



Kinship and Deep History: Exploring Connections between Culture Areas, Genes, and Languages

ABSTRACT Large-scale geographic variation in kinship systems may have deep roots. A number of authors now argue for an “emerging synthesis,” with genetic, linguistic, and archeological findings coming together to paint a consistent picture of large-scale population spreads in prehistory. This article explores a social structural dimension of this synthesis: Major culture areas based on variation in kinship systems correspond closely—yet not perfectly—to genetic and linguistic clusters identified by other researchers. Thus it may be possible to reconstruct: (1) a set of “primary” culture areas corresponding to major population blocs and associated with ancient demic expansions and parallel transmission of genes and culture, and (2) a smaller set of overlying “secondary” culture areas of more recent origin that do not map onto genetic subdivisions and result from changes in subsistence or political economy independent of large-scale demic expansions. I also review latitudinal variation in kinship systems. [Keywords: culture areas, demic expansions, kinship (prehistory), protolanguages]

AT THE END OF HIS BOOK *Lewis Henry Morgan and the Invention of Kinship* (1987), Thomas Trautmann suggests that “in some respects anthropology has yet to catch up with Morgan” (1987:265). Lewis Henry Morgan is often remembered as a pioneer in the study of kinship, but a central aim of his early work—the reconstruction of the deep genealogy of the world’s kinship systems—was relatively neglected in later 20th-century cultural anthropology. The 19th-century founders of kinship theory were deeply influenced by the earlier success of historical linguistics in identifying a far-flung Indo-European language family rooted in prehistory. Morgan (1870), Henry Maine (1864), and Numa Denis Fustel de Coulanges (1864) all tried to follow up on the recovery of the lost Proto-Indo-European language by reconstructing Proto-Indo-European kinship. Morgan was the most ambitious: In his investigations of kinship in Europe, native North America, Asia, and Oceania, he aimed to discover the genealogy of kinship systems, languages, and peoples on a global scale. In the present article I argue that the time may be ripe for a revival of this program. But before presenting the case in detail, it is worth reviewing briefly both how this approach fell out of favor and how recent developments in archeology, biological anthropology, and linguistics encourage a reassessment.

In retrospect it is clear that Morgan’s work not only far outdistanced the data available to him but also suffered from several theoretical weaknesses characteristic of his

times. Like many 19th-century scholars he lumped together two very different conceptions of evolution: evolution as a process of descent with modification creating near and distant genealogical connections and evolution as a progression through universal stages from simple to complex. Also, again like many other 19th-century scholars (Stocking 2001:3–23) including Darwin, Morgan tended to merge “blood” and culture in a single channel of descent: He believed both in the racial determination of cultural characteristics and in the cultural determination of biological heredity through the inheritance of acquired traits. This single-channel view of heredity could not survive the early-20th-century rejection of Lamarckism and the multiple demonstrations by Franz Boas and others that language, genes, and culture can be, and often are, transmitted independently of one another.

The differences between Morganian and Boasian approaches should not be exaggerated, however. A multiple channel view of heredity still leaves open the possibility that genes, language, and culture have been transmitted in parallel often enough that their current distributions partly reflect common causes in the past. Boas himself (1940:525–529) made this argument in discussing the archeology of the region most familiar to him, northwestern and Arctic North America. He argued that population replacements had played an important role in prehistory, and that later genetic and cultural exchanges had blurred but not erased the resulting correspondences between

physical type, language, and culture. Specifically, he cited archeological evidence for a major shift along the southern part of the Northwest coast, with populations there being assimilated both biologically and culturally (but not linguistically) by more northerly coastal tribes. And in the far north he argued that the evidence showed that an earlier cultural and physical continuum between northwestern North America and northeastern Siberia had been interrupted by the intrusion of Eskimos from outside the area, different both in culture and in physical type. (We will see below that these hypotheses are generally consistent with current views regarding the Na Dene contribution to the Northwest Coast culture area and Eskimo–Aleut origins.)

Thus, Boas did not reject reconstructions of the prehistory of populations and cultures and their associations out of hand, although he tended to be skeptical of hypotheses on a large scale—reasonably enough, given the scanty knowledge available at the time. Other early-20th-century scholars were less cautious. William H. R. Rivers (1914) offered a detailed scheme of population movements, innovation, loss of innovation, and borrowing to explain cultural variation in Oceania. The German–Austrian *Kulturkreis* school of Fritz Graebner and Wilhelm Schmidt proposed that migrations and cultural diffusion from a limited number of centers had played a major role in generating spatial patterns of cultural variation, with contact and borrowing as an important secondary complicating factor. The spread of these founding culture circles resulted in the diffusion not only of new subsistence techniques and material culture but also of varied patterns of social organization, including patriliney and matriliney, endogamy and exogamy (Harris 1968; Lowie 1937; Schmidt 1939).

Rivers's, Graebner's, and Schmidt's accounts were clearly speculative and their methodologies less powerful than they claimed, so for the most part their specific conclusions were not taken up by later anthropologists and archeologists. Even Robert Lowie's (1937:169–195) generally sympathetic account falls short of endorsing specifics. Nevertheless, a later generation of anthropologists hewed closely enough to diffusionism to propose a series of "culture areas" for North America and other regions that reflected partly prehistoric diffusion and contact and partly environmental influences (Kroeber 1939; Wissler 1926). By the mid-20th century, Ralph Linton could summarize the state of knowledge in a popular book, *The Tree of Culture* (1956), which was organized around a collection of world culture areas defined by differences in kinship and gender relations (among other things) in some cases tracing back to ancient population movements.

Nevertheless, it is undeniable that this topic was mostly bypassed by the mainstream of 20th-century Anglo-American cultural anthropology. Partly this reflected the contemporary underdevelopment of cognate disciplines. Cultural anthropologists hoping for evidence of past migrations and population histories to anchor their accounts of culture and prehistory could expect only limited help

from biological anthropologists: The inadequacies of older racial typologies based on somatic variation were increasingly evident, but the alternative approach based on variation in gene frequencies took some time to mature. Linguists concerned with language families and protolanguages increasingly worked in isolation from anthropologists and archeologists. And cultural anthropology from at least the mid-century was caught up in a larger antihistorical turn in social theory. British social anthropology and later Boasian and post-Boasian cultural and symbolic anthropology took a strongly synchronic tack, indifferent to "conjectural histories" of cultural variation and its possible connections with the past histories of populations. The various schools of materialist anthropology were generally more interested in technological and ecological determinants of social variation, often treating historical influences as noise rather than data (although the delineation of cultural genealogies continued to be an important part of archeology).

Why return to this old topic today? There has been a submerged current of interest throughout the 20th century. Yet researchers found themselves facing not only an indifferent intellectual climate but also tremendous limitations in available data that made it difficult to move from speculation to hypothesis testing. In this respect, the situation has changed enormously in the last decade or two—so much that many researchers now argue that we are seeing the birth of an "emerging synthesis" in the study of prehistory. Rapidly accumulating information and new theoretical perspectives in population genetics, historical linguistics, and archeology seem to be coming together at last to tell a consistent story of the ancient human past, including the origin of modern humans, domestication and other innovations in subsistence, large-scale demic expansions, genetic and cultural diffusion, and the origins and spread of major language families (Bellwood 1995, 2001; Cavalli-Sforza et al. 1988; Cavalli-Sforza et al. 1994; Diamond 1997; Renfrew 1992, 1996). The emerging synthesis is based on significant correlations in the distributions of genetic, linguistic, and archeological variation. Of course these correlations are imperfect: The Boasian conventional wisdom that there are many cases of language replacement without gene flow, culture shifts without language change, and so on, still stands. But the emerging synthesis suggests parallel transmission has happened often enough to leave traces in current distributions of genes, language, and culture that point back to common causes in prehistory.

So far the emerging synthesis has embraced three of the traditional four subfields of anthropology: biological anthropology, linguistic anthropology, and archeology. The fourth subfield, cultural anthropology, has often (but not always) been neglected by researchers in this new area. Consider, for example, Jared Diamond's deservedly influential popularization *Guns, Germs and Steel* (1997). In discussing the settlement of Polynesia, Diamond brings in relevant evidence from archeology, linguistics, and genetics (1997:334–353). Yet his discussion of Polynesian social

organization is mostly limited to showing how different Polynesian societies occupy different positions on a universal evolutionary scale running from hunting-and-gathering bands to complex chiefdoms (1997:53–66). Missing is any account of how generations of researchers have put together a detailed picture of an ancestral Proto-Polynesian social organization which strongly influenced later cultural evolution (Hage 1999). Without disparaging efforts to identify universal stages and ecological adaptation in cultural evolution, I suggest that the emerging synthesis may be especially valuable in helping to reconstruct prehistoric genealogies of culture.

The rest of this article considers one direction such reconstruction might take, concentrating on the deep history of kinship systems. I review recent work (Burton et al. 1996; Whiting et al. 1988), showcasing improved methods for using information about geographic variation in kinship and social organization to construct world culture areas. I then discuss how this seems to mesh both with one environmental variable (latitude) and with our emerging understanding of prehistory.

KINSHIP AND CULTURE AREAS

Michael Burton et al. (1996) propose a division of the world into nine or ten major culture areas based on variation in social structure, especially kinship systems. Their work is especially valuable in the present context for several reasons. First, it represents an important methodological advance over earlier proposals for global culture areas. By comparison, George Murdock's (1957, 1967) world culture areas, although based on wide reading in the ethnographic literature and experience in coding cultural traits, were created impressionistically, rather than treated as hypotheses subject to formal validation and refinement. Second, Burton et al.'s culture areas are based on variation in social structure, especially variables related to kinship. Although their methods could be applied to other cultural domains—to devising regions based on, say, religion and cosmology, or political organization—there is no reason to think that this would yield the same set of geographic divisions. The focus on kinship is important because anthropologists have long noted that kinship is a particularly conservative cultural domain. This conservatism is attested, for example, in a recent quantitative study of cultural variation in Africa (Guglielmino et al. 1995), which shows that cultural variables relating to kinship and family structure show especially strong associations with cultural phylogeny, as inferred from historical linguistics. Meanwhile, cultural variables relating to economy and religion and other sorts of social variation show relatively greater effects of cross-cultural diffusion and ecological adaptation. This means that kinship is an especially important cultural domain for those interested in reconstructing the distant past.

The work of Burton et al. builds on earlier cross-cultural research by the same researchers (Whiting et al. 1988) using

optimal scaling, a relative of multidimensional scaling, to investigate empirically the major underlying dimensions of cross-cultural variation in social structure. They begin with data for a standard sample of 351 societies (Murdock 1967, 1970). The data for each society consists of coded information about the presence or absence of 32 social organization traits and 31 features of kinship terminology. The social organization traits have to do with kinship, marriage, settlement and community organization and also include the choices between: bride price, bride service, and no marital exchange; nuclear versus extended families; monogamy versus several varieties of polygamy; alternative rules of marital residence; and alternative types of suprafamilial kin groups. When the authors subject this data to optimal scaling they discover two major dimensions of social-structural variation. The first dimension relates to gender and contrasts patricentric and matricentric societies. Traits characterizing patricentric societies include brideprice, sororal polygyny, patrilocal residence, exogamous or clan communities, and transhumance or nomadism, while matricentric traits include matrilocality, segmented communities, nonextended families, monogamy, and the absence of marriage exchange. The second dimension relates to the strength of unilineal kin groups. Traits characterizing unilineal societies include clan communities, unilineal kin groups, nonsororal polygyny and cousin marriage, while bilateral (nonunilineal) traits include bilateral descent groups or ego-centered kindreds, bilocal or virilocal residence, monogamy, and the absence of marriage exchange and cousin marriage (see Murdock 1967 for trait definitions). This research confirms the intuitions of many ethnologists that gender and lineality constitute two major axes of variation in systems of kinship and marriage.

Not only social structural traits and kin terms but also individual societies may be characterized as more or less patricentric or matricentric, unilineal or bilateral, according to their positions on Dimensions 1 and 2. This allows Burton et al. (1996) to produce a set of world culture areas based on similarities in social structure among neighboring societies. They set three criteria for culture areas: areas should be few in number; they should be physically contiguous; and they should be internally homogenous in social structure but significantly different from neighboring regions. Homogeneity in social structure is measured by calculating the average distance on Dimensions 1 and 2 among the societies within a proposed region. The authors proceed by provisionally aggregating neighboring societies into regions, merging regions similar in social structure, splitting up heterogeneous regions, and moving individual societies and adjacent groups of societies between neighboring regions. They repeat this process until they arrive at a stable set of culture areas that minimizes average social-structural distances within regions. In the end they divide the world into nine or ten culture areas, five largely in the Old World (with the North Eurasia and Circumpolar region extending from Eurasia into the American Arctic)

and another four or five in the New World. (The southern South America region is more tentative than the others because it contains just three societies.)

Figures 1 and 2 show Burton et al.'s culture areas. The boundaries between areas are necessarily approximate because the 351 societies cover parts of the globe somewhat sparsely. The graphs at the tops of the figures show the average social structures of each region. The regions are strongly supported by statistical tests. Average distances among societies within regions have a mean of 1.20 and a range of 1.07 to 1.44, compared with a mean distance of 1.81 among societies within the sample as a whole. Murdock's earlier set of six world culture areas does substantially worse by this test, with mean distance among societies within his regions of 1.57.

Burton et al. provide strong evidence for global-scale patterning of cultural variation. Their work immediately raises the question of what forces have generated their culture areas. They argue that culture areas do not correspond very closely to particular ecologies and subsistence regimes and, instead, emphasize historical connections reflected in shared language family membership and participation in different regional precapitalist "world systems." A subsequent publication by Andrey Korotayev and Alexander Kazankov (2000) considers these culture areas in

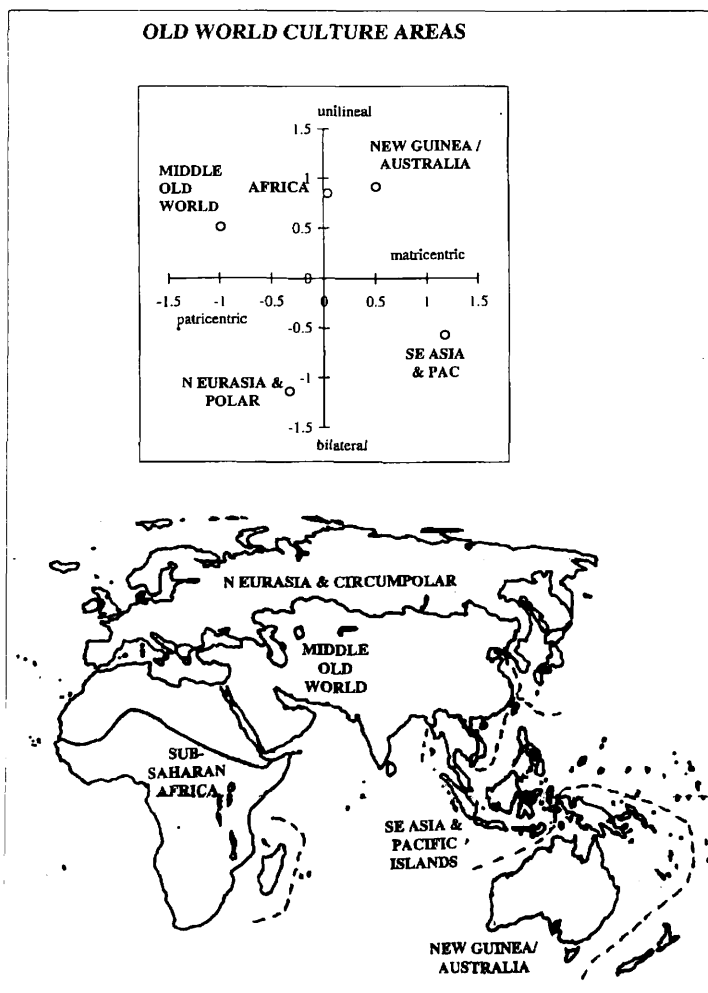


FIGURE 1. Old World culture areas.

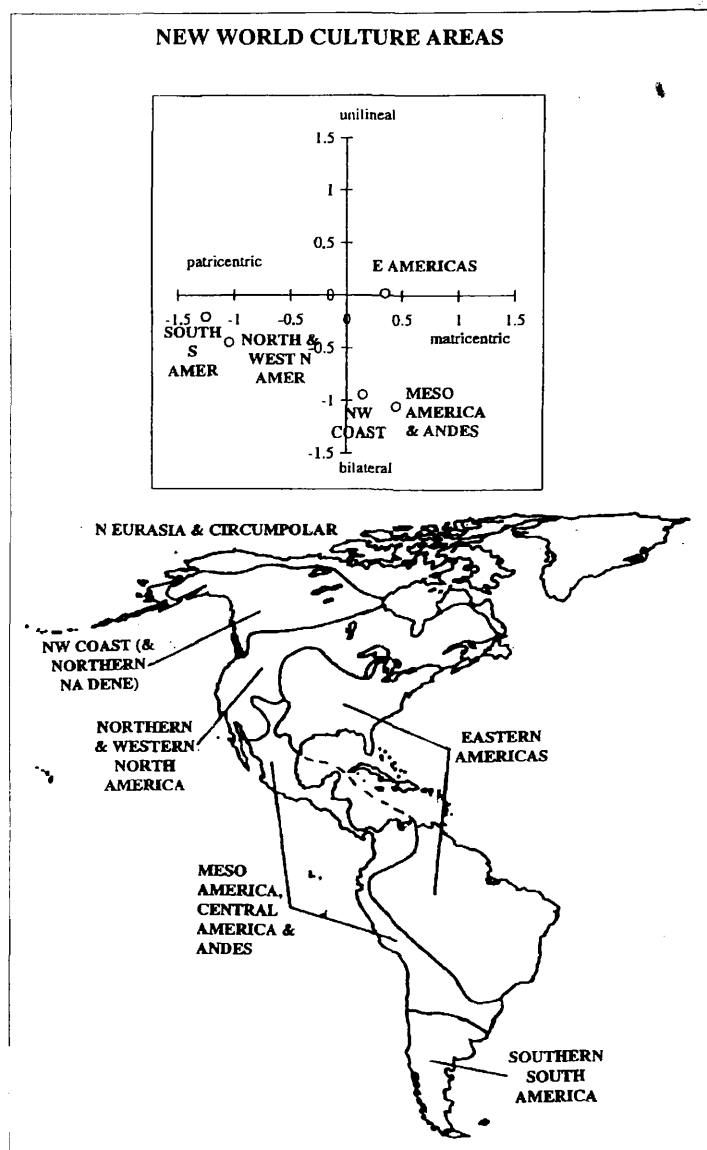


FIGURE 2. New World culture areas.

relation to controversial large-scale language families in Eurasia and the North America. The rest of this article develops these ideas further. The next section briefly considers latitude, a physical-ecological variable not discussed by the preceding authors and argues that latitudinal influences on social structure (at most) complement rather than supersede regional historical influences. Another section introduces the "emerging synthesis" in prehistory and proposes a division between *primary* culture areas that map onto genetic and linguistic clusters identified by the new synthesis and *secondary* culture areas that do not. A further section proceeds with a region-by-region review of culture areas in relation to the demic expansions and genetic and cultural diffusion proposed by the emerging synthesis. A final section gives a summary and considers future prospects.

CULTURE AND LATITUDE

In contrast to some materialist schools of anthropology, proponents of culture area approaches have generally argued

that ecological variables merely constrain rather than strongly determine social variation. Burton et al. argue that their culture areas are only loosely tied to ecological and technological variation; Korotayev and Kazankov (2000) support this with a statistical comparison of culture and subsistence in Eurasia and Southeast Asia and the Pacific Islands. In this section I consider latitude, showing that it predicts variation *among* but not (consistently) *within* culture areas. Insofar as latitude influences social structure, it does so by influencing the average social structure of culture areas rather than that of individual cultures. This provides further support for Burton et al.'s regions, without denying some influence from ecology and subsistence regimes.

Both of Burton et al.'s dimensions of cultural variation correlate with latitude, as shown in Figure 3. Cultures tend to be more matricentric and unilineal the closer they are to the equator. The correlations of Dimensions 1 and 2 with degrees of latitude from the equator are $-.34$ and $-.39$, both $p < .001$. Significant correlations with latitude also hold for the Old World and the New World considered separately, and for northern and southern hemispheres.¹

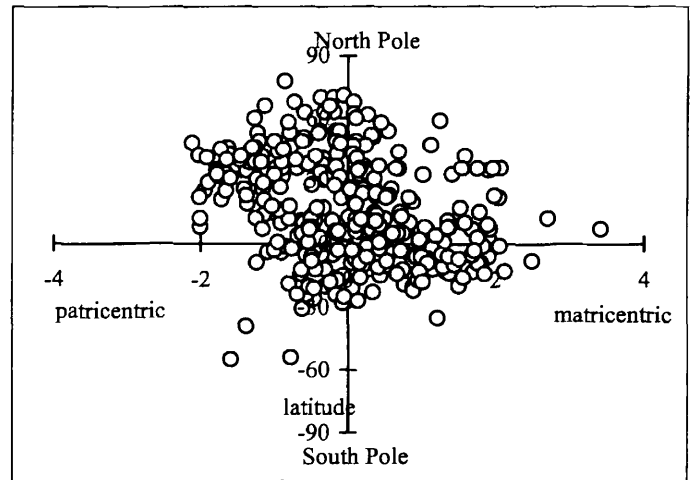
These correlations suggest that Burton et al.'s culture areas might be merely a proxy for latitude, but this is not the case. The analysis of covariance shown in Table 1 demonstrates that (1) culture areas continue to predict cultural variation even when latitude is included in the analysis as a covariate, and (2) within culture areas there is no consistent relationship between latitude and social structure; regression coefficients within different areas vary so widely that they fail the test of homogeneity of regression coefficients, as shown by substantial area-by-latitude interactions (Sokal and Rolf 1981:499–509). The first result is not surprising: Consider, for example, that sub-Saharan African and Southeast Asian and Pacific areas span similar latitudes but differ markedly in social structure. The second result implies that the place to look for consistent effects of latitude on social structure is *among* rather than *within* culture areas. Thus, the average absolute latitudes of culture areas are highly correlated with their average scores

TABLE 1. Latitude and culture area: Ancova.

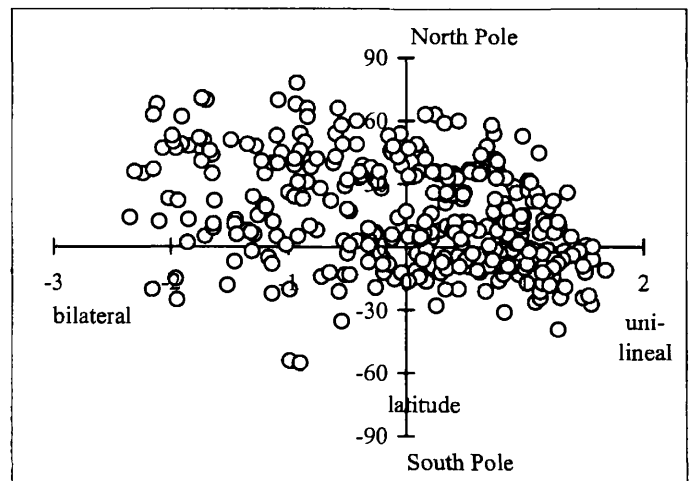
Patri-Matricentricity Ancova					
Source	DF	Sum of Squares	Mean Square	F-Value	P-Value
Culture area	9	28.7	3.19	6.40	< .001
Absolute latitude	1	0.0	0.20	0.03	n.s.
Area* Abs[Latitude]	9	11.3	1.26	2.53	0.008
Residual	##	164.9	0.50		

Lineality Ancova					
Source	DF	Sum of Squares	Mean Square	F-Value	P-Value
Culture area	9	51.4	5.71	12.84	< .001
Absolute latitude	1	1.4	1.39	3.12	0.079
Area* Abs[Latitude]	9	16.5	1.84	4.13	< .001
Residual	##	147.1	0.44		

LATITUDE AND CULTURES



A. Patri-/matricentricity and latitude
Correlation with absolute latitude = $-.34$



B. Lineality and latitude
Correlation with absolute latitude = $-.39$

FIGURE 3. Latitude and cultures.

on Dimensions 1 and 2 ($r = .59$ and $.60$), although with just ten culture areas the correlations are only marginally significant ($.1 < p < .05$).

These results are summarized in Figure 4. The R^2 values in the second column are based on Anova with latitude omitted. To the extent that there is a relationship between latitude and social structure, it is an indirect one mediated by the influence of latitude on average scores of whole culture areas. In other words, there is no direct and consistent relationship between latitude and individual cultures; one can predict a culture's social structure better by knowing the average latitude of its culture area than by knowing the latitude of the culture itself. The forces leading to the formation of culture areas remain to be explored.

LATITUDE	? ->	CULTURE AREA	->	CULTURE
	R ² =			R ² =
MATRI/ PATRI CENTRICITY	.35			.51
LINEALITY	.36			.53
	marginally significant .1 < p < .05			highly significant p < .001

FIGURE 4. Latitude, culture areas, cultures: a summary.

CULTURE AREAS AND THE EMERGING SYNTHESIS

At least within geographic regions, it is fairly common to find that kinship systems correlate with "cultural phylogeny" (Guglielmino et al. 1995). Are there similar correlations on a global scale? Figure 5 suggests an affirmative answer. The tree on the left-hand side of the figure is taken from the population genetic research of Cavalli-Sforza et al. (1988; 1994). It shows genetic similarities between 42 world populations based on data for gene frequencies of 120 alleles. Five European populations have been collapsed into

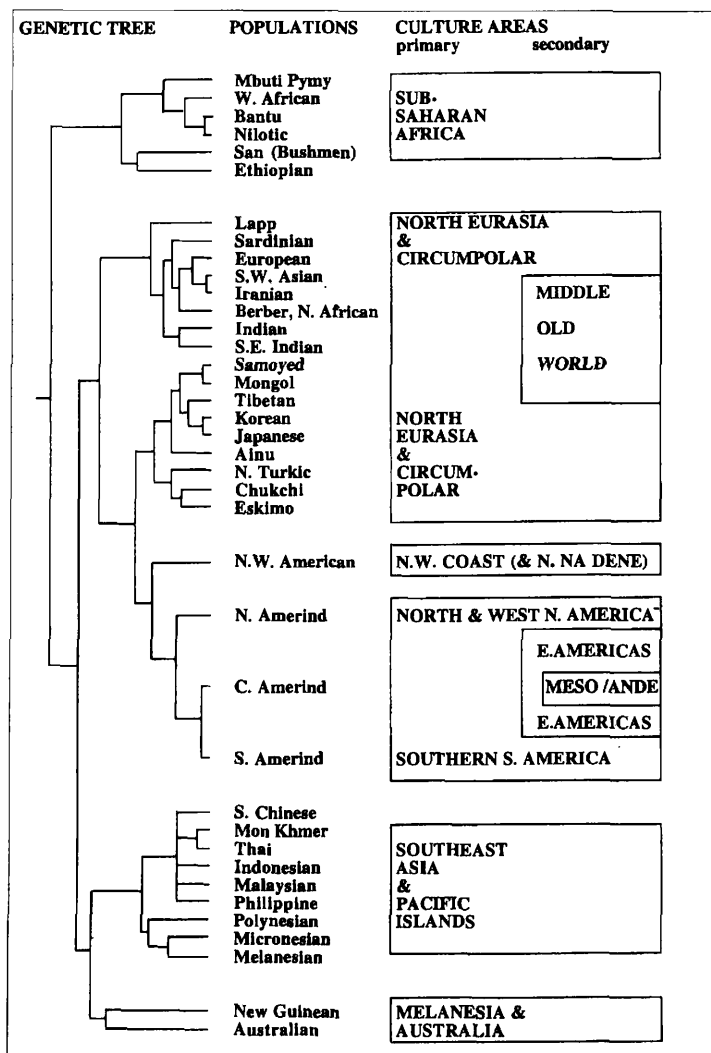


FIGURE 5. Population clusters and culture areas.

a single branch. Genetic similarities between populations are measured by Nei's genetic distance, and the tree is built from the bottom up by the method of unpaired group mean averages (UPGMA). Using a tree based on an alternative measure of genetic distance (FST; Cavalli-Sforza et al. 1994) would not affect the discussion below.

Cavalli-Sforza et al. (1988; 1994) argue that genes and language are correlated: that many population clusters in their tree correspond to well-established language families or to more speculative macro-families (but cf. Bateman et al. 1990 for a negative reaction; and Chen et al. 1995 for an equivocal one). Figure 5 demonstrates a similar correlation between genes and kinship systems, with Burton et al.'s ten world culture areas arranged to show how population genetic clusters correspond to culture areas. There are three sorts of exceptions to the correspondences. First, a few transitional populations are discrepant. South Chinese and Melanesians cluster genetically with Southeast Asians but fall outside the Southeast Asia and Pacific Island culture area. Ethiopians are distantly associated genetically with the African population cluster; yet, culturally, they associate weakly with the Middle Old World. (However, the apparent discrepancy involving the San [Bushmen] is misleading, as discussed below.) Second, within the super-cluster comprising West Eurasian, Northeast Asian, and Native American clusters, Northeast Asians show greater genetic affinities with Native Americans but greater cultural affinities with West Eurasians. Third, and most important, within two population clusters—West Eurasia/Northeast Asia and Amerind—there are major cultural divisions that do not correspond to major genetic divisions. As the figure shows, these seem to entail divisions between primary and secondary culture areas, with the former more geographically peripheral and presumably more ancient.

Some concordance between genetic and cultural variation is expected simply because neighbors tend to be similar both culturally and genetically. But Figure 5 shows something more than this: It shows that divisions between culture areas tend to coincide with divisions between major population clusters. The correspondence—although not without exception—is striking enough to suggest that the forces creating culture areas have often (but not always) run in parallel with those creating population clusters. Several processes might be involved here. On a local scale, genetic and cultural diffusion may work in parallel, and barriers to gene flow may coincide with barriers to cultural diffusion. On a larger scale, population movements can result in genes, languages, and cultures being carried together to new locations. On its own, Figure 5 does not show how either of these processes has operated, or when. However, as discussed above, the reconstruction of population histories and their associations with linguistics and archeology is now a very active field of research. For some major population clusters and language families, we seem to be approaching a consensus on how they were formed; for others, the set of plausible hypotheses is at least limited. The next section reviews this field on a region-by-

TABLE 2. Old World populations and culture areas.

Culture Areas		Causes: Demic Expansions/Changes in Political Economy	Some Associated Language Families
primary	secondary		
Subsaharan Africa (strongly unilineal)		Pastoralism, farming (from Sahel, West Africa)	Nilo-Saharan. Niger-Kordofanian (incl. Bantu)
North Eurasia and Circumpolar (strongly bilateral, patricentric)		Initial settlement? Post-glacial climate change/intensified foraging? Farming (from Near East)?	"Nostratic"/"Eurasianic"
	Middle Old World (strongly patricentric and unilineal)	Pastoralism. Rule by pastoral nomads & state support of patrilineages? Intensive agriculture?	subset of "Nostratic." Sino-Tibetan
Southeast Asia and Pacific Islands (strongly matricentric, bilateral)		Farming (from southern China)	"Austric" (incl. Austronesian)
New Guinea, Melanesia		Farming (from New Guinea)	"Papuan"/Trans-New Guinea
and Australia (strongly unilineal)		Initial settlement? Post-glacial climate change/intensified foraging? (from North Australia)	Australian (incl. Pama-Nyungan)

region basis with an eye to explaining both primary culture areas, which may have been generated by the same processes that have produced population clusters and major language families, and secondary culture areas, which are generated independently.

REGIONS

Modern humans apparently spread out of Africa sometime between 200,000 and 50,000 years ago, largely or entirely replacing Neanderthals and other regional populations (Harpending et al. 1998). This initial demic expansion has left its mark on current gene frequencies. But the last 10,000 years have seen tremendous cultural innovations—especially domestication—and further demic expansions on continent wide scales, as well as genetic and cultural diffusion. Below, for a number of regions, I first review the most widely accepted accounts of the major occurrences in prehistory that have generated correlated genetic, linguistic, and archeological clustering. Then I consider how

the distribution of kinship systems does or does not fit these patterns. The discussion is summarized at the beginning of the next section and in Tables 2 and 3.

Sub-Saharan Africa

This region is a good place to introduce the emerging synthesis because there is a substantial consensus on the role of Holocene demic expansions in shaping the genetic, linguistic, and cultural landscape. While an initial migration of modern humans out of Africa is probably responsible for the genetic division between sub-Saharan Africans and other populations (Nei and Takezaki 1996), more recent population movements within the region have played a major role in generating patterns observed in the ethnographic present. Many of these movements are associated with the spread of farming and herding economies at the expense of hunting and gathering. Two areas, the Sahel just south of the Sahara and the tropical forest of West Africa, are centers of origin of food production and also of

TABLE 3. New World populations and culture areas.

Culture Areas		Causes: Demic Expansions/Changes in Political Economy	Some Associated Language Families
primary	secondary		
North Eurasia and Circumpolar		See previous table	See previous table
Northwest Coast (revised to include Northern Na Dene) (matricentric, bilateral)		Post-glacial climate change/intensified foraging? (from Southwest Alaska?)	Na Dene
Northern and Western North America		Initial settlement (from Beringia/Northeast Asia)	"Amerind"
Southern South America (both strongly patricentric)		Initial settlement (from Beringia/Northeast Asia)	"Amerind"
	Eastern Americas (moderately matricentric)	Farming	subset of "Amerind"
	Mesoamerica, Central America and Andes (bilateral, matricentric)	Intensive agriculture? Spanish rule?	subset of "Amerind"

two major language families, Nilo-Saharan and Niger-Kordofanian (including Bantu), which now cover most of the continent (Ehret 1998; Iliffe 1995). Groups deriving from expansions out of these two areas form a tight cluster in Cavalli-Sforza et al.'s tree. Further evidence of the genetic character of these expansions comes from the distribution of unilineally inherited genetic variation, which shows especially strong population bottlenecks for the patrilineally transmitted nonrecombining portion of the Y chromosome, relative to mitochondrial and non-Y-linked nuclear DNA. This pattern is more marked in Africa, probably as a result of high frequencies of polygyny or more extensive migrations of males, than in Europe or Asia (Hammer and Zegura 1996; Scozzari et al. 1997; Seielstad 1998). Just a few populations within sub-Saharan Africa are genetic and linguistic outliers. These include some Ethiopian groups like the Amhara, who probably adopted agriculture independently, and Khoi-San groups like the !Kung, who were among the last peoples affected by the great migrations of farmers and herders. The hunting and gathering Mbuti Pygmies are also genetic outliers but they have adopted the languages of their Bantu neighbors.

These demic expansions have also shaped the modern distribution of kinship systems in sub-Saharan Africa. Christopher Ehret (1998) offers detailed reconstructions of ancestral kinship systems and cultures, and C. Rosalba Guglielmino et al. (1995) demonstrate that cultural phylogeny (assessed by language family), not ecology or the culture of neighboring groups, is the major determinant of geographic variation in kinship systems. This work implies that many of the social traits like strong unilineal kin groups and nonsororal polygyny that define Burton et al.'s sub-Saharan Africa culture area were carried by early pastoralists and farmers along with their languages and agricultural skills. The sociological importance of demic expansions in Africa, both in ancient and more recent times, is further emphasized by Igor Kopytoff (1989). He argues that expansion along an "African frontier" has played a conservative role in social evolution, reinforcing a complex of traits including strong corporate kin groups, some patrilineal and some matrilineal.

Consistent with this, the Amhara and !Kung San (Bushmen) are outliers not only genetically and linguistically but also in their social structure, with bilateral rather than unilineal kinship. (However, Burton et al. put the !Kung in their sub-Saharan African culture area to avoid creating a separate culture area just for them. The Mbuti Pygmies, also with bilateral kinship, are not in their data set.) Thus genes, languages, and kinship systems have often expanded in tandem over the last 5,000 years of African history, giving most of the continent a degree of genetic and cultural uniformity it probably did not possess earlier.

Southeast Asia and the Pacific Islands

With this region, as with sub-Saharan Africa, there is substantial consensus on the importance of demic expansions

associated with the origin and spread of agriculture (cf. Terrell et al. 1997 for a dissenting view). Southern China, especially around the middle Yangzi River, is a major center of domestication, notably of rice. Expansions out of this area carried farmers through Southeast Asia and, ultimately, to Polynesia and Micronesia. These movements are associated with the expansion of several language families: Miao-Yao, Austroasiatic, and Daic on the mainland, and Austronesian largely on the islands (Gray and Jordan 2000). Some or all of these may constitute a single macrofamily labeled Austric (Blust 1995; Ruhlen 1991). Robert Blust (1995), Peter Bellwood (1996a, 1997), and Bellwood et al. (1995) summarize the linguistic, archeological, and cultural evidence for Austronesian and related expansions. Both skeletal anthropology and genetics demonstrate a substantial genetic component to these expansions (Bellwood 1997; Melton et al. 1998).

In the genetic cluster associated with demic expansions out of southern China, almost all populations also belong to Burton et al.'s Southeast Asia and Pacific Island culture area. This culture area is characterized by matricentric social structures, of varying degrees of unilineality, consistent with ethnohistoric and linguistic evidence implying cognatic or matrilineal descent groups among founding populations (Hage 1998). The importance of matrilineal descent in the Austronesian expansion is further supported by genetic evidence. The Southeast Asian roots of the Austronesian colonization of the Pacific show up more clearly in the distribution of matrilineally inherited mitochondrial haplotypes than in the distribution of nonmatrilineal genetic variation (Lum et al. 1998). The opposite pattern is found with the Indo-European, Semitic, and Niger-Kordofanian language families, which are more associated with variants on patrilineally inherited regions of the Y chromosome than with mitochondrial variants (Poloni et al. 1997).

Two populations from the Southeast Asian genetic cluster fall outside the associated culture area. Southern China, once the center of origin for the demic expansion, has since been transformed linguistically and culturally by Han influences from the north. And Vietnam and some other heavily sinicized border areas (not shown on the genetic tree) have also shifted toward the strong patrilineal emphasis of the Middle Old World. Yet even in southern China, scattered enclaves of pre-Han language groups and matricentric social systems remain: for example, the highly matrilineal Na, who are reported to lack even the institution of marriage (Hua 2001).

Finally, Melanesia is a transitional zone. Originally settled from New Guinea, the region has largely adopted Austronesian languages brought by later Southeast Asian immigrants. There has been substantial and complicated genetic and cultural diffusion in both directions between original inhabitants and newcomers, but Melanesian social structures on average show somewhat stronger affinities with New Guinea than with the Southeast Asia and Pacific Island culture area (Bellwood et al. 1995).

Australia and New Guinea

Australia and New Guinea were occupied by modern humans more than 40,000 years ago; their rather distant genetic connection with one another and their genetic separation from other parts of the world may partly reflect this original settlement. However, later events may be more important for the spread of kinship systems. In New Guinea, a demic expansion associated with the development of agriculture probably helped to spread languages of the Trans-New Guinea phylum across most of the island and to create an East–West gradient in gene frequencies (Cavalli-Sforza et al. 1994; Wurm 1982).

In Australia, language and genes covary in a suggestive fashion. Aboriginal languages are generally grouped together in an ancient Australian family. Yet almost all the fourteen or so subfamilies within Australian are found only in and around a small area in the center north, while a single subfamily, Pama-Nyungan, sprawls over about 85 percent of the continent. Multiple genetic clines, too, radiate from the center north (Cavalli-Sforza et al. 1994: 354–355). Taken at face value, this pattern suggests a demic expansion out of a small core area—most likely during the Holocene, given the strong similarities among Pama-Nyungan languages. This looks a lot like the patterns observed in Africa and Southeast Asia. Of course, aboriginal Australia, in contrast to other regions, saw no spread of agriculture before European contact. Yet there is a clear candidate for the material culture associated with Proto-Pama-Nyungan (McConvell and Evans 1997). Australian hunting and gathering was not a static tradition: The archeological record shows a major discontinuity beginning 6,000 years ago, including considerable advances in technology (the small-tool tradition); an abrupt jump in the density of sites; and, probably, the introduction of the dingo. These changes may reflect influences originating outside Australia—from New Guinea, Southeast Asia, or even India (Flood 1983; McConvell and Evans 1997). The first possibility is consistent with Burton et al.'s culture areas. The last possibility is consistent with parallels between Dravidian and Australian kinship (Trautmann 1981:434–437) and has received recent support from analyses of both mitochondrial (Redd and Stoneking 1999) and Y-chromosome DNA (Redd et al. 2002).

The role of demic expansions, cultural diffusion, and outside contact in the recent prehistory of New Guinea and Australia is still unsettled, but the number of plausible hypotheses is limited. Ongoing research is likely to settle which of these is correct, with implications for the spread of distinctive unilineal kinship systems over large areas (McConvell and Evans 1997).

Eurasia

Eurasia (plus North Africa, minus Southeast Asia) presents a complex picture: an East–West divide in population structure, a North–South divide in kinship systems, and a number of language families. Several phases of demic

expansion associated with initial settlement and the spread of farming, as well as later culture shifts without major demic expansion, may all have contributed to this spatial pattern.

Both genetic and linguistic evidence indicate a substratum of shared ancestry and culture stretching from Europe and North Africa through West, Central, and South Asia to Northeast Asia. Genetic distances based on frequencies of classical polymorphisms show that (1) circum-Pacific populations ranging from Australia through East Asia to the New World have some genetic similarity to one another but (2) among these populations, it is Northeast Asians who are most similar to Europeans and West Asians. These results demonstrate the difficulty of drawing up a single correct racial taxonomy for modern humans. They imply significant gene flow both between Northeast Asia and Southeast Asia and between Northeast Asia and West Eurasia; the latter connection dominates Cavalli-Sforza et al.'s population tree. (But see Nei and Roychouduri 1993 for somewhat different results using a different method of tree construction.)

Further evidence for ancient connections between Northeast Asia and West Eurasia comes from similarities among many major language families of the region, which have often been noted and seem to be too striking to be accidental. Some authors argue that these similarities reflect convergence resulting from contact and borrowing (Nichols 1994), others that they reflect descent from an ancestral protolanguage. Joseph Greenberg (2000) assigns a number of North Eurasian and Circumpolar language families and languages—including Indo-European, Uralic-Yukaghir, Altaic, Korean, Japanese, Chukchi-Kamchatkan, and Eskimo-Aleut—to a macrofamily he calls “Eurasian.” Other linguists have independently argued that the language families above—with the possible exception of the last two—together with Kartvelian (South Caucasian), Elamo-Dravidian, and, maybe, Afro-Asiatic, belong to an even larger macrofamily labeled “Nostratic” (Kaiser and Shevoroshkin 1988; Renfrew and Netting 1999).

Genetic and linguistic connections across Northern Eurasia might date back to the initial settlement of the region by modern humans around forty thousand years ago or to later population movements and contacts among hunter-gatherers. But lately, a number of researchers within the emerging synthesis have suggested that demic expansions associated with the spread of agriculture, similar to those in Africa and Southeast Asia, were probably also important (Barbujani and Pilastro 1993; Bellwood 2001; Renfrew 1996). In one scenario, Proto-Nostratic was spoken by a preagricultural population somewhere around the Fertile Crescent; farming populations moving out of the Near East carried different Nostratic daughter languages with them. Possible secondary homelands for some resulting language families are (1) Anatolia for Indo-European broadly defined and Southeast or East Europe for Indo-European narrowly defined (excluding the Anatolian languages), (2) southern Central Asia for Altaic, (3) southern

Iran for Elamo-Dravidian, and (4) the African shore of the Red Sea for Afro-Asiatic. Barbujani and colleagues (Barbujani et al. 1994; Barbujani and Pilastro 1993) find evidence for genetic clines radiating out from the Near East consistent with this scenario, except for Afro-Asiatic, which may have split off earlier. More recent research also shows moderate-to-major contributions from Near Eastern agriculturalists to gene pools in Europe (Lounés et al. 2002), especially for the patrilineally inherited portion of the Y chromosome. In East Asia, farming dispersals out of northern China probably contributed to the spread of the Sino-Tibetan language family.

Burton et al. identify a North Eurasian and circumpolar culture area with moderately patricentric and mostly bilateral kinship systems that covers most of Europe and Siberia, Korea, Japan, and the circumpolar New World. They also identify a Middle Old World culture area with strongly patricentric and unilineal kinship systems which covers North Africa, part of the Balkans, the Middle East, the Indian subcontinent, much of the Eurasian steppe, and China and its neighboring areas. With the marginal exceptions of Ethiopia and sinicized South China and Southeast Asia, almost all the populations of these two culture areas, and only these populations, fall within the Old World portion of Cavalli-Sforza et al.'s North Eurasian genetic cluster, and most speak languages from the proposed Nostratic or Eurasiatic macrofamilies or the Sino-Tibetan family.²

The North-South bilateral-patrilineal divide in Eurasia does not correspond to any major genetic or linguistic division or to any one inferred demic expansion. The divide *does* relate to mode of subsistence: Northern hunter-gatherers largely belong to the North Eurasian and Circumpolar culture area, while pastoral nomads overwhelmingly belong to the Middle Old World. The association with hunting and gathering, together with a peripheral geographic position, suggest that the North Eurasian and Circumpolar culture area is likely to be the more ancient of the two: It may be a relic of population movements and cultural and genetic exchanges among hunter-gatherers or early farmers or both that fostered a degree of homogeneity in kinship systems as well as genes and language across much of Eurasia.

The formation of the Middle Old World is probably a later development, associated in part with the rise of pastoralism. Among the pastoral nomads who make up part of the Middle Old World, patrilineal kin groups normally play a central military and political role (Barfield 1993). And among almost all of the stratified, centralized agrarian societies that make up most of the rest of the culture area, tribal patrilineal pastoral nomads or their sedentarized descendants have repeatedly established themselves as ruling elites. Perhaps partly in consequence, patrilineal kin groups have traditionally received strong "top-down" political and ideological support, with the regulation of female sexuality central to group honor and

wife givers and wife takers accorded unequal status (Ortner 1996:43–58).

Several recent genetic studies tell something about the development of the Middle Old World culture area. In India, a social system combining patrilineal descent, hereditary stratification, and hypergamy (females marrying up, but not males)—probably partly the legacy of outside conquests—has left an enduring mark on differential distributions of Y-chromosome and mtDNA variation across castes (Bamshad et al. 1998). At least in Andhra Pradesh, upper-caste males still carry elevated frequencies of Y-chromosome haplotypes probably deriving from East Europe or Central Asia (Bamshad et al. 2001). And in Central Asia, the explosive spread of a young patrilineage (around a thousand years old)—which was probably tied to the exploits of Genghis Khan—has left a substantial mark on the distribution of Y-chromosome haplotypes (Zerjal et al. 2003). The genetic evidence is consistent with historical reconstructions suggesting that the spread of pastoralism and segmentary lineage systems in Eurasia and the adoption of patrilineal ideologies in agrarian societies did not result from a demic expansion from a single area but instead involved a number of societies of varied linguistic and genetic backgrounds (Barfield 1993).

Thus, continent-scale demic expansions and parallel diffusion of genes, language, and social structure probably played an important role in the origin of the North Eurasia and Circumpolar culture area and the establishment of moderate patricentricity through most of Eurasia. But any demic expansions and language shifts associated with the formation of the Middle Old World were more numerous, more recent, and more limited in geographic scale and genetic impact.

Eskimo-Aleuts and Northern Na Dene

Two population blocs, Eskimo-Aleuts and Na Dene, are clearly separate from the remainder of New World populations, with distinctive gene frequencies and language families (Bonato and Salzano 1997; Forster et al. 1996; Greenberg et al. 1986). Either the ancestors of these two blocs migrated from Asia later than the ancestors of other populations or they were isolated from the main body of Amerinds in Beringia or Pacific coast refugia during the last Ice Age. (For present purposes, I consider only the "Northern Na Dene," a contiguous bloc of populations in Alaska and Northwest Canada, including Tlingit, Eyak, northern Athabaskans, and, probably, Haida, ignoring a scattering of Athabaskan speakers in Oregon, California, and the Southwest.)

Eskimo-Aleut and Northern Na Dene are distinctive not only in their gene frequencies and languages but also in their social structures. Burton et al. place Eskimo and Aleuts in the North Eurasian and circumpolar culture area, in line with genetic and linguistic evidence linking them with Eurasian circumpolar groups. The Northern Na Dene have their own distinct sociological profile, with matricentric

kinship systems that contrast with the patricentric systems of most of their Amerind neighbors; linguists and ethnographers argue that the ancestral kinship system for the Athabaskans and for the Na Dene as a whole was matrilineal and matrilineal (Dyen and Aberle 1974; Rubel and Rosman 1983).

To show more clearly the cultural distinctiveness of the northern Na Dene, I propose a modest revision in Burton et al.'s New World culture areas. In Burton et al.'s classification, northern Na Dene near the coast are assigned to the northwest Coast culture area while others are assigned to the northern and western North American culture area. But the four inland northern Na Dene groups allocated to the latter area (Nabesna, Carrier, Kutchin, and Sarsi) are some of the least patricentric in an otherwise strongly patricentric area. Reassigning them to the Northwest Coast area actually improves the categorization: The average distance between cultures in the revised Northwest Coast area drops from 1.33 to 1.30, while the average distance in the revised northern and western North American area also drops, albeit by a negligible amount. In other words, I suggest that the Northwest Coast culture area should be turned into a northern Na Dene and Northwest Coast culture area, including (1) the northern Na Dene both on the Northwest Coast and inland and (2) some non-Na Dene groups along the Northwest Coast who have been shifted away from a patricentric orientation, perhaps as a result of intensive cultural and genetic exchanges with coastal Na Dene. (For evidence for substantial gene exchange between Na Dene and non-Na Dene along the Northwest Coast, see Greenberg et al. 1986.) This revision, supported by Burton et al.'s own methodology and by ethnohistory, implies that the New World's two most genetically distinctive population clusters are strongly associated with two of the New World's major culture areas.

Amerinds

The Amerinds are the third major population cluster in the native New World. There may also be an Amerind language macrofamily (Greenberg 1987), although this is controversial. Like the North Eurasian population cluster in the Old World, the Amerinds seem to display a central-peripheral pattern in their social geography. Northern and Western North America and Southern South America lie far apart at the peripheries of the Amerind range. Both areas are inhabited by populations whose members mostly subsist by hunting and gathering and whose kinship systems are strongly patricentric and variable in their degree of unilineality. The peripheral geographic distribution of these culture areas and their association with hunting and gathering suggest that this pattern may represent the ancestral economic and social system for Amerinds. However, it has been superseded in more central regions. The Eastern Americas are home to a number of horticultural or secondarily equestrian populations with a moderately matricentric and unilineal orientation. The North and South

American portions of the Eastern Americas have a connection through the Caribbean, but on the mainland they are separated by a still more central region of intensive agriculture, centralized polities, Spanish colonial influence, and bilateral kinship that extends from Meso-America through the Andes.

These nested culture areas do not correspond to major genetic or linguistic divisions among Amerinds (leaving aside the Spanish contribution to the Meso-America and Andes area). The transitions from foraging to agriculture and from low- to high-intensity agriculture seem to have resulted in changes in social structure but not in areawide population spreads. This is consistent with evidence from archeology and historical linguistics: Because the spread of agriculture in the New World involved a limited stock of domesticates (especially animals), it happened more gradually and with more cultural diffusion, less demic expansion, and less thorough language replacement than in the Old World (Bellwood 1996a; Diamond 1997).

CONCLUSION

Burton et al. did not set out to demonstrate that world culture areas map onto major genetic subdivisions of humanity, and it is unlikely that the correspondences shown in Figure 5 are an artifact of bias in ethnographic reporting (Burton et al. 1996:116–119). Nor are coincident clusters simply a predictable consequence of the fact that neighbors tend to resemble each other both culturally and genetically.

This article takes a different tack. Many prehistorians now argue that demic expansions are an important source of correlations between genes, language families, and archeological cultures. I take this idea a step further by arguing that demic expansions, in combination with local diffusion of social structure in parallel with genes and languages, have also generated most, but not all, of the world's "regions based on social structure" (Burton et al. 1996). While Figure 5 is suggestive in this regard, ultimately the argument must stand or fall for each region on its own. The evidence is especially strong in some cases. For sub-Saharan Africa and Southeast Asia there is considerable agreement regarding centers of agricultural innovation, homelands of major language families, and ancestral kinship systems carried by prehistoric migrants. These two distinctive culture areas seem pretty clearly to have their origins in large-scale migrations of agriculturalists through the Old World tropics. For Na Dene speakers in North America, too, there is substantial agreement on linguistic relationships and ancestral kinship systems, and Burton et al.'s scheme can be bettered with a modest revision that reflects the consensus on the Na Dene expansion, together with later genetic and cultural diffusion southward along the Northwest Coast.

For New Guinea and Australia, the role of demic expansions and genetic and cultural diffusion in the origin of population clusters, language families, and culture areas

is less certain, although a provisional case can be made for parallel transmission. Australia is particularly interesting: Although not widely known, there is quite suggestive genetic, linguistic, and archeological evidence for a fairly recent (from about six k.y.a.) demic expansion. This obviously may bear on the origin of the continent's distinctive social organization.

For the two remaining population clusters, Eurasia (minus Southeast Asia, but including North Africa and the circumpolar New World) and the Amerinds, the situation is more complicated. In both cases, there are peripheral culture areas having some association with hunting and gathering economies and controversial language macrofamilies. These areas may date back to the initial modern human expansion into these regions or later periods of genetic and cultural diffusion. In both cases, however, there are additional culture areas that do not result from area-wide demic expansions. In Eurasia, the development of agriculture is associated with population spreads and probably with the origin of major language families, but not with a lasting social structural divide. Instead, the secondary Middle Old World culture area is related to later developments, including pastoralism and conquest by pastoralists. Among Amerinds two other secondary culture areas are associated with changes in subsistence and political economy. But none of these secondary culture areas correspond to major genetic or linguistic divides.

The distinction suggested here—between primary culture areas which can be tied at least provisionally to area-wide demic expansions or parallel diffusion of genes and culture, and secondary culture areas which cannot—is similar to a pattern noted by Renfrew (1992, 1996) regarding language family spreads. Some (e.g., Bantu and Austronesian) are associated with major demic expansions; others stemming from trade or elite dominance in stratified societies (e.g., Turkic) are not. Only in the former cases are genes and language substantially correlated. Both cultural and linguistic patterns are a reminder that although genes, language, and culture can be and often are transmitted in parallel, they do not *have* to be.

The present article suggests several future lines of investigation. Insofar as similarities in kinship systems within major culture areas reflect descent from cultural common ancestors, it should be possible to move beyond the two-dimensional classification of Burton et al. to reconstruct ancestral systems in more detail. Connections between kinship systems, kin terminology, and language families will be of particular value in this regard.

The connections with genetic variation are also worth pursuing, particularly because different kinship systems may have different consequences for patrilineally and matrilineally transmitted genes. For example, compare West Eurasia and Central Asia, where population expansions and social stratification seem to show up especially in the patrilineally transmitted region of the Y chromosome, with Southeast Asia, where the Austronesian expansion seems

to show up especially in matrilineally transmitted mitochondrial DNA.

Finally, the *interaction* between kinship as a social institution and population processes like migration and diffusion may be a particularly rewarding topic for future investigation. For example, prehistorians commonly argue that demic expansions are driven by innovations in subsistence, especially domestication. But which groups spread and both when and how they did is sometimes a function not just of material technology but of social structure. The Austronesian expansion, Bellwood (1996b:18–40) argues, was driven not just by subsistence pressures, but by a system of ranking based on birth order that encouraged low-ranking descent groups to strike off for new territory even before old territory was demographically saturated. And in Africa and Eurasia, segmentary lineages have sometimes played a role in the “predatory expansion” of populations (Kelly 1985; Kopytoff 1989; Sahlins 1961). Instead of kinship systems being passively carried along by population expansions and diffusion like neutral genetic polymorphisms, they may play an active role in these processes, which may in turn feed back to influence kinship. This article has argued that demic expansions have been associated with the spread of particular social systems; future research may demonstrate that these social systems have played some role in causing these expansions. If so, then cultural anthropology's long-standing interest in kinship systems and their structural consequences may contribute to explaining some of the major events in prehistory.

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NOTES

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1. In all analyses I use absolute latitudes—specifically, degrees of latitude from the equator. Using negative latitudes for the Southern Hemisphere does not substantially affect results.

2. Korotayev and Kazankov (2000) put Nostratic and Sino-Tibetan together in an even more speculative macromacrofamily that also includes a few other Eurasian languages, and the Na Dene family in North America.

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