References Cited

KRIGE, E. JENSEN, AND J. D. KRIGE. 1943. *The realm of a rain-queen.* London: Oxford University Press for the International African Institute.

KUPER, ADAM. 1970. *Kalahari village politics: An African democracy.* Cambridge: Cambridge University Press.

———. 1973. *Anthropology and anthropologists.* London: Routledge and Kegan Paul.

———. 1976. *Changing Jamaica.* London: Routledge and Kegan Paul.

———. 1982. *Wives for cattle: Bridewealth and marriage in southern Africa.* London: Routledge and Kegal Paul.

———. 1987. *South Africa and the anthropologist.* London: Routledge.

———. 1988. *The invention of primitive society: Transformation of an illusion.* London: Routledge.

———. 1994. *The chosen primate: Human nature and cultural diversity.* Cambridge: Harvard University Press.

———. 1999a. *Among the anthropologists.* London: Athlone Press.

———. 1999b. *Culture: The anthropologisits' account.* Cambridge: Harvard University Press.

Semes and Genes in Africa[1]

BARRY S. HEWLETT, ANNALISA DE SILVESTRI, AND C. ROSALBA GUGLIELMINO
Department of Anthropology, Washington State University, Vancouver, Wash. 98686, U.S.A. (hewlett@vancouver.wsn.edu)/Dipartimento di Genetica e Microbiologica, Università di Pavia, Pavia, Italy/Dipartimento di Genetica e Microbiologia, Università di Pavia and Istituto di Genetica Biochimica ed Evoluzionistica, C.N.R. Pavia, Italy. 4 IX 01

This report has two general aims: to explain the distribution of cultural practices and beliefs across the landscape in Africa and to demonstrate how genetic, linguistic, and geographic information can be used to understand the nature of culture. We focus on ethnic groups that share cultural units (schemas or practices) and utilize genetic, linguistic, and geographic data to evaluate the processes that help to explain this sharing. Following Cavalli-Sforza, we call these units "semes" rather than "memes" (Dawkins 1976, Durham 1991,

Boyd and Richerson 1985) because "seme" comes from "sign" and emphasizes the symbolic nature of culture. Our approach is sometimes called "coevolutionary" or "dual-inheritance" because it identifies relationships between genes and culture. We prefer to call it evolutionary cultural anthropology (Hewlett and Lamb n.d.) because the major theoretical contributions to date (Cavalli-Sforza and Feldman 1981, Boyd and Richerson 1985, Durham 1991) emphasize understanding the evolutionary mechanisms and properties of culture.

Studies of the relationships between biology and culture are not looked upon favorably in anthropology, partly because they tend to be linked with discussions of race and culture. Franz Boas countered racism in the early 1900s by demonstrating that "races" had no inherently different biologies and cultures. He saw the processes as unconnected because biological mechanisms were so slow to change while culture could change very rapidly. Boas was interested in explaining cultural diversity and rejected the notion that race or biological differences could help explain this diversity. Discussions of race and culture were major components of early anthropology textbooks (Boas 1938, Kroeber 1923), and combating racism and ethnocentrism continues to be important in most anthropology courses. We suggest that cultural mechanisms can help to explain why genes and culture may coincide. This does *not* mean that the biology determines culture; indeed, culture often determines genes, as in the case of adult lactose absorption (Cavalli-Sforza and Feldman 1976, Durham 1991). Our work is consistent with a Boasian perspective in that we are interested in trying to understand how particular culture histories can help explain cultural diversity in Africa, but in contrast to Boas we use genes and language as tools for interpreting that diversity. This study extends Boas's and Kroeber's work by identifying specific cultural mechanisms and models which help to explain cultural diversity and interpret cultural histories.

EXPLANATORY MODELS

Why do cultures share semes? Three broad explanatory models are usually offered: (1) cultural diffusion, borrowing or diffusion of the seme from neighbors, (2) local adaptations, in which individuals develop similar semes to adapt to similar natural and social environments, and (3) demic diffusion, the movement of peoples and their semes to new areas. The first model is a trademark of the Boasian and Kroeberian cultural relativist tradition in anthropology. This tradition deemphasizes the adaptive nature of culture (i.e., the impact of natural and social ecologies) and suggests that semes arise primarily from human imagination and mindful play and may take their own courses. The second model is common in cultural anthropology and has its roots in Julian Steward's (1955) cultural ecology. In the 1970s, cultural ecology was modified and called "cultural materialism" by Marvin Harris, and in the 1980s and 1990s it was modified further and reemerged as "evolutionary ecology." These approaches consider most semes adaptive (i.e., enhancing

the Darwinian fitness of individuals or groups). The third model is characteristic of studies such as those of Cavalli-Sforza, Menozzi, and Piazza (1993), where it describes the repeated expansions of a group generated by the development of an innovative technology or type of social organization. The innovation leads to population growth, migration, and intermarriage with those without the innovation (i.e., gene flow in the direction of those with the innovation). Genes, semes, and language move with the innovation. The semes that move with people may or may not be adaptive; many are likely to be neutral. Some semes may be adaptive in some environments or circumstances and neutral or nonadaptive in others. Semes are conserved through specific mechanisms of cultural transmission. The demic-diffusion model is seldom used by cultural anthropologists. Cultural diffusion may be popular among postmodern and ethnohistorical anthropologists because it is so easy to see in today's world.

MECHANISMS OF CULTURAL TRANSMISSION

Four mechanisms of transmission underlie these models (table 1). The first, vertical transmission, is most similar to genetic transmission. Mathematical analysis has shown that semes transmitted in this way are highly conserved (Cavalli-Sforza and Feldman 1981). Vertical transmission is especially pronounced in infancy and early childhood, in part because of parent-child proximity and attachment. The second, called the group effect by Cavalli-Sforza and Feldman (1973) and frequency-dependent bias by Boyd and Richerson (1985), is the process whereby individuals acquire semes that occur frequently in the population on the assumption that they are likely to be adaptive. This mechanism also tends to maintain the status quo. Henrich and Boyd (1998) argue that vertical transmission alone is not sufficient to explain group-level conservation of semes and that the group effect increases the frequency of a seme beyond what is expected from vertical transmission. Vertical transmission and the group effect are the mechanisms by which semes are conserved in demic diffusion.

The third mechanism, horizontal transmission, is based upon epidemiological models of disease transmission. As the frequency of interaction with or exposure to an unrelated individual with a seme or disease increases, it becomes more likely that one will adopt a seme or catch a disease. As the frequency of interactions between individuals of different communities increases, it becomes more likely that they will adopt aspects of each other's culture. Horizontal transmission may be (1) between generations (called oblique), (2) within a generation (the origin of the term "horizontal"), or (3) one-to-many (characteristic of highly stratified urban industrial societies in which teachers, leaders, TV, and the Internet transmit information). Culture change with horizontal transmission can be rapid; the one-to-many form is especially conducive to rapid culture change and, though common today, was rare in the past. Horizontal transmission is the prime mechanism of cultural diffusion.

Trial and error is a process that contributes to local innovation and adaptation. Individuals observe or hear about alternative semes and critically evaluate their advantages and disadvantages. This evaluation may lead to a synthesis of existing semes (i.e., recombination) or the development of an entirely new seme. The innovative seme is, at first, often transmitted horizontally. The trial-and-error process takes place from infancy on, but a sub-

TABLE 1
Three Explanatory Models for the Sharing of Semes across Cultures

Model	Mechanism	Features	Age Most Pronounced	Rate of Culture Change	Favoring Environmental Conditions
Demic diffusion	Vertical	Similar to genetic transmission; parent-to-child; preserves status quo	Infancy and early childhood	Slow	Stable
	Group effect	Frequency of seme in population impacts acquisition; preserves status quo	Late childhood and adolescence	Slow	Stable
Cultural diffusion	Horizontal	Frequency of interaction impacts acquisition; epidemiological model; route of innovation	Early childhood (between generations); late childhood and adolescence (within generations)	Can be rapid	Rapidly changing
Local adaptation	Trial and error	Evaluation of alternatives; cost-benefit; source of innovation; leads to convergence	Adolescence	Slow	Rapidly changing

stantial synthetic or innovative seme that is transmitted to others is more likely to emerge in adolescence or early adulthood. The use of trial and error by peoples in similar but distant natural and social environments may lead to the development of similar semes, a process similar to evolutionary convergence.

The stability of the environment influences the utility of these mechanisms. When environments change very slowly, adaptive knowledge can be obtained at the level of vertical transmission because only modest updating of knowledge is needed. It may, in fact, be difficult to distinguish between genetic and vertical cultural transmission mechanisms that are responsible for a particular behavior, since both are vertical and conservative. This has probably led some researchers to attribute genetic causes to human behaviors in error. In contrast, where environmental change is very rapid, individuals should favor horizontal (within-generation) transmission and trial and error. In such environments, genetic systems will change too slowly to cope, and information from the parental generation is likely to be outdated and error-prone.

PATTERNS OF GENETIC, LINGUISTIC, AND GEOGRAPHIC DATA

Eight patterns of genetic, linguistic, and geographic data that emerge from the three explanatory models are shown in table 2. Demic diffusion assumes that cultures share semes because they have a common past, and therefore genetic and/or linguistic similarities are predicted. To control for the effects of cultural diffusion, the cultures should also be geographically distant from each other. Cultures are likely to share semes because of demic diffusion and associated mechanisms of cultural transmission (vertical and group effect) when they exhibit the first three patterns of genetic, linguistic and geographic data. With these patterns, cultures that share semes are far apart and share genes and/or language. Cultural diffusion assumes that cultures share semes because they regularly interact with each other, so cultures that are geographically close to one another are expected to share more semes. In order to control for other factors, the cultures should not share a language or many genes. The fourth, fifth, and sixth patterns are most likely to demonstrate cultural diffusion and horizontal transmission. Pattern 6 is the best measure of cultural diffusion, while 4 and 5 are potentially confounded by factors of demic diffusion. The last pattern indicates that cultural similarities could be explained by any of the three models, while the next-to-last is the best for predicting local adaptations.

DISTANCE MEASURES

Our study required cultural (seme), genetic, linguistic, and geographic data on the same ethnic groups, and the primary limiting factor in selecting a sample was the availability of genetic data. The *Ethnographic Atlas* (Murdock 1967, Gray 1999) provides cultural data on over a thousand ethnic groups; Ruhlen (1991) and Grimes (1978) provide linguistic classification data on most of the world's languages, and it is easy to determine geographic distances between any two ethnic groups. To calculate genetic distances we decided to use autosomal genetic markers rather than DNA markers because only a few African populations have been examined for the latter. (For instance, the most recent study of African mtDNA genetic distances was based upon 20 individuals from 13 ethnic groups [Ingman et al. 2000], and the most recent study of African Y-chromosome genetic distances was based upon 13 individuals from 8 ethnic groups [Underhill et al. 2000].) From the genetic database maintained at Stanford University we were able to identify genetic data on 42 ethnic groups. [Additional information on methods appears in the electronic edition of this issue on the journal's web page]. Six cases had to be eliminated because there were no corresponding cultural data in the *Ethnographic Atlas*, and the remaining 36 cultures became the basis for all comparisons. The 36 ethnic groups had data on 13.97 loci on average (range 7–26) and 34.5 independent alleles (range 16–74). Genetic distances between pairs of ethnic groups were based upon an average of 22.7 independent alleles (range 14–70). Nei and Roychoudhury's (1972) method was utilized to calculate the genetic distance for each pair.

Cultural distances between pairs of societies were calculated with a method similar to Driver and Kroeber's (1932) "G" statistic. Each of the 630 pairs was compared for similarities and differences with regard to the 42 traits (e.g., mode of marriage) in the *Ethnographic Atlas*. Each trait had several alternative semes, and each culture was coded for one seme in each category. If either of the cultures had missing data for a trait, no comparison was made on that trait. A total of 109 semes were compared for each pair of societies.

Since no Swadesh word list was available for most of the cultures and no other method for measuring linguistic distance exists (see Chen, Sokal, and Ruhlen 1995), we developed a method somewhat similar to that described above for cultural distances. From Ruhlen's (1991) classification of languages we determined the number of linguistic categories in which two languages were similar and different.

Geographic distances between two cultures were calculated using the haversine formula (Sinnott 1984), which uses spherical trigonometry to calculate great-circle arcs. This "as the crow flies" measure is limited in that it does not take into account physical features such as mountain ranges, rivers, swamps, and other things that may help or hinder the movement of peoples or semes.

This paper also utilizes another measure, called the "clustering index" (Guglielmino et al. 1995), to evaluate the opportunities that members of one culture might have of acquiring the seme in question from neighboring cultures. It assesses the density of and geographic proximity to other cultures with the same seme.

TABLE 2
Patterns of Data Generated by the Models

Model	Data Pattern			
	Genetic	Linguistic	Geographic	Features
Demic diffusion	Similar	Similar	Distant	Peoples with same language and semes moved some distance from each other
	Similar	Similar	Distant	Peoples intermarried or shared semes in the past but either spoke different languages then or adopted a new language when they moved some distance from each other
	Different	Similar	Distant	No or limited intermarriage in the past, but peoples spoke similar languages and shared semes; one may have moved to a new area and intermarried with new neighbors but retained language and semes
Cultural diffusion	Similar	Different	Close	Intermarriage between peoples that speak different languages but have acquired seme from common neighbors or each other
	Different	Similar	Close	No or limited intermarriage but peoples share language and semes with common neighbors or each other
	Different	Different	Close	No or limited intermarriage and different languages but peoples have acquired semes from common neighbors or each other
Local adaptation	Different	Different	Distant	–
Multiple confounds	Similar	Similar	Close	–

RESULTS

Trees. The genetic tree for the 36 populations demonstrates that genetic distances between most African populations are relatively low by comparison with similar trees in the Americas because of the frequent intermarriage between ethnic groups noted by several ethnographers (e.g., Goody 1976) and the relatively recent Bantu expansion. The linguistic tree has four distinct branches consistent with the four linguistic phyla in Africa. This was expected, given our use of Ruhlen's classification system, but it did support the usefulness of our linguistic-distance methodology. The cultural tree is of course more complex, in part because it is influenced more by horizontal transmission than the other two trees, but the branches did identify three modes of production: hunting-gathering, farming, and pastoralism. This suggests that the semes coded by Murdock are often linked to a particular mode of production in Africa.

Language, ecology, and mode of production. Table 3 lists the means and standard deviations of the four dis-

TABLE 3
Means of Distance Measures and Clustering Index

	Number of Cultural Pairs	Mean	S.D.
Genetic distance	630	0.038	0.046
Cultural distance	630	0.600	0.124
Linguistic distance	630	0.879	0.239
Geographic distance (km)	630	2,988	1,681
Clustering index (mean of 109 semes)		0.385	0.195

tance measures and the clustering index. As genetic, linguistic, and cultural distance increases, the similarities for those values decrease. For instance, the average genetic distance is 0.038; this means that the 36 African cultures share 96.2% of their genes for the alleles measured in this study. The average geographic distance of 29.88 means that cultures are, on average, 2,988 km apart. (The measure in degrees can be converted approximately into kilometers by multiplying by 100.) Africa is huge, and most ethnic groups in this study are far from one another. Consequently, it is unlikely that geographic distance will be a useful measure of potential cultural diffusion between cultural pairs in this study. The clustering index for a particular seme, which is based upon all African cultures in the *Ethnographic Atlas*, will therefore be utilized to evaluate the opportunity for cultural diffusion.

The linguistic distance of 0.88 indicates that two African languages in this sample have, on average, 12% of linguistic features in common. While our distance method seems appropriate for evaluating general relative

differences in languages, it exaggerates the differences, in particular, those between languages of different phyla, which are assigned a distance of 1.0 and a similarity score of 0. Most of the distance scores were based upon languages from different phyla, and this contributed to relatively high linguistic distances. If Swadesh or similar word lists were available for each language, the measure would be more precise. Even languages from different phyla are likely to have some cognates.

Tables 4–6 summarize the four distance measures for linguistic phyla, natural environments, and modes of subsistence for the 36 ethnic groups. (The clustering index is not listed because it is not linked to a specific ethnic group.)

Table 4 shows that the Niger-Kordofanian ethnic groups are near the mean for all measures but tend to be closer genetically than the ethnic groups in the other phyla. The Afro-Asiatic ethnic groups are slightly more heterogeneous in genes and culture than ethnic groups in the other three phyla. Khoisan-speakers have more in common culturally than do Niger-Kordofanian- and Afro-Asiatic-speakers. The Nilo-Saharan cultures in this study are closer genetically and culturally than those of other linguistic groups. While it is possible that this is because they are somewhat closer geographically, on average, it is more likely to be a result of the relatively recent emergence of this group. The fact that the Sahara is a relatively recent desert and the genes, languages, and cultures in this group show low variance makes this especially likely.

Table 5 suggests that ecology has little influence on any of these measures. Cultural ecologists might predict that cultures that share similar natural ecologies should be culturally similar, but no pattern emerges from these admittedly limited data. Table 6 examines the three

TABLE 4
Genetic, Geographic, and Cultural Distances for Cultures in the Same Language Phylum

	Niger-Kordofanian			Khoisan			Nilo-Saharan			Afro-Asiatic		
	n	Mean	S.D.	*n*	Mean	S.D.	*n*	Mean	S.D.	*n*	Mean	S.D.
Genetic distance	18	0.020	0.015	4	0.032	0.018	7	0.013	0.006	7	0.054	0.045
Geographic distance (km)	18	3,210	1,837	4	1,940	1,181	7	1,218	610	7	2,881	1,472
Cultural distance	18	0.587	0.135	4	0.483	0.140	7	0.456	0.121	7	0.684	0.087

TABLE 5
Genetic, Geographic, Cultural, and Linguistic Distances for Cultures in Similar Natural Environments

	Sahel Semidesert			Wet Savannah			Tropical Forest		
	n	Mean	S.D.	*n*	Mean	S.D.	*n*	Mean	S.D.
Genetic distance	12	0.039	0.039	18	0.037	0.0551	6	0.023	0.016
Geographic distance	12	3,734	1,795	18	2,889	1,734	6	2,431	1,214
Cultural distance	12	0.591	0.118	18	0.540	0.126	6	0.663	0.118
Linguistic distance	12	0.891	0.298	18	0.805	0.325	6	0.791	0.282

TABLE 6
Genetic, Geographic, Cultural, and Linguistic Distances for Three Modes of Production

	Hunter-Gatherers			Farmers			Pastoralists		
	n	Mean	S.D.	n	Mean	S.D.	n	Mean	S.D.
Genetic distance	3	0.036	0.015	23	0.029	0.044	10	0.047	0.045
Geographic distance	3	1,939	871	23	3,267	1,705	10	3,341	1,618
Cultural distance	3	0.297	0.067	23	0.562	0.115	10	0.569	0.103
Linguistic distance	3	0.889	0.192	23	0.793	0.296	10	0.914	0.212

modes of production among the groups. The only pattern to emerge is that the three hunter-gatherer groups (San, Mbuti, and Hadza) are the most likely to share many elements of culture.

Explanatory models. The determination of which seme fit a particular explanatory model was based upon z-scores for genetic distance, linguistic distance, and the clustering index. The z-scores provide a measure of how different the mean score for a particular seme is from the overall mean and also indicate the direction of the difference. A negative z-score indicates that the cultures are genetically or linguistically close, while a positive z-score indicates that they are distant in relation to the overall mean distance. A negative z-score for the clustering index means that the cultures that share the seme are relatively distant from each other, while a positive z-score means that they are more clustered. The criteria for determining the fit between a seme and an explanatory model were as follows: (1) If two or three z-scores were below 0.5, no fit could be determined; (2) if two of the three z-scores were above 0.5 it was considered a trend; (3) if one of the z-scores was greater than 1.0 and another greater than 0.5 it was considered a pattern; and (4) if two z-scores were above 1.0 and the third above 0.6 it was considered a strong pattern. A z-score of 0.5 was selected as the minimum because about 70% of the other seme averages would be below or above the overall mean.

It was not possible to discern an explanatory model for 35 semes (32%), and 29 of the semes (27%) had two potential explanatory models because one of the distance measures or the clustering index did not reach 0.5. We were able to identify a primary explanatory model for 45 (41%) of the semes in this study. Given the complex nature of cultural processes, it is not surprising that semes are influenced by several mechanisms and models.

Table 7 lists the semes that fit a particular model, and table 8 summarizes the data by seme category. The demic-diffusion model explained the greatest number of semes (20) and was especially important for explaining kinship, family, and community semes. The data are consistent with the results of recent studies (Guglielmino et al. 1995, Pocklington 1996, Burton et al. 1996, and Jones 1999) indicating that kinship and social organization in Africa and other culture areas reflect the expansion of groups with particular kinds of kinship and social organization. The semes explained by demic diffusion and represented by the greatest number of cultures

are often thought of as classic features of sub-Saharan African social structure: independent polygynous families with wives in separate dwellings, no marriage with first or second cousins, clan-based neighborhoods, and shifting cultivation (i.e., horticulture). The demic-diffusion model was also particularly important for explaining political stratification above the community. The data indicate that political complexity in Africa is primarily due to expansion of particular peoples rather than cultural diffusion or local adaptation.

Cultural diffusion explained 12 semes and was especially useful for explaining the distribution of house construction and the postpartum sex taboo. Since the clustering index is relatively high for these semes, it is also possible that the availability of particular materials in a local ecology may influence the seme.

Semes that have multiple confounds are equally distributed over all six seme categories. These semes could be a later stage of demic diffusion in that groups that slowly expanded, shared semes, and continued to live in proximity to one another or groups that had always lived next to each other may have frequently intermarried and shared semes. Matrilineal clans are a good example of this pattern, as there is a well-known "matrilineal belt" across south-central Africa, but we are unable to determine from these data whether the distribution of matrilineal clans is due to the expansion of a group with matrilineal descent or to the development of this descent system by one group and its gradual incorporation into the cultural systems of neighbors, possibly in order to marry into the group.

Semes linked to local adaptation are particularly interesting because they are the aspects of culture that Steward (1955) was trying to understand with his concept of "multilinear evolution." The four semes listed appear to be variations of demically diffused semes. Particular natural and social conditions have led to the independent development of small (versus large) extended families, the democratic (versus hereditary) election of a headman, class elites based upon their control of scarce resources (versus hereditary classes), and male circumcision in late childhood (versus adolescence).

Table 9 examines the means of genetic and linguistic distances and the clustering indexes of the 45 semes that fit into only one explanatory model. As expected, they fit the patterns described in table 2. The linguistic distances between two groups do not help to distinguish

TABLE 7
Semes and Explanatory Models

Number of Cultures Sharing Seme	Description of Seme and Model	Seme Category
	Demic Diffusion	
3	Bride service	KIN
6	Large extended families	KIN
12	Independent polygynous families, wives with separate rooms	KIN
10	Agamous communities	KIN
11	Exogamous clan communities	KIN
15	No marriage with first or second cousins	KIN
3	Inheritance of real property: to children, sons more	KIN
3	Inheritance of movable property: patrilineal heirs over sons	KIN
5	Inheritance of movable property: to children, sons more	KIN
24	Level of community organization: clan neighborhoods	KIN
4	House making: m + f different tasks, equal participation	SEX
8	Fishing: men only	SEX
5	Fishing: both genders participate, men do more	SEX
4	House wall material: wattle or mats	HOUSE
3	Slavery	STRAT
9	Hierarchy above community, stateless	STRAT
11	Hierarchy above community, petty chiefdom	STRAT
11	Hierarchy above community, small state	STRAT
18	Shifting cultivation	SUBS
7	Premarital sex prohibited but weakly sanctioned	VAR
	Cultural Diffusion	
3	Inheritance of movable property: matrilineal, to sister's son	KIN
3	Level of community organization: villages	KIN
5	House ground plan: rectangular	HOUSE
12	House wall material: walls indistinguishable from roof	HOUSE
3	House roof shape: flat	HOUSE
3	House roof shape: gabled	HOUSE
3	House roof material: earth or turf	HOUSE
7	Agriculture: m + f equal participation, no task differences	SEX
3	Weaving: m + f different tasks, equal participation	STRAT
8	Intensive agriculture	SUBS
5	Postpartum sex taboo, 1–6 months	VAR
8	Postpartum sex taboo, 1–2 years	VAR
	Multiple Confounds	
5	Matrilineal clans	KIN
6	Duolateral cross-cousin marriage	KIN
8	Iroquois kin terms for cousins	KIN
9	House making: men only	HOUSE
4	House roof shape: beehive with pointed peak	HOUSE
5	Boat making: men only	SEX
11	Agriculture: both genders participate, women do more	SEX
6	Weaving: men only	STRAT
11	High god: not concerned with human affairs	VAR

TABLE 7
(*Continued*)

Number of Cultures Sharing Seme	Description of Seme and Model	Seme Category
	Local Adaptation	
9	Small extended families	KIN
3	Headman succession: nonhereditary, through election or consensus	KIN
3	Elite stratification; elite control scarce resources, land	STRAT
7	Circumcision, in late childhood	VAR

NOTE: KIN, kinship, family, and community; SEX, sexual division of labor; HOUSE, house construction; STRAT, social stratification; SUBS, subsistence and settlement; VAR, various.

demic from cultural diffusion; genetic distance and the clustering index are better predictors for these two models. All three measures are important for understanding and predicting the other two explanatory models.

Table 10 examines the relationships between genetic distances, linguistic distances, and the clustering indexes. Significant relationships exist between language and culture, genes and culture, and language and the clustering index. The relationship between genes and language is high but does not reach significance ($p = .09$). Cultural anthropologists often play down the relationship between language and culture because they can always point to instances in which they clearly do not go together (e.g., Bantu-speaking foragers and farmers in Central Africa have dramatically different cultures). While there are several exceptions, these admittedly limited data indicate a significant relationship between language and culture in Africa.

Cultural anthropologists argue even more strongly against a relationship between genes and culture, but again these data indicate otherwise. We hope to have made it clear why semes and genes may coincide: It is *not* because semes are hard-wired to biology but because both are affected by the conservatism of vertical transmission.

The relationship between language and the clustering index indicates that as the proximity between two cultures increases the likelihood that they speak similar languages increases. This is not surprising, because most linguistic families and branches tend to be geographically clustered. While cultural diffusion may explain some cases, demic diffusion (e.g., expansion of Bantu- or Nilotic-speaking peoples) is more likely to explain the clustering of African language families.

This study has provided limited data on the relationship between semes and natural environments. As mentioned above, the natural environment is likely to confound cultural-diffusion semes because peoples that live next to each other may share semes as well as natural environments. Ecology may also confound demic-diffusion semes because people originating in one natural en-

TABLE 8
Summary of Explanatory Models by Seme Category

Seme Category	Explanatory Models				
	Demic Diffusion	Cultural Diffusion	Local Adaptation	Multiple Confounds	Total
Kinship, family, and community	10	2	2	3	17
Sexual division of labor	3	1	0	2	6
House construction	1	5	0	2	8
Social stratification	4	1	1	1	7
Subsistence and settlement	1	1	0	0	2
Various	1	2	1	1	6
Total	20	12	4	9	45

vironment may move to a new location with a similar ecology. Elsewhere we have found (Guglielmino et al. 1995) that semes that fit the demic-diffusion model were much less likely to be influenced by ecology than semes that fit the cultural-diffusion model (6 of 20 semes under demic model, 9 of 12 semes under cultural diffusion; chi square = 6.11, 1 d.f., $p < .01$).

DISCUSSION AND CONCLUSION

In summary, the use of genetic, linguistic, and geographic data has provided a better understanding of cultural diversity in Africa. The seme analysis has indicated that (1) demic diffusion is important for understanding the distribution of semes in the categories of kinship, family, and community and political stratification; (2) cultural diffusion is particularly influential in the distribution of house construction and postpartum sex taboo semes; (3) natural and social environments appear to have led to local adaptations and development of small extended families, the democratic election of a headman, class elites based upon their control of scarce resources, and male circumcision in late childhood; and (4) significant relationships exist between language and culture, genes and culture, and language and the clustering index.

We have been cautious in interpreting these data because our sample is small. In particular, we have limited interpretation of specific semes because of the relatively small numbers of cultures involved. The size and quality of the genetic database is improving, and we hope to conduct more precise studies in the future. Murdock's cross-cultural data have been questioned, but some have recently taken the time to check, extend, and improve upon this database (Gray 1999). It would be preferable to utilize emically defined semes, such as myths or beliefs regarding sorcery, and to conduct the study in the field rather than relying on the codes of others, but field studies of this type have not been conducted. Also, semes are not always encoded in language; some semes are experienced directly in social interactions and daily activities. Consequently, it may be necessary to define some semes etically.

Kinship and family semes are very conservative by comparison with other semes, and their distribution in Africa (Guglielmino et al. 1995, Pocklington 1996) and other parts of the world (Burton et al. 1996, Jones 1999) appears to be primarily the result of demic diffusion. The conservation is due, in part, to both vertical transmission and group effect. These semes are often transmitted and acquired at an early age and become "market traits" (e.g., ethnic clothing styles [Boyd and Richerson 1985]) that help an individual distinguish in- and out-groups. Demic diffusion and the associated mechanisms of transmission call into question the anthropological effort to demon-

TABLE 9
Mean Genetic Distance, Linguistic Distance, and Clustering Index of Semes That Fit One Explanatory Model

Explanatory Model	n	Genetic Distance	Linguistic Distance	Clustering Index
Demic diffusion	20	2.0 (close)	83.7 (distant)	174.2 (low)
Cultural diffusion	12	4.4 (distant)	84.7 (distant)	610.7 (high)
Multiple confounds	9	1.5 (close)	59.8 (close)	495.9 (high)
Local adaptation	4	7.0 (distant)	93.7 (distant)	218.2 (low)

TABLE 10
Relationship between Distance Measures and Clustering Index for 109 Semes

	Genetic Distance	Linguistic Distance	Cultural Distance
Genetic distance	–	–	–
Linguistic distance	0.165	–	–
Cultural distance	0.184[a]	0.442[c]	–
Clustering index	−0.023	−0.252[b]	−0.013

[a]$p < 0.05$.
[b]$p < 0.01$.
[c]$p < 0.01$.

strate that many of these semes are adaptive or functional in a particular ecology. While more precise studies of the relationships between semes and ecology are needed, this and our previous study indicate that the impact of ecology is limited.

Cultural diffusion and horizontal transmission are of tremendous importance in today's global economy, in part because of new technologies that allow rapid dissemination of semes. Most ethnic groups in this study did not have these technologies at the time they were described; consequently, this study suggests a more limited role for cultural diffusion.

Semes usually do not evolve as discrete units; they often evolve as part of a culture complex or culture core. The models, mechanisms, and methods described in this paper can help evaluate the culture cores or complexes proposed for Africa (e.g., Vansina 1990, Goody 1976), but this would take considerably more analysis. Archaeologists have argued that functional features of artifacts are adaptive whereas stylistic features are neutral and more appropriate for evaluating cultural evolution. What is stylistic and what is functional is not always clear, and the methods used here may be helpful for making this distinction in a particular region. We hope to have provided the theoretical, conceptual, and methodological tools that will allow others to examine the relationships between language, culture, and genes in any region of the world.

References Cited

BOAS, F. Editor. 1938. *General anthropology*. Boston: D. C. Heath.

BOYD, R. AND P. J. RICHERSON. 1985. *Culture and the evolutionary process*. Chicago: University of Chicago Press.

BURTON, M. L., C. C. MOORE, J. W. M. WHITING, AND A. K. ROMNEY. 1996. Regions based on social structure. CURRENT ANTHROPOLOGY 37:87–123.

CAVALLI-SFORZA, L. L., P. MENOZZI, AND A. PIAZZA. 1993. Demic expansions and human evolution. *Science* 259: 639–46.

CAVALLI-SFORZA, L. L., AND M. W. FELDMAN. 1973. Models for cultural inheritance. *Theoretical Population Biology* 4:42–55.

———. 1976. Cultural and biological evolutionary processes: Selection for a trait under complex transmission. *Theoretical Population Biology* 4:42–55.

———. 1981. *Cultural transmission and evolution*. Princeton: Princeton University Press.

CHEN, H., R. R. SOKAL, AND M. RUHLEN. 1995. Worldwide analysis of genetic and linguistic relationships of human populations. *Human Biology* 67:595–612.

DAWKINS, R. 1976. *The selfish gene*. New York: Oxford University Press.

DRIVER, H. E., AND A. L. KROEBER. 1932. Quantitative expression of cultural relationships. *University of California Publications in American Archaeology and Ethnology* 31: 211–56.

DURHAM, W. 1991. *Coevolution*. Stanford: Stanford University Press.

GOODY, J. 1976. *Production and reproduction*. Cambridge: Cambridge University Press.

GRAY, J. P. 1999. A corrected ethnographic atlas. *World Cultures* 10:24–136.

GRIMES, BARBARA. Editor. 1978. *Ethnologue*. Huntington Beach, Calif.: SIL International.

GUGLIELMINO, C. R., C. VIGANOTTI, B. HEWLETT, AND L. L. CAVALLI-SFORZA. 1995. Cultural variation in Africa: Role of mechanisms of transmission and adaptation. *Proceedings of the National Academy of Sciences, U.S.A.* 92:7585–89.

HENRICH, J., AND R. BOYD. 1998. The evolution of conformist transmission and the emergence of between-group differences. *Evolution and Human Behavior* 19:215–42.

HEWLETT, B. S., AND M. E. LAMB. n.d. "Integrating evolution, culture, and developmental psychology: Explaining caregiver-infant proximity and responsiveness in Central Africa and the United States of America," in *Between biology and culture: Perspectives on ontogenetic development*. Edited by H. Keller, Y. Poortinga, and A. Schölmerich. Cambridge: Cambridge University Press. In press.

INGMAN, M., H. KAESSMANN, S. PAABO, AND U. GYLLENSTEN. 2000. Mitochondrial genome variation and the origin of modern humans. *Nature* 408:708–12.

JONES, D. 1999. Culture areas as a product of ancient demic expansions. Paper delivered at annual meeting of the Human Behavior and Evolution Society, Salt Lake City.

KROEBER, A. L. 1923. *Anthropology*. New York: Harcourt, Brace.

MURDOCK, G. P. 1967. *Ethnographic atlas*. Pittsburgh: University of Pittsburgh Press.

NEI, M., AND A. K. ROYCHOUDHURY. 1972. Genetic differences between Caucasian, Negro, and Japanese populations. *Science* 177:434–35.

POCKLINGTON, R. 1996. Population genetics and cultural history. M.A. thesis, Simon Frazer University, Burnaby, B.C.

RUHLEN, MERRITT. 1991. *A guide to the world's languages*. Stanford: Stanford University Press.

SINNOTT, R. W. 1984. Virtues of the haversine. *Sky and Telescope* 68:159.

STEWARD, JULIAN. 1955. *Theory of culture change*. Urbana: University of Illinois Press.

UNDERHILL, P. A., S. PEIDON, A. A. LIN, L. JIN, G. PASSARINO, W. H. YANG, E. KAUFFMAN, B. BONNÉ-TAMIR, J. BERTRANPETIT, P. FRANCALACCI, M. IBRAHIM, R. JENKINS, J. R. KIDD, S. Q. MEHDI, M. T. SEIELSTAD, R. S. WELLS, A. PIAZZA, R. W. DAVIS, M. W. FELDMAN, L. L. CAVALLI-SFORZA, AND P. J. OEFNER. 2000. Y chromosome sequence variation and the history of human populations. *Nature Genetics* 26:358–61.

VANSINA, J. 1990. *Paths in the rainforest*. Madison: University of Wisconsin Press.

The Institutional Maintenance of Celibacy[1]

HECTOR QIRKO
Department of Anthropology, University of Tennessee, 250 South Stadium Hall, Knoxville, Tenn. 37996-0720, U.S.A. (hqirko@utk.edu). 7 IX 01

From a Darwinian perspective, celibacy is a problem worthy of particular attention. After all, reproduction is