

compared to the Yanomama-Guaymí 24% (Migliazza n.d.). While small differences in cognate fractions may not be significant, the linguistic data appear to be consistent with the biological evidence.

With regard to the broader anthropological issues raised by these findings, we have here a "worked example" of a problem which will arise repeatedly as tribal data on genetic markers, anthropometrics, or linguistics accumulate. Perhaps the most important conclusion to be drawn from this experience is that the wealth of genetic markers now available, plus the standard anthropometric measurements, together contain sufficient information that when tribal similarities emerge on the basis of limited data, further research has a high probability of resolving the evolutionary question raised. There should be little room for continuing ambiguity.

SUMMARY

A multidisciplinary study of the Guaymí of western Panama was undertaken to confirm or disprove their apparent similarity to the Yanomama of southern Venezuela and northern Brazil, inferred from allele frequencies for six polymorphic loci studied in the Guaymí by Matson and colleagues in 1965. Gene frequencies were estimated from the present sample of 484, which is more than twice as large as the previous sample and appears to be completely independent of the latter. The findings replicate the gene frequencies obtained earlier, within the error of resampling after a decade. Leukocytes were typed for A and B locus specificities of the HLA system in 22 Guaymí. A specificity (HLA Bw15) absent from the Yanomama is present in high frequency in the Guaymí. Elsewhere we have reported that a polymorphism of serum albumin in the Yanomama is not present in the Guaymí but that the Guaymí possess polymorphisms of acid phosphatase and lactate dehydrogenase not present in the Yanomama. These findings make any close evolutionary relationship between the two tribes unlikely.

Anthropometric data, though not extensive for other tribes, support the conclusion reached from gene frequencies. Of four tribes for which comparable measurements are available, three are more similar to the Guaymí than are the Yanomama, as judged by Mahalanobis's distance. Linguistic studies suggest that the Yanomama language (lexicon) has a larger fraction of cognates with Guaymí than does any other language compared here; however, two other languages in the series (Cashinahua and Shipibo) have higher cognate fractions with Yanomama than does Guaymí.

Comments

by B. K. AVERILL

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The authors present an interesting example of historical guessing, more generally known as microevolution. While I am sympathetic with the conclusions reached, there are other factors which could account for the degree of similarity between the Guaymí and the Yanomama.

In some simulation experiments of small human populations influenced only by drift and mutation (Averill 1977), I found that measures of genetic distance depended on how many loci, and which loci, were used. Although the estimates based on subsets of loci tended to diverge over time, there were periods, say, 100-400 years, when pairs of populations became

more similar. The authors choose not to credit chance as an important factor, but from these experiments I see it operating at two levels: at a biological level in the form of drift and mutation and at the observer level in the choice of loci.

Secondly, the degree of similarity between the Guaymí and the Yanomama on the basis of anthropometric data could be due also to nonselectable ecological factors. For example, differences in the availability of mineral ions and in the intake ratio of carbohydrates to proteins could be responsible partially for dissimilarity between two groups.

The authors conclude that further research in conjunction with previously collected genetic and anthropometric data can likely resolve the question of phylogenetic relatedness. This seems an overly optimistic view, particularly in regard to populations with no recorded history. At best, any conclusions about a recent common history are guesses, and ambiguity will continue to loom large.

by JOSEPH B. BIRDSELL

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This paper is a timely model in methodology for the study of evolutionary relationships between two populations. Earlier data had suggested a possible biological relationship between the Guaymí Indians of Panama and the Yanomama of southern Venezuela and northern Brazil. The present paper represents a retesting of the hypothesis of relationship using many more genetic variants, collecting and analyzing linguistic materials for the two tribes in question as well as others of South America, and, finally, obtaining anthropometric data of a limited sort. Using the parameters in the three discrete fields of investigation, the authors find it possible to exclude any probable biological relationship between the two tribes of Indians well removed in space.

The pleasing things about this study involve a willingness to retest an earlier hypothesis, the bringing to bear upon the task of powerful discriminant variables, and the sophisticated posture of the authors when dealing with the ambiguities of evolutionary relationship. They are clearly aware that similarities between two groups may result from convergent evolution as well as be a by-product of statistical operations. They are not misled by dendrograms in which clustering may simply result in placing "leftovers" together. The pattern of genetic markers present in the two tribes makes it unlikely that they have any close evolutionary relationship. The paper is a classic and should be a model for many future investigations of like type.

by M. H. CRAWFORD

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During the last decade, much of our knowledge of the genetics of the Amerindian populations of South America has been derived from the extensive investigations of J. V. Neel and his associates, among them F. Salzano, N. Chagnon, F. Kotinhammer, R. Ward, R. Spielman, and H. Gershowitz. To date approximately 100 articles have been published on various aspects of the demography, population genetics, disease patterns, serology, and sociocultural anthropology of the Yanomama, Xavante, and Makiritare tribes of Brazil and Venezuela. This article attempts to combine and focus data from different fields of inquiry upon a single question of the ethnogenesis of the Guaymí and the Yanomama.

Fitch and Neel (1969) noted, on the basis of blood marker gene frequencies, that the Yanomama (of southern Venezuela and northern Brazil) clustered together with the Guaymí (of

western Panama and eastern Costa Rica) on the same "branch" of a dendrogram. Spielman et al. investigate the possibility of phylogenetic relationship between these two geographically separated groups on the basis of genetics, linguistics, and anthropometrics. The results of the anthropometric and linguistic comparison suggest that the Guaymí and the Yanomama have no recent phylogenetic relationship, the taxonomic similarities implied by the gene-frequency data being an artifact of the statistical method utilized.

This paper is useful to anthropologists from a number of different perspectives. It provides an example of the convergence of genetics, linguistics, and sociocultural and biological anthropological methods on a question of common interest. In addition, it illustrates the inherent statistical problems of attributing too much biological meaning to dendrograms constructed from heterogeneous groupings. The Guaymí and Yanomama cluster together because both are relatively distant from other groups sampled and not because of gene-frequency similarities. Because cluster algorithms minimize within-cluster variability, groups which differ from most of the populations are clustered together. To their credit, Spielman et al. did not accept the initial clustering of the Yanomama and Guaymí as "biological truth," thus further confusing the prehistory of the area. Instead, they tested the hypothesis, using additional data, and then discarded it.

by RICARDO CRUZ-COKE

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The authors recognize that an HLA specificity found in a single individual might reflect admixture. In fact, antigens A1, B8, and Bw17 are prevalent in Caucasian populations (Bodmer and Bodmer 1973). Nevertheless, they add that the finding of Bw15 in the Guaymí, together with its absence in the Yanomama, "implies a solid genetic difference between the two tribes." It seems to me that this is a very strong statement. The Guaymí sample is very small and obtained in a single isolate. Although nothing is known about the consanguinity of the Guaymí, the relatively high frequency of Bw15 among them may be the result of a founder effect. To support this explanation, I would recall the example of haplotype HLA 12, Bw29, characteristic of Western European Caucasians, which was found in high frequency in a sample of 49 Easter Islanders by Thorsby et al. (1972). Later, Rothhammer and I (1977) published a genealogy of Easter Islanders showing the founder effect of a Caucasian sailor, ca. 1870, and the gene flow of the "Caucasian" haplotype across four generations up to the present time. Before claiming "a solid genetic difference," it would be necessary to increase the number of individuals and isolates.

by C. C. CURTAIN

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Spielman and his colleagues have provided a commendable and significant illustration of the dangers of placing too much reliance on phylogenetic trees based on small numbers of attributes. The case of the Guaymí and the Yanomama is all too familiar to students of the peoples of Melanesia, where populations closely related at first sight are on more detailed examination swallowed in the sea of random and apparently inexplicable diversity which seems characteristic of the region. The only additions I could suggest would be a reference to Simmons's early insights into the causes of blood-group heterogeneity in such populations and an important paper by Gajdusek on factors influencing the genetics of primitive populations (Simmons et al. 1961, Gajdusek 1964).

by PARTHA PRATIM MAJUMDER

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The paper under consideration tackles an important problem rendered the more important by the current fashion of constructing phylogenetic trees from distance matrices. More often than not, such trees are interpreted without adequate reference to the history of the populations under consideration. Spielman et al.'s method of verifying the hypothesis of taxonomic similarity between populations merely as statistical "leftovers," without any real biological similarity, is laudable. Indeed, interpretations in anthropological genetics can be misleading and false if not considered in conjunction with sociohistorical data.

In the case of the Yanomama-Guaymí relationship, Spielman et al. have shown that, despite the fact that on the basis of genetic data the two tribes fall on the same branch of a large phylogenetic tree, there is little evidence for their common ethnic ancestry. In other words, they have shown that the close similarity between the two tribes as obtained from genetic data is not "real." The phylogenetic tree in question, however, was computed from a distance matrix based on only six genetic loci (five of them blood-group loci). Isn't this too few loci to give any proper representation of phylogenetic relationship? In fact, the "provisional nature of the schemata" under consideration was pointed out by Fitch and Neel (1969). The results might have been different if a larger number of loci had been considered. In any case, six is too small a number of loci on which to base the construction of a phylogenetic tree. As table 3 shows, the distance between the Guaymí and the Yanomama computed on the basis of 11 anthropometric traits is, relatively, not small. What I am emphasizing is simply that the question "Does the genetic similarity between these two populations indicate a relatively closely shared evolutionary history?" may not be very meaningful because the computation of the similarity index was based on gene-frequency data at only six loci. If, on the other hand, the computation of genetic distance had been based on a larger number of loci and the distance had still been found to be small, the problem tackled here would have been more meaningful.

In conclusion, I would like to record, once again, my appreciation of the authors' bringing this important problem to the surface and of the method with which they have dealt with it.

by NEWTON E. MORTON

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This paper considers the available evidence, most of it previously unpublished, about the similarity of two geographically isolated tribes for which closely shared evolutionary ancestry was once suggested. The data are presented clearly, the language is precise, and the verdict of "not proven" is cautious and noncontroversial. A casual reader would not guess that as recently as five years ago the genetic structure of populations was a battlefield of conflicting methods and interpretations (Cavalli-Sforza 1973; Morton 1973, 1974). What were the issues, and how was consensus reached?

Investigators who are interested in quantifying and comparing different population structures use *kinship*, a measure of similarity which relates gene frequencies to genotype frequencies and can be predicted from migration and genealogy as well as "bioassayed" from phenotypes, surname or clan concordance (isonymy), and cognate frequencies. Often the matrix of kinship within and between pairs of populations can be adequately summarized by Wright's hierarchical model or Malécot's isolation by distance. The approach to population struc-