in text.)

of the numerical taxonomist, is any characteristic which varies in the group under consideration. In our example, characters which have been coded into two states, plus or minus, have been listed. Certain characters in human beings, such as Rh positive or Rh negative blood types, could easily be coded in this fashion. Coding a character such as height in this manner results in considerable loss of information.

In order to obtain a measure of the degree of resemblance among *A*, *B*, and *C*, a very simple coefficient of association is obtained by counting the number of characters which are the same for each pair of entities. This coefficient may take values from a maximum of 7 (two entities the same in all characters)

to a minimum of o (two entities different in all characters). Values for all combinations are shown in the table in the upper right. This array of coefficients of similarity among entities is known as a Q-matrix. It can be seen that, with respect to the characters measured, A and B are more similar than A and C, C is more similar to B than to A, and B is more similar to A than to C.

Since only three entities are being compared here, it is possible to diagram these relationships in two dimensions as has been done in the lower left. The higher the coefficient of similarity, the shorter the line connecting any two entities. However, Q-matrices containing coefficients among more than three entities cannot be diagrammed in two dimensions. Nor is it easy by inspection to visualize the multi-dimensional relationships inherent in larger matrices. A matrix showing all of the possible comparisons among, say, 100 species of a genus would contain 4,950 different coefficients regardless of the number of characters employed in the comparisons. In order to obtain some grasp of the relationships in such an array, various methods of searching for and diagramming structure in the matrix have been devised.

The dendrogram (lower right) illustrates one method of structuring applied to our small sample matrix. The ordinate is the scale of values of the similarity coefficient. Since each entity has complete similarity with itself, each is placed at the top of the diagram with a value of 7. The highest coefficient in the Q-matrix is 5, between A and B, therefore the lines are joined at that level. The A-B stem is joined to the C stem at the average value of the coefficients of C with A and C with B (3). The diagram gives a more readily grasped picture of relationships, but only at the cost of the loss of some information present in the Q-matrix. For instance, from looking at the diagram one could not know that C is not equally similar to A and B.

The "taxonomy" of these entities could be viewed as one

taxon comprising two entities (or subordinate taxa) and another taxon comprising one. Various methods of applying nomenclature to dendrograms have been employed but their details need not concern us. The decision of how distinctive a group of entities must be before it should be distinguished (with a number or a name) as a "kind" or "species" is a decision which can only be made in the context of a particular investigation. It is important to realize that clusters derived by such analysis are based solely upon resemblances in the characteristics evaluated and are not based upon genetic or phylogenetic hypotheses. They comprise, however, the basic data set upon which such hypotheses may be constructed.

As might have been expected, such procedures have been decried by many taxonomists as being anti-evolutionary or typological. The first criticism is clearly not valid since the system is not concerned with the possible interpretations of the computed similarities. The second is partially true, although, as several authors (Daly 1961, Sokal 1962) have pointed out, there are fewer objectionable typological aspects to numerical taxonomy than there are to so-called phylogenetic taxonomy. A certain amount of the opposition to numerical taxonomy seems to be based on emotional reactions to the growing use of computers. There are dangers from the misuse of computers as with any mechanism extending human capabilities. Such misuse, if it occurs, is the result of a human decision. Emotional reactions to numerical taxonomy can be found even in the anthropological literature. For example (Coon 1962, p. 13):

The determination of species cannot be made by feeding figures into a computer. It is in a sense an art, practiced by men of experience who know, first of all, how species are formed.

It is true that the so-called art or intuition of practicing taxonomists has resulted in classifications of practical and scientific use. These intuitive classifications, however, also

have led to some unfortunate misconceptions as will be discussed below. The rigorous and highly specified procedures of numerical taxonomy largely avoid such problems by limiting greatly the opportunity for personal bias to enter undetected at the stage of gathering data and making comparisons. Coon's statement also illustrates the confusion of data with hypotheses mentioned above.

In some instances, the results of numerical taxonomy have been remarkably congruent with those produced by classical taxonomy. The numerical study retains the advantage, however, of having been done in clearly specified and repeatable steps. The classical taxonomist must depend for the evaluation of a taxonomic work largely upon his personal opinion of its author. Numerical taxonomists may check each other's work by repeating any or all steps. Other advantages of numerical taxonomy, such as precision in estimating relationships and ability to specify questions of character sampling and interrelationships of characters, cannot be discussed here. Most importantly perhaps, numerical taxonomy has retrieved the problem of what is meant by biological relationship from the cloudy realm of art and intuition.

It has long been assumed that satisfactory general classifications of organisms could be based on virtually any sample of the characteristics of individuals. In the past, the majority of these samples consisted of a small number of external characteristics of adult organisms. A few taxonomists have been concerned about the validity of this assumption in holometabolous insects and in plants with alternation of generations. This concern is understandable since larvae and adults or gametophytes and sporophytes may live in quite different environments and may seem strikingly different. Recently, numerical taxonomists have begun to investigate this question. Preliminary results indicate that congruence of taxonomies based on different stages in the life history may not be the

rule. For instance, Rohlf (1963) compared the classifications of larval and adult mosquitos using numerical taxonomic techniques. He found significant (but not large) correlations between larval and adult relationships. The sets of relationships were, however, not congruent. He concluded (p. 116):

... while there is general agreement between the larval and adult interrelationships, there are also many distinct differences between the classifications. It was recommended that characters should be taken from all life-history stages, if possible, in order to form the most general classification.

Similar difficulties may be found when characteristics of different sexes or different parts of the adult are used in establishing phenetic relationships. Michener and Sokal (1963), for example, have found incomplete congruence in comparing the patterns based on males and females and on head and body characteristics of bees. The taxonomist assumes that the phenotypes he studies are representative of genotypes. The fact that more than one representation of the same genotype may be constructed by studying different stages in the life cycle or different sets of characters from the same stage clearly shows how biased our picture of the genotype may be and how poor is our understanding of the genotype-phenotype relationship.

The magnitude of this problem cannot be judged from the data in hand because so few detailed studies have been made. The data which are available give us little reason to feel sanguine about the precision of inferences about relationships estimated on the basis of small samples of characteristics. When it is remembered that paleontology deals with small samples of characteristics of small samples of organisms, the importance of this problem is easily seen. Little credence can be put in attempts to reconstruct phylogenies at the infraspecific level from paleontological data (as has been

attempted by Coon, 1962, in the case of human races). Indeed, the arbitrary subspecific units recognized by Coon almost certainly have no phylogeny to reconstruct. It is difficult enough to trace even major lineages when relatively abundant material is available, as for instance, in the history of horses summarized by Simpson (1951).

A general problem in biology is how to deal with continuous but ever changing phenomena. This problem is especially important for the taxonomist because one of the more unfortunate aspects of the hierarchy inherited from Linnaeus is its requirement for discrete taxa. Therefore continua in space and time must be fragmented by the taxonomist. The patterns created by hybridization, reticulate evolution, apomixis, etc., cannot be adequately expressed by the classical taxonomic structure. Quantified similarities in a Q-matrix are free of this problem, although any *classification* based upon a Q-matrix will inevitably lose some information (but in a predetermined pattern dependent upon the clustering procedure used). Very recently C. D. Michener (1963) has begun to explore ways of making taxonomic classifications more realistic biologically by allowing overlapping taxa. The phylogenetic taxonomist often feels, and always hopes, that his groups represent "real" entities. The numerical taxonomist is always aware of the real source of his groups.

The Subspecies Problem

When one looks at the systems of classification which have been employed by anthropologists, he cannot help but be struck by the diversity of these systems and their tendency to overemphasize differences. Nowhere is this more apparent than in the classification of human subspecies or "races."

The ancient observation that men from different areas may differ in superficial characteristics unfortunately has led to the assumption that man could be divided into some number of biological entities known as races. Beginning as a simple folk taxonomy, the idea of distinct or largely distinct races appears throughout the literature of anthropology. As anthropologists became aware of the new systematics, they naturally attempted to interpret their classifications in the genetic and phylogenetic terms appropriate to this approach.

The genetic definition of taxa seemed particularly suitable since modern *Homo sapiens* is perhaps the only widespread species which has been demonstrated to fit the "biological" species definition. In all probability every significant test of interbreeding within the species has been made under natural conditions and there is no known instance of successful interbreeding with a sympatric species. Indeed, the cytogenetic systems and behavioral mechanisms of the hominoids would seem to preclude the latter. Thus it is convenient to describe man in aggregate as the species *Homo sapiens*. Species is here used to connote *kind* and not to imply some sort of biological equivalence with other species of plants, animals, or microorganisms. We can be certain that *Homo sapiens* is quite a different sort of entity from the coast redwood, the common fruit fly, or *Paramecium aurelia*.

While *Homo sapiens* may qualify (perhaps uniquely) as a biological species, treatment of infraspecific variation in man under the rules of the "new systematics" has not proved so simple. As mentioned above, the arbitrary nature of the subspecies has long been recognized. Two general problems have plagued those who wish to circumscribe infraspecific units in plants and animals. The first is the selection of the characters on whose variation the units will be defined. The second is the decision as to the amount of difference which will be recognized as amounting to subspecific differentiation. This de-
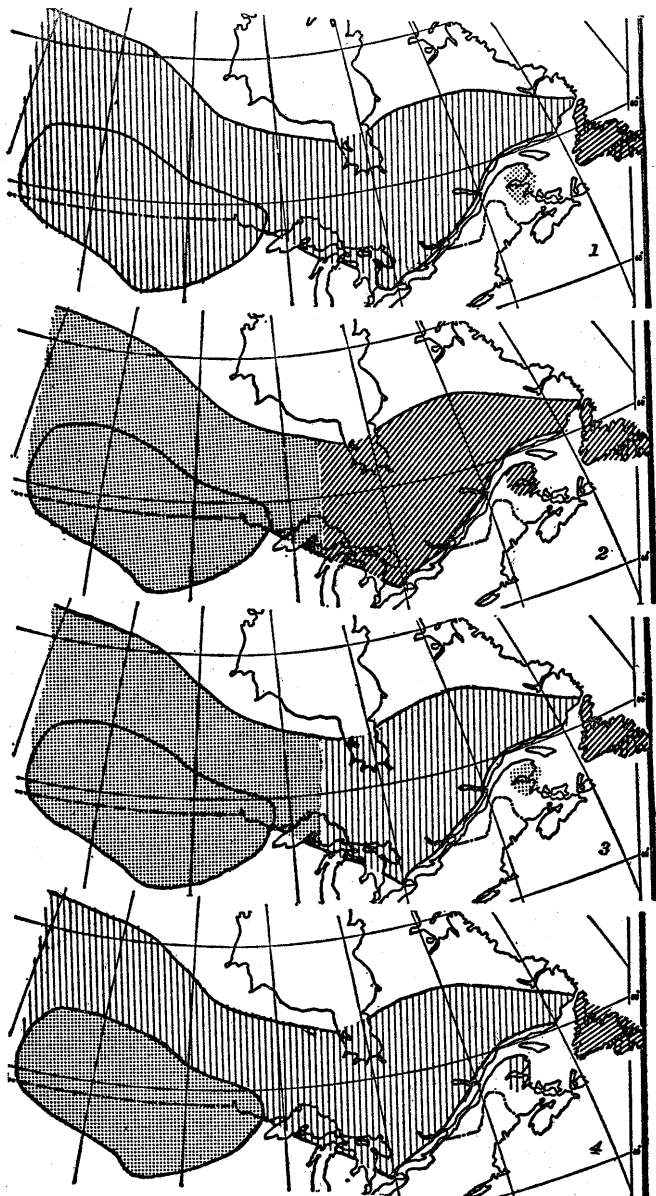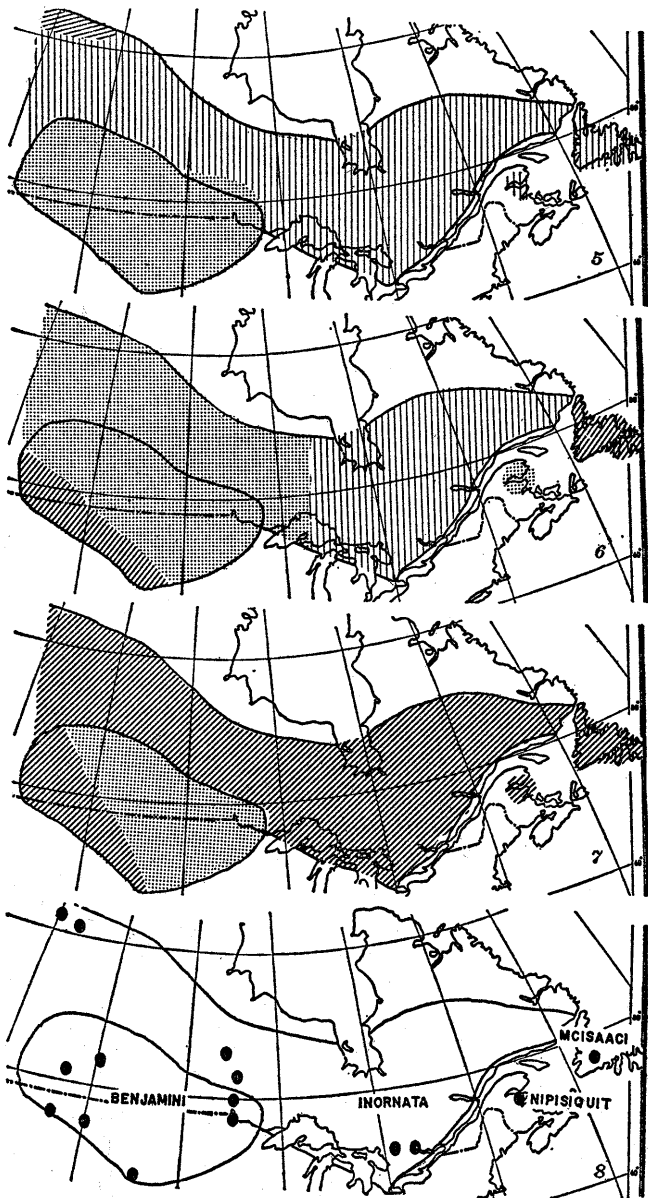
Figure 2. Geographic variation of seven different characters in
the butterfly *Coenonympha inornata*. Junctions between different
kinds of shading indicate that adjacent populations are signifi-
cantly different from one another in the particular character

mapped. The heavy black lines indicate the approximate ranges of
two of the currently recognized continental subspecies, *inornata*
and *benjamini*. *Mcisaaci* and *nipisiquit* are disjunct "subspecies."
(After Gillham.)

cision is a matter of taxonomic judgment and the discussion over percent rules and other guidelines for making decisions need not concern us here.

Concordance and Discordance

The question of character selection is of greater moment. If characters are largely concordant (that is, if they tend to vary together), then the study of the variation in any one character, or a few characters, would reveal the patterns in which population differentiation has occurred. If, on the other hand, variation is mostly discordant (characters are largely independent), then population differentiation must be studied with respect to one variable at a time. With discordance predominating subspecies recognized on the basis of one or a few convenient characters would not be evolutionary units. They would be simply units of convenience for filing specimens. Our zeal for discovering evolutionary units is predicated upon the belief, of course, that such units will have greater information content and hence greater predictive value than units recognized on other bases. Units of convenience for filing would not necessarily have these attributes and are not commonly thought of as useful in this way.

Too few studies have been made to permit a clear statement as to whether concordance or discordance in variation prevails in plants and animals. Subspecies in plants often seem to show concordant variation. In those zoological situations which have been analyzed, however, discordance seems to be the rule. For example, Gillham (1956) has analyzed a series of studies of geographic variation in butterflies in which both continental and insular subspecies have been recognized.

His survey revealed widespread discordance, as exemplified by Figure 2. As Gillham puts it (p. 120):

In view of the prevailing discordance of geographical patterns followed by different variates, racial partition of butterfly species is not only arbitrary, but it must also necessarily weight some variates and ignore others, without regard for the biological significance of any of them. The best that can be hoped for now is an analysis of variation by individual characters, avoiding arbitrary subdivision of the species. Such analysis will eventually yield a less distorted picture of species formation than that to which the artificial subspecies now inevitably leads.

It seems fair to state that, as a tool for understanding biological processes, the subspecies has deservedly lost favor. In the past ten years, only a very few papers in the journal *Evolution* have dealt primarily with the subspecies concept.

The Situation in Homo Sapiens

Is man an exception to this trend of discordance in animals? The problem of taxonomic structure within the species *Homo sapiens* is very complex. Certain statements, however, seem almost beyond dispute:

1. There is geographic variation in numerous human phenotypic traits.
2. This geographic variation has a largely genetic basis.
3. Variation in many instances cuts across cultural lines. Furthermore, there is reason to believe that differences among populations are largely the result of the action of selective agents. An inspection of a series of maps of the geographic distribution of human traits shows that the observed variation

patterns are quite discordant. The problem is not solved even if recent migrations are discounted and only so-called aboriginal populations considered. It is obvious that the choice of a characteristic for the primary division will determine in large measure what races will be recognized. The vast majority of classifications which have been proposed thus far, both folk and scientific, have been based primarily on skin color. Had blood groups, hair type, or body build been the primary standard, the lines would certainly have been drawn differently.

Doubtless there are many internal structural and physiological characteristics which are not immediately obvious, but which show geographic variation. Only a few of these have been studied, especially those relating to metabolism and temperature tolerance. As W. L. Brown has aptly put it (p. 152):

Applied to the wealth of data on the variation of modern *Homo sapiens*, the "no race" idea seems worth considering on this basis [discordance of characters], even though the value of the race concept in studies of man has already been challenged widely on other grounds by anthropologists themselves. In the face of such obvious discordance as, for instance, human skin pigmentation with blood type factors, or hair form with cephalic index (taken on a world basis), the wildly varying opinions of anthropological schools on the racial classification of our species show up as irrelevant and unnecessary.

Psychological characteristics, such as intelligence, drive, and disposition, certainly have a genetic basis (Erlenmeyer-Kimling and Jarvik, 1963). Although there can be no doubt that these psychological attributes are in part determined by the genetic information, the problem of estimating the genetic component of the variation in ability to reason abstractly, for example, is difficult in the extreme. In other words, the hereditary endowment of an individual and his environment interact to produce the psychological phenotype. It is virtually

impossible to separate the two components completely. While most mental characteristics are highly subject to environmental (particularly cultural) modification, it is clear that the range of possible responses is genetically set. One would expect, therefore, the frequency of the genes concerned to vary geographically. Psychological characteristics undoubtedly show basically the same sort of geographical variation as physical characteristics, even though their environmental component may, in many cases, be greater.

It seems very unlikely that satisfactory tests will be devised in the near future which will permit accurate evaluation of the genetic range of psychological characteristics, even within rather close-knit cultural groups, let alone among diverse cultures. One might expect variation in the genetic range of abstract reasoning ability from culture to culture, perhaps based on weak selection for or against individuals showing a high capacity for abstraction. One might hypothesize that, say, a Chinese population would have a slightly higher or lower average genetic ability for abstraction than one from the United States. It is difficult, however, to conceive of any practical way of testing this hypothesis in the face of overriding cultural influences.

It is generally accepted that attributes like intelligence are composite in nature. There would seem to be *a priori* no reason to expect concordant variation in the frequencies of genes controlling these various components (if they could be estimated), any more than in those controlling so-called physical characters. It also seems quite clear that geographic variation in genetic components of intellectual traits must be relatively insignificant in comparison with the variation induced by social and cultural environments.

This does not mean that the differences observed among men are some sort of mirage. Eskimos and Ubangis are obviously different in many respects. The crucial question is
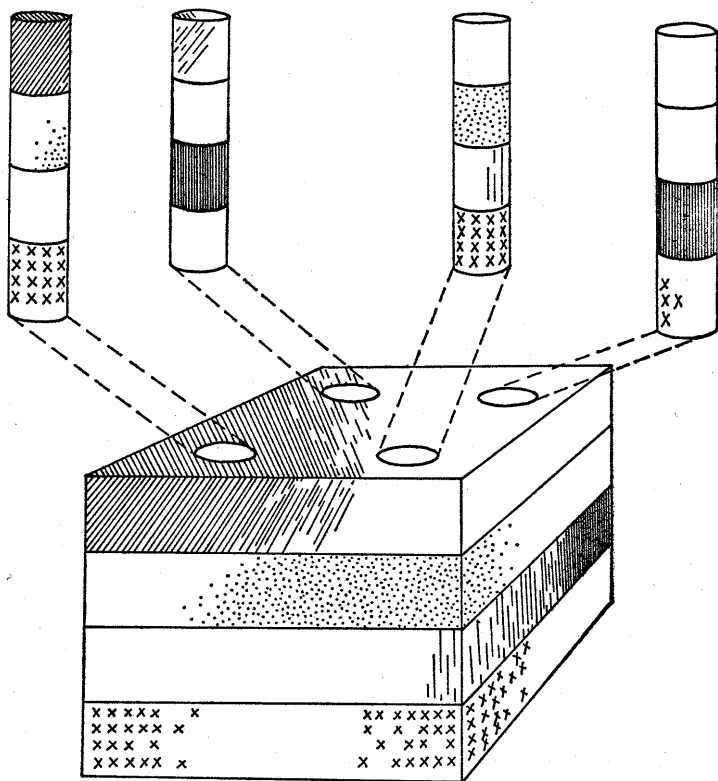
Figure 3. Diagram of discordant variation in four characters. (Explanation in text.)

whether or not one can classify human populations into discrete biological units (races or subspecies) one of which contains, say, the Eskimos and the other the Ubangis. This point is clarified in Figure 3. Each layer in the cube represents the geographic variation in a single hypothetical character. For example, if the top layer represented skin color, individuals in the near left-hand corner would have the darkest skin, those in the righthand half of the cube would have light skin, and so

forth. The cores extracted from the cube each represent a sample of individuals taken in that geographic area. Each sample is different; indeed, one might say that each represents a different "race." However, a set of four samples taken at any four places in the "character cube" would also produce four different "races." There is no "natural" racial division because the abundant geographic variation is in discordant characters.

The goal of any system of classification is, or should be, to abstract patterns of variation in such ways that they may be comprehended. Hiernaux (1963) has clearly expressed the crux of the matter (p. 199):

Classification is not a goal in itself, but a tool, a very useful one indeed when it works. When it does not, discarding it will not withdraw any scrap of knowledge, but on the contrary force us to face the facts as they are, in their full complexity.

Present-day subspecific classifications of man do not satisfactorily abstract the patterns of infraspecific variation apparent in *Homo sapiens*. Numerical taxonomic techniques will permit the evaluation of phenetic relationships among different geographic samples of men. It seems unlikely, however, that such analysis would result in sets of relationships which could reasonably be structured into discrete subspecific entities. It would be interesting to determine if discrete clusters exist at any level and if any indication of hierarchical structure exists.

Thing-Concept Confusion

Why then, in the face of these difficulties, do many biologists still feel that "good species" and "good subspecies" must exist in nature and, that, given the time and tools, such entities will be discovered or delimited? The answer may be found

in what might be called the "thing-concept confusion." The average biologist, when he says bird, flower, or Negro, feels that he is referring to a real, clearly delimited, biological entity. Although certain items may be referred unambiguously to one or another of these concepts, even a cursory consideration of them reveals that their unity resides primarily in the mind. How are the penguin, the ostrich, and the sparrow related? The systematist would say that they belong to a unit, birds, because of recency of descent from a common ancestor. Unfortunately this answer ignores the question of when, in time, birdlike reptiles became reptilelike birds. The limits of the entity bird become indefinite when the paleontological dimension is considered. The question of how to determine recency of descent is also ignored. One might assert that a penguin's most important biological relationships are with other organisms in their ecological situation such as killer whales, seals, and Antarctic fishes. These relationships at least have the advantage of being amenable to a certain degree of definition. It is only by making value judgments that one can decide which of these sorts of relationship are more important. Many biologists feel that phylogenetic relationship is more important because they can conceive of the transfer of genetic information along lineages back through time. We would not care to make this judgment. The transfer of energy in ecosystems seems equally (or more) significant than transfer of genetic information. In addition little is known about the structure and evolution of ecosystems and the possibilities of exchange of genetic information across what are considered to be phylogenetic lines.

The word flower might be considered to refer unambiguously to a morphological unit. In some plants, however, it is difficult to delimit one flower from another because they are reduced and crowded together in the inflorescence. From the point of view of function, the situation is even more complex.

The familiar poinsettia is an example of a group of very specialized flowers arranged in an inflorescence with brightly colored leaves or bracts. Just as most of us think of a daisy as a single flower although it is a cluster of small florets, so could we regard an entire flowering branch of poinsettia as the ecological equivalent of a flower. Nearly all of the grasslike sedges are wind-pollinated and have inconspicuous flowers. The highly modified, small, and clustered flowers of the sedge, *Dichromena*, however, are surrounded by colored leaves and the whole complex resembles a single flower. This genus of sedge is insect-pollinated. As soon as one attempts to make an exclusive definition, he immediately perceives borderline situations which do not clearly fit within the limits he wishes to impose.

The concept Negro has much in common with the concepts bird and flower. Sociologically, Negro is defined differently in the United States and Brazil. In the southern United States anyone who is not "pure white" is a Negro. In Brazil, anyone who is not "pure black" is a caucasian. Biologically the concept Negro has even less unity. Heavy skin pigmentation may be associated with a wide variety of other characteristics.

It is all too easy to decide from one's mental patterns and prejudices or one's distorted percepts from nature that there is an actual structure out there waiting to be found. This is the phenomenon of reification of concepts, well-known to the historian of scientific thought. This concept-thing confusion may seem unimportant when dealing with, say, subspecies of butterflies. With *Homo sapiens* such confusion creates not only social problems in the present, but perhaps evolutionary problems in the future. The evolution of man is an interaction between classical "biological" evolution and psychosocial or cultural evolution (Ehrlich and Holm 1963, Montagu 1962). In the realm of psychosocial evolution, conflicting ideas may be analogous to alleles at a genetic locus, their relative frequency

fluctuating through chance effects and what might be termed cultural selection. In this context, one might view the waxing and waning of ideas concerning the significance of races and racism as a problem in population phrenetics.

The Consequences of the Classical Approach

It might be profitable to look more closely at the harm that is done by continuing to use the classical species-subspecies categories and the usual hierarchic structure. Intellectual damage is done at virtually every level of investigation in both theory and practice. It is difficult to specify the extent of "damage" when it involves misfiling of specimens of grosbeak study skins as pointed out by West (1962) or the arbitrary pigeonholing of butterfly populations as was done by Ehrlich (1955). It is even more difficult to determine the extent to which our understanding of the process of evolution has been distorted by the imposition of the rigid set of taxonomic categories. In a recent textbook on evolution, one finds the statement: "The very hierarchy of genera, families, orders, and so forth is in itself evidence for the correctness of the theory of evolution, for that is the pattern that evolution should cause to develop." Since evolutionary theory has almost always been dealt with in terms of this hierarchical structure it is hardly surprising that our present theory may be misconstrued as automatically leading to such a structure. The systems of relationship established by unbiased procedures lend little comfort to the view that the structure of nature is inherently hierarchic.

There is no question, however, about the harm which has resulted from the extension of this taxonomic approach to considerations of the nature of geographic variation in *Homo*

sapiens. It has, among other things, led to the mistaken assumption that arbitrary racial subdivisions of *Homo sapiens* can be considered as evolutionary units in space and time. As has been discussed above, there is no basis for assuming, without extensive genetic study, that any population or any taxonomic group is an evolutionary unit. Discussions of the biological origins and characteristics of subjectively determined races (e.g., Coon, 1963), based exclusively, as they must be, on evolutionary misconceptions, are useful only for strengthening culturally determined prejudices against groups which have reality only in a social, rather than a biological, sense.

One unfortunate aspect of persisting in considering races to be discrete biological entities is seen in discussions of the consequences of interbreeding between supposed races of *Homo sapiens.* Many of these discussions do not accurately represent what is known about the genetics of interfertile ("infraspecific") populations in other organisms. For example, much attention has been drawn to the problem of the supposedly deleterious effects of "racial intermixture." Zoologists and some botanists, by their use of a "biological" species concept, are constrained to regard exchange of genetic material between what they call species as somehow detrimental to the continued existence of the species. Such interchange in effect becomes an illicit process and the biologist may unconsciously regard it as "unnatural." In the minds of some, hybridization comes to be thought of as a process deleterious to further evolutionary differentiation and not as a part of the evolutionary repertoire of the populations involved.

Biologists do not take this point of view about genetic interchange among populations of the same species. Indeed, the presumed existence of such interchange of genes is critical to the so-called biological species concept. Anthropologists and others have sometimes proposed that the supposedly harmful effects of gene exchange at the species level in other organisms

occur at the racial level in man. The term hybridization with its psychologically based overtones, or the ugly word miscegenation, are then used to describe what is presumed to be happening.

There is evidence that some infraspecific crosses made in the laboratory between geographically distant populations produce offspring which are relatively inviable. This has been found in butterflies, moths, frogs, and some plants. Such evidence seems largely lacking for crosses within *Homo sapiens*, although it is possible to construct models involving such phenomena as Rh incompatibility in which crossing might prove deleterious to a population. However, there is also some reason to believe that progeny of parents drawn from two different human populations would be, on the average, more fit in the sense of the population geneticist than the offspring of individuals from the same population. There would appear to be no genetic support either for the encouragement or the repression of intergroup gene exchange in man. Indeed, the situation of partially differentiated populations with some gene exchange among them has been postulated to be the ideal state for further evolution.

It is not necessary here to dignify the George Report and similar tracts with a point-for-point refutation. The pertinent facts are well known to biologists and anthropologists and are widely available to the interested layman (Commoner, et al. 1963). It might be maintained by any scientist that it is his duty to publish facts in his discipline as he sees them. This presumably would include speculations based on these facts. While this is clearly so for the more abstruse ideas of basic science, it does not seem reasonable to absolve the scientist of all social responsibility for his views. The question would rarely arise in the domain of pure science, but it arises frequently wherever *Homo sapiens* is concerned. The situation with race finds an interesting parallel in the discussions of the

responsibility of nuclear physicists in designing and building nuclear weapons. Surely no one would wish to prescribe rules of conduct in such matters; one must depend upon the judgment and good faith of the scientist.

It seems little enough to ask, however, that the scientist working in areas where any results are of great social consequence should follow the behavioral pattern of scientists in general. His results should first be published in the scholarly literature. Potential social effects of the results should be considered thoroughly. This would be true whether the scientific results concern nuclear fission, cancer-related viruses, extrasensory perception, organic poisons of potential use as pesticides, or the evolution of *Homo sapiens*. Should the work be misinterpreted or be used to further causes which it does not support, it surely is the responsibility of the scientist immediately to make clear the misinterpretation and to disavow the misuse of his work. In the absence of such a disavowal, it may properly be assumed that the scientist supports such use of his work. Definition of the areas of a scientist's responsibility is an important and vexing question and deserves further discussion. It seems obvious, however, that certain types of behavior are to be avoided. A scientific idea of merit does not become part of the formal structure of science by its acceptance by the public at large. Rather, it must be weighed and reworked by the scientific community. It must not become the basis for social actions until it has passed this important test.

In conclusion it may be said that so-called subspecies or races in man, as in many other organisms, are not evolutionary units. They are arbitrarily created to describe certain variation patterns in one or a few characteristics. They have no common genetic pattern nor may their genetic future be predicted. It is an error to believe that human subspecies or races are *things* that may be discussed and compared or whose separate evolutionary development may be traced. Whereas in

other organisms use of the subspecies concept may do only intellectual damage by creating a distorted view of nature, in *Homo sapiens* the results are very different. Promulgation of views of races and their supposed properties may have serious and far-reaching consequences both for man's present behavior and for his future psychosocial evolution. In 1768 the botanist von Haller said:

Natura in reticulum sua genera connexit, non in catenam: homines non possint nisi catenam sequi, cum non plura simul sermone exponere.[1]

His words have even greater cogency today when we know so much more about man's evolutionary background, his behavior and culture, and at least some of the possible consequences of his activities.

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1. Nature has linked her kinds into a net, not into a chain; men are incapable of following anything but a chain since they cannot express in words more than one thing at a time. *Historia stirpium indigenarum Helvetiae.*

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