matters arising

Culture and genetic variability

CHAKRABORTY found[1], by using gene frequencies for seven serological markers to compute genetic distance, that 'only geographical distance seems to be important, explaining the trend in genetic variabilities' in seven Chilean Indian populations. The correlation coefficients he presented were 0.716, 0.775, and 0.901, for correlations between genetic distance–geographical distance, genetic distance–cultural dissimilarity, and geographical distance–cultural dissimilarity, respectively. He then presented the results from a stepwise regression, and found that while geographical distance explained 51.31% of the genetic variation, cultural dissimilarity explained only an additional 8.88%. He did not, however, use as the first variable in the stepwise regression the one which had the highest correlation with the dependent variable. Culture alone accounts for 60.06% (r^2) of the genetic variation in these data. If geographical distance is then added, the additional variation explained would be less than 0.2%. These figures are, of course, approximations subject to slight rounding error from the published tables. It is indeed difficult to assess the relative importance of variables which are themselves highly correlated, as Chakraborty states. But his data clearly do not support his conclusion that of the variables measured, only geographical distance is an important correlate of genetic distance. From these data, culture is at least of equal importance.

It would be profitable to use these data to consider the relative effects of genetic and geographical distance upon culture. Geographical distance apparently explains 81.18% of cultural diversity as measured in this study. This leaves a smaller, but possibly significant, proportion of cultural variation which might be explained by the genetic measure.

PENELOPE J. GREENE

Population and Developmental Biology Group,
School of Biological Sciences,
University of Sussex,
Brighton, Sussex, UK

1 Chakraborty, R. *Nature* 264, 350–352 (1976).

CHAKRABORTY REPLIES—Greene[1] contests my assertion regarding the relative importance of geographical versus cultural separation as a correlate of genetic variation in seven Chilean populations[2]. In so doing, she notes that in the stepwise regression procedure I used geographic distance as the first variable even when the cultural dissimilarity index had a higher product moment correlation with genetic distance (the dependent variable). Two reasons justify my choice of geography as the first independent variable to be entered in the regression analysis, one being theoretical, the other pragmatic.

Take, for instance, cultural variability as the dependent variable. Evaluation of the relative effects of geographical and genetic distances on cultural variability indicate that 82.41% of the cultural variability is explained by geographical distance ($P < 0.0005$), whereas the additional effect of genetic distance is 4.01%, which is statistically insignificant ($0.10 > P > 0.05$). This alone may suggest that geographical distance should be the first variable of interest.

The pragmatic view concerns the choice of the characteristics determining cultural diversity. As elaborated elsewhere[3], it is difficult to ascertain that cultural attributes are independent of geography. For example, we classified the seven populations on the basis of their types of subsistence, housing and architecture, economics, mode of gathering food, etc., which do have strong geographic components embedded in them. Thus, the strong association between cultural affinity and geographic proximity is indeed historical in these seven populations.

Furthermore, a stepwise regression method often under-represents the importance of the last variable to go in, particularly when the independent variables are significantly correlated with the dependent one. A logical explanation of causal relationship in such an event has to based on an understanding of the process producing the covariation between the variables, and not based on which independent variable has the highest correlation with the dependent one.

Greene's criticism, therefore, should be viewed with caution, although any generality of my analysis needs further examination, possibly from studies of other populations with comparable ethnographic accounts.

RANAJIT CHAKRABORTY

Center for Demographic and Population Genetics,
University of Texas Health Science Center,
Houston, Texas 77030

1 Greene, P. J. *Nature* 267, 375 (1977).
2 Chakraborty, R. *Nature* 264, 350–352 (1976).
3 Chakraborty, R., Blanco, R., Rothhammer, F. & Llop, E. *Soc. Biol.* 23, 73–82 (1976).

Do viruses use calcium ions to shut off host cell functions?

IN discussing the shut-off of host cell functions by poliovirus, Carrasco and Smith[1] ask: "How does a viral protein change the ionic environment inside the cell?" Perhaps it forms channels across the external membrane[2]. For example, a viral structural protein might generate holes by assembling into hexamers, pentamers, or extended lattices in a membrane.

Although Carrasco and Smith emphasised Na^+ ions, divalent ions are probably more important controllers of metabolism. In general, Ca^{2+}, Mg^{2+} and polyamine ions tend to form much more specific links with polyelectrolytes than Na^+ or K^+ do[3], and the Debye–Hückel concept of ionic strength grossly underestimates the relative binding of, say, Ca^{2+} compared with K^+, to membranes and viruses[4]. Many enzymic activities depend upon divalent ions, while relatively few respond to physiological changes in monovalent ion concentrations.

Of the two main divalent ions in biology, it is Ca^{2+}, not Mg^{2+}, that usually acts as a signal. This is because Ca^{2+} is actively pumped to at least a thousandfold concentration difference across membranes[5], whereas Mg^{2+} is much nearer equilibrium[6], probably because it permeates more easily. The fact that cells respond more to changes in extracellular Mg^{2+} than Ca^{2+} has misled some workers into putting a false emphasis upon the ions' relative roles[7].

The early effects of many lytic viruses can readily be interpreted as a consequence of increased flow of Ca^{2+} into