

is inappropriate. The first and fifth clusters are clearly consistent with traditional explanations for the peopling of the New World and for the differences seen by most scholars between Indians and Eskimos. While Szathmary and Ossenberg single out the second cluster as supporting their argument, Brennan and Howells argue convincingly for gene flow, citing both linguistic and historical data in confirmation. They point out that their analysis supports the traditional, multiple-migration model for the peopling of the New World as elaborated by Neumann.

Szathmary and Ossenberg present data on a relatively small number of groups that are widely distributed in space and time and definable as populations on very different levels, for example, Cibecue Apache versus Japan, Korea (table 1). Since distance and cluster statistics are based on the comparison of within- and between-group variance, the use of samples ranging from small communities to regional and national aggregates is cavalier at best. The effect of the nature of the samples on the results should be assessed, and some effort should be expended in finding Asiatic Mongoloid samples that are more appropriately matched in scale to the North American data. It is unclear why the study was limited to the groups chosen here when other, more appropriate samples are available (Brennan and Howells n.d., Spuhler 1972, and South American sources).

Scale is important in the interpretation of these results in another way. Small-scale studies of the congruence of linguistic and biological attributes have generally been quite successful. For example, Spielman (1973; Spielman, Migliazza, and Neel 1974) compared serological, anthropometric, and linguistic data on Yanomama villages and found good agreement among the resulting dendrograms, and both Ossenberg (1977) and Zegura (1975) have reported good congruence between linguistic and cranial data on Eskimo populations. In contrast, Spuhler's (1972) extensive analysis of serological, linguistic, and geographic data on North American aboriginal groups fails to demonstrate a significant correlation between biological distance and glottochronological distance. Instead, Spuhler finds that geographic distance and, by extension, gene flow are highly correlated with biological distance. Studies on the correspondence between biological and cultural trees are analogous to the biological-clock problem and as such are based on, among others, two assumptions: that nonphylogenetic sources of resemblance such as gene flow and diffusion are unimportant and that the chance reappearance of similarities in two diverging lines is rare (Spuhler 1972, Byles 1976). As time depth increases in the absence of efficient isolating mechanisms, these assumptions must become less and less tenable. Given the geographic distances, great time depth, and relatively small numbers of groups used in the Szathmary and Ossenberg study, it is not surprising that the results are not entirely consistent with the traditional picture of Eskimo-Indian relationships. The problem at hand, however, is not whether the traditional model fits all available data perfectly, but whether it provides a better explanation than do alternative models. A research strategy like that used by Spuhler, in which more than one model explaining population relationships is applied to the data and the fit of these models is compared using an explicit statistical evaluation, provides a satisfactory solution to the problem. Szathmary and Ossenberg use neither simulation techniques nor correlation to test the correspondence of their dendrograms to the various historical models they present. Their results would be better presented if these models were stated in a testable form, for example, as trees, and fit to the biological data in an explicit fashion. Post-hoc explanations appealing to gene flow, to incomplete summaries of the archeological record, and to ecological oversimplifications (for example, Haida and Maritime Archaic are maritime Indians, Barren Grounds and Brooks Range are inland Eskimo) are no substitute, and the time involved in the necessary computations is no excuse.

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In science, the constant challenging of old dogma is a sign of intellectual health and vitality. Uncritical and premature acceptance of explanatory hypotheses as fact can retard the progress of investigation. All too often, research becomes stagnant when established theories remain unchallenged and are passed on from one intellectual generation to another as "truths." Szathmary and Ossenberg raise some significant questions concerning one of the established truths, namely, that "Eskimos and Indians are descendants of different populations that entered the New World at different times, following different routes." Implicit in this "truth" is that the Eskimos are latecomers into the New World, which was peopled earlier by the Amerindians. While the questions posed by the authors may not be answerable at this time, it is hoped that their synthesis will stimulate additional research.

On the basis of multivariate statistical analyses of blood-marker frequencies and discrete cranial traits, an affinity is noted between the Eskimo and the Indian Na-Dene-speakers. The affinity is interpreted in two possible ways; (1) the two groups had a common founding or ancestral group some 10,000 years ago, or (2) the founding group had two components that were linguistically and biologically distinct.

In studies of gene flow and racial admixture, gamma globulin (Gm) haplotypes are particularly informative as to ethnic origin (Schanfield 1976). Unfortunately, such data were not available to Szathmary and Ossenberg in evaluating the affinities of the Na-Dene-speaking Indian and Eskimo groups. The Gm distribution patterns of Alaskan, Siberian, and Indian groups suggest that the New World Eskimo haplotypes are unique. Unhybridized New World Eskimos totally lack  $Gm^{2a:2}$  but exhibit  $Gm^{2a:1}$  and  $Gm^{2a:1b:1}$  at moderate frequencies. Siberian indigenous populations have a high incidence of  $Gm^{2a:1}$  with lower frequencies of  $Gm^{2a:2}$  and  $Gm^{2a:1b:1}$  (Schanfield and Crawford, unpublished data). The absence of  $Gm^{2a:2}$  in New World Eskimos better supports the second of the two interpretations proposed by Szathmary and Ossenberg, namely, that the founding group had two components which were biologically distinct—the parental Amerindian group possessing the  $Gm^{2a:2}$  haplotype while the founding Eskimo group lacked it. It is possible that the founding Eskimo population was small and did not represent the Siberian indigenous gene pool.

As information on more genetic markers becomes available, the likelihood of these alternative explanatory hypotheses may have to be amended. In addition, other explanations may become more plausible with the addition of genetic and morphological information from Siberia.

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Although most initial reservations against the authors' use of specifically archaeological data are in the long run too insignificant to mention, I do wish to raise two points by way of supplement rather than criticism.

1. The citation (Laughlin 1963, 1975) of work said to set out the "most favoured current view" of Eskimo and Aleut origins fails entirely to do justice to the recent recognition and attempted treatment of a most complex set of related problems by a number of investigators (e.g., Clark 1974, 1975; Dumond 1970, 1974, 1977, 1978; Dumond, Conton, and Shields 1975; Dumond, Henn, and Stuckenrath 1976; Irving 1970; McCartney 1971; McGhee 1976, 1978; Turner and Turner 1974). These problems involve relationships not alone between Eskimos and Aleuts, but also between the somewhat anomalous "Pacific Eskimos" and their northern brethren.