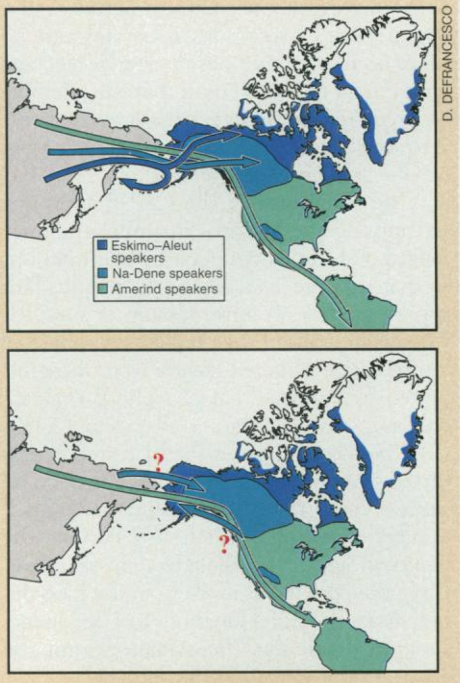
LETTERS



"Lines of evidence"

How strong is the evidence "that the Americas were peopled by three waves of migrations"? (Above, possible migration routes about 12,000 years ago; top, the Greenberg hypothesis; below, alternative proposed routes.) Can researchers "who model protein structure" make "accurate predictions before a structure is determined by experiment"? Is another study needed about "low-level radiation risk"? Is there "consensus" about the effects of electromagnetic fields? And did "mere absence" of men during World War I turn "more women to drink"?

The "Greenberg Hypothesis"

I would like to comment on the article "The peopling of the Americas" by Ann Gibbons, whose reporting I respect (Research News, 4 Oct., p. 31), concerning what is therein called the "Greenberg hypothesis"—that the Americas were peopled by three waves of migrations. It is said that this hypothesis is challenged by new genetics data suggesting two waves, or one wave. In this case, it appears that pertinent evidence was not taken into account.

Regarding the dating of the Amerind language, the impression may have been given that the linguistic age based on glottochronology is wedded to the Clovis culture of about 12,000 years before the present (B.P.). What we stated in 1986 (*1*) was that glottochronological dating has major problems, that long dates are seriously underestimated, and that "for Amerind we are dealing with a time period greater than 11,000 B.P. and beyond the limits of glottochronology."

Regarding genetic dates, Peter Forster, who is cited at the end of the article in a context of suggesting doubt regarding the three-migration scenario, has stated (*2*), "I was very excited to find that my results match your findings so closely."

If we evaluate the various lines of evidence, Eskimo-Aleut must be very recent and separate, given the mutual intelligibility of Alaskan and Greenlandic Eskimo and the undisputed acceptance of Eskimo-Aleut, even by conservative linguists. Eskimo and Na-Dene have entirely separate linguistic relatives in the Old World, Na-Dene being most closely related to Ket in Siberia, and Eskimo to quite other groups in northern Asia—for example, Chukchi.

Of all the sciences concerned, archaeology has the most assured dating. In a recent massive work (*2*), the editor Frederick West of the Harvard Peabody Museum points out (*2*, p. 525) the "striking parallelism" of the archaeological evidence to the three-migration theory." No one has seriously discredited Turner's dental evidence. The massive material on population genetics assembled by Cavalli-Sforza shows essential agreement, as does the early mitochondrial DNA evidence of Wallace and Torroni. A scientist should abandon an incorrect theory, but a fair appraisal of evidence from four independent sources, including new archaeological evidence, shows that this would be premature in the case of the "Greenberg hypothesis."

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References

1. J. Greenberg, C. Turner, S. Zegura, *Curr. Anthropol.* **27**, 477 (1986).
2. P. Forster, personal communication.
3. F. H. West, Ed., *American Beginnings* (Univ. of Chicago Press, Chicago, IL, 1996).

Gibbons's description of the objections to Greenberg's hypothesis (that virtually all the

indigenous languages of the Americas have a common ancestry) has linguists saying that "it's impossible to trace the family tree of Amerind languages back to one 12,000-year-old ancestor, because written records go back only 5000 years." But tracing linguistic family trees is not based on written records. For most Amerindian languages, there are no such records. Language families are established by systematic comparison of phonetic data from currently spoken languages. Sometimes (although not in Amerindian linguistics), written records have been peripherally relevant to substantiating the validity of the methods used (as when 4000-year-old Hittite inscriptions turned out to confirm certain conclusions about early Indo-European).

What linguists typically disagree with Greenberg about is whether phonetic comparison of present-day languages could ever provide a warrant for suggesting a relationship going back 12,000 years. It is extremely unlikely. Languages appear to change fast enough that over that sort of time scale the phonetic similarities within a group of languages would be irretrievably obscured. That conclusion is (contra Greenberg) fairly secure, and is quite independent of the existence of writing.

The languages of the Americas could, of course, have had a common northeast Asian ancestor spoken tens of millennia ago. Historical linguists don't dislike that idea; they just feel obliged to point out that linguistic evidence cannot confirm it.

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Response: The article's brief mention of written records was not intended to imply that these were used to trace the origin of American Indian languages, but simply to point out that, even in the best cases, where written records exist, many linguists think that it is impossible to trace languages back to a 12,000-year-old ancestral language.

—***Ann Gibbons***

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Protein Structure Prediction

Elizabeth Pennisi's Research News article "Teams tackle protein prediction" (26 July, p. 426) describes an ongoing project, known as CASP (for Critical Assessment of Techniques for Protein Structure Prediction) (*1*), to provide researchers who model protein structures with the opportunity to jointly make bona fide predictions, announced before a structure is determined by experiment. The theme of the article, that collaboration is needed for progress, is indisputable. We do not agree, however, that, among those who participated in the ab initio part of the first prediction contest "nobody really came close to predicting an accurate structure," that "predictions [of secondary structure] were no more accurate than ones made a decade ago with cruder methods," and that the assembly of predicted secondary structural elements into "a complete 3D structure" "didn't work at all," as John Moult alleges.

One advantage of the CASP approach is that the predictions are independently judged and the judges publish their opinions so that they are available to the public. This was so for the ab initio session of CASP1. The evaluations of the predictions published by the judges differed greatly from those reported by Pennisi. "For phospho-β-D-galactosidase," wrote judges DeFay and Cohen (*2*), "Benner and Sader [both] correctly predicted this protein to be an α/β barrel." The success came from "an exceptionally small number of 'wrong' predictions." Further, the judges wrote, "it . . . would have been unlikely if a prediction was made from the [decade-old, cruder] GOR [method for] secondary structure prediction." For synaptotagmin, the