When Two Worlds Collide

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This special issue of *Human Biology* commemorates the quincentennial of Christopher Columbus's journeys to the New World. This historical event, the collision of New and Old World cultures, forever altered the demography of the world. As a result of this contact, the native peoples of the Americas experienced innumerable hardships, disease, death, and the destruction of civilizations, tribes, and a way of life. However, Europe was enriched by the acquisition of an assortment of agricultural products, gold, and a haven for millions of immigrants fleeing persecution and poverty. This collision of the worlds also resulted in the creation of a unique social experiment, democracy under a constitution, but at a phenomenal cost to the natives of the Americas and to the Africans brought to work the land. We should not celebrate this so-called discovery of the New World, but we can reflect on the 500th anniversary of a profound historic event.

This commemorative volume of *Human Biology* summarizes the available information on the biology of New World populations. Given spatial constraints, I solicited contributions that examined the controversial issues of late versus early peopling of the New World and the effects of cultural contacts. The eight articles are grouped temporally; that is, the first section deals with Amerindian populations before European contact, and the second section describes contemporary genetic and morphological variation.

Precontact Amerindian Populations

The first contribution, by R.A. Rogers et al., provides a relatively balanced evaluation of theories concerning the early versus late entry of Siberians into the New World and their probable pathways of entry. Rogers and colleagues have synthesized information on the peopling of the Americas from diverse fields, such as linguistics, ecology, archeology, and geology. They conclude that a pre-Clovis occupation occurred in the Western Hemisphere. On the basis of linguistic and ecological data, they argue that the coastal route of entry into the New World was the most significant. Rogers et al. also point out that multiple migrations are fea-

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tures of technologically sophisticated societies, not of hunters and gatherers. They stress the role of geological barriers, such as glaciers and oceans, to explain the observed genetic and linguistic variation among New World populations.

Recently, an apparent multidisciplinary consensus was forged around the chronology and number of Siberian migrations entering the New World. In a series of articles by Greenberg, Zegura, and Turner it appeared that the genetic, dental, and linguistic evidence was reconciled in favor of a late entry (no later than 12,000 years B.P.) by three population movements from Siberia (Greenberg et al. 1986; Turner 1985; Zegura 1985). This so-called tripartite theory of the peopling of the New World was constructed around Greenberg's massive comparison of basic vocabulary and word similarities in American Indian groups (approximately 600 different languages surviving to the present). Greenberg concluded that American Indian languages can be classified into three linguistic phyla (Na-Dene, Aleut-Eskimo, and Amerind) and that each of these groups resulted from a separate migration into the Americas. The dental evidence was offered as further support for the three-migration theory, despite the failure of Turner to statistically test this alleged relationship. Instead, Turner eye-balled the affinities and pronounced "a remarkably good fit." Turner's selective use of the dental evidence prompted Szathmary (1986, p. 490) to remark:

> Turner's equating the label Na-Dene with the Greater Northwest Coast group suggests that he is not prepared to question, let alone reject, the three-migration hypothesis. . . . Rather, he interprets his analytical results in the light of a preexisting hypothesis that he simply assumes to be true.

Zegura (1985) presents the genetic interpretation in a more guarded fashion, stating that he views the genetic data as a secondary support for the primary inferences based on linguistic and dental evidence. He also indicates that the genetic data can and have been interpreted by various researchers to be indicative of other patterns of migration and evidence for an earlier peopling of the New World. Indeed, Schanfield et al. (1990) have interpreted the geographic distribution of immunoglobulin allotypes to suggest a minimum of four migrations into the New World.

Recently, this consensus has begun to rapidly unravel (Morell 1990). The mitochondrial DNA sequences observed in Amerindian tribal populations is suggestive of an early peopling of the New World. The DNA lineages can be traced on average to 60,000 years B.P., indicating the differentiation of mtDNA into lineage clusters before an expansion of Siberian groups into the New World (Ward et al. 1991). A recent linguistic analysis by Nichols (1990) argues against the creation of a single Amerind phylum and concludes that the linguistic diversity in the New

World dates back to at least 35,000 years B.P. Because the dental and genetic aspects of the tripartite model rested uneasily on the linguistic foundation, the loss of credibility of this part of the model has caused this theory to collapse much like the proverbial house of cards.

The second paper, by D.G. Steele and J.F. Powell, summarizes the earliest available skeletal evidence from North America. Steele and Powell employ an assortment of statistical techniques to compare the Paleo-Indian specimens with modern northern Asians and North American Indians. During the Holocene, trends in increasing brachycephalization (head broadening) and the development of a larger, broader face were observed in Amerindian skeletal remains. Apparently, these morphological features were "made in America" and indicate either genetic adaptation or the action of plasticity in native populations facing vastly different environmental conditions during their tenure in the New World. Unfortunately, these skeletal data have insufficient sample sizes to provide a chronology of entry into the New World and to suggest the number of founding populations.

The application of molecular and immunoglobulin approaches to skeletal pathological conditions in Amerindian populations may prove useful in resolving questions of disease etiology. What diseases were present in the New World before European contact? What evidence exists for the reconstruction of pre-Columbian disease patterns? Until recently, there were four primary sources of information on the disease state of precontact Amerindians:

1. Observations by settlers, priests, and conquistadors at initial contact. However, the reliability of most of these reports is in question. Often, fevers and rashes were confused, and some diseases went totally unrecognized.
2. A few native accounts, such as the *Book of Chilam Balam*, a Mayan description of a disease-free society before the Spanish conquest. Considering the skeletal evidence for disease in precontact Amerindian populations, these native reports are nostalgic.
3. Paleopathological observations. Some diseases, such as syphilis, tuberculosis, and arthritis, leave markings on the bones of their victims. Unfortunately, there are some diseases that leave no osseous evidence for their presence.
4. The study of coprolites, which permits the recognition of intestinal parasites.

The recent developments in the methods for the extraction and identification of DNA from contaminating pathogens should provide more precision in the identification of pre-Columbian disease.

The third article, by D.J. Ortner et al., applies molecular genetic and immunologic methods to questions concerning the role of disease in the evolution of Amerindian populations. These techniques were used to identify treponemal antibodies from osseous materials marked by lesions suggestive of treponematosis. Out of 30 Amerindian skeletal remains from different archeological sites, Ortner and colleagues found 1 individual who reacted immunologically to the treponemal antigen. This person, with a carbon-14 date of more than 1200 years B.P., exhibited proliferative periostosis (a condition suggestive of treponematosis). Thus, using immunological techniques, Ortner et al. have found evidence of treponemes in the New World before European contact. Similarly, Ortner et al. review the molecular evidence and note DNA sequence homology in subspecies of *Treponema* thought to cause syphilis and yaws.

D.H. Ubelaker's contribution straddles the temporal divide between pre- and postcontact population studies. It examines the demographic changes in New World populations before and after 1492. Ubelaker points out that morbidity and mortality in native populations were increasing in response to higher population densities, increased sedentism, and changing subsistence. Ubelaker interprets the archeological and skeletal evidence to suggest that the population decreases were caused by regional epidemics rather than by continental pandemics.

My research with three New World populations (Tlaxcaltecan Indians, Eskimos of St. Lawrence Island and coastal Alaska, and Black Caribs of St. Vincent Island and Central America) supports Ubelaker's conclusion that depopulation was primarily a result of regional epidemics. However, it should be stressed that unique historical events played an important role in the variation of the population response to epidemics. Some groups became extinct, for example, the Chono of Chile (Steward and Faron 1959) and many tribes of the eastern coast of the United States and most of the Caribbean. Other groups suffered an initial diminution, then a nadir, followed by recovery; eventually these populations regained their precontact sizes. The magnitude of the survivorship varied by culture, population density, and unique historical events. For example, the Tlaxcaltecan Indians from Mexico experienced a population reduction from approximately 300,000 at contact to 100,000 in fewer than 200 years of Spanish conquest. This survivorship of 1 in 3 is generally considered low for the New World compared to the estimates of 1 in 20 or 1 in 25 postulated by Dobyns (1966). This greater rate of survival is a reflection of the unique historical role that the Tlaxcaltecans played in the conquest of Mexico and their partial exemption from colonization and exploitation (Halberstein et al. 1973). In contrast, the Eskimos of St. Lawrence Island were reduced from approximately 4000 to 222 individuals at the population nadir in 1917 (Byard et al. 1983). Partly because of the inhospitable nature of the Arctic environment, these pop-

ulations were geographically isolated until the development of the whaling industry. In 1878 a combination of famine and epidemic struck St. Lawrence Island with a devastating force. By 1880 only 500 individuals remained alive. The survivorship rate for this population at its nadir was 1 in 20. The Carib and Arawak Indians of the Caribbean islands became extinct early in the history of European colonization. The genetic remnants of these populations can be detected in Black Carib gene pools of St. Vincent Island, Dominica, and the coast of Central America. The hybridization of Amerindian and West African genes provides a classic example of human adaptation in Black Carib colonizing populations (Crawford 1984).

Postcontact Genetic Variation

The second section of this special issue focuses on the genetic and morphological variation observed in contemporary Amerindian populations. Included in this section is an assessment of New World peopling based on traditional blood markers, immunoglobulins, and mitochondrial DNA restriction fragment length polymorphisms (RFLPs). In addition, the morphological variation of North American Indian populations of the 1890s is summarized by the last contribution to this section.

The first article of this section, by M. Schanfield, examines the variation of the immunoglobulin systems (GM and KM) geographically distributed over the two Americas. Schanfield argues for a minimum of four distinct GM patterns representing at least four migrations into the New World. He argues that the South American non-Nadene populations, characterized by *GM*A G* and *GM*X G* haplotypes, represent the initial migrants into the New World. A later migration, non-Nadene Amerindians, contained populations with high frequencies of *GM*A G* and low frequencies of *GM*A T*. The Nadene speakers have *GM*X G* and *GM*A T* in approximately equal frequencies. The final Siberian migrants into the New World, the Eskimo-Aleuts, possess only the *GM*A G* and *GM*A T* haplotypes. Schanfield argues that the earliest Siberian populations entered the New World before 17,000 years B.P. and that the non-Nadene crossed Beringia during the postglacial period, preceding the Nadene and the Eskimo-Aleuts.

D.C. Wallace and A. Torroni base their interpretation of New and Old World phylogenetic affinities on mtDNA RFLPs. They observed four mtDNA lineages in 6 Amerindian tribes representing North, Central, and South America. Each lineage contains a rare Asian mtDNA marker. Wallace and Torroni interpret these data to suggest one or two Asian migrations that were distinct from the Nadene. They also suggest that the Amerind populations (represented by the Pima, Maya, and Ti-

cuna populations) are approximately four times more ancient than the Nadene. This study does not support the postglacial entry of the Nadene and Amerinds into the New World. The mtDNA clock suggests that the 4 Amerindian lineages are 21,000–42,000 years old. These results are consistent with the mtDNA-sequence-based time of 60,000 years for the lineages observed among the Nootka Indians (Ward et al. 1991) and the 35,000 years B.P. migration necessary to account for the observed linguistic variation (Nichols 1990). It is tempting to consider the possibility of a new consensus forming. However, science does not usually operate by consensus or by the popularity of a particular explanatory theory—or does it?

D.H. O'Rourke et al. examine the patterns of genetic variation in Native American populations. They use 7 polymorphic blood group loci frequencies from 144 populations geographically distributed over 2 continents, approximately 6000 miles. This research is a further development of their earlier synthetic map analyses (Suarez et al. 1985; O'Rourke and Suarez 1986; O'Rourke and Lichty 1989). Genetic distance analyses reveal a slightly higher mean value among the South American samples compared to the North American genetic distances. Similarly, the average genetic distances are smaller among the Central American Indian groups. The F_{ST} values indicate a similar pattern of degree of population differentiation with the North and South continental groupings being approximately equal, whereas there is less genetic heterogeneity in Central America. On the basis of spatial autocorrelation, O'Rourke et al. argue for the existence of distinct genetic structures in North and South America. The correlation between genetic and geographic distances is higher for North America than for South America. In contrast to the findings of Salzano and Callegari-Jacques (1988), O'Rourke et al. found little evidence for clinal distributions of genes in South America and less of an association between geography and genetics.

When the effects of the massive New World depopulation are considered, with survival rates as low as 1 in 25, it is surprising that any pre-Columbian genetic structure is revealed. In addition to the depopulation, most contemporary Amerindian groups experienced considerable gene flow from European settlers or African slaves. This gene flow should lower the genetic distances between admixed Amerindian populations. The most careful selection of unmixed populations may fail to detect gene flow that may have occurred hundreds of years earlier. If admixture is the primary determinant of the observed genetic variation in contemporary Amerindians, then my prediction is that the North American populations should be least heterogeneous (given that they have experienced the most admixture), Central Americans should be next, and South Americans should exhibit the least gene flow and the highest genetic distances between the populations. However, this prediction is compli-

cated by possible biases that many of the Central American samples described in the literature have considerable admixture and that the least admixed have not been studied.

In attempting to explain the apparent lack of correspondence between geography and genetic distances in the South America, O'Rourke et al. suggest and then dismiss a hypothesis that its colonization was too recent. However, recent ecological and geological evidence suggests that during the Pleistocene the Amazonian basin was an inland sea (L. Martin, personal communication, 1991). As a result, humans immigrated into this region after the Wisconsinan glaciation when the inland sea was drained and desiccated. This late arrival of Amazonian populations, together with their unique population structure, may account for the poor fit between geography and genetics.

R.L. Jantz et al. examine the morphological variation in North American Indians at their numerical nadir, approximately 100 years ago. Jantz and co-workers secured anthropometric measurements on approximately 15,000 Amerindians; the data were collected for the World's Columbian Exposition in 1892. F.W. Putnam organized a series of field expeditions that were to be the bases of exhibits at this exposition. Franz Boas (a noted anthropologist) was employed to coordinate the massive task of measuring this sample. To date, this data set had not been analyzed by any multivariate statistical techniques. Jantz et al.'s analysis reveals a significant geographic patterning of body morphology similar to that observed for blood markers. The less plastic and probably more genetic traits, such as the head and face dimensions, exhibit considerable intertribal variation. This preliminary analysis does not provide evidence that the Nadene and Eskimos are differentiated from other language phyla and thus fails to support the tripartite theory.

Discussion

Science should be viewed in probabilistic rather than absolute terms. When specific data or evidence is uncovered (such as osseous materials), a number of explanations may be equally likely. As more information is compiled, the likelihood of some of these explanations changes and some become more probable. The peopling of the New World can be used as an example of such a probabilistic approach. Until the 1920s, without accurate dating, most of the explanations for the presence of Amerindian skeletal and archeological remains contended that the New World was peopled less than 5000 years ago (Hrdlička 1917; Holmes 1925). However, in the mid-1920s several sites in the southwestern United States revealed an association between projectile points and the skeletal remains of extinct Pleistocene mammals. Most notable of these sites was

Folsom, New Mexico, where a projectile point was discovered embedded between the ribs of an extinct Pleistocene bison. This Folsom discovery pushed the date of human arrival in the New World back to 12,000 years B.P. With the recent discoveries of well-excavated and dated sites, such as Meadowcroft Rock Shelter in Pennsylvania and the Monte Verde site in Chile, the probability of pre-Clovis human habitation in the New World has increased. This likelihood has continued to soar as data from linguistics, mitochondrial DNA, and geology have been added to the evidence derived from archeological excavations.

At this time, massive evidence strongly supports an early peopling of the New World, although the exact number of migrations and the exact geographic Siberian origins of the early Amerindians remain unresolved. Additional genetic data from Siberian indigenous people and a more complete sampling of Native American populations will undoubtedly alter the likelihood of the present hypotheses. The tripartite theory appeared to be highly probable a few years ago. Now, as additional data appear, the likelihood of this explanation is decreasing markedly, particularly with regard to the three postglacial migrations. Finally, the mitochondrial sequence data for the Nootka reveal such high genetic variation on a tribal level that the founding gene pools were extremely variable (Ward et al. 1991). This finding challenges the notion that a small number of Siberians followed herds of Pleistocene fauna into the New World. The more likely explanation is that the Siberian populations expanded across Beringia because of population pressures associated with technological innovation.

It is our obligation as scientists to examine the evidence dispassionately before concluding which explanation is the most likely. As additional data surface, we should be willing to change our minds and accept the dictates of the evidence. Theories that are disproven or at least shown to be unlikely should be discarded for the most likely explanations. Colleagues who continue to argue their personal positions, despite the evidence, retard scientific progress. There is no room for personality cults in science!

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