MORPHOLOGICAL VARIATION OF THE LATE PRECONTACT AND CONTACT PERIOD GUALE

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ABSTRACT

Griffin, Mark C. Ph.D., Purdue University, August 1993. Morphological Variation of the Late Precontact and Contact Period Guale. Major Professor: Clark Spencer Larsen.

The primary purpose of this study is to estimate biological distances among a time-successive series of Native American skeletal samples from the southeastern U.S. Atlantic coastal region (Georgia and Florida) using dental and cranial morphological traits as the principal comparative features. Biological distance, in the sense used here, refers to a statistical expression of morphological similarity between populations which is derived from genetically controlled traits.

The population distances are estimated here in order to (1) delineate the biological relationship between the three primary (Guale) skeletal samples, (2) explore the relationship between these three samples and other biologically or linguistically related groups, (3) compare all of these samples with biologically distinct and geographically distant populations, and (4) compare the five southeast Amerindian samples to Turner's Sinodont dental classification (Turner 1990). These comparisons are

important because (1) no investigator has studied the biological relationships between Native American groups in this geographic area, (2) prior research has indicated that the Guale population samples used here underwent profound biological changes after European contact, but it is unclear the extent to which these changes represent in-migration of other populations, (3) it is unclear what the biological relationships are between the Guale and other Southeast Amerindian groups, and (4) it is unknown how Native American groups from the southeastern U.S. compare to Turner's Sinodont division of the Mongoloid dental classification because he has not included populations from this region in his analyses.

The results of this study indicate that the Guale of the southeast U.S. were a particularly diverse group in terms of dental and cranial morphology. The degree of biological dissimilarity between some of the Guale samples cannot be fully explained in terms of genetic drift. Other mechanisms of biological change are suggested. In comparison to other Amerindian groups and Asian Sinodont population samples, the American southeast populations separate as a distinct group. Not unexpectedly, they are more similar to north Amerindian samples than to the Asian Sinodont samples.

CHAPTER I - INTRODUCTION

The Problem

The primary purpose of this study is to estimate biological distances among a time-successive series of Native American skeletal samples from the southeastern United States Atlantic coastal region (Georgia and Florida). Dental and cranial morphological traits are used as the principal comparative features. Biological distance, in the sense used here, refers to a statistical expression of morphological similarity between populations which is derived from genetically controlled traits (Ubelaker 1984). Dental (e.g., Haeussler et al. 1989, Lukacs and Hemphill 1991, Nichol 1989, 1990, Sofaer et al. 1986, Townsend et al. 1990, Turner 1986a and b, 1990) and cranial (Dodo 1987, Dodo et al. 1992, Ishida 1990, Katayama 1988, Pietrusewsky 1981, 1984, Saunders and Popovich 1978, Sawyer et al. 1978, Sciulli 1990a) morphological traits have recently been used to assess population affinity and microevolution. Given the extensive archaeological, biocultural, and historic documentation for this area of the southeastern United States (see Larsen 1990), this region provides an ideal test case for addressing issues related to biological distance.

The population distances are estimated here in order to (1) delineate the biological relationship between the three primary (Guale) skeletal samples, (2) explore the relationship between these three samples and other biologically or linguistically related groups, (3) compare all of these samples with biologically distinct and geographically distant populations, and (4) compare the five southeast Amerindian samples to Turner's Sinodont dental classification (Turner 1990).

The primary samples used for this analysis represent Native American populations of the Georgia and Florida coasts, spanning a time period from ca. A.D. 1150 to A.D. 1702. Ethnographic and archaeological data indicate that these Guale population samples are: (1) temporally successive, (2) derived from the same prehistoric population, and (3) represent three distinct periods of cultural history (precontact agricultural: A.D. 1150 - 1550, early postcontact: A.D. 1608 - 1680, and late postcontact: A. D. 1686 - 1702) (Larsen 1982, 1990, Thomas 1987).

The secondary samples are comprised of groups which are culturally and linguistically related to the Guale, and groups which are not culturally related to the Guale (Figure 1). The Amerindian groups from the southeastern United States were selected not only because of their geographical

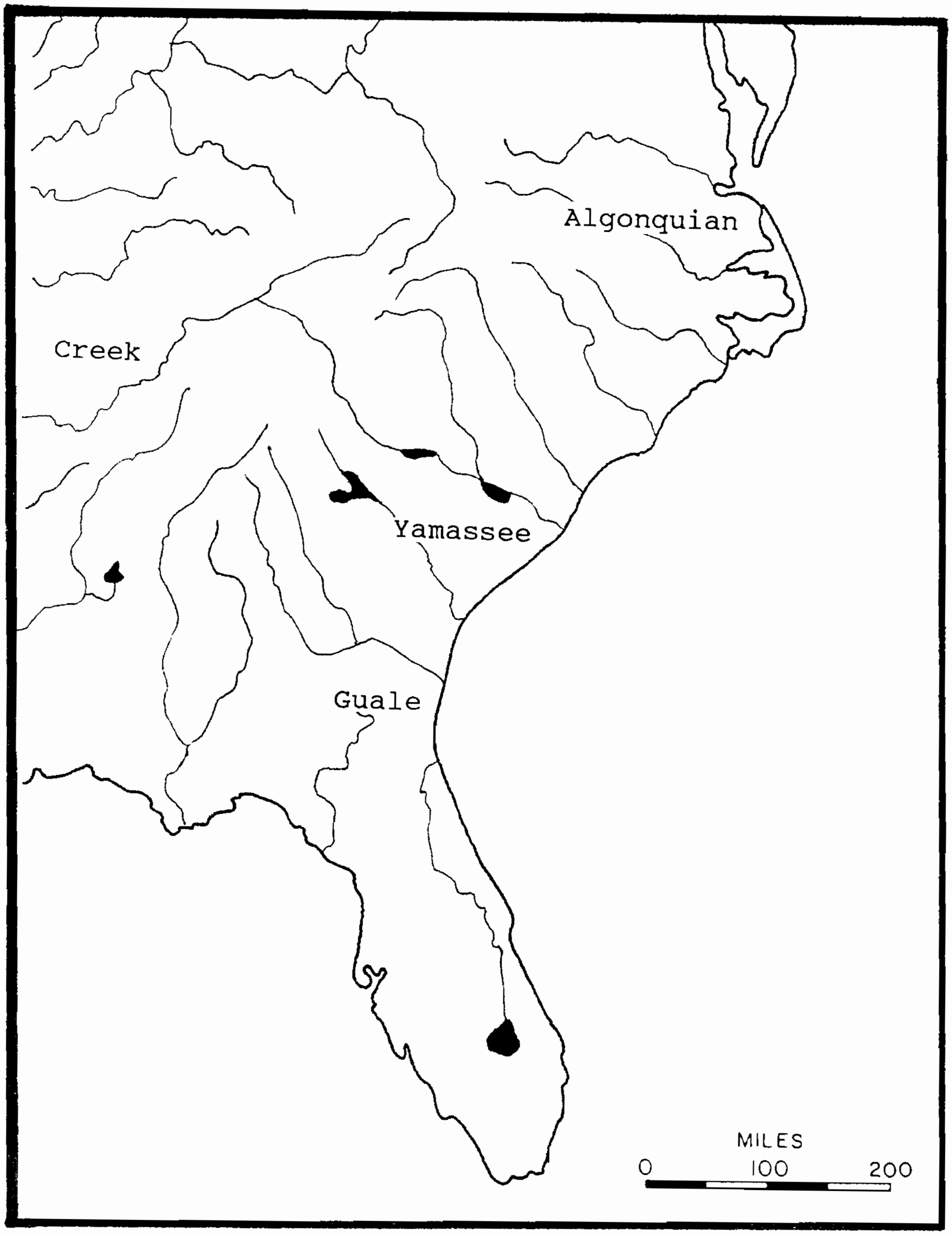

Figure 1. Geographic Location of Southeast Amerindian Population Samples.

(Yamassee, Creek, and Algonquian) and cultural (Yamassee and Creek) affinity to the Guale, but also for their temporal closeness to the late precontact and contact Guale. The Sinodont population samples were chosen for comparison in this study because Turner (1987) asserts that all Amerindians belong to this division of the Mongoloid dental classification, yet no southeast Amerindian groups from this area have been compared to Sinodonts.

Significance

This study is important because it focuses on a series of population samples which (1) are temporally, archaeologically, and spatially well defined, and (2) have been well documented through numerous biocultural studies (Choi 1986, Griffin and Larsen 1989, Harn 1992, Hutchinson 1986, Hutchinson and Larsen 1988, Larsen 1982, 1990, Larsen and Russell 1989, Larsen et al. 1991, 1992, Ruff and Larsen 1990, Russell 1987, Shavit 1988). Recent research using dental and cranial morphological traits has focused on population microdifferentiation (e.g., Dodo 1987, Dodo et al. 1992, Greene 1982, Haeussler 1985, Ishida 1990, Katayama 1988, Lukacs 1983, Pietrusewsky 1981, 1984, Richards and Telfer 1979, Saunders and Popovich 1978, Sawyer et al. 1978, Sciulli 1990a, Sofaer et al. 1986, Turner 1985, 1987a and b). That is, dental and cranial traits in recent research have been used to differentiate between local populations rather than between large aggregate geographically defined populations (e.g., between groups of Amerindians rather than between Amerindians and Europeans). The present study is also focused on population microdifferentiation. No biological distance studies have been done for this part of the southeastern United States, and the actual biological relationships between groups in the area are virtually unknown. The Guale population samples used here reportedly represent a more or less genetically continuous group, but this assumption has never been tested with a biological analysis.

Although extensive research has been done on the biological adaptation of the Guale (e.g., Griffin and Larsen 1989, Hutchinson 1986, Hutchinson and Larsen 1988, Larsen 1990, Ruff and Larsen 1989, Larsen et al. 1990), only limited study has been done on the biological relationship between the Guale from different time periods or their relationship to other populations. However, a pilot study was conducted to delineate some of these relationships (Griffin 1989). The primary focus of the pilot study was to establish the genetic affinity between two Guale skeletal population samples (*Santa Catalina de Guale* and *Santa Catalina de Guale de Santa Maria*) and to assess the population distance between them. The results from the examination of trait frequencies, discriminant function analysis, and other multivariate procedures indicates that the population samples from *Santa Catalina de Guale* and *Santa Catalina de Guale de Santa Maria* are almost certainly derived from the same deme. Although there were statistically significant ($p<0.05$) differences in the frequency of expression for some of the dental traits, these can likely be explained by genetic drift. As for the actual population distance between the samples, the mean measures of divergence were calculated and compared with other unrelated Native American groups from the southwest. As expected, these distances revealed that the distance between the Guale samples and the southwest samples was greater than that between the two Guale samples. These statistics will become more meaningful with comparison to the other southeast Amerindian samples in this study. Principle component analysis elucidated a number of traits which will be particularly useful for the present studies.

The three Guale temporal periods included in the present study (late precontact, early contact, and late contact) are characterized by a series of profound changes in subsistence strategies and general lifeway (Larsen 1982, 1990). Prior to European contact, the period of transition from a hunting and gathering mode of subsistence to an agricultural one was reportedly accompanied by increasing levels of biological stress (Larsen 1982, 1990). The biological stress posed by this dramatic change in lifeway may have been further exacerbated by extensive European contact in the two postcontact periods (Larsen et al. 1990). Although the data are more problematic for the postcontact Guale, the evidence indicates a further overall decline in health after European contact (Larsen et al. 1990). Hutchinson (1986) concludes that the early contact population at *Santa Catalina de Guale* was under a greater amount of stress than the earlier, precontact Guale. Hutchinson surmises that this stress very likely resulted from (1) an increase in aggregation of the population, precipitating the rapid spread of European introduced diseases; and (2) the increased focus on maize as a primary constituent of the diet after the arrival of Europeans, and the concomitant decline in nutrition. Evidence from the analysis of the frequency of carious lesions and the patterns of osteoarthritis indicates that the later contact period Guale at *Santa Catalina de Guale de Santa Maria* were under even more stress (Shavit 1988, Griffin and Larsen 1989). Other studies on the precontact Guale have examined demography, growth disruption, pathology, morphology, and size. These examinations of Guale skeletal remains from the precontact and postcontact Georgia coast also suggest a pattern of declining health after European contact. Evidence for this decline comes primarily from observation of the prevalence of dental caries (Larsen 1982, Shavit

1988, Larsen et al. 1991), dental enamel hypoplasias (Hutchinson 1986, Hutchinson and Larsen 1988), infection (Larsen 1984), and degenerative joint disease (Griffin and Larsen 1989). Additional evidence is provided by the examination of demography (Larsen 1982, Russell 1987, Larsen and Russell 1989), postcranial structural morphology (Ruff and Larsen 1990), and bone chemistry (Schoeninger et al. 1990). The present study will, in part, test for the possibility that these changes represent the in-migration of non-Guale populations. Dissimilar trait frequencies and population distance estimates among the Guale samples may indicate such an in-migration.

CHAPTER II - MATERIALS

Introduction

The three primary population samples used in this study represent the pre- and postcontact Guale of coastal Georgia and Florida. The Guale skeletal samples examined here were recovered from three sites: (1) Irene Mound in Chatham County, Georgia, (2) *Santa Catalina de Guale* on St. Catherines Island, Georgia (hereafter referred to as Santa Catalina), and (3) *Santa Catalina de Guale de Santa Maria* on Amelia Island, Florida (hereafter referred to as Santa Maria).

The secondary samples used for comparison with the Guale consist of population samples from the same geographic region (southeastern U.S.) and from regions which fall into Turner's Sinodont classification (Turner 1987a). The southeast U.S. samples were recovered from four sites: (1) *Santa Maria de Yamassee* on Amelia Island, Florida (hereafter referred to as SMdY), (2) the Baum site in Currituck County, North Carolina, (3) the Piggot site in Carteret County, North Carolina, and (4) the Ledford Island site in east Tennessee. The Sinodont samples represent recent populations from insular and mainland Asia and are described by Turner (1987a).

This combination of samples will provide a broad comparative view of the Guale from a regional and pan-geographic perspective. This broad perspective will help define the biological relationship of the Guale (1) specifically with some of the major Amerindian linguistic groups from the Southeastern United States, (2) generally with other Amerindian groups from North America, and (3) in general with Turner’s Sinodont classification. The population samples used in this study are summarized in Table 1. The ethnohistoric and biocultural contexts of these population samples are briefly described in this chapter.

Primary Population Samples

Guale

Humans have occupied the Georgia coast for some 4000 years prior to the arrival of Europeans (Thomas et al. 1978, Larsen 1982). The Guale population samples under consideration here occupied the mid-section of the Georgia Bight (Larsen et al. 1992). The Georgia Bight, a large continental embayment extending from Cape Hatteras, North Carolina, to Cape Canaveral, Florida, is dominated by a

Table 1. Summary of Population Samples

Site	n	Temporal Period	References
Guale			
Irene Mound	248	A.D. 1150-1550	Caldwell and McCann 1941; Hulse 1941; Larsen 1982; Anderson 1990a
Santa Catalina de Guale	431	A.D. 1608-1680	Thomas 1987; Larsen 1990; Larsen et al. 1990
Santa Catalina de Guale de Santa Maria	112	A.D. 1686-1702	Saunders 1988; Larsen 1991
Yamassee			
Santa Maria de Yamassee	105	A.D. 1675-1683	Saunders 1988
Carolina Algonquian			
Baum, Burial 1	55	A.D. 1315±70	Phelps 1980a, b
Baum, Burial 5	33	A.D. 1315±70	Phelps 1980a, b
Baum, Burial 7	27	A.D. 1425±70	Phelps 1980a, b
Piggot	40	A.D. 1230±65	Phelps 1980a, b
Creek			
Ledford Island	456	≈A.D. 1400-1600	Lewis and Kneberg 1945; Boyd 1984; Sullivan 1986
Sinodont			
NE Siberia	264	recent	Turner 1987a
Amur	106	recent	Turner 1987a
Lake Baikal	32	recent	Turner 1987a
N China-Mongolia	514	recent	Turner 1987a
Japan	522	recent	Turner 1987a
Hong Kong	319	recent	Turner 1987a
S China	124	recent	Turner 1987a

large complex of barrier and marsh islands that lie seaward of an extensive estuarine system (Frey and Howard 1986, Reitz 1988). The islands of the Georgia Bight are barriers, large constructional landforms as much as 1 kilometer wide and 100 meters high which receive sand from offshore and longshore drifting (Bloom 1978). Borehole testing has demonstrated that this barrier system has been in place for the last 6000 years and originated during postglacial submergence, not during coastal emergence as was previously maintained (Otvos 1972).

The early inhabitants of the Georgia coast were hunter-gatherers whose seasonal migrations followed the availability of food resources. Due to the abundance of marine resources in this type of estuarine habitat, these foodstuffs represented a large portion of the native diet. In the mid-1500s, after brief contact with French and Spanish explorers earlier in the century, the inhabitants of the Georgia coast came under an extensive period of contact with European colonists. The mid-1500s marked the beginning of the ill-fated Spanish mission effort in *La Florida*. *La Florida*, as used here, follows the definition outlined by Thomas (1987) for the First Spanish Period of St. Augustine (1566-1763), and so encompasses parts of the modern states of Georgia and South Carolina, in addition to most of Florida. European contact had a tremendous impact on the native inhabitants of this area, especially in terms of the native subsistence strategy. The changes brought about by this early contact were to spell the virtual extinction of native American populations and cultural traditions of the Georgia coast.

The term *Guale* refers to a geographic region and a Muskhogean speaking aboriginal group. From 2200 B.C. to A.D. 1684, the Guale occupied areas of coastal Florida and Georgia from the mouth of the Savannah River to the mouth of the St. Marys River (Jones 1978). The Guale Indians were named by the Spanish for the chiefdom centered at the village of the same name on St. Catherines Island, Georgia. The Franciscan mission on St. Catherines Island was thus christened *Santa Catalina de Guale*.

Much of the early archaeological research on the Georgia coast was concerned with constructing chronological sequences based on ceramic types (see Table 2). Later research focused on the reconstruction of past lifeways by the examination of subsistence patterns (Reitz 1982a, 1982b, 1985, 1988, Reitz and Scarry 1985, Reitz and Quitmyer 1988, Quitmyer et al. 1985), settlement patterns (Crook 1978, 1984, Thomas 1987, Wood et al. 1989), and ethnohistoric data (Bushnell 1987, Hann 1986, 1988, Jones 1978, Loucks 1979, Milanich and Proctor 1978).

Table 2. Cultural Sequence for the Georgia Coast*

Period	Ceramic Types	Dates
		A.D. 1700
Altamaha	Altamaha-Line Block, Incised, Plain, Check Stamped, Red Filmed	
		A.D. 1550
Irene	Irene-Incised, Complicated Stamped, Burnished Plain, Plain, Corn Cob Impressed	
		A.D. 1330
Savannah	Savannah-Complicated Stamped, Check Stamped, Fine cord Marked, Plain, Corn Cob Roughened	
		A.D. 1150
St. Catherines	St. Catherines-Plain, Net Marked, Fine Cord Marked, Burnished Plain	
		A.D. 1000
Wilmington	Wilmington-Plain, Burnished, Heavy Cord Marked, Check Stamped, Complicated Stamped	
		A.D. 500
Deptford	Deptford-Complicated Stamped, Cord Marked, Check Stamped, Refuge Simple Stamped, Refuge-Plain	
		400 B.C
Refuge	Deptford-Linear Check Stamped, Check Stamped; Refuge-Plain, Simple Stamped, Dentate Stamped, Punctated, Incised	
		1100 B.C.
St. Simons	St. Simons-Incised and Punctated, Incised, Punctated, Plain	
		2200 B.C.

*after DePratter 1979

Late Precontact Guale

Until about A.D. 1150, the inhabitants of the Georgia coast were primarily hunter-gatherers, with a diet consisting of marine, mammal, and plant foods (Larsen 1990). Reitz (1985) asserts that the Georgia coast has some of the richest marine resources in the world. Accordingly, until about 800 B.C., marine resources constituted a large portion of the native subsistence. In fact, Reitz (1988) has demonstrated from analysis of archaeological faunal remains that fish and shellfish provided most of the dietary protein. Around 800 B.C. a lowering of sea level precipitated a shift in local subsistence strategy to an increased focus on hunting (DePratter 1979). Schoeninger and coworkers (1990), using carbon and nitrogen stable isotopes, have demonstrated a heavy focus on wild plant and animal resources among the Guale for the period prior to the twelfth century A.D. After A.D. 1150, the native subsistence strategy began an irreversible shift to agriculture, although according to Reitz and Scarry (1985), fish still represented a large percentage of the native diet. Stable isotope analysis has confirmed this contention (Schoeninger et al. 1990, Larsen et al. 1992). Fish, along with wild plants and shellfish, probably helped to sustain the Guale during years of failure of the maize crop.

Botanical evidence as well as settlement pattern analysis have indicated the adoption of maize agriculture among the Guale during the twelfth century A.D. This is consistent with changes in subsistence strategy and social organization throughout the eastern United States during this time period (J. Griffin 1967, Steponaitis 1986, Smith 1986, 1989). Concomitant with this apparent shift in subsistence strategy, there appears to have been an increase in cultural complexity and the emergence of some form of chiefdom level of social organization (Anderson 1990a and b). Evidence presented by Anderson (1990a and b) from the Irene period mortuary practices and interment patterns (ca. A.D. 1300) may indicate a transition towards more egalitarian social organization resulting in part from environmental stress (e.g., reduced rainfall, increased warfare). After A.D. 1450, the area surrounding the mouth of the Savannah River was completely abandoned, probably due to social developments and stress factors (Anderson 1990a).

The Guale population sample representing the late precontact period (A.D. 1150-1550) was recovered from the Savannah-Irene period Irene Mound site (9Ch1) located at the mouth of the Savannah River in coastal Georgia (Table 1). The Irene Mound site is located near the Savannah River mouth just south of the confluence with Pipemaker Creek. The site was occupied from ca. A.D. 1150 to 1450.

The Irene Mound site was originally examined by C.B. Moore in 1897 (Caldwell and McCann 1941). The site was later almost completely excavated during a period from September 1937 to January 1940 under the auspices of the Works Progress Administration (Caldwell and McCann 1941). The site consisted of two mounds and an associated village area. Eight construction stages with associated structures were found in the larger of the two mounds, which was approximately 48.8 meters in diameter and 4.7 meters high in 1937 (Anderson 1990a). A low circular burial mound was located to the west of the large mound. The burial mound contained the skeletal remains of 106 individuals.

An apparent mortuary dating to the Irene period was located on a low rise approximately 25 meters south of the primary mound (Anderson 1990a). A semi-subterranean structure inset 30 to 40 centimeters into the ground was in the central part of this complex which was surrounded by two circular pallisade lines. The structure had apparently been destroyed by fire during the site occupation and was subsequently covered with a low sand mound. The immediate area around the mortuary structure and the low mound that covered it was used as a cemetery. The cemetery area was demarcated by two successive circular enclosures measuring 13.7 and 18.3 meters in diameter. The skeletal remains of a total of 267 individuals were recovered from the burial mound, the mortuary area, and the cemetery (Caldwell and McCann 1943, Larsen 1982).

The late precontact period represents a period of subsistence and social change for the Guale. The changes were characterized by the addition of plant domesticates, in particular maize, which was added to the dietary regime of hunting, gathering, and fishing (primarily in estuary and marsh biotopes), as well as shifts in level of social organization (Larsen et al. 1992). The shift from a primarily hunting and gathering mode of subsistence to one incorporating agriculture occasioned a number of pathological and morphological changes in the Guale. Larsen (1982) has demonstrated that not only did the frequency of infectious and noninfectious disease increase after the adoption of agriculture by the Guale, but also the decrease in functional demand on the masticatory and postcranial skeleton resulted in an overall reduction in size and robusticity of the skeleton.

Postcontact Guale

The population samples representing the postcontact Guale (A.D. 1608 - 1702) were recovered from two Spanish mission cemeteries (*Santa Catalina de Guale and Santa Catalina de Guale de Santa Maria*) located respectively on the Georgia and Florida coasts (Table 1). A combined skeletal sample representing 550 individuals were collected from these two cemeteries.

The Guale of coastal Georgia were subject to "a long, intensive period of Spanish colonization" beginning in 1566 (Thomas 1988). By the mid-seventeenth century, *La Florida* had about 70 Franciscans serving approximately 25,000 Indians in 38 missions (Arana and Manucy 1977, Hann 1988, Thomas 1988). The size and scope of the Spanish missions in the Southeast, Thomas points out, was certainly comparable to the Franciscan missions flourishing in California and the Southwest at the same time. By 1680, prompted by the expansion of the Carolina colony southward and the consequent withdrawal of the Spanish to the south, the reduced Guale population was relocated. Only two small villages of Christianized Indians remained outside of St. Augustine by the 1750s. When the Spaniards turned over rule to the British in 1763, the remaining Native American converts fled from Florida as well (Siebert 1940, Deagan 1983).

Santa Catalina de Guale

In the mid- to late-1500s, the Spanish mission efforts in *La Florida* were minimal; only four Franciscan friars were stationed throughout the entire area. By 1597, however, 14 friars were stationed in La Florida and several of these served among the Guale (Geiger 1940). That same year, the Guale staged a major revolt, partly on St. Catherines Island. On St. Catherines Island, the *iglesia* (church) was burnt to the ground and the site abandoned, later to be resettled in 1604.

After the Spanish resettled northern coastal Georgia in the 1600s, they remained its sovereign rulers until 1670 when the English settled at Charles Town, South Carolina (Ross 1926). The area from St. Catherines Island in the north to St. Augustine in the south became known as "the debatable land," a territory of contention between England and Spain that was to remain so until 1763 (Bolton and Ross 1925).

In 1680, seven years after an unsuccessful attempt to attack Charles Town by the Spanish and their establishment of a garrison on St. Catherines Island, the English began a steady southward push down the coast and westward across the Mississippi (Thomas 1988:19). That same year, a British-led force of 300 Yamassee Indians staged an attack on the mission which precipitated its immediate abandonment. At this point, the remaining Guale began a retreat toward the relative safety of St. Augustine. After a brief stay in a refugee camp on Sapelo Island, the Guale from Santa Catalina and Satouche, another Spanish mission located on Sapelo Island, were persuaded to move to Santa Maria on Amelia Island, Florida (Jones 1978, Bushnell 1986, Milanich and Saunders 1986).

Anthropological research on St. Catherines Island has been conducted by the American Museum of Natural History since 1974 (Thomas 1987). Most of the early research was concerned with the excavation and analysis of prehistoric mortuary sites. The archaeological search for the Spanish mission site of *Santa Catalina de Guale* (9Li274) began in 1981 (Thomas 1988). After extensive survey and testing, the remains of several structures were unearthed (see Figure 2 for location of *Santa Catalina de Guale*). Among the structures discovered were a church, kitchen, well, priest's quarters, and infantry barracks.

The church at Santa Catalina was a rectangular structure measuring 20 meters long and 11 meters wide. Three of the church walls were constructed of daub, and the fourth, the facade, was built of wattle and daub (Thomas 1988). During excavations directed by C.S. Larsen from 1982 to 1986, the remains of 431 individuals were recovered from beneath the floor of the nave and the sanctuary within the church. An additional burial was discovered in 1991 (Larsen 1993). The mortuary pattern of the burials conformed to

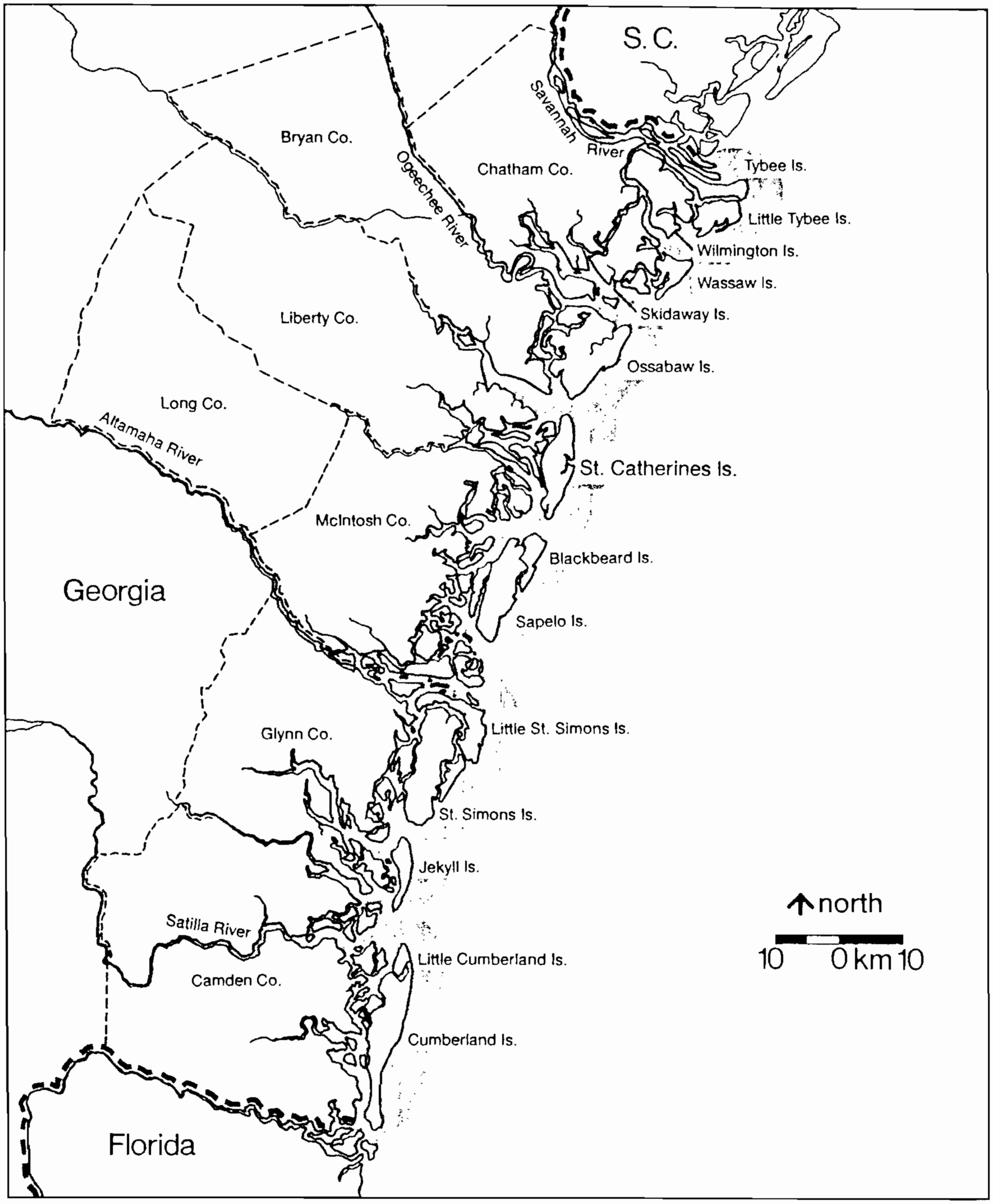

Figure 2. Location of *Santa Catalina de Guale* on St. Catherines Island, Georgia (from Thomas et al. 1978).

that observed at most Spanish mission sites. According to Larsen (1990:20), "one-third of the burials occurred in primary context, buried in a supine position with feet toward the altar and hands across the chest or abdomen" (Figure 3). The rest of the individuals were found scattered and disarticulated in the upper grave fill. These remains probably represent a zone of disturbance created as new interments impacted earlier ones. The cemetery at Santa Catalina produced a huge array of grave goods. The artifacts recovered include majolica plates, projectile points, a chunky stone, a rattlesnake shell gorget, wood and metal crosses, religious medals, mirrors, rings, bells, shroud pins, religious plaques, and tens of thousands of trade beads (Thomas 1988). The quantity and distribution of grave goods indicates a considerable wealth and possibly a social hierarchy at Santa Catalina (Thomas 1988).

Biocultural studies on the Santa Catalina population sample have focused primarily on human adaptation (Hutchinson 1986, Larsen 1990, Ruff and Larsen 1990, Shavit 1988). Preliminary findings indicate that although the native inhabitants must have experienced a great deal of biological stress with the arrival of Europeans, the initial changes were apparently cultural and not biological (Larsen 1990). Research has indicated that there was a greater biological change in the native inhabitants prehistorically

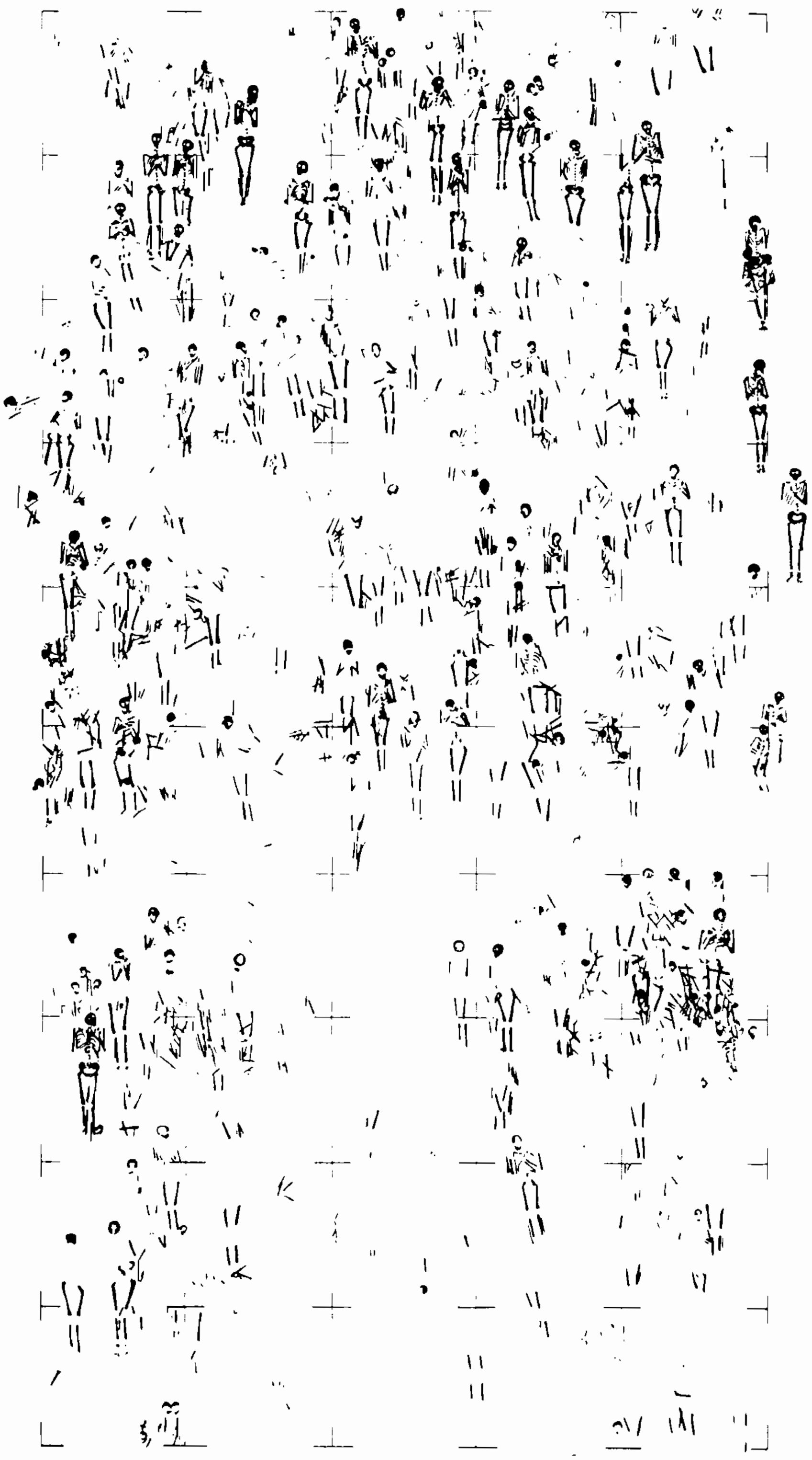

Figure 3. *Santa Catalina de Guale*: Location of Burials (from Larsen 1990).

with the shift to an agricultural subsistence pattern than with the initial contact with Europeans (Hutchinson 1986).

Santa Catalina de Guale de Santa Maria

The island of Santa Maria (Amelia Island) had been the general location of several largely unsuccessful Spanish missions since the early 1600s. The earliest mission, *Santa Maria de la Sena*, was originally located on the mainland, on the banks of the St. Mary's River (Thomas 1987). The later missions were located on the island itself in order to protect the residents from marauding pirates. The missions of Santa Maria were not associated exclusively with the Guale. From 1675-1683, the mission was occupied by the Yamassee, who were distant inland relatives of the Guale (Bushnell 1986). After a bloody raid by English and French pirates in 1683, the Yamassee fled north.

In 1684, Santa Catalina was re-established by the Guale from Santa Catalina and Satouche. Mission *Santa Catalina de Guale de Santa Maria* served the relocated residents from 1686 to 1702 (Figure 4). The 1680s and 1690s were relatively peaceful for the inhabitants of the mission. Even so, supplies were scarce and the Guale became increasingly intolerant of the Spanish demands on them (Bushnell 1986). Between 1702 and 1713, during the War of the Spanish Succession, continued harassment by the British

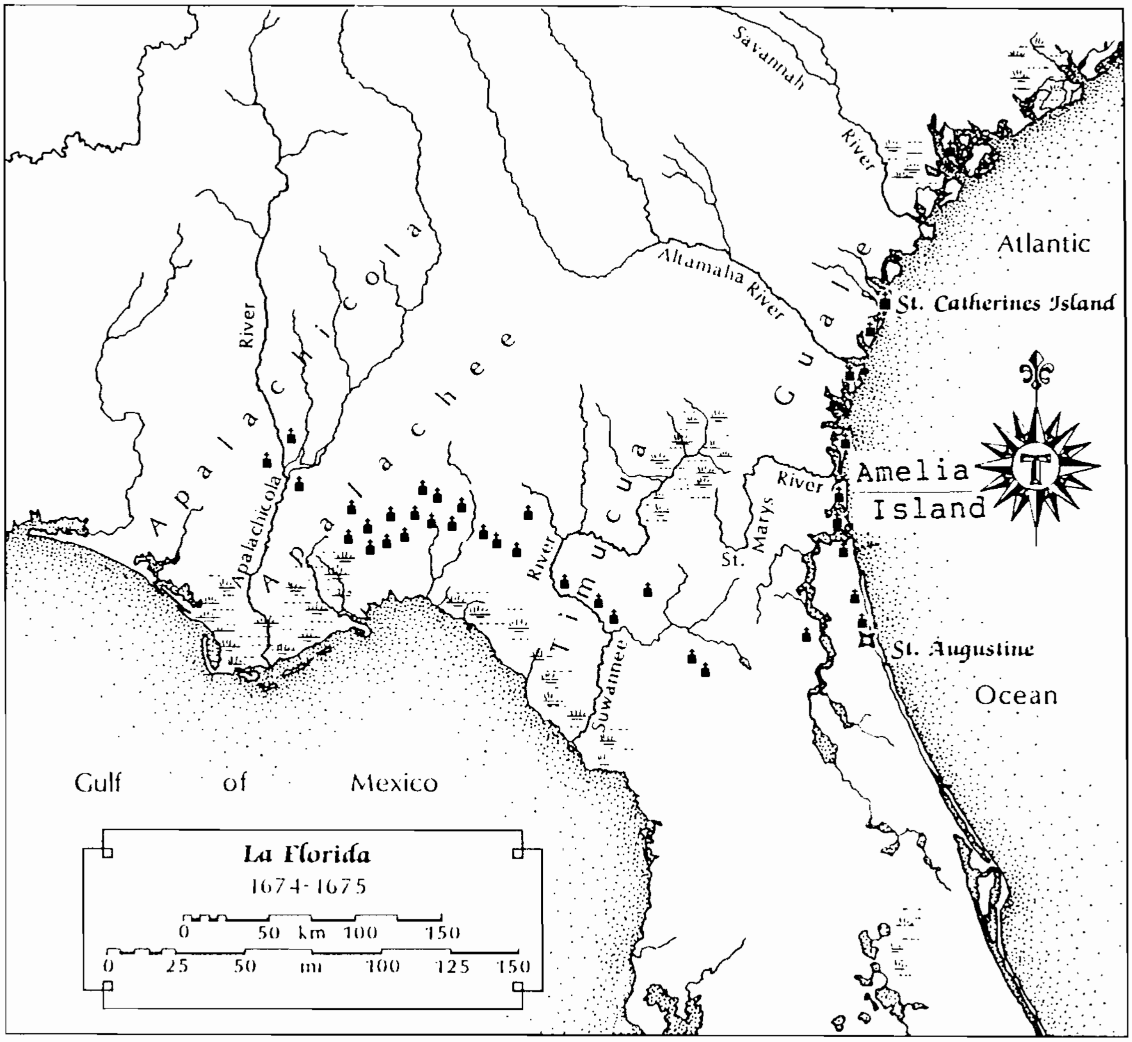

Figure 4. Location of *Santa Catalina de Guale de Santa Maria* on Amelia Island, Florida (from Thomas 1987).

from Carolina and their native allies routed nearly all of northern Florida's missions (Wood 1989). These raids culminated in the successful disruption of the Spanish borderland and the enslavement of the native populations. As part of this effort, in November 1702, Santa Maria was overrun and destroyed by British troops several days prior to Governor James Moore's siege of St. Augustine. The Franciscans and Guale fled with what they could carry and sought shelter at *San Juan del Puerto*, located just south of Amelia Island on Fort George Island. After the siege of St. Augustine, the remaining Guale were assimilated into the surrounding tribal groups. "The last information that we have of their existence as a group is in 1735 when one Fray Tomas de Aguilar was reappointed professor of the Indian language of Guale" (Larson 1978:120).

The mission period represented another change in lifeway for the Guale. With the arrival of the Spanish, it appears that there was a radical change in Guale settlement and subsistence patterns. Officially, the Spanish missions were established as "a place where tribal economies were reorganized, new crops and European methods of cultivation were introduced, scattered Native American groups were nucleated into new settlements, where instruction included music, reading, and writing" (Thomas 1987:75). More likely, the Spanish molded the Native American cultures to suit their needs and exploited the native populations as a source of virtually free labor. The missionaries forced sedentism and intensive agriculture on the native populations in order to "promote Christianity, make allies, and generate stable supply lines" (Milanich 1978:82) -- or as Bolton (1917) suggests, to "convert, civilize and exploit."

This major shift in lifeway precipitated a number of changes that were to eventually spell the extinction of the Guale as a distinct group. Among these changes were the obliteration of tribal boundaries by nucleation of the native populations and the interruption of seasonal migrations by establishing large permanent settlements. These changes resulted in a profound degree of biological stress stemming from epidemics, chronic food shortages, and military action by Spanish, British, and aboriginal forces (Larsen et al. 1990). Increased sedentism, demographic nucleation, and agricultural intensification were also an aggravating influence on the presence and severity of disease and nutritional stress. During the final years of missionization, the Guale were increasingly exploited by the Spanish. As Bushnell relates, even in times of severe food shortages, the natives were called upon "to provision whole boatloads of persons travelling north on government business, even foreigners" (1986:9). After a visit to Santa Maria in 1700, Governor Don Jose de Zuniga y Cerda reported that there were no more than two hundred natives on the whole of the island and that they were "a miserable, low-spirited people, very poor and humble" (Bushnell 1986:11). On November 4, 1702, Governor James Moore routed Santa Maria two days prior to his siege of St. Augustine. This effectively marked the end of the Guale as a culturally distinct group.

The site of *Santa Catalina de Guale de Santa Maria* (8Na41) was discovered in 1985 when a backhoe operator unearthed human bone while removing a tree on a resident's property (Hardin 1986). Archaeological excavations revealed architectural features at this site (hereafter referred to as Santa Maria), including part of a building 30 meters north of the cemetery, and possibly a moat and palisade. During excavation of the cemetery, an ossuary comprised of mostly disarticulated remains was encountered in the northeast corner. Although the human remains from this ossuary are currently being studied, their relationship to the cemetery population remains unclear.

The skeletal remains of 119 individuals were recovered from the Santa Maria cemetery in 1986 during excavations directed by R. Saunders and C.S. Larsen (Saunders 1992). The individuals were buried within a simple church structure in a supine position with hands folded over the chest. The orientation of the cemetery was 110 degrees east of north, and the individuals were buried with heads oriented to the southeast (Figure 5). In contrast to the cemetery at Santa Catalina, there were few disturbed burials. The lack of disturbance probably reflects the shorter duration of Santa Maria (about sixteen years).

A pattern of age segregation was apparent at the Santa Maria cemetery. That is, most of the immature individuals were buried on the western side of the cemetery. This age-based segregation was not evident at Santa Catalina. There is also a radical difference in the number of grave goods found at each site. The quantity of grave goods found at Santa Catalina far outnumbers those found at Santa Maria. Thomas (1988) posits that the abundance and variety of grave goods at Santa Catalina and the relative paucity of grave goods at Santa Maria may simply be an artifact of sampling or sample size. He argues that one would naturally expect to find a greater number and variety of grave goods at Santa Catalina (with 431 individuals) than at Santa Maria (with 119 individuals) because there are simply more people represented at the former. Other factors were almost certainly involved (see Thomas 1988).

Saunders (1988) suggests that the paucity of grave goods at Santa Maria might reflect certain aspects of the

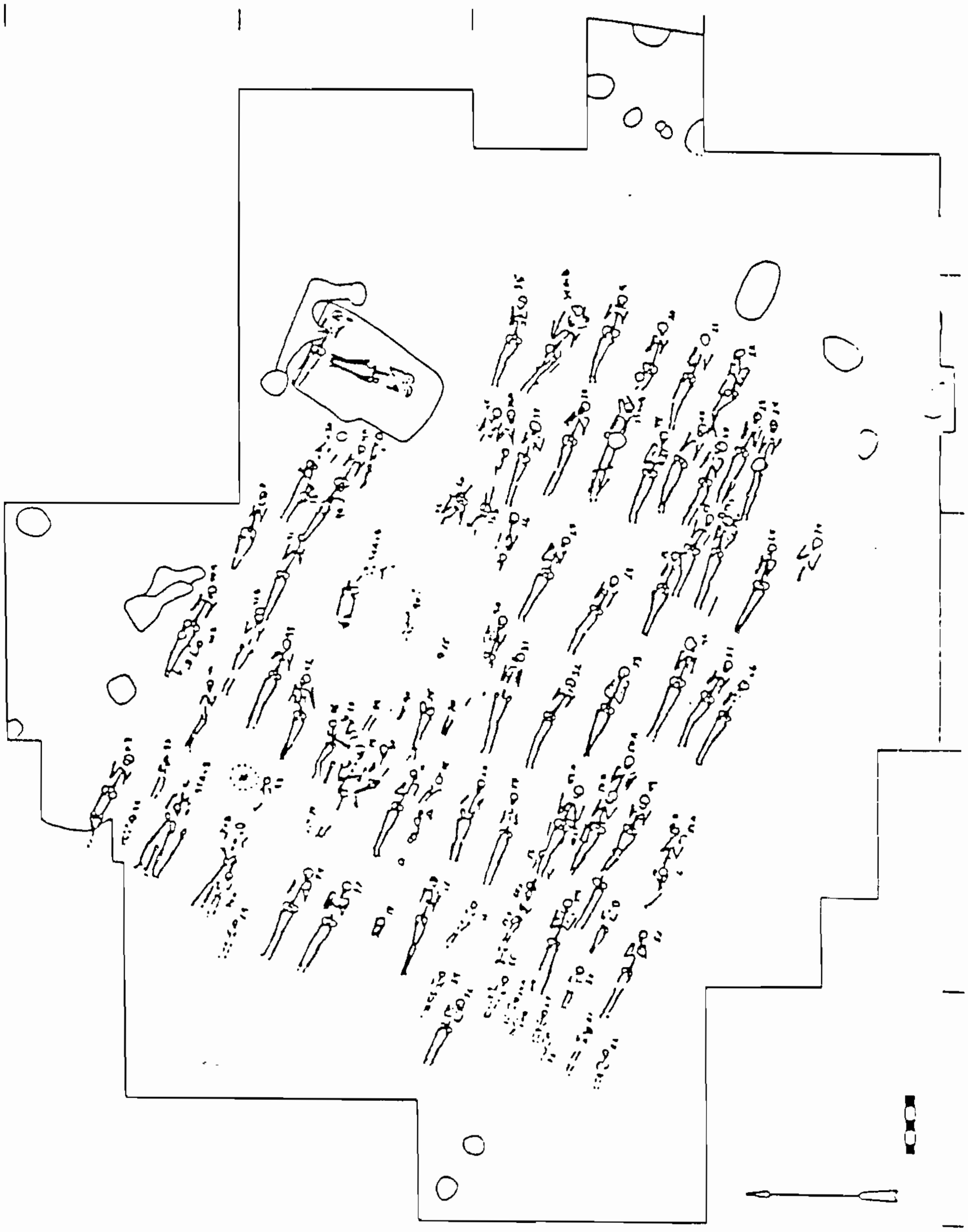

Figure 5. *Santa Catalina de Guale de Santa Maria*: Location of Burials (from Saunders 1988).

social climate. In particular, because St. Catherines Island was the regional administrative center, burial in the church cemetery may have been restricted to high status individuals who had access to European trade goods. Alternatively, Saunders adds that "the lack of grave goods at Amelia Island may reflect the scarcity of trade goods and religious commodities in the later period and/or a break down in the social mechanisms that previously supported elaborate burial goods" (1988:10). Regardless, it is clear that the burial practices at the two missions differed somewhat. Whether these differences reflect modern scientific biases or the social biases of the original inhabitants is not clear.

Biocultural Research of the Guale

The results from previous biological studies of the Guale suggest an overall reduction in health and quality of life as they changed from a hunting and gathering mode of subsistence to an agricultural one prior to the contact period (Larsen 1982). Although the data are more problematic for the postcontact Guale, the evidence indicates a further decline in health after European contact (Larsen et al. 1990). Hutchinson (1986) concludes that the population at *Santa Catalina de Guale* was under a greater amount of stress than the earlier, precontact Guale. This stress very likely resulted from (1) an increase in aggregation of the population, precipitating the rapid spread of European introduced diseases; and (2) the increased focus on maize as a primary constituent of the diet after the arrival of Europeans, and the concomitant decline in nutrition. Evidence from the analysis of the frequency of carious lesions and the patterns of osteoarthritis indicates that the Guale were under even more stress at Santa Maria (Shavit 1988, Griffin and Larsen 1989). Other studies on the precontact Guale have examined demography, growth disruption, pathology, morphology, and size. These examinations of Guale skeletal remains from the precontact and postcontact Georgia coast also reveal a pattern of declining health after European contact. Evidence for this decline comes primarily from observation of the prevalence of dental caries (Larsen 1982, Shavit 1988, Larsen et al. 1991), dental enamel hypoplasias (Hutchinson 1986, Hutchinson and Larsen 1988), infection (Larsen 1990), and degenerative joint disease (Griffin and Larsen 1989). Additional evidence is provided by the examination of demography (Larsen 1982, Russell 1987, Larsen and Russell 1989), postcranial structural morphology (Ruff and Larsen 1990), and bone chemistry (Schoeninger et al. 1990).

Secondary Population Samples

Yamassee

Yamassee, a tribal name of uncertain etymology, refers to a Muskhogean-speaking people which originally occupied the coast region and islands of south Georgia and northern Florida (Mooney 1969). From their residence near the Savannah River, they have frequently been confused with the Shawano and Yuchi, sometimes referred to as the "Savannahs." Spanish missions were established among the Yamassee around 1570 under whose jurisdiction they remained until 1687 (Mooney 1969). In 1687 an attempt by the Spanish government of Florida to transport a number of Yamassee as laborers to the West Indies resulted in revolt. After attacking a number of mission settlements, the Yamassee fled north to the English colony of South Carolina. They remained in the vicinity of Beaufort County until 1715 when disputes with local traders resulted in the large scale massacre of English colonists at the hands of the Yamassee and other local tribes. They were subsequently driven south to Florida by Governor Craven of South Carolina (Mooney 1969). The Yamassee reportedly resided near St. Augustine until around 1812 when after repeated enslavement and destruction by the Seminoles they disappeared as a distinct tribal group.

The skeletal sample used in this study - which has been tentatively identified as Yamassee - was recovered immediately south of the *Santa Catalina de Guale de Santa Maria* cemetery on Amelia Island, Florida (8Na41). The population sample is referred to here as *Santa Maria de Yamassee*. Human remains have been reported eroding out of the banks at this location since at least the 1900s (Saunders 1988). During the excavation of the *Santa Catalina de Guale de Santa Maria* cemetery in 1986, excavators were led to some of the eroding remains by a local resident. Excavations in 1987 revealed the presence of a church structure and the skeletal remains of a considerable number of individuals contained therein (Saunders 1988). At least 118 individuals are included in this sample. Saunders (1988) estimates that the original cemetery may have contained the remains of as many as least 250 individuals. Approximately half of these were lost due to extensive bluff erosion along the adjacent waterway, Harrison Creek.

Saunders (1988) has tentatively identified this population sample as Yamassee. Evidence for this identification comes from the work of Bushnell (1986). Bushnell's research indicates that a church called *Santa Maria de la Sena* was originally established on the north end of the island prior to 1602. At that time it served a predominantly Timucuan population. There is little mention of the church after this date, until 1675, when the mission census of Bishop Calderón reported a Santa Maria in the center of the island (Bushnell 1986). The Calderón document indicates that the population at that time was Yamassee. This Amerindian group, like the Guale, were refugees from northern Georgia and lower South Carolina, and are considered inland relatives of the coastal Guale. Although it is clear that the Yamassee were probably close linguistic and cultural relatives of the Guale, the biological affinity of these two groups is unclear.

The Yamassee had little contact with the Spanish until 1675. They remained at Santa Maria until 1683, when the Spanish crown decided to relocate them to the area of the mission of Santa Catalina on St. Catherines Island, which had been abandoned after 1680. The Yamassee did not believe the area was safe, and refused to settle there; this disagreement resulted in the abandonment of Santa Maria on Amelia Island (Bushnell 1986:5).

The burials of Santa Maria de Yamassee were apparently interred within a church structure like the burials from *Santa Catalina de Guale*. The orientation of the long axis of the structure was parallel to the adjacent bluff overlooking Harrison creek, about 30 degrees east of magnetic north. This type of orientation in relation to an adjacent waterway is also reminiscent of *Santa Catalina de Guale*. The church appears to have been constructed of wood and was built on shell sleepers and shell filled postholes. This type of construction is unique among contemporaneous Spanish mission churches. However, as Saunders (1988:18) points out, "...mission construction involved a great deal of experimentation in the adaptation of an ideal design to the soil matrices and available resources in each area." Saunders postulates that the shell sleepers may have served to elevate the structure above surface runoff. The shell filled postmolds probably retarded deterioration of the wooden posts by neutralizing the surrounding acidic soil.

Saunders reports that the interment pattern at *Santa Maria de Yamassee* is consistent with that found at other mission cemeteries. That is, the burials were extended, aligned with the long axis of the church, with heads to the southwest and feet to the northeast, and hands folded either under the chin, over the midsection, or along the top of the pelvis. There were four exceptions to this pattern. Two extended burials were aligned perpendicular to the other burials and two burials were tightly flexed. All four of these burials overlay extended burials aligned north-south. Saunders interprets the two extended burials to indicate a change in the preference for orientation to one similar to that used at *Santa Catalina de Guale de Santa Maria* to the north. She interprets the flexed burials to indicate continued use of the mission cemetery after it was abandoned by the friars.

The burials at *Santa Maria de Yamassee* varied greatly in terms of depth of burial pit and there were many cases of multiple burials in the same pit (Saunders 1988). In many of these multiple burials, the lower interments were not disturbed by the upper ones. This has been interpreted to indicate a more intensive use of the cemetery compared to the *Santa Catalina de Guale de Santa Maria* cemetery immediately to the north. Saunders (1988) reports that artifacts intentionally interred with individuals at the *Santa Maria de Yamassee* cemetery were conspicuous in their paucity. Only three undisturbed burials were recovered with *in situ* artifacts. This is even fewer artifacts than from the *Santa Catalina de Guale de Santa Maria* cemetery. There was no apparent age or sex segregation in the *Santa Maria de Yamassee* cemetery. The evidence for segregation according to social status is not compelling (Saunders 1988).

North Carolina Algonquian

Prior to European contact, the North Carolina coastal region was occupied by two distinct cultures, the Carolina Algonquians, who inhabited the Tidewater zone, and the

Tuscarora, on the Inner Coastal Plain (Phelps 1983). Ethnohistoric information has suggested political-territorial boundaries for these groups. These boundaries have been partially confirmed archaeologically, as shown in Figure 6. Two local phases have been established for these Late Woodland cultures of the North Coastal region: Colington is the phase name given the Algonquian culture of the Tidewater zone, and Cashie is applied to the territory of the Tuscarora, Meherrin, and Nottaway in the interior Coastal Plain (Phelps 1983). Current radiocarbon dates for the Colington phase range from A.D. 860±85 to 1315±70 (Phelps 1977). The North Carolina population samples used here are all from the Colington phase Algonquian cultural tradition.

The Carolina Algonquians were the southernmost representatives of a linguistic family distributed from North Carolina to Canada (Goddard 1978). The Carolina Algonquians lived in scattered villages along the North Carolina coast, on islands, river estuaries, or further upstream on smaller tributaries in the area of the Outer Banks (Hulton and Quinn 1964). The typical subsistence pattern was a seasonal round which consisted of a spring and summer planting period, yielding three sequential crops, followed by a period of winter movement away from the village site, involving hunting of game, fishing, and

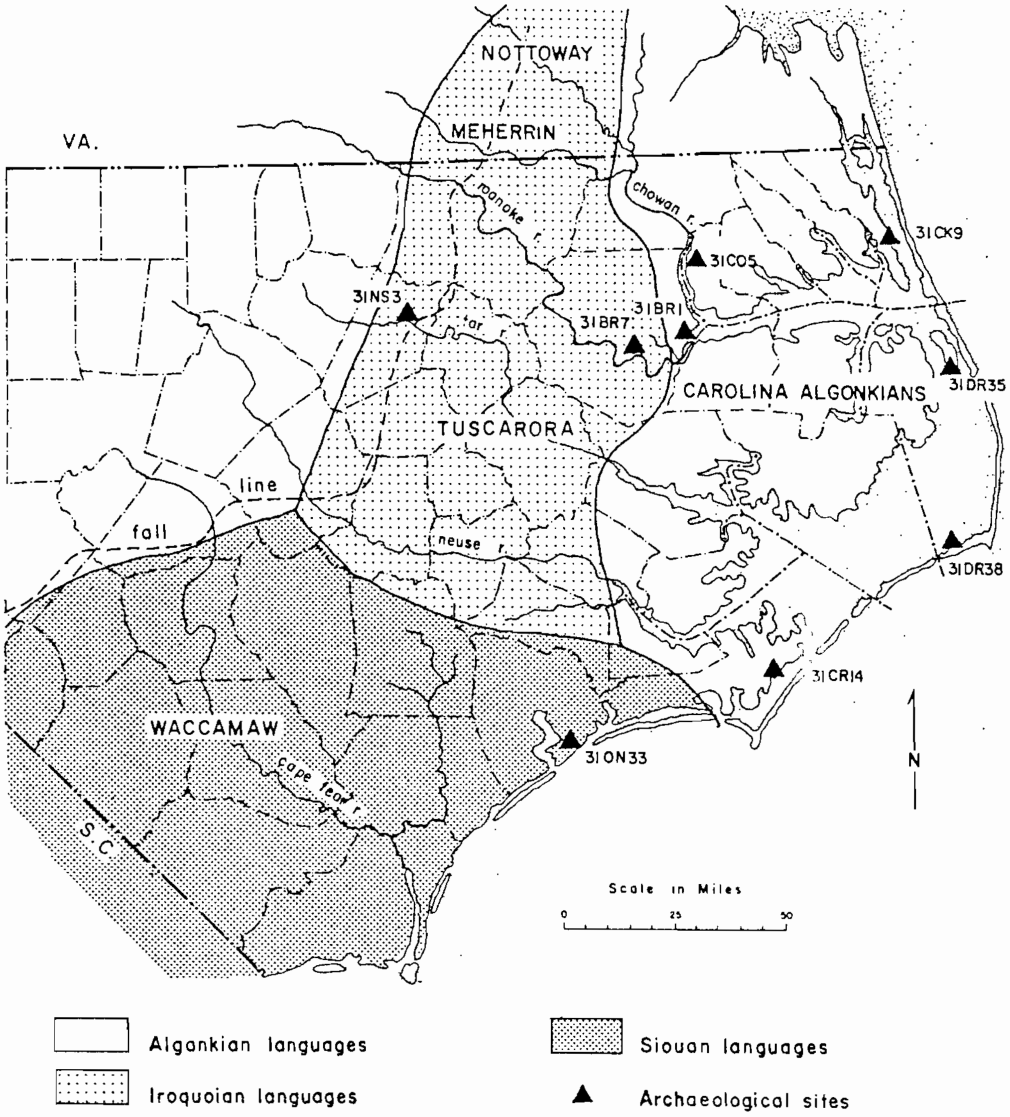

Figure 6. Protohistoric Ethnic and Linguistic Groups of the North Carolina Coastal Plain (from Phelps 1983).

gathering of fruit, berries, nuts, and roots (Feest 1978). There is no evidence for seasonal dispersal as has been suggested for other Southeastern groups. Marine resources (i.e., clams, oysters, mussels, and fish) also made up an important part of the Algonquian diet. The traditional burial pattern for the Colington phase Algonquians is the ossuary. These mass interments are typical of both the Algonquian cultures and their Iroquoian neighbors (Ubelaker 1974). Phelps has suggested that the Carolina Algonquian ossuaries "represent the periodic redisposal of accumulated dead, stored somewhere by each family until the time of burial and placed by each family in the ossuary pit" (1980a:8). This periodic disposal likely involved not only the dead from the village but also those from its peripherally dispersed farmsteads. If this is the case, each ossuary should represent a synchronic cross-section of the village population, and the total number of ossuaries at a site may be diagnostic for its diachronic occupational sequence. Although this assertion has not been fully tested, it will be assumed for the purposes of this study that the ossuary samples discussed here are representative of the Algonquian populations from which they derived.

The Carolina Algonquian samples were chosen for this study because (1) the remains were well preserved, (2) the samples consist of both genders and all ages, (3) the samples have clearly defined temporal and ethnic affiliation, and (4) the Algonquian represent a culturally distinct group in comparison to the Guale. Three of the Algonquian population samples included in this study were recovered from the Baum site. The Baum site (31Ck9), located in coastal North Carolina, covers at least five acres and contains a Middle Woodland period component (300 B.C. - A.D. 800) and a Late Woodland component (A.D. 800 - 1650). Five ossuary type burials have been recovered from the Baum site in excavations from 1972 to 1983. All five ossuaries have been found overlying the Middle Woodland component, indicating a Late Woodland, Colington phase affiliation. A radiocarbon date for Burial 1 of A.D. 1315 ± 70 confirms this association (Phelps 1980b). The prehistoric residents of this area are believed to be of the Algonquian-speaking tribes of northeastern North Carolina (Feest 1978:271). The location of the ossuaries suggests a cemetery area near the northern site periphery which may be a standard part of the intrasite pattern in Colington villages (Phelps 1983).

The remaining ossuary sample was recovered from the Piggot site (31CR14). The Piggot site is located in Carteret County, North Carolina, near the southern boundary of the traditional Algonquian distribution (Phelps 1980a). The ossuary (Burial 1) was an oval pit measuring 1.8 meters by 3.4 meters and containing the partially articulated remains of 40 individuals. The individuals were in bundles arranged in five distinct groups. No artifacts were associated with the burial pit. The burial pit was located on the eastern edge of the site and appears to have intruded on an earlier palisade. Most of the site has been lost to extensive wave erosion and the remainder has been subjected to major disturbance from historic activity dating from the early 1700s to present.

Creek

The people known to European settlers as the Creek were a composite group comprised of the Muskogee from the northwest, the Alabama from northwest and southwest, the Koasati and Tuskegee from the north, and the Hitchiti from the Gulf region (Spencer and Jennings 1965, Swanton 1922). The name Creek likely derives from the old name of one of the rivers in the area (Swanton 1946). Archaeologically and historically, they were principally a people of the interior plateau, situated at the margin of Piedmont and Coastal Plain (Spencer and Jennings 1965). Spencer and Jennings (1965) suggest that the Guale of the Georgia coast may have derived from inland Creek ancestors.

The Creek lived in towns ranging in size from one hundred to a thousand persons. The towns, physically comprised of thirty to one hundred houses, were distributed in hamlets along rivers and loosely clustered around ceremonial centers (Spencer and Jennings 1965). Early Creek towns were defended by stockades (Lewis 1907). Structures were rectangular, constructed of wattle-and-daub, and roofed with cypress bark or shingles held down by poles. Town life revolved around the ceremonial square or rotunda where the chief and his council were to be seen in daily session partaking of the "black drink" (cassina emetic), smoking, and conducting civil affairs (Bartram 1958).

Kinship among the Creek was reckoned using the Crow system (Murdock 1949), merging parents' parallel siblings and their spouses with each other, and classifying their offspring with their own siblings. The basic household unit was the family, comprising a woman, who owned the house, her husband, and their children. The woman's classificatory "uncles", "brothers", and "sons" were also included in this household unit. Local groups were divided into matrilineal clans, phratries (including from two to nine clans), and moities. Within each town, clans were divided into moieties, termed *white* and *chiloki* (of different speech). Moities formed the basis of a dual division into civil and war officials in each town (Adair 1930).

The Creek subsistence pattern was characterized by a seasonal round comprised of five to six months of agricultural production followed by six to seven months of hunting and gathering (Schoolcraft 1856). The hunting and gathering season usually began in early October, and all able-bodied persons dispersed leaving the aged and infirm behind to watch the village. The heavy reliance on hunting and gathering likely reflects the abundance of wild game in settlement areas rather than ineffective farming methods (Spencer and Jennings 1965). Plant domesticates included three varieties of corn, beans, squashes, pumpkins, melons, and sunflowers. Gathered plants included wild rice, cane seed, persimmon, sweet potatoes, and a variety of fruits, berries, and nuts (Spencer and Jennings 1965). Hunted fauna included deer, bear, fish, numerous small mammals, and birds. Bows and arrows were used to hunt large game; blowguns, clubs, traps, and snares for smaller animals; and a variety of methods were employed for catching fish including hooks and line, spears, weirs, and narcotic roots.

Burial customs varied among the Creek. Traditional burial involved the digging of a hole in the house floor beneath the decedent's bed, lining the hole with cypress bark, and placing the corpse in a sitting position into the burial pit along with personal items, such as tomahawks, pipes, and bows (Bartram 1958). In this type of burial, the family often built a new house, but might instead purify the old one by kindling a new fire in the hearth and exorcising the ghost (Swanton 1928).

The Creek population sample used for this study was recovered from the Ledford Island site (16By13) in east Tennessee. The Ledford Island site was a large Mississippian town located on an island of the same name in the Hiwassee River. The site is affiliated with the Mouse Creek phase (≈A.D. 1400-1600) of the east Tennessee Mississippian. The skeletal remains of 456 individuals were recovered from the Ledford Island site (Lewis and Kneberg 1945, D. Boyd 1984, Sullivan 1986).

East Tennessee Mississippian settlements were centered in areas of easily worked fertile soils, which were found in the floodplain and on low terraces and levees along the major rivers and streams. A village economy agriculture was practiced in the gardens and fields in and around the town. Beans, maize, squashes, and several varieties of native seed plants were cultivated. This production was complemented by hunting, particularly white-tailed deer, fishing, and the gathering of a wide variety of seasonal natural flora, especially arboreal nuts.

The Ledford Island town was enclosed by a stockade and, as was the case for many other Mississippian towns in this region, the stockade was abandoned long before the town was vacated (Sullivan 1986). The town is comprised of community buildings, plazas, and status differentiated burial zones, but no large earthworks (possibly because of a shorter chronology than other Mississippian towns). By far the largest building in the complex was the community building (250 square meters). To the southeast of the community building was a plaza area of about 1600 square meters. Surrounding the plaza were at least two rows of houses, some of them slightly larger than the average Mouse Creek Mississippian dwelling, but all less than half the size of the community building. Also located in the circumplaza area were two cemetery-like concentrations of burials. The cluster on the east side of the plaza contained 78 individuals and was more clearly defined than the group on the west side. The group on the west side included 28 individuals. Conch shell products, effigy pipes and pottery, and long ceremonial chert blades were exclusive to these circumplaza cemetery areas.

Sinodont

Culturally and linguistically it is difficult to ascertain relationships between native inhabitants of Asia and native Americans. Because the dentition is genetically conservative, teeth may offer a tool by which the relationships between these groups can be deciphered (Scott and Turner 1988). Turner (1985, 1986a, 1987a) has specifically addressed this contention. Using dental morphology, Turner has proposed two distinct Asian population groups, Sundadonts and Sinodonts. Each of these groups is characterized by a distinct set of dental features. Sundadonts now populate Southeast Asia and Polynesia; Sinodonts represent the native peoples of China, Japan, Siberia, and the Americas (Turner 1989). The specific dental morphological features which define Sundadonts and Sinodonts include in the maxillary dentition, central incisor shoveling and double shoveling, first premolar root number, first molar enamel extensions, and third molar reduction or absence (Turner 1985, 1986a, 1987a). In the mandibular dentition, these traits include first molar deflecting wrinkle, first molar root number, and second molar cusp number.

According to Turner's reconstruction of population history, in Southeast Asia, there are, and have been for several thousand years, Mongoloid peoples whose teeth are relatively simple and possess crown and root characteristics thought to be retained from late Pleistocene populations (Turner 1987a). Turner has named these Southeast Asian groups Sundadonts in recognition of the fact that both island and mainland peoples have a similar pattern of dental trait frequencies. The name Sundadont derives from the central geographic feature of the area, the now-submerged Sunda Shelf, a continental plain that once bridged insular and mainland southeast Asia. Turner postulates that Sundadonty originated sometime between 30,000 and 17,000 years ago based on the observation that this dental pattern is first observed in the Minatogawans of Okinawa during this period and the fact that early migrants to Australia 30,000 years ago do not have this dental pattern (Turner 1985).

The Sinodonts were so named because this relatively more complicated dental pattern was first recognized in a large skeletal series originating from the Shang Dynasty site of An-yang in northern China excavated by the late Li Chi (Yang 1970). Turner maintains that all northeast Asians (excluding recent Russians) and Native Americans possess the Sinodont pattern, with the exception of some Ainu and all Jomonese of Japan (Turner 1985). Population samples which Turner has assigned to the Sinodont classification will be used in this study and are summarized in Table 1.

The Sundadont dental pattern is basically the retention of early human dental characteristics. The Sinodont pattern in contrast represents a departure from the Sundadont characteristics. Sinodonty is characterized by specialization and intensification of several features of the roots and crowns of the dentition. To explain the origination of Sinodonty, a weak case can be made for the hypothesis that selection favored dental architectural strengthening. Under the arctic-like conditions of late Pleistocene North China and Mongolia, minor structural additions to the teeth might have provided small but significant advantages. Thus, the added mass of enamel ridging on the mesial and distal borders of incisors and canines may have enabled these teeth to wear slightly longer. Under harsh arctic conditions, crushing of bones with one's teeth to extract the last possible bit of nutrition was not uncommon, even in children, and teeth often had to be resorted to as survival tools when a hunter's hands were nearly frozen. The same strength and wear advantage may have favored more lower molar cusps which Sinodonts have. The occurrence of the supernumerary third root on lower first molars would surely help hold this important tooth in proper occlusion for more years than would be the case without it (Turner 1987).

On the other hand, Sinodonty is also characterized by relatively high frequencies of weakly socketed one-rooted upper first premolars, missing or diminutive third molars, fewer instances of upper molar cusp 5, fewer Carabelli's cusps, and more examples of one-rooted lower second molars than is Sundadonty. These conditions which reduce the robusticity of the masticatory apparatus suggest a reduction in dental fitness in the context of a harsh environment. Given this adaptive inconsistency, direct selection on dental morphology does not seem to be the prime mechanism that caused the characteristics of Sinodonty.

Drift or founder's effect is a much more parsimonious way to explain the co-occurrence of positive and negative changes. This is particularly true in a small, relatively isolated population system that was likely the human demographic situation in late Pleistocene North China and Mongolia. Boyd's (1953) review of studies on the decay of genetic variability showed that it can be directional and occur by chance alone, especially in small populations. The greater dental homogeneity in the New World than in eastern Asia is consistent with an hypothesis of genetic drift or founder's effect being primarily responsible for the Sinodont dental pattern. Turner (1987a:319) derives this from the assertion that "all Native Americans have to be descended from a limited number of North China hunting bands that drifted into severely restrictive late Pleistocene northeast Siberia."

Turner (1989) has postulated that the Sinodont populations which migrated to the Americas derived from a region bounded on the west by Lake Baikal and on the south by northern China. Greenberg and coworkers (1986) estimate that three major migrations took place, one of which included the Paleo-Indians who were ancestral to all South American and most North American natives with the exception of Aleuts, Eskimos, the ancestors of the Navajo and Apache, and the native groups that populate the interior of Alaska and parts of British Columbia. These exceptions derived from later migrations.

Turner has used dental morphological traits and the multivariate mean measure of divergence to estimate the date of genetic separation between American Indians and Asians, and between Pacific Islanders (Polynesians) and Southeast Asians (Turner 1986a). Turner refers to this methodology as dentochronology. These estimates are compared with other independent estimates of separation. This method gives an American Indian fission date from Asians of about 13,000 ± 3,000 years ago, which Turner maintains agrees with archaeological data. The data also suggests that Polynesians split from Southeast Asians 5,000 ± 2,200 years ago and are not derived from Melanesians; and that Ainu-Jomon originated in Sundaland 14,000 ± 3,300 years ago. These dates generally correspond well with independent dates derived from archaeological or other data. Turner maintains that using the mean measure of divergence to derive "microevolutionary rates" provides reliable dates of fission between populations. He also maintains that these "microevolutionary rates" are fairly constant. The dentochronological dates which do not correspond with independently derived dates he explains as effects of admixture in one of the branch pairs. Turner concludes that the average world dental microevolution rate is ≈ 0.0003 ± 0.004 MMD per 1,000 years. This may help in estimating the antiquity of other skeletal population samples.

CHAPTER III - THEORY AND METHOD

Introduction

Nonmetric traits have been recognized and cited in anthropological literature as descriptive features in human populations since the turn of the century (Chambellan 1883, Dorsey 1897, Gregory 1916, Le Double 1903, 1906, 1912, Hrdlicka 1920, 1921, 1924, Russell 1900). Nonmetric traits offer a useful tool in determining population distance (e.g., Balakrishan and Sanghvi 1968, Ossenberg 1976, Sjovold 1973, Kellock and Parsons 1970a and b, Konigsberg 1987, Sjovold 1984, Suchey 1975). Population distance, as used here, is an expression of morphological similarity between two or more populations, based on a statistical treatment of selected variables. In choosing these variables, one assumes that they are (1) largely under genetic control and (2) minimally affected by environmental or nutritional conditions. Also, the variables should be (1) reliably scored to ensure that population differences in trait frequency reflect biological not observational variance, (2) sufficiently variable to provide information to measure population distance, and (3) independent of one another in order to be useful in a multivariate analysis (Molto 1983).

Furthermore, the sample must represent the population and be of adequate size (Rösing 1982, 1984). Distance measures between populations are useful in anthropology for inferring residence patterns, patterns of diffusion and migration, and microevolutionary changes through time (Ubelaker 1989).

Much time has been devoted to debating the relative usefulness of nonmetric traits as opposed to so called "metric" traits for the estimation of biological distance (e.g., Berry and Berry 1967, Carpenter 1976, Cheverud et al. 1979, Pietrusewsky 1981, Rightmire 1972). "Metric" traits, as used here, refer to linear measurements of skeletal elements or indices derived from these linear measurements. Essentially, the debate has focused on the degree of environmental influence on trait expression in each of these classes of traits. As Kennedy (1981) has pointed out, existing information suggests that neither nonmetric traits nor metric data are of superior value in studies of biological relationships. Both are likely influenced by environmental factors such as climate, nutrition, maternal physiology, or biomechanical stress. More importantly, considering the probable polygenic nature of many of both classes of traits, the effect of environmental factors is probably minimal (A.C. Berry 1972, Corruccini et al. 1986, DeVilliers 1968, Kolakowski et al. 1980, Moller 1967, Nichol 1989). Interestingly, researchers have found that both sets of traits seem to vary systematically and have proposed a common developmental pathway (Benfer 1970, Cheverud et al. 1979, Corruccini 1975, Richtsmeier et al. 1984).

A key difference in the usefulness of nonmetric traits versus metric traits lies in the context of the population samples under examination. For skeletal populations derived from an archaeological context, nonmetric traits offer a distinct advantage over metric data. Nonmetric data can be collected from fragmentary or incomplete skeletons. This condition most typically represents the condition of skeletal remains from archaeological contexts. In such a situation nonmetric data represent a distinct advantage over metric measurements which often require a high degree of skeletal integrity and thereby markedly reduce sample sizes. Statistical analyses commonly used for biological distance studies typically require large skeletal samples (Rösing 1982, 1984). Owing to the generally fragmentary nature of much of the skeletal material considered here, nonmetric traits offer a crucial advantage over metric variables.

The Hypothesis

This study will examine the biological relationships between a time-successive series of Guale population samples compared to other culturally and linguistically distinct Native American groups from the southeastern and southwestern United States. The present study is important because (1) only one study has been done on the biological relationships of Native American groups in this area (i.e., Griffin 1989), (2) prior research has suggested that the Guale population samples considered here underwent profound biological changes after European contact, but it is unclear if these changes instead represent in-migration of other populations, (3) the biological relationships between the Guale and other Amerindian groups has not been established, and (4) it is unclear how Native American groups from the southeast U.S. compare to Turner's Sinodont classification because he did not include populations from this region in his analysis. This study will help provide answers to these questions.

The assumption made when calculating population distance is that one is dealing with large, panmictic populations with little or no in- or out-migration (i.e., an essentially static gene pool). A change in this gene pool will directly affect the frequency of genotypes in the populations and will be reflected in the expression of morphological characteristics (Turner 1969). Therefore, if the difference in gene pools is small, the population distance will be correspondingly small. Because the three Guale population samples being examined here should be closely genetically affiliated (being derived from essentially the same population), a great disparity in dental morphology may indicate a change in the genetic composition of the population. This change could stem from in- or out-migration, selection against certain members (as in epidemic disease), or artificial selective pressures (e.g. warfare, circumscription). Any or all of these factors could significantly change the gene pool of the Guale reflected by each of the population samples.

It has been inferred from ethnographic and archaeological evidence that the precontact Guale of the Georgia coast and the postcontact Guale of the Georgia and Florida coasts represent a single temporally continuous population. If this is indeed the case, the results of this study should indicate a homogeneous population over all of the temporal periods with few significant differences in frequency for the cranial and dental morphological traits. Likewise, if the population samples in this study represent a temporally continuous population, it is expected that the biological distance between the Guale samples will be small in comparison to those from other non-Guale groups. In this case, comparison with the non-Guale population samples should reveal a significant difference in trait frequencies and in biological distance. It is expected that the differences will be greater for those groups that are geographically more distant from the Guale (e.g., Algonquian and Creek) than for the closer populations (e.g., Yamassee) which have a greater chance to experience gene flow between local groups.

Concomitant to the shift in lifeway the Guale experienced between the late precontact and the late postcontact periods, there were increases in frequencies of infectious and non-infectious diseases and a reduction in size and robusticity of the skeleton (Larsen et al. 1990). It has been suggested that these changes were the result of radical changes in lifeway (Larsen 1993). It may be, however, that these changes were the result of in-migration of non-Guale populations and not change in lifeway. Dissimilar trait frequencies and population distance estimates among the Guale samples may indicate such an in-migration.

The Genetic Basis of Nonmetric Traits

Introduction

Traditionally, researchers have used metric variables, in particular cranial indices, to estimate population distance (e.g., Cybulski 1972, Hanihara 1985, Howells 1966, 1973, Jantz 1970, 1974). Recently, nonmetric variables have been more frequently used for population distance studies (e.g., Buikstra 1972a, 1980, Corruccini 1974, Dodo 1987, Finnegan 1978, Greene 1982, Haeussler 1985, Haeussler et al. 1989, Kennedy 1981, Lukacs 1983, Pietrusewsky 1981, 1984, Richards and Telfer 1979, Sciulli 1990a and b, Sofaer et al. 1986). Although nonmetric traits have been recognized and described since the turn of the century (Chambellan 1883, Gregory 1916, Le Double 1903, 1906, 1912, Hrdlicka 1920, 1921, 1924, Russell 1900), their population specificity was held in question until investigations into the genetic nature of nonmetric variation was undertaken in the 1950s and 1960s (Deol et al. 1957, Truslove 1954, Grüneberg 1952, Searle 1954a and b, Howe and Parsons 1967, Berry and Berry 1967). In particular, Berry and Berry (1967) proposed that, nonmetric variables offered a more reliable estimation of population similarity than metric variables, and researchers began employing these traits for human population distance studies (e.g., Balakrishan and Sanghvi 1968, Ossenberg 1976, Sjovold 1973, Kellock and Parsons 1970a and b, Konigsberg 1987, Sjovold 1984, Suchey 1975).

Nonmetric traits are generally considered to be morphological characteristics which have a finite range of expression and can usually be classified in two to six categories. This is in contrast to metric variables which are typically linear measurements or indices derived from linear measurements and are considered to be continuous variates. Nonmetric variables take the form of accessory ridges, tubercles, extra-sutural bones, accessory foramina, differing positions of foramina, and in the case of teeth, sizes and shapes of cusps expressed on the lingual, buccal, or occlusal surface. Often, nonmetric variation can exhibit a range of expression from slight to pronounced. This type of expression has been termed "quasi-continuous" rather than discontinuous (Grüneberg 1952). Although "quasi-continuous" is a better descriptive term for most nonmetric variation, the term "nonmetric" will be used here because it is more commonly used in the literature.

As mentioned previously, nonmetric traits have been recognized and cited as descriptive features in human populations for nearly a century. However, not until the 1950s did researchers begin investigating the genetic nature of nonmetric variables (Deol et al. 1957, Truslove 1954, Grüneberg 1952, Searle 1954a and b, Howe and Parsons 1967, and Berry and Berry 1967). This early research initiated the wide-spread use of nonmetric traits for estimation of population distance between skeletal populations (Balakrishan and Sanghvi 1968, A.C. Berry 1974, Greene 1982, Kennedy 1981, Laughlin and Jorgensen 1956, 1957, Lundy 1980, Ossenberg 1976, Spence 1971, 1974).

Some of the first research concerning the genetic nature of nonmetric traits began in 1952 when Hans Grüneberg initiated a series of studies using laboratory mice. This series, entitled: "Genetical Studies on the Skeleton of the Mouse," was concerned with finding to what extent skeletal morphology is genetically controlled. Grüneberg (1952) crossbred two strains of laboratory mice to assess the genetic behavior of each. His conclusions, from the study of vertebral and pelvic variations, were that these variations were multifactorally inherited and that they were sensitive to environmental influences. At this point, it was unclear how much of an effect the environment has on the expression of nonmetric traits.

One of the most important principles enumerated by Grüneberg was the principle of quasi-continuity. This tenet, based on a model by Sewall Wright (1934a and b), proposed that inheritance of a nearly discontinuous character was due to the segregation of multiple genes in conjunction with a threshold of manifestation. As an illustration of this, Grüneberg cited the expression of the third molar in mice. In mice, "additive" genes affected the size of the tooth germ, bringing it to a "threshold of manifestation"; falling below this threshold meant no expression of the third molar. After the threshold is reached, tooth size varied within a finite range.

The importance of this finding lies in its implications for the study of nonmetric variables. Indeed, nonmetric variables are often not exclusively present or absent, but rather are of a quasi-continuous nature, even beyond their threshold of manifestation (Reich et al. 1972). Therefore, scoring techniques should reflect not only the variable's presence or absence, but also the degree of expression (number, size, shape).

Other studies in the mouse series focused on the environmental impact on trait expression. Searle (1954a) found that non-genetic factors (maternal and postnatal) accounted for 80% of the variance in 75% of vertebral nonmetric traits. In an extension of this study, Deol and Truslove (1957) found that maternal physiology (in particular, factors related to malnutrition) affected the litter size and the size of the offspring. This later effect greatly influenced the expression of nonmetric traits.

In a later study by Richtsmeier and McGrath (1986), postnatal effects were considered in a crossfostering experiment using laboratory mice. Although the results were largely inconclusive, Richtsmeier and McGrath found that there is a distinct correlation between the functional type of trait being scored and its heritability. They separated nonmetric traits into three types: foraminal, hyperstotic/hypostotic, and fusion. Of 35 traits examined, four showed significant heritability values. Three of the four traits were hyperstotic/hypostotic, and one trait was foraminal. From these results, Richtsmeier and McGrath concluded that nonmetric traits follow the principles of the Functional Matrix Hypothesis: that is, as the number of developmental sources of trait variation increase, heritability values decrease. In the case of foraminal traits, factors such as the number of bundles of nerves or blood vessels and their position in relation to the bone exert additional influence over the expression of a trait (Richtsmeier and McGrath 1986).

Studies of nonmetric traits in non-primate species have provided some useful guidelines for the selection and use of traits for population distance studies. Perhaps the most important among these contributions are the quasi-continuous nature of nonmetric traits (Grüneberg 1952) and the possibly significant influence of environmental factors in the expression of these traits (Searle 1954a, Deol and Truslove 1957, Richtsmeier and McGrath 1986). Other researchers have confirmed these early findings and have further emphasized the significant effect of environmental conditions (R.J. Berry 1968, Berry and Searle 1963, Deol et al. 1957, Grewal

1962, Grüneberg 1963, 1965, Rees 1969, Searle 1954a, Self and Leamy 1978, Truslove 1954).

Nonmetric traits in research concerning humans were used primarily as descriptive features in physical anthropology in the early twentieth century (Akabori 1934, Bolk 1931, Hooton 1930, Hrdlicka 1920, Wood Jones 1930). However, later authors began to examine the genetic nature, heritability, and the usefulness of nonmetric traits for population studies (Bennett 1965, A.C. Berry 1974, 1975, Birkby 1973, Blakely 1973, Buikstra 1972a, 1980, Corruccini 1974, Finnegan 1978, Finnegan and Faust 1974, Kennedy 1981, Korey 1970, Ossenberg 1969, Rightmire 1972, Saunders 1978, Sjovold 1973). These later works have helped to clarify the place of nonmetric variation in the analysis of skeletal populations and have also raised some important questions about their use in population distance studies.

Dental Traits

Dental nonmetric variables have been found to be particularly sensitive for determining population affinities and genetic relationships between groups (e.g., Axelsson and Kirveskari 1977, 1982, Dahlberg 1963a and b, 1965a and b, 1986, Greene 1982, Haeussler 1985, Lukacs 1983, 1986, Richards and Telfer 1979, Sofaer et al. 1986, Turner 1967a and b, 1987a and b, Yamada and Kawamoto 1988). The human dentition is genetically conservative and changes little over many generations (Scott and Turner 1988). Teeth are also extremely durable and are often the only intact skeletal remains recovered from archaeological contexts. This, combined with the fact that dental nonmetric traits are easily and reliably observed as well as numerous make this type of characteristic ideally suited to population distance studies involving skeletal remains from archaeological contexts.

The use of dental morphology to study the relationships between populations dates to the first half of this century (e.g., Dahlberg 1945, Gregory 1916, Hellman 1929, Hrdlicka 1920, 1921). More recent research in dental morphology has focused on the genetic nature of dental traits and microdifferentiation of population samples (Greene 1982, Hanihara 1992a and b, Haeussler 1985, Lukacs 1983, Nichol 1989, 1990, Richards and Telfer 1979, Sofaer et al. 1986, Townsend et al. 1990, Turner 1985, 1987a and b).

Scott and Dahlberg (1982) give a general overview of recent studies and developments in the study of dental morphology. The nature of many of these studies has been to ascertain the extent to which dental morphology, specifically tooth crown morphology, can be used to determine predictable patterns of biological relationships among human populations. The methods of these studies as well as the sample characteristics have varied widely but they have been in general agreement that the utility of such traits can be viewed with "cautious optimism." However, this caution is not necessarily related to disagreements over the genetic stability and population specificity of the traits, but more to the general lack of standardization in scoring and analysis of frequencies of dental morphological traits. These observations echo those made by Brothwell (1967) over a decade earlier. Some of the problems noted by Scott and Dahlberg are (1) a lack of standardization in trait definition and scoring procedures, (2) the scoring of variable teeth in a given field, instead of only "key" teeth, which introduces "unnecessary, environmentally induced variation," (3) the difficulty involved in recording subtle traits, which are often key features for an analysis, and (4) inter-observer error. As will be discussed, most of these problems are currently being addressed.

As Scott and Turner point out, "a biological trait can be useful in historical-evolutionary analyses only if a significant component of its variation is genetic" (1988:100). Research has shown that although dental morphology does not adhere to a simple mode of inheritance, there is a sufficiently strong genetic component to make dental morphological traits useful for assessing biological relationships and microevolutionary trends (Biggerstaff 1975, Corruccini et al. 1986, Garn 1977, Goose and Lee 1971, Lundstrom 1977).

Since the 1950s, much research has been done on the description and genetic basis of nonmetric dental characteristics (Baume and Lapin 1983, A.C. Berry 1976, Biggerstaff 1968, Brothwell et al. 1963, Carbonell 1963, Corruccini et al. 1986, Dahlberg 1951, 1956, 1960, 1961, Goose and Lee 1971, Hanihara 1967, Harris and Bailit 1980, Jacob 1967, Lunt 1967, Moorrees 1967, Potter et al. 1968, Sakai 1967, Zubov 1968, 1973, 1977). Most of these works have concentrated on the description of dental features and have dealt only in a minor way with the genetic basis of these variations. Later research provides some evidence for the reliability of dental characteristics for population distance studies (Dahlberg 1963a, Garn et al. 1966b, Christensen 1967, Haseman and Elston 1970, Lundstrom 1977, Zubov 1973, Staley and Green 1974, Potter and Nance 1976, Harris and Bailit 1980, Butler 1982, Dahlberg et al. 1982, Corruccini et al. 1986).

Early researchers assumed that nonmetric dental traits were Mendelian (Devoto et al. 1968, Turner 1967a and b, 1969). As Sofaer (1970) has suggested, this assumption is incorrect. Attempts have been made to support the contention that various human dental morphologic characteristics are controlled by single autosomal genes, merely by an examination of the frequencies in populations of different rather arbitrarily defined manifestations of nonmetric traits (Devoto et al. 1968, Turner 1967a and b, 1969). No reference to individual relationships within the populations were made, and yet conclusions were drawn about the way in which the characteristics are transmitted from one generation to the next. As Sofaer (1970) points out, such conclusions can only be valid if they are drawn from family data, because the study of inheritance clearly demands the use of related individuals. In these studies, explanations of the genetic control of human dental morphologic variation in terms of single autosomal genes, the expression of each character has been divided into three classes: nonaffected, minimally to moderately affected, and moderately to maximally affected. Sofaer contends that this procedure is valid from the phenotypic point of view; but because all three classes appear to represent ranges on the same continuous scale there is, at present, no reason to suspect any qualitative biologic difference between them. However, the assumption has been made in these explanations that the three classes of expression correspond to three distinct genotypes produced by the segregation of two alleles at a single autosomal locus. All non-affected individuals have been presumed homozygous for one allele;

minimally to moderately affected individuals have been presumed heterozygous; and moderately to maximally affected individuals have been presumed homozygous for the other allele. The agreement of the frequencies of these three hypothetical genotypes in populations with the expectation derived from the application of a fundamental theorem of population genetics, the Hardy-Weinberg Law, has then been taken as evidence of single gene control.

The fallacy of this approach lies in the misconception that the appearance in a population of three arbitrarily defined classes in the proportions p^2, $2pq$, and q^2 constitutes evidence of single gene control. Sofaer (1970) asserts that there is no good reason to suppose that these classes represent genotypes. He also points out that testing observed and expected frequencies with the chi-square statistic may be misleading. The chi-square test for goodness of fit with the Hardy-Weinberg expectation is concerned only with whether the numbers of each of the three types of individual are distributed according to the binomial expansion. It is clearly incapable of providing any information about the nature of each of these three types of individuals. The test is only meaningful if it is applied to a known locus, identified through a study of related individuals, when its purpose is to see how closely a population resembles the ideal. Recent research has suggested that nonmetric dental traits are in fact under complex genetic control and not Mendelian in nature.

Harris and Bailit (1980), in an effort to establish the genetic nature of dental variation, recorded the incidence and size variability of the metaconule in a series of 1217 living Melanesians. The results of their study were the following: (1) the incidence decreased along a gradient from the first molar to the third molar; (2) when the metaconule occurred on distal molars it tended to be larger; (3) the additive genetic component for the first molar was 65%; and (4) the additive genetic component for second molar was 15% and almost negligible for the third molar. They interpreted these to mean that the first molar is under more complex genetic control than distal molars, and once the initial threshold of expression is reached, the increments between subsequent thresholds are smaller (see Reich et al. 1972).

Human twin studies have offered some evidence for the genetic nature of nonmetric dental traits. In a series of studies with monozygotic and dizygotic twins, Lundstrom (1977) found that variances in tooth morphology compared between twins and the general population suggested a good genetic basis for tooth morphology. In fact, the correlations were strong enough to determine whether two individuals were twins and what type of twins. Corruccini et al. (1986) found, upon initial analysis, that about 50% simple heritability was suggested for dental occlusal variables in mono- and dizygotic twins. However, upon reexamination, it was found that environmental factors may heavily bias these estimates. Corruccini cautions that this is a twin study and observations of the general population in controlled circumstances should be made. Haseman and Elston (1970) tout twin data as a very useful means of estimating the genetic basis of characters, but also caution that the results do not always apply to the general population. This concern is shared by other researchers (Potter and Nance 1976, Staley and Green 1974).

From a genetic and biological perspective, the dentition is part of a complex system which is under relatively tight genetic control. Biggerstaff (1979) has suggested that tooth size and morphology represent two variables in the complex system of human craniofacial development, and that all craniofacial components generally show interrelated variations. Biggerstaff also suggests that the probability is high that direction and stability during ontogenetic processes is achieved by continuous feedback and modulating systems which insure that development will proceed normally despite a variety of environmental conditions.

According to Biggerstaff, the compatible interactions of the teeth, jaws, and masticatory muscles express the extent to which organisms and populations are adapted to their habitats. He cites evidence that the functional adaptations of the molar cusps of fruit eaters, leaf eaters, insect eaters, and omnivores are correlated to muscle and jaw function. From this, Biggerstaff concludes that it is the morphogenetic control of the intricate developmental patterns that integrates the components of the head and face. In the case of humans, the selective pressures that initially shaped the craniofacial complex have been somewhat relaxed, allowing for more variation to emerge despite the genetic controls inherent to the system. These conclusions are important for nonmetric dental traits because they suggest that (1) the dentition is under tight genetic control and (2) the allowance for variation in humans provides the basis for inter- and intra-populational differences.

Moller (1967) has suggested that environmental influences may have only a minor effect on the expression of dental morphological traits. This study reports on the effects of nutritional and environmental stressors on the gross morphology, micromorphology, and ultrastructure of the human dentition. Nutritional stress is demonstrated to have an adverse effect on the size and quality of the pits, fissures, proximal contacts, buccal and lingual surfaces, and the incidence of gross enamel defects. In terms of micromorphology, tooth form was also adversely affected by nutritional stress, the detrimental effects including increased surface roughness, perikymata, and incidence of internal defects in micromorphology. Ultrastructure was also detrimentally effected in terms of surface texture, prism harmony, and crystallinity. However, except in terms of gross size, nutritional stress did not seem to affect the expression of morphological dental features. The detrimental effects were primarily confined to the structural aspects of the dentition. One should bear in mind, however, that the stressors studied here are neo- and post-natal and not pre-natal. There may be significant differences between these growth stages.

More recent research has suggested some probable modes of inheritance for dental nonmetric traits. In order to examine probable mode of inheritance for a set of 24 morphological variants of the dental crown, Nichol (1989) used a complex segregation analysis. Models tested included three two-allele single-locus models (dominant, codominant, and recessive) and a polygenic model, with transmissibility estimated via maximum likelihood. The results of the analysis suggest major genes for 13 of the 24 traits examined. Five traits give good evidence of being polygenic in origin: winging, canine distal accessory ridge, molar groove pattern, entoconulid, and mandibular torus. Six are likely of quasi-continuous origin: central incisor procumbency, double-shoveling, premolar lingual cusp number, deflecting wrinkle, protostylid, and maxillary torus. Five are likely influenced by a single dominant gene: lateral incisor insetting, interruption grooves, Carabelli's cusp, hypoconulid, and metaconulid. Three are likely influenced by a single recessive gene: incisor labial convexity, hypocone, and transverse ridge. Estimates of transmissibility for all of the twenty-four traits examined ranged from 0 to 1, with a mean of 0.36. Nichol concludes that many of these traits may be under significant influence of sex-linked genes, or under significant influence of familial environmental effects on development and expression. Kolakowski and others (1980) have confirmed this assertion.

In a familial complex segregation analysis of Carabelli's trait in Melanesians, Kolakowski and others (1980) found that while Carabelli's trait appears to be under the control of a single dominant gene, its expression was significantly effected by maternal pre- and post-natal conditions. In fact, these environmental factors accounted for over 19% of the variance for this dental trait. Thus, it can be seen that distances obtained from the frequencies of many nonmetric dental traits reflect phenotypic rather than genotypic affinity because of their probable polygenic mode of inheritance (Scott and Turner 1988:102). However, many of the other variables studied by physical anthropologists are also polygenically inherited (that is, more than one gene controls their expression).

Some researchers have expressed concerns over dental "field effects." In the field model of embryological development, tissues are seen to develop in organizational fields. Influences on the tissues vary in a sense of "polarity" with the greatest effect being at a particular pole (site) within a field (Weiss 1937, Butler 1939). Variations in form and size of the individual members within the group are directly correlated with their respective distances from the pole of the field. In modern humans, the first molars, first premolars, canines, upper central incisors, and lower lateral incisors are marked as "poles" of their individual fields (Dahlberg 1962). The expression of a particular trait is strongest in the first tooth in a particular "field" (e.g., first molars usually have a stronger expression for a trait than third molars).

Townsend and others (1990) examined the field effect and the genetic basis of the entoconulid (sixth cusp) on mandibular molars of Australian aboriginals. Four grades of trait expression (trace, small, medium, and large) were defined on dental casts of 399 subjects. Approximately 80% of deciduous second molars exhibited the trait, whereas frequencies in the permanent dentition ranged from 50% on the second molar to 70% on the first molar and 80% on the third molar. The degree of expression increased distally along the molar series, with only 3% of the deciduous second molars showing large cusps compared with 25% of third molars. Based on a quasi-continuous threshold model, a genetic contribution to entoconulid variability was observed that was strongest for the first molar. Similar findings were reported by Sofaer and others (1972a) for a broader range of traits, including shovel form, Carabelli's trait, cusp number, and groove pattern. In their study, analysis of the resemblance between relatives from these two Melanesian population samples indicated that for each of the morphological characters scored on an earlier and a later developing member of a tooth class, the later developing tooth showed a smaller component of additive genetic variation. This finding suggests that the greater morphological variability generally observed at the distal ends of tooth classes may be due primarily to a difference between the environmental conditions experienced by earlier and later developing teeth within a morphological class coupled with a smaller additive genetic component for the distal members of the class. The implications of these findings for studies using dental nonmetric traits is that it may be more informative to use only the first tooth in a specific field for certain traits.

It should be clear from this brief overview of the literature that dental morphological traits present a reliable and genetically stable means of estimating biological affinity between populations. Evidence from twin studies indicate a high degree of reliability (in relation to the influence of environmental stress) for dental nonmetric variation. Sofaer et al. (1986) have also shown the genetic stability over space and time of dental morphology. Other researchers have explored the genetic stability and population specificity of dental characters and come to similar conclusions (e.g., Dahlberg 1945, Garn et al. 1963, 1966a, Kirveskari 1977, Saunders and Mayhall 1982, Scott 1980, Scott and Dahlberg 1982, Smith 1977, Snyder et al. 1969). These and other studies suggest that although the exact mode of inheritance and the number of genes involved are not known, twin data, chromosomal studies, and other lines of evidence clearly support a strong genetic influence on variation in dental morphology. This evidence suggests that dental characteristics present a stable and reliable means of population distance estimation.

Microevolutionary Perspective

Mammals rely on an intact dentition for their survival. "When the teeth fail to function through extreme wear or loss ... death soon follows" (Scott and Turner 1988:105). This has been true for much of our distant past as evolving hominids. Somewhere in our past, however, humans began to utilize culture as a buffer against the environment, thereby reducing the absolute dependency on the dentition. Although natural selection has been demonstrated to be the directing factor in some dental traits (e.g., shovel-shaped incisors), genetic drift may be a more plausible explanation for much of the dental variation observed in modern humans (Smith 1982, Taylor 1982).

Aberrant maxillary third molars have been described by Taylor (1982) as molars having the normal number of cusps but having a "compressed" shape. In most situations, the cusps are simply modified with respect to their relative locations to one another, and to a lesser degree, their size and shape. This condition is believed to be the result of a number of factors. The ontological development of the surrounding supporting structures may be the most influential factor. A shift in cusp location has been observed to occur as a result of the "invasion" of supporting or adjoining structures, reducing or modifying the space in which the tooth bud can grow. A similar process has been suggested for the groove pattern of the lower molars (Taylor 1982).

The dominant groove pattern for the hominoid lower molar in primate evolution has been the "Y-5" pattern. This pattern is characterized by the presence of a well developed hypoconulid and a distinct contact between the second and third cusps (metaconid and hypoconid). Until fully modern *Homo* appears, this pattern is highly stable, becoming a criterion for designation as hominoid. With the appearance of modern *Homo sapiens sapiens*, the groove pattern of the lower molar becomes considerably less stable (Hellman 1929). Although the lower first molar typically retains the "Y-5" pattern, the second and third molars exhibit significant variation. The predominant types of variation include contact between the protoconid and entoconid (referred to as the "X" pattern) and contact between all four cusps, described as a "+" pattern (Jorgenson 1955). The former is much more common than the latter (Scott and Turner 1988). This shift may be due to the same type of process observed for aberrant maxillary third molars.

It may also be the case that these are simply the secondary results of a relaxation of selective pressures. It has been proposed that an increase in dental variation may occur when it is no longer neccessary for the teeth to be genetically stable (Scott and Turner 1988). This condition seems to characterize an evolutionary trend in *Homo* in general. In this sense, it appears that the wide range of dental variation in humans may simply be the effect of non-selective factors. It should be emphasized here that although the human dentition is highly variable in a macroevolutionary sense, it tends to be conservative in a microevolutionary perspective. Thus, characteristics of the teeth are useful for the estimation of population distances and group affiliation.

Cranial Traits

Over 200 nonmetric cranial traits have been described for the human cranium (Hauser and De Stefano 1989). Nonmetric cranial traits have been observed and recorded from at least the time of ancient Greeks and the early European Anatomists (Ossenberg 1969). However, their use as "racial markers" was not suggested until the turn of this century (Chambellan 1883, Dixon 1900, 1904, Gregory 1916, Le Double 1903, 1906, 1912, Hrdlicka 1920, 1921, 1924, Russell 1900, Sullivan 1925). Nonmetric cranial traits were used primarily as descriptive features in biological anthropology in the early twentieth century (Akabori 1934, Bolk 1931, Hooton 1930, Hrdlicka 1920, Wood Jones 1930, 1933). However, later authors began to examine the genetic nature, heritability, and the usefulness of nonmetric cranial traits for population studies (Ardito 1977, Bennett 1965, A.C. Berry 1974, 1975, Birkby 1973, Blakely 1973, Buikstra 1972a, 1980, Corruccini 1974, Kennedy 1981, Korey 1970, Ossenberg 1969, Rightmire 1972, Saunders 1978, Sjovold 1973). Recently, as with dental nonmetric traits, research using cranial nonmetric traits has focused on population differentiation (Dodo 1987, Dodo et al. 1992, Ishida 1990, Ishida and Dodo 1993, Katayama 1988, Pietrusewsky 1981, 1984, Saunders and Popovich 1978, Sawyer et al. 1978, Sciulli 1990a).

The use of nonmetric cranial traits for population studies was pioneered by Laughlin and Jorgensen (1956). In their study, the assumption was made that the characters were largely under genetic control and that the distribution of expression was Mendelian. As Sofaer (1970) has suggested, the assumption that nonmetric traits exhibit Mendelian distributions is erroneous. However, the assertions that nonmetric traits are largely under genetic control made them particularly attractive for population studies in part because traditional metric variables were losing favor as measures of population distance (Molto 1983).

Most of the significant work on nonmetric skeletal morphology comes from studies of *Mus musculus* (Searle 1954a, b, Grüneberg 1955, Carpenter et al. 1957, Deol et al. 1957, Deol and Truslove 1957, Deol 1958, Truslove 1961, Grewal 1962, R.J. Berry 1963, 1964, 1967, and 1968). These studies provide evidence for nonmetric skeletal variation being the product of multiple alleles acting at a large number of loci, in conjunction with the influence of non-genetic factors, all under the action of some sort of threshold mechanism (Grüneberg 1963). Sjovold (1977) contends that the large number of factors influencing the expression of nonmetric skeletal traits makes it reasonable to assume that they are normally distributed.

A study by Berry and Berry (1967) is generally cited as being the major stimulus for recent human population studies using cranial nonmetric traits. Although earlier authors had written extensive descriptions of many nonmetric traits, these were written as typological classifications of "interesting anomalies." Berry and Berry (1967) examined a total of 585 adult crania using 30 nonmetric cranial variants recognized for human populations and used these traits to estimate biological distances between large geographical groups. The sample consisted of crania from North and South America, Burma, India, Nigeria, Palestine, and Egypt. The researchers found several good correlations between populations but also some "odd likenesses" such as those found between Egyptians and the Ashanti of Nigeria.

No distinction could be made between West Africans and North American Indians. The Berrys dismissed these later findings as mere aberrations, and contended that cranial nonmetrics were still a reliable measure of population divergence. The Berrys' major contribution incluided a list of reliably observed cranial traits and the application of the multivariate Smith-Grewal statistic, which is an estimation of biological distance. The Berrys proposed that the traits used in this study were minimally affected by sex, age, side, and environmental factors and were, therefore, superior to metric variables for estimating population distance. This did not go unnoticed by the scientific community and a number of comparative studies between metric and nonmetric traits were published (e.g., Rightmire 1972, Carpenter 1976, Cheverud et al. 1979). Opinions coalesced into two factions: those who thought nonmetric traits were a better discriminating tool for biological distance than metric traits and those who clearly felt the opposite. What most of these studies tended to obscure was the fact that the major problems with the Berry's and other contemporaneous studies were methodological, not necessarily theoretical.

Many researchers have criticized the Berrys' early study for methodological problems. Perhaps the most comprehensive and useful of these critiques is provided by

Corruccini (1974). Corruccini argues that the Berrys did not consider a variety of parameters which can greatly influence the outcome of population distance studies using nonmetric traits. The first of these is their examination of sex differences. The Berrys have proposed that there are no significant differences between sexes in the expression of nonmetric traits. Corruccini points out that they did not separate populations to look for sexual dimorphism and that the intermingling of populations can have a "cancelling effect" on populations with differential sexual dimorphism. Corruccini also points out that the Berrys did not consider age differences or side asymmetry in their study, and that these factors could very well bias their results.

Although there are some problems with the Berrys' early study, it does offer a clear and fairly precise description of cranial nonmetric traits. This type of standardization is crucial for the correct interpretation of other researchers work (see Dahlberg 1956). The Berrys' work represents a landmark in the study of human nonmetric variation. Later studies have offered both support and challenges to the use of nonmetric traits in population distance research. After the Berrys' study, a plethora of studies using nonmetric cranial traits and the Grewal-Smith statistic were published (e.g., Pietrusewsky 1969, 1971, Jantz 1970, Kellock and Parsons 1970b, Buikstra 1972a, Finnegan 1972, Lane and Sublett 1972, Birkby 1973, Gaherty 1974, Cybulski 1975, McWilliams 1974, Corruccini 1974).

The Berrys' study created a great deal of interest in nonmetric cranial morphology, but many of the subsequent studies were heavily influenced by the work of J.E. Anderson (1964, 1968a, b, 1969, 1972, Wright and Anderson 1963). A considerable volume of work was generated by researchers either trained or influenced by Anderson (i.e., Ossenberg 1969, 1974, 1976, Pietrusewsky 1969, Webb 1969, Gaherty 1970, Lane and Sublett 1972, Cybulski 1975). Ossenberg's landmark study (1969) particularly reflected the tenor of this research. Ossenberg estimated the inter- and intra-regional distance of 23 Amerindian population samples using a battery of 37 nonmetric cranial traits. Her study was among the first to demonstrate considerable biological diversity within a geographical region, which led her to conclude that the diversity was largely due to genetic differences caused by inbreeding and genetic drift. This conclusion gave good evidence that nonmetric cranial traits offered great potential for regional studies because of the detectable variance in trait expression between closely related groups. Others have supported this position (R.J. Berry 1968, Kennedy 1981, Korey 1970, Molto 1983, Suchey 1975). Ossenberg was also the first to closely examine the effects of age, sex, and side on cranial nonmetric trait expression.

Most early research on the genetic basis of nonmetric cranial variation was done using animals not closely biologically related to humans (i.e., nonprimates). However, later researchers began looking at primate species to test the reliability of nonmetric traits for population distance studies (e.g., Berry and Berry 1971, Cheverud and Buikstra 1978, 1981, 1982, Chiarelli 1971, McGrath et al. 1984, and others). It remains unclear what the proportion of genetic determination is for nonmetric cranial traits in humans. No large human pedigree samples, living or dead, have been compiled for these traits.

Berry and Berry (1971) examined four species of primates including *Hylobates lar*, *Pan troglodytes*, *Pongo pymaeus*, and *Gorilla gorilla*. Thirty variants were recorded and the C.A.B. Smith Mean Measure of Divergence (Grewal 1962) was used to assess biological distance. The authors found that subspecies within each species differed systematically. This systematic difference was attributed to geographic and spatial reproductive barriers. In the case of *Gorilla gorilla*, subspecies separated by a mountain range exhibited a higher measure of divergence than those separated by a greater geographical distance along a river drainage basin. The Berrys used this finding to further bolster their claims of the reliability of nonmetric variants for estimation of population distance. Later studies by Cheverud and Buikstra (1981, 1982) appear to support this contention.

In 1981, Cheverud and Buikstra initiated a series of studies using a skeletal collection of rhesus macaques from Cayo Santiago. This population was collected over a 25-year period (1956-1981) and was comprised of 297 individuals, representing both sexes and all ages. Using 24 cranial nonmetric traits, Cheverud and Buikstra examined the genetic nature of these variables. Their results resembled much of the earlier nonprimate research in nonmetric variation. They found that heritability values for all of the variations fell in the significant range and that both hyperstotic and hypostotic variables tended to have higher values than other classes of traits. This was again attributed to the functional differences of traits (i.e., the Functional Matrix Model).

In an examination of relative heritability values by Cheverud and Buikstra (1982) between foraminal and hyperstotic traits, it was found that hyperstotic values were significantly higher (h^2=0.798) than those for foraminal traits (h^2=0.352). It was also found that, overall, nonmetric traits tended to have higher heritability values (h^2=0.528) than metric variables (h^2=0.317). This last finding should be accepted cautiously because of the significantly different number of traits in each category (56 metric traits and 14 nonmetric traits, respectively). Richtsmeier et al. (1984) extended this study, again using the rhesus macaques of Cayo Santiago, to look at the correlations between metric and nonmetric variations. Canonical correlations ranging between 0.80 and 0.95 were obtained, indicating a very close relationship between the two sets of variables. Richtsmeier and co-workers interpreted this finding to reflect a common developmental pathway shared by cranial size and shape characteristics and nonmetric traits.

Overall, studies of nonhuman primates have given a slightly different picture of the reliability of nonmetric traits for population distance studies. Genetic factors seem to be somewhat more important than nongenetic factors in the expression of nonmetric traits (Cheverud and Buikstra 1981), and all of the nonmetric traits examined showed significant heritability values. A common developmental pathway for metric and nonmetric variants has also been proposed (Richtsmeier et al. 1984).

Discussion

Much time has been devoted to debating the relative utility of metric versus nonmetric traits for the estimation of population distance (e.g., Berry and Berry 1967, Carpenter 1976, Cheverud et al. 1979, Ossenberg 1977, Rightmire 1972). As discussed above, it is probably the case that neither is free from environmental influence, and both types of traits are likely polygenic in origin. Thus, in my opinion, neither metric nor nonmetric traits are inherently more useful for estimating biological distance. It has been suggested by many researchers that metric and nonmetric data produce complementary results (e.g., Sanghvi 1953, Laughlin and Jorgensen 1956, Pollitzer 1958, Brothwell 1959, DeVilliers 1968, Howells 1970, 1972, Jantz 1970, 1974, Rightmire 1972, Corruccini 1974, Trinkaus 1978, Kennedy 1981, Molto 1983). Although this approach is certainly more desirable than reliance on one type of trait, the selection of variables for this study was influenced by the nature of the skeletal remains. Selection of traits, nonmetric versus metric, was largely dependent here on the relative preservation of the samples which ranged from extremely poor in the *Santa Catalina de Guale* sample to excellent in the Irene mound series and the *Santa Catalina de Guale de Santa Maria* sample. Because metric variables require relatively complete skeletons, their use here was not appropriate.

As Scott and Turner point out, "a biological trait can be useful in historical-evolutionary analyses only if a significant component of its variation is genetic" (1988:100). Research suggests that nonmetric dental traits are under complex genetic control and have a sufficiently strong genetic component to make them useful for assessing biological relationships and microevolutionary trends (Goose and Lee 1971, Lundstrom 1977, Biggerstaff 1975, Garn 1977, Harris and Bailit 1980, Kolakowski et al. 1980, Corruccini et al. 1986, Nichol 1989, Townsend et al. 1990). The distances obtained from the frequencies of many of these traits reflect phenotypic rather genotypic affinity because of their probable polygenic mode of inheritance. However, many of the other variables studied by physical anthropologists are also polygenically inherited (that is, more than one gene controls their expression).

Saunders (1989:104) has also pointed out that "the biological validity of distance studies of prehistoric samples is difficult to verify." Just because distance statistics suggest that two populations are biologically dissimilar does not necessarily indicate that they are genetically unrelated. Indeed, environmental differences in time and space may cause such differences. Similarly, small biological distances do not necessarily imply genetic relatedness if the populations experienced like environmental conditions. However, these constraints are no different for any other type of traits currently used for discriminating between skeletal populations.

Morphological traits of the tooth crown have been successfully used to discriminate between major geographic groups (e.g., Dahlberg 1945, 1951, Hellman 1929, Hrdlicka 1920, Lasker 1950, Lukacs and Hemphill 1991, Turner 1987a, 1990). Some traits are population specific to the degree that one trait alone can be used to distinguish between groups (e.g., shovel-shaped incisors, Carabelli's trait, and cusp 6) (Scott and Turner 1988). Although ethnic affiliation is useful for many areas of inquiry, morphological dental traits have not been limited strictly to discriminating major geographical groups. Distance statistics derived from tooth morphology can be used to estimate relative degrees of similarity among groups that "diverged from common ancestors many hundreds or thousands of years in the past" (Scott and Turner 1988:103). Most recent dental morphologic studies have focused on this level of differentiation (Greene 1982, Haeussler 1985, Haeussler et al. 1989, Ismagulov and Sekhmbieva 1989, Lukacs 1983, Richards and Telfer 1979, Sciulli 1990b, Sofaer et al. 1986, Turner 1985, 1987a and b). The bulk of this research has concentrated on the delineation of dental variation in Asian and Asian-derived groups. Groups of Asian descent are easily differentiated, in part, because of their morphologically complex dentitions (Scott and Turner 1988:105).

The exact etiology for nonmetric cranial traits remains unclear (Hauser and De Stefano 1989). However, many researchers have argued that the multifactorial hypothesis, which argues for the involvement of many genes and environmental influences, makes these traits acceptable as measures of biological distance (Corruccini 1974, Molto 1983). As with dental nonmetric traits, cranial traits reflect phenotypes and not genotypes. This does not lessen their reliability for estimation of population distance. As Molto (1983:8) observes, "there is ample evidence to support the contention that under natural conditions the genome plays a significant role in the phenotypic manifestation of skeletal variation." Despite the apparent paucity of genetic research involving nonmetric cranial traits in humans, there is ample evidence to support the significant control of expression of these traits by multiple alleles at a large number of loci (Searle 1954a, b, Grüneberg 1955, Carpenter et al. 1957, Deol et al. 1957, Deol and Truslove 1957, Deol 1958, Truslove 1961, Grewal 1962, Grüneberg 1965, R.J. Berry 1963, 1964, 1967, and 1968). As with the expression of dental traits, the expression is likely influenced by environmental factors. Sjovold (1977) has suggested that these factors make it reasonable to assume that nonmetric skeletal traits are normally distributed.

It has been suggested that skeletal population studies should include as many types of traits as possible (e.g., Sanghvi 1953, Laughlin and Jorgensen 1956, Pollitzer 1958, Brothwell 1959, DeVilliers 1968, Howells 1970, 1972, Jantz 1970, 1974, Rightmire 1972, Corruccini 1974, Trinkaus 1978, Kennedy 1981, Molto 1983, Hanihara 1992a). Sokal and Sneath (1963:97) state that "there are no distinct large classes of genes affecting exclusively one class of characters, or affecting special regions of the organism." Thus, no single class of traits should be inherently better than any other class of traits for distinguishing populations. This fact, coupled with evidence that skeletal and dental tissues exhibit differing responses to the environment (A.C. Berry 1976, Sinclair 1978), argues for the inclusion of different classes of traits in distance studies. Cranial nonmetric traits were chosen in addition to dental traits in the present study in part because they have been successfully and extensively used for population microdifferentiation.

The investigation of nonmetric traits in human skeletal remains has undergone a transformation from the descriptive, typological approach used in the first half of this century to a more processual approach currently being applied by most researchers. The focus of this research has been to delineate population movement and change over time (cf., Greene 1982, Haeussler 1985, Lukacs 1983, Richards and Telfer 1979, Sofaer et al. 1986, Turner 1985, 1987a and b). Although in recent years biological distance studies have taken somewhat of a back seat to investigations of health and diet, they remain of crucial importance in deciphering evolutionary histories of peoples, the nature of residence patterns, and appropriate perspectives in which to place paleodemographic and paleopathologic studies (Buikstra et al. 1990). Nonmetric traits offer a unique research tool in these endeavors because (1) they survive well in an archaeological context, (2) they are easily and reliably observed, (3) they are numerous, facilitating polythetic classifications, and (4) they are evolutionarily stable and under relatively tight genetic control.

Nonmetric Trait Selection

Dental Traits

Morphological observations were made on 100 dental crown and root variables using the standardized Arizona State University dental anthropology system (Turner et al. 1991). This system is comprised of a wide range of dental morphological variables, including multitooth expression of a single trait and traits involving a single pair of antimeres. This information facilitates the identification of the most variable tooth or site for trait expression. The ASU system has proved particularly useful for distinguishing between local populations as well as larger regional series (Turner 1985, Scott and Dahlberg 1982). Most of the traits in this study are observed using ordinal scales with several grades, and many are tested using more than one dichotomy of their scale. These multiple analyses allow for an examination of such factors as trait incidence on the results of the statistical analysis.

A pilot study was conducted in April 1988 by the author to determine which traits would be most applicable to the two study populations. Forty-one traits were examined from the ASU system using the *Santa Catalina de Guale de Santa Maria* population sample as a test case. Thirty-five traits from the ASU system were selected on the basis of intra-observer reliability, wear sensitivity, and ease of observation (see Griffin 1989). None of the traits were deleted because of low intraobserver reliability. One trait (radical number) was deleted because of low numbers of observations (i.e., it normally cannot be seen without full exposure of the root). Three of the traits were deleted due to excessive wear sensitivity (in most cases, they could not be observed after the age of 27). Traits deleted due to wear sensitivity included the premolar mesial and distal accessory cusps, the tri-cusped premolar, and the distosagittal ridge. The resulting battery of traits consists of thirty-five dental nonmetric traits and two cranial nonmetric traits along with observations on the presence/absence of teeth, periodontal disease and overall dental wear. The dental morphological traits used in the present study are summarized in Table 3.

Cranial Traits

Morphological observations were made on twenty-four nonmetric cranial traits described by Berry and Berry (1967). There are a great many nonmetric cranial traits which have been described in the literature, but these descriptions generally lack information on the reliability of specific traits in describing and comparing populations. This creates a situation where the researcher must rely to a large degree on precedents set by other workers or on personal preference.

The cranial traits used in this study were chosen from those described by Berry and Berry (1967). The traits selected from this study were chosen on the basis of three criteria: (1) reliability of scoring and observation, (2) demonstrated ability to discriminate populations, and (3) low intercorrelation with sex and age (see Kennedy 1981). The twenty-five traits included in this study are listed in

Table 3. Dental Morphological Traits

Trait		Teeth Observed	References
winging	[WING]	upper central incisors	Enoki and Dahlberg 1958; Dahlberg 1963; Scott 1973
shoveling	[SHOV1] [SHOV2]	upper incisors	Hrdlicka 1920; Dahlberg 1956; 1963; Moorrees 1957; Scott 1973
curvature	[CURV]	upper central incisors	Nichol et al. 1984
double-shoveling	[DSHOV]	upper central incisors	Dahlberg 1956; Turner 1967
interruption groove	[IGROV]	upper lateral incisors	Turner 1967
tuberculum dentale	[TD]	upper lateral incisors	Scott 1973; Turner et al. 1991
canine mesial ridge	[CMR]	upper canines	Morris 1975; Turner et al. 1991
canine distal accessory ridge	[DAR]	upper canines	Scott 1973; 1980; Turner 1967
premolar mesial and distal accessory cusps		upper premolars	Turner 1967
tri-cusped premolars		upper premolars	Turner et al. 1991
distosaggital ridge		upper premolars	Morris et al. 1978
metacone	[METAC]	upper 3rd molars	Turner et al. 1991
hypocone	[HYPO1] [HYPO2]	upper 1st and 2nd molars	Larson 1970; 1978; Scott 1973; Turner et al. 1991
metaconule	[M1C5] [M2C5]	upper 1st and 2nd molars	Harris 1977; Harris and Bailit 1980
Carabelli’s trait	[CARAM1] [CARAM2]	upper 1st and 2nd molars	Dahlberg 1956; 1963; Scott 1973; 1980
parastyle	[PARA]	upper 3rd molar	Katich 1975; Turner et al. 1991
enamel extensions	[EEM1] [EEM2]	upper 1st and 2nd molars	Pedersen 1949
premolar root number	[PRN]	upper premolar 3	Turner 1967; 1981
molar root number	[MRN]	upper 2nd molars	Turner 1967
radical number		all teeth	Turner 1967
peg-shaped incisor	[PSI]	upper lateral incisor	Turner et al. 1991
peg-shaped molar	[PSM]	upper 3rd molar	Turner et al. 1991

(continued on following page)

Table 3, continued

Trait		Teeth Observed	References
odontome	[ODONT]	premolars	Pedersen 1949; Alexandersen 1970
first lower premolar lingual cusp variation	[LP3V]	lower 1st premolars	Pedersen 1949; Kraus and Furr 1953; Scott 1973
second lower premolar lingual cusp variation	[LP4V]	lower 2nd premolars	Pedersen 1949; Kraus and Furr 1953; Scott 1973
anterior fovea	[AF]	lower 1st molar	Hrdlicka 1924; Turner et al. 1991
groove pattern	[GPM1] [GPM2]	lower 1st and 2nd molars	Gregory 1916; Hellman 1929; Jorgensen 1955
cusp number	[CNM1] [CNM2]	lower 1st and 2nd molars	Gregory 1916; Hellman 1929; Turner 1967
deflecting wrinkle	[DW]	lower 1st molars	Weidenreich 1937; Scott and Dahlberg 1982; Turner et al. 1991
distal trigonid crest	[DTC]	lower 1st molars	Hrdlicka 1924
protostylid	[PM1] [PM2]	lower 1st and 2nd molars	Dahlberg 1950; 1956; 1963; Turner 1967; Scott 1973
cusp 5	[C5M1] [C5M2]	lower 1st and 2nd molars	Turner 1970; Scott and Dahlberg 1982; Turner et al. 1991
cusp 6	[C6M1] [C6M2]	lower 1st and 2nd molars	Turner 1970; Scott 1973; Scott and Dahlberg 1982; Turner et al. 1991
cusp 7	[C7M1] [C7M2]	lower 1st and 2nd molars	Turner 1970; Turner et al. 1991
canine root number		lower canines	Turner 1967
Tomes' root	[TR]	lower 1st premolar	Tomes 1923; Turner et al. 1991
first molar root number		lower 1st molar	Turner 1967; Turner et al. 1991
second molar root number		lower 2nd molar	Turner 1967; Turner et al. 1991
torsomolar angle	[TA]	lower 3rd molar	Neiberger 1978; Turner et al. 1991
palatine torus	[PTOR]	palate	Miller and Roth 1940; Turner et al. 1991
mandibular torus	[MTOR]	mandible	Johnson et al. 1965; Morris 1970

Table 4 using an organizational schema devised by Ossenberg (1970). Ossenberg's schema organizes traits according to major regions of the skull and hypostotic-hyperstotic classification. Twenty of the traits fit into Ossenberg's schema, the other five traits are emissary foramina. All of the traits used here are observed recording presence or absence of the trait. No ordinal scales are used because these tend to be highly subjective (see Kennedy 1981).

The computer coding forms are contained in Appendix A. The coding forms record information on age, sex, tooth presence and condition, and both cranial and dental trait observations from both left and right sides (the latter facilitates side asymmetry analysis). Some of the traits used in this study are observable in some populations but not in others. This is mainly due to differential preservation. Although these traits are not particularly useful for the present analysis, they may be important for future comparative studies.

Bilateral Asymmetry

Many nonmetric variables can occur bilaterally. That is, a trait occurring on the left side of the skeleton is usually mirrored on the right reflecting the general bilaterally symmetrical nature of vertebrates. Occasionally a trait will occur on one side only, making the expression

Table 4. Cranial Morphological Traits

Trait	Abreviation	References
I. Sutural bones of the cranial vault		
posterior		
(1) ossicle at lambda	[OAL]	Bennett 1965; Berry and Berry 1967; Molto 1983
(2) lambdoid ossicles	[LO]	Bennett 1965; Berry and Berry 1967; Herzog 1968
(3) ossicle at asterion	[OAA]	Berry and Berry 1967; Suchey 1975; Molto 1983
anterior		
(4) parietal notch bone	[PNB]	Oetteking 1930; Berry and Berry 1967; Ossenberg 1969; Molto 1983
(5) epipteric bone	[EPB]	Wood-Jones 1930; Berry and Berry 1967; Molto 1983
(6) bregmatic bone	[BB]	Wood-Jones 1930; Berry and Berry 1967
(7) coronal ossicle	[CO]	Wood-Jones 1930; Sublett 1966; Berry and Berry 1967
II. Frontal bone observations		
(8) metopism	[MET]	Limson 1924; Bolk 1931; Torgersen 1951; Berry and Berry 1967
(9) fronto-temporal articulation	[FTA]	Collins 1926; 1930; Berry and Berry 1967; Ossenberg 1969
(10) supraorbital foramen	[SF]	LeDouble 1903; Berry and Berry 1967; Ossenberg 1969; Korey 1970
(11) frontal notch	[FN]	Wood-Jones 1930; Berry and Berry 1967
III. Variations of the cranial base and maxilla		
(12) auditory torus	[AT]	Wood-Jones 1930; Berry and Berry 1967
(13) foramen of Huschke	[FOH]	Anderson 1962; Berry and Berry 1967; Molto 1983
(14) condylar facet double	[CFD]	Anderson 1962; Berry and Berry 1967; Kennedy 1981
(15) precondylar tubercle	[PT]	Inglemark 1947; Berry and Berry 1967
(16) foramen ovale	[FO]	Wood-Jones 1930; Berry and Berry 1967
(17) foramen spinosum	[FS]	Berry and Berry 1967; Korey 1970; Suchey 1975
(18) accessory lessor palatine foramen	[APF]	Berry and Berry 1967
(19) palatine torus	[PAT]	Suzuki and Sakai 1960; Berry and Berry 1967; Turner et al. 1991
(20) maxillary torus	[MAT]	Berry and Berry 1967
IV. Emissary foramina		
(21) parietal foramen	[PF]	Berry and Berry 1967; Ossenberg 1969; Molto 1983
(22) posterior condylar canal patent	[PCC]	Boyd 1930; Berry and Berry 1967; Ossenberg 1969; Korey 1970
(23) mastoid foramen exs.	[MF]	Berry and Berry 1967
(24) anterior condylar canal double	[ACC]	Berry and Berry 1967; Korey 1970; Ossenberg 1969; Molto 1983
(25) zygomatico-facial foramen	[ZFF]	Berry and Berry 1967; Molto 1983

bilaterally asymmetrical. The implications of asymmetrical trait expression is unclear.

Ossenberg (1981) has proposed that unilateral trait expression is genetic in origin. She suggests that as genetic liability for a trait increases so does the probability of bilateral occurrence. This has been disputed by McGrath et al. (1984). They point out that no apparent physical or mechanical process could explain the progression from unilateral to bilateral expression, if the trait fits the liability model for quasi-continuous traits. Other authors have suggested that bilateral expression may be developmentally progressive, increasing in incidence with developmental age (Korey 1970, 1980, Saunders 1978, Winder 1981). Saunders (1989) has also suggested that unilateral occurrence appears to be a transitional developmental stage in which individuals may remain permanently due to "random environmental disruptions."

In early research, investigators, while realizing that bilateral asymmetry was present, did not determine how commonly unilateral expression occurs. Trinkaus (1978) examined skeletal samples of African, European, and Amerindian origin, to study just this problem. His finding was that unilateral frequencies of over 10% occurred for over 50% of nonmetric traits. Trinkaus believes, although he gives no direct evidence, that unilateral expression is the result of environmental stress, resulting in physiological stresses on individual tissues. Earlier research gives some evidence for this assertion (see Chamay and Tschantz 1972, and Hoyte and Enlow 1966).

Research using nonhuman species also lends some evidence for environmental influence on bilateral asymmetry (Bader 1965, Howe and Parsons 1967, Nass 1982, Siegal and Doyle 1975a and b, Siegal et al. 1977). Korey (1980) echoes the opinion of Trinkaus that unilateral expression is possibly stress related and also proposes that it could be related to age. Ossenberg (1981) presents another explanation for this phenomenon by proposing a theory of multiple thresholds (see Reich et al. 1972). She proposes that the difference between unilateral expression for a trait and bilateral expression for a trait depends on ones relationship to a second additive genetic threshold (the first assumed to determine expression/nonexpression). Although not unplausible, theories of this type are inherently difficult to prove beyond a strictly theoretical framework.

Studies with human subjects have come to two disparate conclusions regarding the cause of bilateral asymmetry. Sellevold (1980) and Axelesson and Hedegard (1981) studied mandibular tori in prehistoric Norse and historic Eskimo, and Icelandic school children, respectively. Both studies concluded that unilateral expression was primarily the result of environmental stress. On the other side of the issue, Noss and others (1983) and Mayhall and Saunders (1986), in studies among Pima Indians and Eskimos, found that there was no conclusive evidence for environmental stress as the causal agent in bilateral trait expression in molar teeth. The differences in these studies may simply reflect the relative genetic stability of the human dentition (see Sofaer et al. 1986).

In another aspect of the same issue, Green et al. (1979) propose that a new approach in the study of bilateral asymmetry is necessary. They contend that to test for independence between sides, one cannot base an opinion, as some investigators have (e.g., Finnegan 1978), on whether the frequencies are the same on both sides. This is analogous to saying: "if the frequency of right blue eyes and the frequency of left blue eyes is the same then the traits are independent." Nor can one say that if the frequencies are different then the traits are independent. In fact, Green and others (1979) suggest that independence has nothing to do with bilateral trait expression and the appropriate way to study bilateral traits is to consider both sides and use the total number of times the trait occurs divided by the total number of sides observed. In retrospect, this may seem to be the obvious approach. However, early researchers simply scored whether a trait occurred at all on either side or considered only one side, ignoring the implications of unilateral expression.

Each tooth in the normal human dentition exists in two copies. That is, each tooth on the left side is duplicated on the right. Scott (1980) outlines three commonly employed counting procedures used for dental morphologic traits. The first procedure, total tooth count, scores all antimeres for each trait (Hellman 1929, Dahlberg 1963a, Sofaer et al. 1972b, Harris 1977). This method tends to inflate sample size unnecessarily. For the type of statistical analyses typically used for nonmetric dental traits, it is desirable not to artificially inflate the sample by counting both antimeres. Some researchers have chosen to overcome this problem by scoring only one side of the dentition in each individual. This procedure, referred to as the unilateral count method, restricts scoring entirely to right or left antimeres (Smith 1977, Goose 1977, Kirveskari 1977, Axelsson and Kirveskari 1977). As some teeth will not be observable for various reasons (e.g., tooth loss, attrition, carious lesions), this approach tends to reduce sample size. This method seems to unnecessarily restrict the sample size, although some authors (e.g., Zubov and Kahldeyeva 1979) have surmounted this difficulty by observing the antimere if the tooth on the selected side is missing. Turner and Scott (1977) have recommended observation of both antimeres, and the recording of the highest of the two scores as the observation for that individual. This approach, referred to as the individual count method, assumes that the member of a pair of asymmetric antimeres that exhibits the greatest degree of trait expression best represents the genetic potential for that character in that individual (Turner 1967, Turner and Scott 1977, Scott 1977, 1980). Turner and Scott's procedure eliminates any artificial inflation of the sample while at the same time maximizing the available information.

For the present investigation, twenty of the cranial nonmetric traits are bilateral (occurring on left and right sides). For bilateral traits, presence on either side is considered "present". This method was chosen instead of "total side frequency" (Ossenberg 1981). Researchers that favor the individual scoring method used here rather than "total side frequency" (e.g., Korey 1970, Buikstra 1972a, Birkby 1973, Suchey 1975, Saunders 1978) point out that (1) it is more realistic to treat individuals, rather than sides, as members of a population, (2) because of the age-dependency of the proportion of bilateral occurrence, the side method exaggerates the effect of age-regression in variant incidence, and (3) the side method artificially inflates sample size and introduces redundant information deriving from the strong positive correlation in trait frequency between sides.

It should also be noted that the total side incidence method may bias the sample. When calculating distance statistics, the variance is stabilized by angular transformations of trait frequencies to remove sampling error. It would seem, then, that the total side incidence method would maximize sample size without affecting distance calculations. However, considering that the archaeological skeletal record may be biased towards robust, young, males (because their remains are more durable than other members of the population) this method may amplify an already pervasive problem. That is, because robust, young, males will likely have more "sides" that are observable compared to less robust individuals (which may at best have only one side to observe), the samples will obviously overrepresent a segment of the population. Thus, total side incidence may needlessly introduce yet another source of bias where there are already many sources of sampling error.

Age and Sex Estimation

One of the assumptions made when choosing traits for population distance studies is that groups belonging to the same population will exhibit no significant differences in trait expression. Comparisons which make use of traits with a known bias towards members of a particular group (e.g., sex, age, status) whould be considered invalid (Spence 1971, Kennedy 1981).

Some researchers have suggested that nonmetric traits vary independently of sex and age (Berry and Berry 1967). It has been demonstrated that sex and age dependence was tested inappropriately in their study (Corrucini 1974). Other researchers have demonstrated that there are significant inter- and intrapopulation sex and age variation in nonmetric trait frequencies (A.C. Berry 1975, Buikstra 1972b, Corruccini 1974, Finnegan 1978, Garn et al. 1966b, Green et al. 1979, Konigsberg 1987, Ossenberg 1969, 1970, Scott 1977, Sjovold 1973). Of these, Corruccini (1974) offers, perhaps, the broadest and most useful critique of methodology in nonmetric trait research. For his review, Corruccini examined 321 crania from the Terry Collection, controlling for sex, age, and population affiliation. Seventy-two cranial traits were used, consisting of those from the Berrys' (1967) research and others deemed useful from later research. Sexual dimorphism was found to be significant within and between populations, and Corruccini points out that this was a major problem with earlier research (e.g., Berry and Berry 1967). The second parameter, that of age, was also found to have an influence on the value obtained from the final distance equation. The ages considered ranged from nineteen to sixty-five. It was found that there is a systematic change of large magnitude for a few traits and significant cumulative age divergence over many traits. Other researchers have encountered similar age and sex biases (Kennedy 1981, Molto 1983, Pietrusewsky 1984, Ossenberg 1969). Because of these relationships, sex and age were estimated for each individual in the samples and were considered as possible biases in estimation of population affinity.

There are three methods of dealing with the problem of age and sex bias in nonmetric trait analysis (Kennedy 1981). These are: (1) eliminate those traits which display a bias from distance calculations, (2) use statistical procedures which account for any existing bias, or (3) structure the analysis so as to avoid the affects of any bias. The first option was chosen here, and all traits which demonstrated an age or sex influence in expression were deleted from the estimation of population distance.

Age Estimation

The ages for the Santa Maria sample were estimated by K.F. Russell (Larsen and Russell 1989). Ages for the Santa Catalina sample were provided by Russell and coworkers

(1990). The ages for the *Santa Maria de Yamassee* sample were estimated by K.F. Russell and Scott W. Simpson (1992). There were no accurate age estimations available for the Ledford Island series or the North Carolina coastal population samples. Ages were therefore estimated by the author. For all of the population samples except for Santa Catalina and the North Carolina coastal populations, preadult ages were estimated based on epiphyseal union, dental calcification, and dental eruption (Ubelaker 1989). The standards used for epiphyseal union were those described by Krogman and Iscan (1986:50-83), and the standards for dental calcification and dental eruption were those set by Ubelaker (1984:46-47). Due to the overall poor bone preservation of the Santa Catalina sample and the nature of ossuary interments in the case of the North Carolina coastal samples, only dental remains could be used to systematically estimate the ages-at-death. Therefore, dental eruption and dental wear were the primary criteria for estimation of age-at-death for these samples.

The adults from the Santa Maria, *Santa Maria de Yamassee*, and Ledford Island cemeteries were assigned ages-at-death based on a number of criteria. The primary criteria were dental functional wear (Miles 1963, 1978) and the metamorphosis of the auricular surface of the innominate (Lovejoy et al. 1985b). The Miles method utilizes preadult erupted dentitions to approximate the number of years an individual's teeth have been in functional occlusion. The advantage of this method is that it is specifically suited for each population to which it is applied. Using the above criteria and a number of other independent indicators of age, the ages-at-death for the Santa Maria and *Santa Maria de Yamassee* samples were calculated using a multifactorial aging technique (see Lovejoy et al. 1985a). Age estimation was possible for 955 individuals out of a total of 1537 across all of the population samples. Table 5 reports the individual sample age-at-death summaries.

Because age-at-death was estimated by more than one observer, inter-observer error for age estimation was tested between estimates of the author and the estimates of Russell and coworkers. The Santa Maria and *Santa Maria de Yamassee* population samples were used as test cases. Over 75% of the age-at-death estimates for the *Santa Maria de Yamassee* sample (N=73) varied by less than 5 years and 94.5% by less than 10 years. For the Santa Maria sample (N=112) 81.3% of the estimates varied by less than 5 years and 98.2% by less than 10 years. Table 6 presents the results of this test. For the purposes of this analysis this degree of interobserver error is not significant.

Table 5. Age-at-Death Summaries

Age Class	Irene Md	SCdG[1]	SCdG-SM[2]	SMdY[3]	N.Carolina Ossuaries	Ledford Is
0-5	25 (14.4)	33 (11.3)	23 (19.7)	20 (24.1)	15 (16.7)	69 (34.0)
6-10	13 (7.5)	39 (13.4)	8 (6.8)	11 (13.3)	5 (5.5)	21 (10.3)
11-15	18 (10.4)	23 (7.9)	4 (3.4)	4 (4.8)	2 (2.3)	8 (3.9)
16-20	42 (24.3)	50 (17.1)	7 (6.0)	3 (3.6)	6 (6.7)	15 (7.4)
21-25	35 (20.2)	44 (15.0)	3 (2.6)	14 (16.9)	7 (7.8)	30 (14.8)
26-30	12 (7.0)	43 (14.7)	5 (4.3)	3 (3.6)	5 (5.5)	28 (13.8)
31-35	7 (4.0)	32 (11.0)	8 (6.8)	5 (6.0)	27 (30.0)	18 (8.9)
36-40	11 (6.4)	24 (8.2)	15 (12.8)	11 (13.2)	17 (18.9)	10 (4.9)
41-45	6 (3.5)	4 (1.4)	22 (18.8)	9 (10.8)	5 (5.5)	4 (2.0)
46-50	4 (2.3)	0 (0.0)	14 (12.0)	3 (3.6)	1 (1.1)	0 (0.0)
51-55	0 (0.0)	0 (0.0)	7 (6.0)	0 (0.0)	0 (0.0)	0 (0.0)
56-60	0 (0.0)	0 (0.0)	1 (0.8)	0 (0.0)	0 (0.0)	0 (0.0)
Totals	173 100.0	292 100.0	117 100.0	83 100.0	90 100.0	203 100.0

[1] Santa Catalina de Guale
[2] Santa Catalina de Guale de Santa Maria
[3] Santa Maria de Yamassee

Table 6. Results of Interobserver Reliability Analysis

Estimate varied by	SCdG-SM*			SMdY**		
	N	%	cum. %	N	%	cum. %
0	41	36.6	36.6	21	28.7	28.7
±1	9	8.0	44.6	12	0.8	29.5
±2	11	9.9	54.5	9	28.0	57.5
±3	11	9.8	64.3	6	8.2	65.7
±4	7	6.2	70.5	2	2.7	68.5
±5	12	10.8	81.3	5	6.8	75.3
<10	19	16.9	98.2	14	19.2	94.5
>10	2	1.8	100.0	4	5.5	100.0

*Santa Catalina de Guale de Santa Maria
**Santa Maria de Yamassee

Researchers have come to various conclusions regarding the relationship between age and the expression of nonmetric traits. Ossenberg (1970) has noted a slight tendency for hyperostotic cranial traits to be age progressive, whereas hypostotic cranial traits seem to be slightly age regressive. She suggests that such a slight dependency may be ignored, because it does not greatly alter the significance of group comparisons. Korey (1970) has demonstrated age correlations for several nonmetric traits when immature individuals are included in population samples. Buikstra (1972a) has come to similar conclusions and recommends that individuals younger than twelve years of age be deleted from analyses. As noted earlier, Corruccini (1974) encountered age correlations for some nonmetric traits causing significant cumulative effects on the final distance statistics. Corruccini found that there is a systematic change of large magnitude for a few traits and a significant cumulative age divergence over many traits. It was observed that distances between younger and older members of each sex and population group were statistically significant ($p<0.01$). This finding substantiates earlier claims of age dependence for nonmetric trait expression (Akabori 1934, Ossenberg 1969, Buikstra 1972b).

Obviously, age influence on cranial nonmetric traits has a different meaning from age influence on dental nonmetric traits. Because the osseous skeleton can remodel throughout an individual's life, nonmetric cranial traits may change form according to age. The teeth, however, do not undergo alteration, other than attrition, after they are calcified. Age differences in dental trait expression may indicate a genetic difference between age cohorts. This could substantially alter the outcome of distance equations.

Intrasite age influence on trait incidence was examined via two-dimensional contingency tables. Chi-square and Tau-b statistics were computed for each trait in each sample. The Chi-square statistic calculates the statistical probability that the null hypotheses of no association between variables is true (Thomas 1986). The Tau-b statistic calculates the degree of association between variables (Thomas 1986). Stated differently, the Tau-b statistic gives an indication of how much the knowledge of variable A (age-at-death in this case) improves the estimation of the value of B (each nonmetric trait here) for any given individual. If there is no association, the τ_b should be zero, and a knowledge of A (age-at-death) would not reduce the errors of assigning values for traits. If there is a perfect positive association, the τ_b would be 1. For purposes of analysis, each population was divided into five distinct age categories: 0-10, 11-20, 21-30, 31-40, and

41-60 years of age. The results of this analysis are reported in Table 7.

Examination of Table 7 reveals a number of traits which are influenced by age. Some traits in the Santa Maria and the North Carolina coastal samples show an apparent directional influence of large magnitude, indicated by high τ_b values, but the relationship is not statistically significant ($p<0.05$). These traits include lower first molar cusp six and anterior fovea in the Santa Maria sample, and deflecting wrinkle, distal trigonid crest, lower first molar protostylid, and lower first molar cusp five in the North Carolina coastal samples. Small sample size is likely the cause for these apparent relationships.

There are also a number of traits which show statistically significant relationships between trait incidence and age-at-death but have low τ_b values, indicating a weak association. These traits are indicated in Table 7. As Thomas (1986:426) cautions "even relatively weak associations can prove statistically significant, provided a large enough sample is involved." While these relationships are clearly statistically significant, they are also clearly weak. This type of association will be disregarded here.

Table 7. Intrasite Variations with Age

		Irene Mound					Santa Catalina					Santa Maria			
Trait	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p
SHOV1	53	0.125	10.623	4	0.031[1]	62	-0.163	23.574	20	0.261	43	0.077	20.061	16	0.217
SHOV2	53	0.194	8.263	12	0.764	86	0.155	24.952	32	0.808	42	0.203	24.367	20	0.227
CURV	53	0.123	1.367	2	0.505	65	0.204	9.836	8	0.277	49	-0.121	7.852	12	0.797
DSHOV	52	0.195	9.479	10	0.487	65	-0.141	31.981	20	0.044[1]	48	0.120	24.610	20	0.217
IGROV	53	0.065	6.682	6	0.351	67	-0.107	9.947	16	0.301	44	-0.011	10.580	12	0.565
METAC	58	0.077	4.948	8	0.763	116	0.022	20.603	18	0.300	34	0.227	16.988	16	0.386
HYPO1	68	0.212	3.518	2	0.172	173	0.088	13.188	12	0.356	51	0.318	15.070	12	0.238
HYPO2	66	0.317	15.836	8	0.045[1]	149	0.255	38.907	24	0.028[1]	38	0.176	18.356	16	0.303
M1C5	58	-0.299	8.460	6	0.206	113	0.107	12.549	16	0.705	34	-0.020	9.132	8	0.331
M2C5	57	-0.170	2.682	4	0.612	101	0.184	18.955	20	0.525	25	0.163	4.578	4	0.333
CARAM1	66	-0.063	6.514	12	0.888	97	0.051	33.855	21	0.038[1]	31	-0.123	13.138	12	0.359
CARAM2	64	-0.186	3.395	4	0.494	72	0.009	1.238	3	0.744	24	-0.270	3.310	4	0.507
PARA	58	*	*	*	*	95	-0.109	13.304	15	0.579	37	0.015	2.493	4	0.646
PSI	53	*	*	*	*	80	0.144	3.701	4	0.448	50	*	*	*	*
PSM	58	-0.118	1.204	2	0.548	101	-0.388	22.021	3	0.000[1]	41	0.013	2.055	4	0.726
AF	38	0.092	0.549	1	0.459	82	0.322	20.434	8	0.009[1]	27	-0.571	19.137	12	0.085
GPM1	57	-0.155	2.116	2	0.347	142	-0.001	8.656	6	0.194	31	-0.109	6.617	8	0.578
GPM2	58	0.309	8.284	4	0.082	140	0.066	10.641	6	0.100	24	-0.077	3.651	6	0.724
CNM1	54	-0.249	6.927	6	0.328	130	-0.182	7.973	6	0.240	36	-0.156	1.703	3	0.636
CNM2	54	-0.215	7.311	4	0.120	117	-0.225	13.012	6	0.043[1]	27	-0.081	10.583	8	0.226
DW	3	*	*	*	*	56	-0.192	3.544	3	0.315	22	-0.279	2.729	3	0.435
DTC	15	-0.196	0.967	1	0.325	82	0.125	2.950	2	0.229	22	-0.048	0.095	1	0.758
PM1	57	-0.104	5.917	4	0.205	71	-0.137	4.970	4	0.290	21	-0.043	9.468	8	0.304
C5M1	54	0.199	3.518	6	0.742	128	-0.002	5.800	6	0.446	35	-0.163	11.127	12	0.518
C5M2	54	0.145	5.372	8	0.717	114	0.263	41.447	15	0.000[1]	24	0.204	14.069	12	0.296
C6M1	54	-0.251	5.529	8	0.700	128	-0.122	23.862	12	0.021[1]	30	-0.478	13.144	12	0.359
C6M2	54	-0.286	7.079	6	0.314	114	-0.240	19.003	15	0.214	21	-0.056	10.008	16	0.866
C7M1	54	-0.160	2.146	2	0.342	128	-0.162	10.222	9	0.333	31	*	*	*	*
C7M2	54	*	*	*	*	114	*	*	*	*	23	*	*	*	*
HNL	67	-0.006	0.618	3	0.892	0	*	*	*	*	68	0.284	12.115	4	0.017[1]
OAL	69	-0.179	3.448	3	0.328	0	*	*	*	*	63	0.028	5.221	4	0.265
LO	69	-0.010	1.169	3	0.760	0	*	*	*	*	63	0.019	2.473	4	0.650
PF	66	-0.053	1.424	3	0.700	0	*	*	*	*	65	0.011	5.855	4	0.210
BB	66	*	*	*	*	0	*	*	*	*	62	-0.046	2.403	4	0.622
MET	68	*	*	*	*	0	*	*	*	*	70	*	*	*	*
CO	66	0.092	3.098	3	0.377	0	*	*	*	*	62	0.120	1.610	4	0.807
EPB	51	-0.205	4.276	3	0.233	0	*	*	*	*	36	0.130	1.098	4	0.895
FTA	50	-0.010	1.668	3	0.644	0	*	*	*	*	38	*	*	*	*
PNB	63	0.019	0.089	3	0.993	0	*	*	*	*	64	0.144	2.378	4	0.667
OAA	61	0.077	2.841	3	0.417	0	*	*	*	*	62	0.083	4.414	4	0.353
AT	68	*	*	*	*	0	*	*	*	*	66	*	*	*	*
FOH	68	-0.083	0.762	3	0.859	0	*	*	*	*	68	-0.056	7.801	4	0.099
MFE	60	0.008	12.157	3	0.007[1]	0	*	*	*	*	63	0.050	4.452	4	0.348
MFA	60	-0.072	2.868	3	0.412	0	*	*	*	*	63	0.130	4.000	4	0.406
CFD	47	*	*	*	*	0	*	*	*	*	36	*	*	*	*
PT	44	*	*	*	*	0	*	*	*	*	33	-0.036	1.040	4	0.904
ACC	47	0.028	2.257	3	0.521	0	*	*	*	*	33	0.155	2.689	4	0.611
FO	48	0.005	1.495	3	0.684	0	*	*	*	*	53	0.121	1.367	4	0.850
FS	44	0.049	4.485	3	0.214	0	*	*	*	*	55	-0.064	4.439	4	0.350
APF	45	-0.117	2.748	3	0.432	0	*	*	*	*	42	-0.132	5.790	4	0.215
PAT	56	0.003	4.176	3	0.243	0	*	*	*	*	57	0.157	3.892	4	0.421
MAT	58	-0.087	1.062	3	0.786	0	*	*	*	*	58	0.451	17.863	4	0.001
ZFF	60	0.104	4.058	3	0.255	0	*	*	*	*	56	-0.117	3.288	4	0.511
SF	66	-0.077	2.370	3	0.499	0	*	*	*	*	66	0.160	6.061	4	0.195
FN	65	0.007	1.802	3	0.614	0	*	*	*	*	65	0.163	4.300	4	0.367
AIF	46	0.141	4.734	3	0.192	0	*	*	*	*	49	0.048	5.162	4	0.271

continued

Table 7, continued

	SMdY					Algonquian					Ledford Island				
Trait	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p
SHOV1	35	-0.387	25.978	12	0.011[1]	5	0.118	7.777	6	0.255	76	-0.202	22.487	12	0.032[1]
SHOV2	33	-0.045	20.301	15	0.161	11	0.305	16.343	15	0.360	72	-0.003	9.306	15	0.861
CURV	34	-0.128	7.034	6	0.318	5	0.144	3.950	2	0.138	77	0.164	4.140	6	0.658
DSHOV	33	-0.089	20.611	18	0.299	5	-0.110	7.777	6	0.255	77	-0.165	21.579	18	0.251
IGROV	29	-0.040	7.061	9	0.631	11	-0.276	9.751	6	0.136	62	-0.136	5.012	9	0.833
METAC	21	0.027	23.519	15	0.074	12	0.084	8.179	8	0.416	37	0.005	1.648	4	0.800
HYPO1	46	0.290	18.414	8	0.018[1]	16	0.170	4.982	6	0.546	90	0.179	6.549	9	0.684
HYPO2	36	0.275	23.115	20	0.283	14	0.316	13.783	12	0.315	66	0.260	26.457	6	0.000[1]
M1C5	40	0.025	14.261	12	0.284	16	0.387	13.300	9	0.150	83	-0.204	12.131	9	0.206
M2C5	31	0.244	4.337	4	0.362	14	0.384	12.105	9	0.207	58	0.020	5.161	6	0.523
CARAM1	40	-0.183	17.892	20	0.595	15	-0.204	11.734	9	0.229	84	-0.239	36.025	21	0.022[1]
CARAM2	30	-0.224	2.740	4	0.602	13	*	*	*	*	60	-0.193	5.163	6	0.523
PARA	21	-0.317	3.542	3	0.315	12	*	*	*	*	37	0.117	1.059	2	0.589
PSI	32	*	*	*	*	11	*	*	*	*	73	*	*	*	*
PSM	24	-0.227	2.567	4	0.633	13	*	*	*	*	39	*	*	*	*
AF	24	0.091	5.822	8	0.667	11	-0.223	2.118	3	0.548	84	-0.003	10.047	9	0.347
GPM1	34	-0.007	3.376	4	0.497	14	0.312	3.386	3	0.336	86	0.121	5.545	3	0.136
GPM2	27	-0.077	3.651	6	0.724	11	0.227	0.960	2	0.619	59	-0.051	1.063	4	0.900
CNM1	35	-0.156	1.703	3	0.636	14	-0.125	2.209	3	0.530	88	-0.312	12.900	6	0.045[1]
CNM2	25	-0.352	12.986	6	0.043[1]	11	-0.092	2.284	4	0.684	59	-0.289	5.782	2	0.056
DW	19	0.098	6.085	6	0.414	5	-0.408	1.185	1	0.276	55	-0.184	9.669	6	0.139
DTC	21	*	*	*	*	6	-0.447	1.588	1	0.208	67	-0.019	0.720	3	0.868
PM1	34	-0.027	2.965	3	0.397	14	-0.498	8.514	6	0.203	88	-0.162	19.038	6	0.004[1]
C5M1	34	-0.157	1.203	4	0.878	14	-0.466	4.869	3	0.182	88	0.181	15.170	9	0.086
C5M2	25	-0.036	21.310	15	0.127	11	0.055	9.417	8	0.308	59	0.161	6.253	6	0.395
C6M1	34	-0.099	4.489	6	0.611	14	0.016	6.225	9	0.717	88	-0.232	19.840	15	0.178
C6M2	25	-0.338	14.451	15	0.492	11	-0.254	2.767	4	0.598	59	-0.291	12.842	6	0.046[1]
C7M1	34	*	*	*	*	14	*	*	*	*	88	-0.099	1.492	3	0.684
C7M2	25	-0.223	2.118	3	0.548	11	*	*	*	*	59	*	*	*	*
HNL	19	0.347	8.270	4	0.082	69	0.122	8.278	4	0.082	29	0.087	6.344	4	0.175
OAL	18	0.311	3.225	4	0.521	68	0.066	3.926	4	0.416	29	-0.436	14.902	4	0.005
LO	19	-0.020	13.150	4	0.011[1]	67	0.104	2.554	4	0.635	30	-0.345	8.514	4	0.074
PF	21	0.057	3.193	4	0.526	69	0.139	4.075	4	0.396	32	0.211	2.975	4	0.562
BB	21	*	*	*	*	69	*	*	*	*	32	*	*	*	*
MET	21	*	*	*	*	69	*	*	*	*	32	*	*	*	*
CO	21	*	*	*	*	67	0.113	3.189	4	0.527	32	-0.030	1.293	4	0.862
EPB	18	*	*	*	*	56	*	*	*	*	26	0.106	2.109	4	0.716
FTA	18	*	*	*	*	60	*	*	*	*	28	*	*	*	*
PNB	20	-0.028	5.732	4	0.220	65	0.011	2.561	4	0.634	29	-0.017	2.499	4	0.645
OAA	20	0.208	3.842	4	0.428	67	0.071	4.731	4	0.316	25	-0.062	2.318	4	0.677
AT	21	*	*	*	*	69	*	*	*	*	32	*	*	*	*
FOH	21	-0.625	13.975	4	0.007	65	-0.011	5.553	4	0.235	32	-0.309	6.890	4	0.142
MFE	17	-0.182	1.694	4	0.792	66	0.065	2.427	4	0.658	24	-0.070	14.252	4	0.007[1]
MFA	16	0.294	2.626	4	0.622	67	0.013	1.519	4	0.823	24	-0.043	2.955	4	0.565
CFD	16	*	*	*	*	45	*	*	*	*	19	*	*	*	*
PT	16	*	*	*	*	47	-0.027	0.946	4	0.918	18	0.000	3.561	4	0.469
ACC	14	0.018	1.243	3	0.743	50	0.177	5.092	4	0.278	20	-0.028	3.469	4	0.483
FO	16	*	*	*	*	62	0.194	7.409	4	0.116	25	0.000	1.049	4	0.902
FS	16	0.181	1.718	4	0.787	60	-0.224	4.697	4	0.320	25	0.000	2.158	4	0.707
APF	12	-0.306	4.164	2	0.125	45	0.227	5.584	4	0.232	21	-0.221	3.590	4	0.464
PAT	18	-0.082	6.717	4	0.152	54	-0.118	1.921	4	0.750	29	*	*	*	*
MAT	18	0.228	4.182	4	0.382	51	*	*	*	*	31	0.169	5.268	4	0.261
ZFF	18	0.040	7.223	4	0.125	64	-0.027	6.534	4	0.163	29	-0.282	10.495	4	0.033[1]
SF	20	0.305	3.452	4	0.485	67	0.058	2.595	4	0.628	32	0.063	2.528	4	0.640
FN	20	-0.051	7.029	4	0.134	68	0.034	7.197	4	0.126	32	0.204	3.989	4	0.407
AIF	12	*	*	*	*	46	0.169	4.954	4	0.292	27	0.033	6.000	4	0.199

*no variation in trait score

[1] low Tau-b, statistically significant

Examination of Table 7 reveals several traits which are both strongly (high τ_b) and significantly ($p<0.05$) affected by age in at least one of the samples. These traits are maxillary torus in the Santa Maria sample, foramen of Huschke in the *Santa Maria de Yamassee* sample, and ossicle at lambda in the Ledford Island sample. These traits will be dropped from the estimation of population distance.

Sex Estimation

A number of criteria were used to estimate the sex of individuals from each sample (Russell et al. 1990, Larsen and Russell 1989). Sex was estimated for the adults only, because of the difficulties of deriving sex estimation in preadults (Ubelaker 1989). The primary criteria for sex estimation involved sex-specific characteristics of the os pubis (Phenice 1969) and overall pelvic morphology, including characteristics of the sciatic notch, subpubic angle, size of the obturator foramen and acetabulum, the type and morphology of the preauricular sulcus, and the presence or absence of pubic parturition scars (Bass 1987). The pubic ventral arc and subpubic concavity are present in females and absent in males. The ischio-pubic ramus consists of a sharp ridge in females, although it is flat in males. The sciatic notch, subpubic angle, and pubic symphysis are wide in females and narrow in males. With regard to cranial features, females tend to have smaller mastoid processes and supraorbital tori and a smooth nuchal area compared to males. If the innominate was fragmented or missing for an individual, then robusticity or gracility and size of the cranial and postcranial skeleton were used to estimate sex. In consideration of these morphological characteristics, generally females are more gracile than are males.

Due to the extremely poor preservation for the Santa Catalina sample, only 66 of the 223 adults could be assigned a sex (39 female, 27 male). As many as possible of the above-mentioned methods were used for these estimations. Because of better preservation, 84 of 85 adult individuals from the Santa Maria sample could be assigned a sex (43 female, 41 male), 173 of 198 adults from the Irene Mound series (106 female, 67 male), 52 of 71 adults from the *Santa Maria de Yamass*ee cemetery (28 female, 24 male), 70 of 72 adults from the North Carolina ossuary samples (26 female, 44 male), and 113 of 116 adults from the Ledford Island sample (52 female, 61 male). Again, as many as possible of the above-mentioned methods of sex estimation were used for each individual.

Sexual dimorphism in nonmetric trait expression has been demonstrated to be significant within and between populations (Scott 1973, Corruccini 1974, Konigsberg 1987).

Up to 31% of the traits studied by Corruccini (1974) differed at $p<0.05$ between the sexes within populations and each population tends to exhibit a different pattern of sexual dimorphism (i.e., different traits are dimorphic for each population). Many researchers (Howe and Parsons 1967, Ossenberg 1970, Corruccini 1975, Scott 1977, Cheverud et al. 1979) have observed a general tendency for body size to be positively correlated with expression of traits which increase mass (e.g., hyperostotic traits). Tooth size and tooth form have also been shown to be positively correlated (Keene 1965, Scott 1977). Grüneberg (1963) alluded to this type of relationship in his pioneering work on nonmetric traits.

A male bias has been suggested for accessory lessor palatine foramina (A.C. Berry 1975), ossicles at lambda (Akabori 1934, DeVilliers 1968, Ossenberg 1969), lambdoidal ossicles (Sublett 1966, Ossenberg 1969), presence of parietal foramina (Sublett 1966, Ossenberg 1969), and canine distal accessory ridge (Scott 1973, 1977). A female bias has been suggested for absence of mastoid foramina (Akabori 1934, Corruccini 1974, A.C. Berry 1975), metopism (Akabori 1934, Ossenberg 1969, A.C. Berry 1975), palatine tori (Woo 1950, Sublett 1966, DeVilliers 1968), and precondylar tubercles (A.C. Berry 1975). Other studies have found that in many populations, for these same traits, there is no apparent sexual dimorphism in trait expression. For example, A.C. Berry (1975) found no bias for expression of ossicles at lambda, lambdoid ossicles, or metopism in certain populations; Suzuki and Sakai (1960) found no bias for expression of palatine tori; and Akabori (1934) and DeVilliers (1968) found no bias for expression of parietal foramina. Evidence has been presented for sexual dimorphism in cusp number (Garn et al. 1966b, Biggerstaff 1975) partly paralleling dimorphism in tooth size (i.e., larger teeth correspond with more cusps). However, Garn and coworkers (1966b) found that females also tended to have more cusps for the same crown diameter compared to males. In regard to Carabelli's trait, Garn and coworkers (1966c) found no evidence of sexual dimorphism. Likewise, Scott (1973, 1977) reports no evidence of sexual dimorphism for nineteen of twenty standard nonmetric dental traits. Obviously, there is an overall lack of consistency in the patterns of sexual variation in nonmetric trait expression (Kennedy 1981, A.C. Berry 1975, Corruccini 1974). It is apparent that sexual dimorphism in trait expression should be tested on a population by population basis in order to determine its nature and extent.

As with intrasite age variation, intrasite sex influence on trait incidence was tested via two-dimensional contingency tables. Chi-square and Tau-b statistics were computed for each trait in each sample. Because sex cannot be accurately estimated for immature skeletal remains (<16 years of age), only the adults were included in this analysis. The results of this analysis are reported in Table 8.

Examination of Table 8 reveals a number of traits which are apparently influenced by sex. As with the examination of age influence, there are several instances in which there is an apparent directional influence of large magnitude, yet the chi-square statistic indicates that the relationship is not statistically significant. Traits with these characteristics include anterior fovea in the Santa Catalina sample, lower first molar protostylid in the Santa Maria sample, lower second molar groove pattern and maxillary torus in the *Santa Maria de Yamassee* sample, and central incisor shoveling and double-shoveling in the North Carolina coastal samples. Again, this type of apparent relationship tends to coincide with low sample size, making the statistics suspect.

There are also a number of traits which show statistically significant relationships between trait expression and sex but have low τ_b values indicating a weak correlation. These traits are indicated in Table 8. As pointed out earlier, this type of statistical relationship

Table 8. Intrasite Variations with Sex

	Irene Mound					Santa Catalina					Santa Maria				
Trait	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p
SHOV1	53	-0.084	0.460	2	0.795	16	0.048	3.977	4	0.409	32	0.027	2.348	3	0.503
SHOV2	53	-0.044	4.588	6	0.598	20	-0.041	3.078	5	0.688	32	0.000	9.065	5	0.106
CURV	53	0.141	1.444	1	0.229	18	-0.288	2.463	2	0.292	30	0.174	4.398	3	0.222
DSHOV	52	-0.021	2.067	5	0.840	18	0.215	7.963	4	0.093	37	-0.209	6.218	5	0.286
IGROV	53	0.012	3.174	3	0.366	16	0.076	3.568	3	0.312	37	0.228	3.453	3	0.327
METAC	58	-0.038	2.350	4	0.672	35	-0.112	11.702	6	0.069	31	0.296	7.719	4	0.102
HYPO1	68	0.145	1.457	1	0.227	33	0.150	2.904	2	0.234	28	-0.147	0.640	1	0.424
HYPO2	66	-0.084	1.015	4	0.908	33	0.320	6.274	4	0.180	27	0.000	0.824	3	0.844
M1C5	58	-0.157	3.470	3	0.324	13	-0.078	1.818	3	0.611	12	-0.255	1.142	1	0.285
M2C5	57	-0.200	3.400	2	0.183	14	-0.026	4.540	4	0.338	14	0.277	1.463	1	0.226
CARAM1	66	0.002	5.534	6	0.477	13	-0.305	5.638	4	0.228	17	-0.115	2.007	3	0.571
CARAM2	64	-0.195	3.567	2	0.168	13	*	*	*	*	18	*	*	*	*
PARA	58	*	*	*	*	31	0.034	2.793	2	0.247	35	-0.198	1.734	1	0.188
PSI	53	*	*	*	*	22	*	*	*	*	40	*	*	*	*
PSM	58	0.163	1.877	1	0.171	34	-0.068	0.159	1	0.690	39	0.150	1.261	1	0.262
AF	38	-0.193	1.767	1	0.184	3	-0.816	3.819	2	0.148	6	-0.204	3.819	3	0.282
GPM1	57	0.024	0.032	1	0.859	14	*	*	*	*	10	0.272	1.095	1	0.295
GPM2	58	0.075	0.604	2	0.739	23	0.235	2.040	2	0.361	14	0.142	2.692	2	0.260
CNM1	54	0.055	3.379	3	0.337	13	0.228	1.023	1	0.312	15	0.000	2.783	2	0.249
CNM2	54	-0.219	3.599	2	0.165	19	-0.110	2.637	2	0.268	16	0.350	3.005	2	0.223
DW	3	*	*	*	*	0	*	*	*	*	1	*	*	*	*
DTC	15	-0.480	4.142	1	0.042	1	*	*	*	*	1	*	*	*	*
PM1	57	-0.086	0.433	2	0.805	1	*	*	*	*	8	0.560	3.591	2	0.166
C5M1	54	-0.254	4.448	3	0.217	13	0.179	0.491	2	0.782	14	0.237	6.904	3	0.075
C5M2	54	-0.063	5.905	4	0.206	17	0.086	3.054	3	0.383	15	0.322	2.408	2	0.300
C6M1	54	0.064	4.355	4	0.360	13	0.228	1.023	1	0.312	9	*	*	*	*
C6M2	54	-0.103	1.409	3	0.703	17	-0.236	1.327	1	0.249	11	0.347	2.055	2	0.358
C7M1	54	0.211	3.170	1	0.075	13	*	*	*	*	10	*	*	*	*
C7M2	54	*	*	*	*	17	*	*	*	*	12	*	*	*	*
HNL	67	0.156	1.669	1	0.196	0	*	*	*	*	63	0.246	3.896	1	0.048[1]
OAL	69	0.016	0.018	1	0.893	0	*	*	*	*	58	-0.345	7.063	1	0.008[1]
LO	69	0.132	1.214	1	0.271	0	*	*	*	*	58	-0.198	2.294	1	0.130
PF	66	-0.126	1.058	1	0.304	0	*	*	*	*	61	0.090	0.499	1	0.480
BB	66	*	*	*	*	0	*	*	*	*	57	0.127	1.300	1	0.254
MET	68	*	*	*	*	0	*	*	*	*	64	*	*	*	*
CO	66	-0.182	3.255	1	0.071	0	*	*	*	*	57	-0.141	1.514	1	0.218
EPB	51	-0.074	0.287	1	0.592	0	*	*	*	*	35	-0.149	1.141	1	0.285
FTA	50	-0.107	0.904	1	0.342	0	*	*	*	*	36	*	*	*	*
PNB	63	-0.086	0.479	1	0.489	0	*	*	*	*	59	-0.158	1.516	1	0.218
OAA	61	0.094	0.535	1	0.464	0	*	*	*	*	58	-0.011	0.008	1	0.931
AT	68	*	*	*	*	0	*	*	*	*	61	*	*	*	*
FOH	68	-0.238	4.143	1	0.042[1]	0	*	*	*	*	63	-0.087	0.476	1	0.490
MFE	60	0.309	5.844	1	0.016[1]	0	*	*	*	*	58	0.274	4.418	1	0.036[1]
MFA	60	0.045	0.121	1	0.728	0	*	*	*	*	58	-0.028	0.044	1	0.833
CFD	47	*	*	*	*	0	*	*	*	*	34	*	*	*	*
PT	44	*	*	*	*	0	*	*	*	*	32	0.293	4.097	1	0.043[1]
ACC	47	-0.023	0.024	1	0.876	0	*	*	*	*	32	-0.124	0.481	1	0.488
FO	48	-0.129	1.167	1	0.280	0	*	*	*	*	51	0.139	1.367	1	0.242
FS	44	-0.091	0.367	1	0.545	0	*	*	*	*	53	0.080	0.340	1	0.560
APF	45	0.230	2.574	1	0.109	0	*	*	*	*	39	-0.166	1.121	1	0.290
PAT	56	0.082	0.385	1	0.535	0	*	*	*	*	51	0.068	0.237	1	0.626
MAT	58	0.217	3.461	1	0.063	0	*	*	*	*	52	-0.077	0.311	1	0.577
ZFF	60	0.058	0.200	1	0.655	0	*	*	*	*	51	0.044	0.097	1	0.756
SF	66	-0.058	0.229	1	0.632	0	*	*	*	*	62	-0.172	1.844	1	0.175
FN	65	0.432	13.035	1	0.000	0	*	*	*	*	62	0.056	0.194	1	0.660
AIF	46	-0.020	0.018	1	0.892	0	*	*	*	*	44	0.225	3.307	1	0.069

continued

Table 8, continued

		SMdY					Algonquian					Ledford Island			
Trait	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p
SHOV1	23	-0.565	16.502	4	0.002	4	0.516	1.726	2	0.422	46	-0.062	6.027	3	0.110
SHOV2	21	-0.219	4.487	5	0.482	8	-0.258	6.766	5	0.239	46	-0.077	2.833	4	0.586
CURV	22	0.375	3.869	2	0.144	4	*	*	*	*	47	-0.214	2.951	2	0.229
DSHOV	21	-0.278	7.181	5	0.208	4	0.707	4.499	3	0.212	47	-0.113	7.696	6	0.261
IGROV	19	-0.068	1.099	2	0.577	8	0.346	2.267	2	0.322	46	-0.190	3.212	3	0.360
METAC	20	-0.184	5.976	5	0.309	11	-0.233	3.871	4	0.424	36	-0.055	0.360	2	0.835
HYPO1	25	0.040	2.022	2	0.364	13	-0.090	2.839	2	0.242	49	0.212	2.292	1	0.130
HYPO2	24	-0.140	3.492	5	0.625	12	0.121	9.029	3	0.029[1]	53	-0.092	1.245	2	0.537
M1C5	19	-0.304	4.554	4	0.336	13	0.223	3.715	3	0.294	42	0.372	13.040	3	0.005[1]
M2C5	19	-0.180	0.951	1	0.329	12	0.000	5.716	3	0.126	45	0.197	2.466	2	0.291
CARAM1	21	0.093	5.162	3	0.160	12	-0.305	5.638	4	0.228	44	-0.048	3.488	5	0.625
CARAM2	21	*	*	*	*	11	*	*	*	*	47	0.151	1.452	1	0.228
PARA	20	*	*	*	*	11	*	*	*	*	36	-0.160	1.304	1	0.254
PSI	21	*	*	*	*	8	*	*	*	*	47	*	*	*	*
PSM	22	0.000	0.000	1	1.000	12	*	*	*	*	37	*	*	*	*
AF	5	*	*	*	*	7	*	*	*	*	40	0.254	3.243	2	0.198
GPM1	13	-0.247	1.760	2	0.415	10	0.272	1.095	1	0.295	42	0.091	0.350	1	0.554
GPM2	15	0.404	3.976	2	0.137	10	*	*	*	*	37	0.023	0.685	2	0.710
CNM1	14	0.059	0.048	1	0.826	10	0.000	0.000	1	1.000	44	0.334	5.070	1	0.024[1]
CNM2	13	0.000	1.760	2	0.415	10	-0.227	1.185	2	0.553	37	0.135	0.685	1	0.408
DW	2	*	*	*	*	2	*	*	*	*	13	0.548	4.162	1	0.041
DTC	3	*	*	*	*	3	*	*	*	*	23	-0.271	2.428	1	0.119
PM1	15	0.327	1.632	1	0.201	10	-0.102	0.103	1	0.749	45	-0.012	2.935	2	0.230
C5M1	13	0.137	0.768	2	0.681	10	-0.102	0.103	1	0.749	44	-0.059	7.607	2	0.022[1]
C5M2	13	-0.170	4.565	3	0.207	10	0.336	6.189	4	0.185	37	0.136	3.707	3	0.295
C6M1	13	0.033	0.014	1	0.906	10	0.147	2.911	2	0.233	44	0.340	10.248	4	0.036[1]
C6M2	13	0.267	1.309	1	0.253	10	-0.154	0.277	2	0.871	37	0.123	4.504	3	0.212
C7M1	13	*	*	*	*	10	*	*	*	*	44	*	*	*	*
C7M2	13	*	*	*	*	10	*	*	*	*	37	*	*	*	*
HNL	17	0.648	7.758	1	0.005	67	0.184	2.201	1	0.138	27	-0.053	0.075	1	0.784
OAL	16	0.228	1.202	1	0.273	66	0.085	0.488	1	0.485	27	-0.081	0.178	1	0.673
LO	17	-0.290	1.449	1	0.229	65	0.051	0.173	1	0.677	28	-0.084	0.199	1	0.655
PF	18	-0.329	1.983	1	0.159	67	0.164	1.800	1	0.180	30	0.000	0.000	1	1.000
BB	18	*	*	*	*	67	*	*	*	*	30	*	*	*	*
MET	18	*	*	*	*	67	*	*	*	*	30	*	*	*	*
CO	18	*	*	*	*	66	-0.137	1.188	1	0.276	30	-0.152	1.045	1	0.307
EPB	15	*	*	*	*	55	*	*	*	*	24	-0.293	3.073	1	0.080
FTA	15	*	*	*	*	58	*	*	*	*	26	*	*	*	*
PNB	18	0.217	1.222	1	0.269	63	-0.219	2.867	1	0.090	27	-0.217	1.944	1	0.163
OAA	18	0.395	3.023	1	0.082	66	0.117	0.961	1	0.327	23	0.099	0.214	1	0.644
AT	18	*	*	*	*	67	*	*	*	*	30	*	*	*	*
FOH	18	-0.598	7.979	1	0.005	63	0.047	0.144	1	0.705	30	-0.120	0.456	1	0.499
MFE	16	-0.323	1.768	1	0.184	64	0.162	1.641	1	0.200	22	0.171	0.664	1	0.415
MFA	15	0.134	0.273	1	0.601	65	-0.043	0.117	1	0.733	22	-0.263	2.242	1	0.134
CFD	14	*	*	*	*	45	*	*	*	*	17	*	*	*	*
PT	14	*	*	*	*	46	0.035	0.058	1	0.809	16	0.098	0.148	1	0.700
ACC	12	0.169	0.345	1	0.557	49	0.030	0.044	1	0.834	18	-0.282	2.127	1	0.145
FO	14	*	*	*	*	61	-0.077	0.351	1	0.554	23	-0.171	1.022	1	0.312
FS	14	-0.337	1.539	1	0.215	58	-0.091	0.472	1	0.492	23	-0.247	2.107	1	0.147
APF	10	0.089	0.080	1	0.777	43	-0.059	0.149	1	0.699	19	0.258	1.281	1	0.258
PAT	15	0.134	0.273	1	0.601	52	0.073	0.283	1	0.595	27	*	*	*	*
MAT	15	0.419	3.404	1	0.065	50	*	*	*	*	29	0.265	2.018	1	0.155
ZFF	15	-0.134	0.273	1	0.601	62	-0.156	1.489	1	0.222	27	0.225	1.505	1	0.220
SF	17	0.278	1.395	1	0.238	65	-0.043	0.118	1	0.732	30	-0.320	4.491	1	0.034[1]
FN	17	0.029	0.014	1	0.906	66	0.025	0.040	1	0.842	30	0.082	0.201	1	0.654
AIF	10	*	*	*	*	44	-0.270	3.116	1	0.078	25	0.042	0.043	1	0.836

*no variation in trait score

[1] low Tau-b, statistically significant

is to be expected given a large enough sample. However, given that the relationship between sex and trait expression is apparently weak in these cases, this type of association will be disregarded.

Examination of Table 8 reveals several traits which are both strongly (high τ_b) and significantly ($p<0.05$) affected by sex in certain of the population samples. Among these are supraorbital foramen in the Irene Mound sample, central incisor shoveling, foramen of Huschke, and highest nuchal line in the *Santa Maria de Yamassee* sample, and deflecting wrinkle in the Ledford Island sample. Because of the apparent strong and statistically significant influence of sex on trait expression in these cases, the traits involved will be deleted from the estimations of population distance.

Trait Intercorrelation

With the large number of genetic and non-genetic factors influencing the expression of nonmetric traits, it is expected that the number of traits which are statistically correlated would be low. Research has shown this presumption to be generally false (Suzuki and Sakai 1960, DeVilliers 1968, Buikstra 1972a, Corruccini 1974, Ossenberg 1976, Molto 1983). Molto (1983) attributes the higher than expected frequencies of correlations to four major factors: nonmetric traits (1) are often alternative expressions of a single underlying variable, (2) often have a common regional or embryological origin, (3) can be affected by similar developmental phenomenon, and (4) may be affected by the shared interaction of some combination of the above. Given these factors, it is expected that frequencies of nonmetric traits would show a considerable number of positive correlations. It can be argued that nonmetric traits offer redundant information in the real population. Accepting this argument will alter the strategy adopted for dealing with trait correlations as discussed later.

Research has suggested that genes can have pleiotropic effects over the expression of some skeletal variants (Saunders 1989). Pleiotropism as used here is the case in which a trait is controlled by major gene(s) and "is also influenced incidentally and slightly by various other genes" (Grüneberg 1963:16). These "minor genes" are classified as such by virtue of the extent of their effect on the "major" gene which one is studying. Minor genes may govern the expression of groups of traits causing higher than expected levels of intercorrelation. Expression of nonmetric skeletal traits may also be correlated with one another via common developmental pathways or other similar phenomena (e.g., arrested growth). Ossenberg (1969, 1970) has suggested that a common developmental pathway exists between hypostotic traits and accessory sutural bones and that a regional pattern of development may effect the expression of craniobasal variations. Other researchers have identified traits that may be parts of a common variable (Ossenberg 1976, Saunders 1978, Molto 1983). Studies of intertrait correlations in human samples have generally shown them to be low and random (Benfer 1970, Kellock and Parsons 1970b, McWilliams 1974, Suchey 1975).

The statistics commonly used to analyze nonmetric trait variation do not take into account the existence of intertrait correlations and depend on the assumption that the traits used are not statistically correlated (Kennedy 1981). This can present problems for analysis of nonmetric traits.

Many authors have simply assumed *a priori* that correlations between frequency of expression for nonmetric traits are non-existent (Berry and Berry 1967, Benfer 1970, Spence 1971, A.C. Berry 1972). In part, this decision was based on studies of *Mus musculus* (Truslove 1961) and *Homo sapiens* (Berry and Berry 1967, Kellock and Parsons 1970a, Corruccini 1974). Other researchers have suggested significant correlation between classes of traits (Hrdlicka 1940, Woo 1950, DeVilliers 1968, Ossenberg 1976, Suzuki and Sakai 1960). That is, traits which have similar developmental pathways (e.g., hypostotic, hyperstotic, oral tori, basicranial foramina) will have similar degrees of expression in an individual. However for the most part, as Corruccini (1974) has pointed out, the nature of such correlations often differs randomly from group to group.

The real question here is not whether nonmetric traits are correlated. Some very clearly are. The real issue is what to do with those that are significantly correlated. Many approaches have been used to deal with this issue. Kennedy (1981) reasoned that because correlations are usually "random" when compared between populations, they could be ignored. Sjovold (1977) has taken a similar approach claiming that the pattern of low correlation will not cause serious distortion of the results. Buikstra (1972a) has taken a reductionist approach by simply eliminating traits until the matrix was free of all significant correlations. Ossenberg (1976) has taken yet a different approach by amalgamating significantly intercorrelated matrices of common traits as a single trait. A reductionist approach approximating Molto's (1983) will be adopted here. Traits which have significant correlations and clear etiological connections will be eliminated from the analyses of population distance.

Many authors have recommended the use of the phi coefficient to detect the correlations between nonmetric traits in place of other coefficients (Benfer 1970, Sjovold 1977, Molto 1983). Another related statistic, Tau-b (Goodman and Kruskal 1954, 1959, 1963), is used here because many of the traits are not exclusively dichotomous as required for phi correlation analysis. Tau-b, like phi, gives a close approximation to the chi-square distribution, and therefore is more sensitive to this task than other coefficients of association (Thomas 1986). Correlation coefficients were calculated for both classes of traits in this study. The results of this analysis are reported in Tables 9 and 10.

There are a number of strong correlations which are apparent upon examination of Tables 9 and 10. Without exception, these correlations result from the nature of the traits. That is, in each case either the traits involved occur on multiple teeth (i.e., field effects) or the traits are different manifestations of the same complex. An example of the later would be central incisor curvature and central incisor double-shoveling. By definition, these traits vary inversely. Therefore, they are strongly negatively correlated. Two of the traits which show a strong association with one another are central incisor shoveling and lateral incisor shoveling. Central incisor shoveling has already been deleted due to correlations with age-at-death and sex. The other correlations are central

Table 9. Matrix of Kendall Tau-b Coefficients, Nonmetric Cranial Traits

	HNL	OAL	LO	PF	BB	PT	ACC	FO	FS	APF	CO	EPB	PNB	OAA	FOH	MFE	MFA
HNL	1.000																
OAL	-0.061	1.000															
LO	-0.025	0.353	1.000														
PF	0.010	0.006	-0.080	1.000													
BB	0.038	-0.039	-0.057	-0.055	1.000												
PT	-0.003	-0.166	-0.129	0.000	-0.025	1.000											
ACC	-0.068	0.109	0.022	-0.017	-0.037	-0.027	1.000										
FO	0.013	-0.002	0.098	0.082	-0.016	0.052	0.144	1.000									
FS	-0.023	-0.122	0.077	0.050	-0.040	0.121	0.025	0.109	1.000								
APF	-0.042	0.011	0.073	0.010	0.058	-0.013	0.104	-0.021	-0.162	1.000							
CO	-0.052	-0.059	0.116	0.148	-0.012	-0.074	-0.033	0.081	-0.028	0.072	1.000						
EPB	0.003	0.220	0.082	-0.002	-0.021	-0.076	0.002	0.026	0.025	0.073	-0.060	1.000					
PNB	-0.124	0.183	0.075	-0.016	-0.020	-0.042	0.084	0.010	-0.040	0.026	0.195	0.171	1.000				
OAA	0.032	0.189	0.098	-0.008	-0.039	-0.032	0.097	-0.087	-0.051	0.204	-0.058	0.024	0.121	1.000			
FOH	-0.181	0.012	0.109	0.025	-0.035	0.011	0.114	-0.009	0.092	0.045	0.010	0.033	0.103	0.015	1.000		
MFE	0.104	-0.094	-0.049	0.007	-0.082	0.118	0.038	0.044	0.094	0.044	-0.087	-0.138	-0.076	-0.062	-0.092	1.000	
MFA	-0.025	0.122	-0.072	-0.067	-0.026	-0.007	-0.082	-0.031	0.029	-0.017	0.068	0.178	0.141	0.008	-0.080	-0.399	1.000
PCC	0.065	-0.053	-0.105	0.066	-0.069	-0.117	0.035	0.277	0.052	0.020	-0.019	-0.042	0.022	-0.131	-0.173	0.197	-0.062
PAT	0.128	-0.074	-0.206	-0.152	-0.109	0.077	-0.062	-0.237	-0.055	-0.037	-0.111	0.014	0.067	0.161	0.095	-0.141	0.189
MT	0.129	0.022	-0.058	0.072	-0.027	-0.041	-0.033	-0.093	-0.101	-0.067	-0.067	0.014	-0.062	0.034	-0.052	-0.052	0.043
ZFF	0.213	-0.047	0.013	-0.083	0.059	0.105	-0.040	-0.031	-0.045	-0.030	-0.155	0.074	0.070	0.126	0.044	0.013	0.185
SF	-0.066	-0.021	-0.005	-0.022	-0.036	0.101	0.009	0.164	-0.009	-0.124	0.116	-0.066	-0.017	-0.133	-0.108	0.113	0.044
FN	0.126	-0.062	0.043	0.017	-0.072	0.087	-0.027	0.154	0.024	-0.073	-0.017	0.001	-0.139	0.041	0.011	0.181	0.043
AIF	0.026	-0.016	-0.019	0.274	-0.029	0.014	-0.037	0.202	0.002	0.026	0.019	0.018	0.055	-0.164	-0.019	-0.052	-0.184

	PCC	PAT	MT	ZFF	SF	FN	AIF
PCC	1.000						
PAT	-0.371	1.000					
MT	-0.121	0.219	1.000				
ZFF	-0.189	0.299	-0.015	1.000			
SF	0.036	-0.254	-0.095	-0.168	1.000		
FN	0.110	-0.081	-0.045	-0.019	0.047	1.000	
AIF	0.089	-0.113	-0.111	0.024	0.143	0.081	1.000

Table 10. Matrix of Kendall Tau-b Coefficients, Nonmetric Dental Traits

	SHOV1	SHOV2	CURV	DSHOV	IGROV	METAC	HYPO1	HYPO2	M1C5	M2C5	CARAM1	CARAM2	PARA	PSM	AF	GPM1
SHOV1	1.000															
SHOV2	0.475	1.000														
CURV	-0.139	-0.173	1.000													
DSHOV	0.310	0.303	-0.463	1.000												
IGROV	-0.002	-0.003	0.051	-0.007	1.000											
METAC	0.072	0.039	0.018	0.050	-0.103	1.000										
HYPO1	-0.092	0.142	-0.090	0.062	-0.071	0.134	1.000									
HYPO2	0.015	0.082	-0.037	0.052	-0.062	0.073	0.411	1.000								
M1C5	0.234	0.052	-0.078	0.140	-0.089	0.130	-0.088	0.055	1.000							
M2C5	0.013	-0.009	-0.006	0.084	-0.001	0.050	0.042	0.040	0.421	1.000						
CARAM1	0.098	0.070	-0.102	0.122	0.049	0.169	0.126	0.130	0.140	0.084	1.000					
CARAM2	0.075	-0.003	0.064	0.044	0.132	0.016	-0.058	0.049	0.024	-0.011	0.219	1.000				
PARA	0.020	0.005	0.034	-0.051	0.177	0.006	0.057	0.004	-0.123	0.093	0.046	-0.034	1.000			
PSM	-0.032	-0.098	0.070	-0.104	-0.091	-0.162	0.051	-0.147	-0.019	0.204	-0.062	-0.054	0.010	1.000		
AF	0.057	0.161	-0.204	0.151	-0.073	0.268	0.223	0.264	0.064	-0.011	0.199	0.044	-0.058	0.344	1.000	
GPM1	-0.021	-0.052	-0.104	0.033	-0.009	-0.077	-0.003	-0.120	0.041	0.024	0.037	0.048	-0.060	-0.016	-0.085	1.000
GPM2	0.042	0.098	-0.162	0.161	-0.099	-0.057	0.129	0.038	0.038	0.102	0.034	-0.118	0.017	0.001	0.140	0.006
CNM1	0.143	0.068	-0.042	0.120	0.142	0.010	-0.027	-0.024	0.154	0.147	0.138	0.060	0.017	-0.088	0.109	0.008
CNM2	0.098	0.039	0.015	0.102	0.120	0.006	-0.102	-0.087	0.152	0.230	0.080	0.058	0.055	0.154	0.024	0.026
DW	0.017	0.039	0.053	0.046	-0.089	0.217	0.113	0.010	0.023	0.174	-0.001	0.079	.	0.082	0.172	-0.062
DTC	-0.126	-0.139	0.033	-0.077	0.195	0.033	0.125	0.060	0.018	0.222	0.013	-0.114	.	0.253	0.164	-0.094
PM1	0.057	0.103	-0.147	0.163	-0.007	0.123	0.174	0.060	-0.049	0.018	0.178	0.173	-0.103	0.073	0.235	-0.056
C5M1	-0.078	0.029	0.028	-0.016	-0.052	0.129	0.086	0.019	-0.117	-0.106	-0.003	-0.018	-0.040	-0.100	0.020	-0.046
C5M2	0.002	0.164	0.080	-0.054	0.014	0.136	0.107	0.132	0.001	0.053	0.045	-0.020	0.040	-0.040	0.144	-0.065
C6M1	0.153	0.098	-0.081	0.148	0.129	-0.016	-0.020	-0.040	0.167	0.172	0.088	0.051	-0.002	-0.030	0.098	0.026
C6M2	0.095	0.025	-0.062	0.134	0.104	-0.059	-0.026	-0.073	0.099	0.207	0.059	0.041	0.068	0.140	0.007	0.071
C7M1	-0.068	-0.059	-0.021	-0.063	0.011	-0.007	-0.027	-0.016	0.016	-0.043	0.094	-0.024	-0.015	-0.025	0.049	-0.056
C7M2	-0.066	-0.104	0.148	-0.093	0.026	-0.134	-0.042	-0.090	-0.048	-0.034	-0.073	-0.021	-0.012	-0.024	0.047	-0.018

	GPM2	CNM1	CNM2	DW	DTC	PM1	C5M1	C5M2	C6M1	C6M2	C7M1	C7M2
GPM2	1.000											
CNM1	-0.080	1.000										
CNM2	0.045	0.449	1.000									
DW	0.085	0.229	0.178	1.000								
DTC	0.023	0.112	0.165	0.174	1.000							
PM1	-0.015	0.085	0.109	0.173	0.100	1.000						
C5M1	0.051	-0.501	-0.182	-0.052	0.042	0.039	1.000					
C5M2	-0.023	-0.058	-0.004	0.040	0.076	0.112	0.265	1.000				
C6M1	-0.071	0.875	0.434	0.157	0.031	0.073	-0.567	-0.086	1.000			
C6M2	0.077	0.399	0.821	0.198	0.201	0.084	-0.224	-0.235	0.403	1.000		
C7M1	0.014	0.282	-0.005	0.155	0.178	0.084	-0.012	0.043	0.060	-0.012	1.000	
C7M2	0.049	0.091	0.045	0.162	-0.041	-0.014	-0.038	-0.115	0.056	0.039	-0.009	1.000

incisor curvature with central incisor double-shoveling, upper first molar hypocone with upper second molar hypocone, upper first molar metacone with upper second molar metacone, lower first molar cusp number with lower second molar cusp number, lower first molar cusp number with lower first molar cusp five and six, lower second molar cusp number with lower first and second molar cusp six, lower first molar cusp five with lower first molar cusp six, and mastoid foramen exsutural with mastoid foramen absent. Traits were eliminated from the analysis on the basis of which were not included as key traits in Turner's Sinodont classification (Turner 1985, 1986a, 1987a). Therefore, the traits eliminated from the analysis because of intercorrelation are central incisor curvature, upper first molar hypocone, upper second molar metaconule, lower second molar cusp number, lower first molar cusp five, lower first molar cusp six, and mastoid foramen exsutural.

Preservation Bias

An assessment was made of those traits most frequently lost due to damage, poor preservation of particular areas of the skeleton, or excessive dental occlusal wear. Any traits which could not be recorded for the majority of individuals for any single population sample were omitted from the analysis, because the frequency of these traits could not be considered a valid reflection of total sample frequency.

Thus, the following traits were omitted from the analysis: anterior ethmoid foramen, posterior ethmoid foramen, posterior condylar canal, incisor winging, tuberculum dentale, upper canine mesial ridge, upper canine distal accessory ridge, upper molar enamel extensions, upper premolar root number, upper molar root number, ondontome (upper and lower premolars), lower premolar variation, protostylid (second molar), lower canine root number, Tomes' root, lower first and second molar root number, and torsomolar angle.

Inter- and Intra-Observer Error

In any line of research involving measures which can be interpreted as somewhat subjective, the degree of inter- and intra-observer error should be considered (see Landis and Koch 1975a, b). Intra- and interobserver error has been tested for recording craniometrics (Page 1976, Utermohler and Zegura 1982, Utermohle et al. 1983), cranial nonmetric traits (Korey 1970, Suchey 1975, Molto 1979), and dental morphological traits (Turner 1967, Sofaer et al. 1972b, Scott 1973, Nichol et al. 1984, Nichol and Turner 1986. Studies by Page (1976) and Jamison and Zegura (1974) have concluded that interobserver error is significant in the scoring of morphologic traits. Molto (1979) has found that intraobserver error is relatively low (on the order of 20%) and occurs randomly among cranial nonmetric observations.

Nichol and Turner (1986) have found that intra- and interobserver error can be quite high for some dental morphological characters. However, the pattern of error, for the most part, appears to be random. Four traits have consistently high intra- and interobserver errors: tuberculum dentale, canine distal accessory reidge, upper first premolar marginal accessory cusps, and lower first molar anterior fovea.

For the present study, all traits for the southeast U.S. samples were scored by the author. Therefore, the contribution of interobserver error was nil. However, there remains the question of intraobserver reliability. In the aforementioned pilot study (Griffin 1989), thirty-nine dental morphologic traits were scored on the skeletal sample from *Santa Catalina de Guale de Santa Maria* (n=119) using the Arizona State University dental anthropology system (Turner et al. 1991). One month following the completion of the pilot study, the same series was again scored by the author. The methods used to quantify observer variation were selected from those suggested by Nichol and Turner (1986). For each trait, four percentages were calculated: (1) percent of teeth observed in one recording session but not the other, (2) percent of instances in which the score for a trait differed between sessions, (3) percent of instances in which the difference in score was greater than one grade, and (4) percent of cases in which a trait was scored as present in one session but not the other. These calculations are reported in Table 11. The means for these four measures of intraobserver error across thirty-nine traits are 3.3%, 15.0%, 2.7%, and 3.7%, respectively. These percentages are lower than those reported by other examinations of intraobserver error for nonmetric dental traits (Scott 1973, Nichol and Turner 1986, Lukacs and Hemphill 1991). The difference is likely due to the fact that these previous examinations were based on observations of dental casts, whereas the present study relied on actual teeth. As Nichol and Turner (1986) point out, dental casts are generally more difficult to reliably observe nonmetric traits on than actual teeth. Otherwise, the level of intraobserver error is acceptable and consistent with similar studies (Konigsberg 1987, Lukacs and Hemphill 1991, Molto 1979, Nichol and Turner 1986).

Table 11. Results of Intraobserver Reliability Analysis

Trait	n	Observed only one session	Variant scoring	>1 Grade variant scoring	Presence-absence variance
WING	34	0.000	0.000	0.000	0.000
SHOV1	43	0.000	0.186	0.000	0.000
SHOV2	42	0.000	0.238	0.000	0.000
CURV	49	0.000	0.082	0.020	0.020
DSHOV	48	0.000	0.125	0.021	0.000
IGROV	44	0.000	0.000	0.000	0.000
TD	42	0.000	0.238	0.095	0.119
CMR	8	0.000	0.250	0.125	0.125
DAR	6	0.000	0.167	0.000	0.167
METAC	34	0.088	0.193	0.000	0.000
HYPO1	51	0.058	0.208	0.104	0.000
HYPO2	38	0.000	0.105	0.053	0.000
M1C5	34	0.117	0.266	0.100	0.066
M2C5	24	0.000	0.083	0.000	0.000
CARAM1	31	0.000	0.258	0.000	0.000
CARAM2	24	0.000	0.083	0.000	0.000
PARA	37	0.000	0.000	0.000	0.000
PSI	50	0.000	0.000	0.000	0.000
PSM	41	0.000	0.000	0.000	0.000
ODONT	91	0.109	0.000	0.000	0.000
LP3V	18	0.000	0.278	0.222	0.000
LP4V	16	0.000	0.375	0.312	0.000
AF	27	0.148	0.217	0.000	0.000
GPM1	31	0.161	0.231	0.000	0.000
GPM2	24	0.083	0.227	0.000	0.000
CNM1	35	0.000	0.000	0.000	0.000
CNM2	23	0.000	0.000	0.000	0.000
DW	22	0.136	0.421	0.000	0.158
DTC	22	0.136	0.263	0.000	0.263
PM1	21	0.050	0.000	0.000	0.400
PM2	9	0.111	0.000	0.000	0.125
C5M1	35	0.028	0.294	0.000	0.000
C5M2	24	0.000	0.416	0.000	0.000
C6M1	30	0.066	0.178	0.000	0.000
C6M2	21	0.000	0.428	0.000	0.000
C7M1	31	0.000	0.000	0.000	0.000
C7M2	23	0.000	0.000	0.000	0.000
PTOR	74	0.000	0.054	0.000	0.000
MTOR	90	0.000	0.000	0.000	0.000

CHAPTER IV - STATISTICS

Introduction

The preceding chapters have presented the historical, theoretical, and methodological foundations for this study. These chapters provide the framework within which to place an assessment of the biological relationships of the Guale from temporal, regional, and pan-geographic perspectives. This chapter will address the statistical comparison of morphological traits in the Guale and the secondary population samples. A brief overview of the statistical procedures is given here in order to concisely state the strengths and weaknesses of the research design. All of the statistical analyses reported here were performed using SYSTAT (Wilkinson 1988a) and SYGRAPH (Wilkinson 1988b).

Statistical Analysis

The primary purpose of this study is to estimate population distances between a time successive series of Guale samples in comparison to other culturally and linguistically distinct Native American groups. A number of different statistical procedures are employed to compare these groups. Among these procedures are: Chi-square and

Tau-b statistics, cluster analysis (Aldenderfer and Blashfield 1984), estimations of mean measures of divergence (Green and Suchey 1976, Sofaer et al. 1986), multidimensional scaling (Kruskal and Wish 1978), and principal component analysis (Manly 1986).

Biological Distance

A primary objective of this study is to estimate biological distances between population samples. This objective is best achieved by expressing the degree of divergence between the populations with a single numerical value, rather than trying to evaluate relationships on a trait by trait basis using univariate statistics (Cybulski 1975, Molto 1983). The single numerical value is calculated using multivariate statistics and is derived from the sum of the squared differences between corresponding variates of two population samples (Smith 1972). When the populations are similar, the coefficient value should be small, and when the populations are dissimilar, it should be large. Dissimilarity in population studies is equated with biological distance. The distance for population models is usually defined in terms of Euclidean distance.

Most of the distance coefficients used for nonmetric morphological data are based on C.A.B. Smith's Mean Measure of Divergence (Grewal 1962). This statistic uses an angular transformation of the original trait frequencies for each population sample being compared. The angular transformation stabilizes the variance so that sampling error does not distort the estimation of distance. This is necessary with dichotomous traits because the variance of the *sample* proportion is a function of the *population* proportion (Sjovold 1977, Molto 1983). The mathematical foundation of the Mean Measure of Divergence as an appropriate distance measure using nonmetric data has been substantiated by Sjovold (1977). This is the most widely utilized statistic for estimating population distance for nonmetric data (Sjovold 1977, Molto 1983). However, use of the Mean Measure of Divergence without corrective statistics on small population sample sizes has been cautioned against (Sjovold 1977, Green and Suchey 1976). There are a number of transformations currently used to remove the effects of small sample size (e.g., Anscombe 1948, Freeman and Tukey 1950). The usefulness of each technique is dependent on how quickly and effectively they stabilize the variance (Molto 1983).

The transformation devised by Smith (in Grewal 1962) has been widely used (Pietrusewsky 1969, 1971, Jantz 1970, Kellock and Parsons 1970a, b, Buikstra 1972, Finnegan 1972, Rightmire 1972, Lane and Sublett 1972, Cybulski 1972, Birkby

1973, Gaherty 1974, McWilliams 1974, Corruccini 1974, Berry 1974). The formula for this transformation is:

$$\Theta = \arcsin(1 - 2p)$$

where p is the proportion of a trait in a population. Green and Suchey (1976) have demonstrated that this transformation produces inflated variances for small sample sizes combined with small trait frequencies. Thus, the variance is not adequately stabilized and tests of significance between samples are unreliable. Sjovold (1973) has suggested that Bartlett's correction can be used to alleviate the problems caused by the extreme frequencies of 0 or 1. That is, $\frac{1}{4}n$ is substituted for frequency 0 and $1-\frac{1}{4}n$ is substituted for frequency 1. This correction compensates for extreme frequencies, but small sample sizes or greatly differing sample sizes within a comparison present problems (Green and Suchey 1976).

Other researchers have proposed the use of alternate transformations (Green and Suchey 1976, Sjovold 1977, de Souza and Houghton 1977). The best are those of Freeman-Tukey (1950) and Anscombe (1948). According to Molto (1983), there is little empirical difference between the two transformations. However, the Freeman and Tukey transformation is slightly more efficient at stabilizing the variance of very small proportions which are common in archaeological samples (Green and Suchey 1976, Sjovold 1977).

The Mean Measures of Divergence for this study will be calculated using the Freeman and Tukey transformation and the method suggested by Green and Suchey (1976):

$$\mathrm{MMD} = \frac{\sum_{i=1}^{r} (\Theta_{1i} - \Theta_{2i})^2 - [1/(n_{1i} + \tfrac{1}{2}) + 1/(n_{2i} + \tfrac{1}{2})]}{r}$$

where r is the number of traits used in the comparison, Θ_{1i} and Θ_{2i} are the transformed frequencies in radians of the i^{th} trait in the two groups being compared, and n_{1i} and n_{2i} are the numbers of individuals scored for the i^{th} trait in the two groups. For each group comparison, the maximum number of traits was used.

The angular transformation for each trait was carried out using the formula suggested by Freeman and Tukey (1950):

$$\Theta = \tfrac{1}{2}\arcsin(1 - 2k/(n + 1)) + \tfrac{1}{2}\arcsin(1 - 2(k + 1)/(n + 1))$$

where k is the number of individuals scored as positive and n is the total number of individuals scored for the trait in the given population. This transformation stabilizes the variance to approximately $1/(n + \tfrac{1}{2})$ (Green and Suchey 1976).

The standard deviation of the Mean Measures of Divergence was calculated using the method suggested by Sofaer and others (1986):

$$\mathrm{Var}_{\mathrm{MMD}} = 2/r^2 \sum_{i=1}^{r} (1/(n_{1i} + \tfrac{1}{2}) + 1/(n_{2i} + \tfrac{1}{2}))^2$$

and

$$\mathrm{sd}_{\mathrm{MMD}} = \sqrt{\mathrm{Var}_{\mathrm{MMD}}}$$

A mean measure of divergence equal to or greater than twice its standard deviation is considered to be statistically significant at the $p<0.05$ level (Molto 1983). When two samples have identical frequencies of each variant or sample sizes are small, the mean measure of divergence assumes a negative value (Turner and Bird 1981). As Constandse-Westermann points out, "lack of significance usually does point to a close association of populations" (1972:3). However, non-significant distance does not necessarily mean that the samples being compared are drawn from the same population (Rightmire 1972, Constandse-Westermann 1972, Hiernaux 1972, Sjovold 1977). It is equally misleading to interpret statistically significant distances as indicating samples from different populations. As Grüneberg (1952, 1963) has noted, distances between populations may increase at a constant rate over generations due to random genetic drift.

The expression $[1/(n_{1i} + \frac{1}{2}) + 1/(n_{2i} + \frac{1}{2})]$ in the mean measure of divergence equation is the assumed variance of $(\Theta_{1i} - \Theta_{2i})$. By subtracting this term from each $(\Theta_{1i} - \Theta_{2i})$ value, the variance due to random sample fluctuation is removed (Molto 1983). When a sufficient number of measures of divergence are negative, the mean measure of divergence will also be negative. Some researchers (e.g., Constandse-Westermann 1972, Zegura 1971) have questioned this outcome on the basis that theoretically the distance between two points should be either positive or "0". Sjovold (1977) has pointed out that negative values should be expected because the estimations of divergence are based on samples and not populations. It makes mathematical sense to obtain values that fluctuate around zero when there is no significant divergence indicated.

Taxonomic Statistics

Interpreting biological relationships from a large matrix of distance coefficients can be a quite confusing task. In order to make interpretation easier, two related taxonomic statistical techniques have traditionally been employed (Molto 1983, Lukacs and Hemphill 1990). These two techniques are cluster analysis and multidimensional scaling. Both of these procedures are based on the assumed relationship between biological dissimilarity and the concept of Euclidean distance (Molto 1983).

Cluster Analysis

Affinity of the groups is assessed using cluster analysis, a metric approach leading to the establishment of clusters of similar groups (Anderberg 1973, Everitt 1974, Blashfield 1976, Aldenderfer and Blashfield 1984). The object of the analysis is: given a sample of *n* objects, each of which has a score on *p* variables, devise a scheme for grouping the objects into classes so that similar ones are in the same class. The objects here are the population samples and the scores are the arcsine transformed trait frequencies. The method must be completely numerical and, unlike discriminant function analyses, the number of classes is not known.

There are a number of hierarchical methods available for cluster analysis. These methods operate on a distance matrix to construct a dendrogram which illustrates the relationships among the population samples. Agglomerative hierarchical methods in cluster analysis start with the calculation of the distances of each individual to all other individuals. Groups are then formed by a process of agglomeration. All objects start by being alone in groups of one. Close groups are then gradually merged until finally all individuals are in a single group. Of the methods available, Ward's minimum variance provides the most accurate results for the type of data used here (Blashfield

1976, Molto 1983). This method is designed to generate clusters so that the variance within clusters is minimal (Ward 1963). The procedure uses an error sum of squares function which computes the sum of squares of the distance from each point to its parent cluster. At each step, it combines those two clusters which result in the least increase in the within group sum of squares objective function. A cluster formed by this method can, therefore, be defined as a group of entities such that the error sum of squares among the members of each cluster is minimal (Blashfield 1976).

Multidimensional Scaling

The next procedure used to illustrate population distances is multidimensional scaling (Torgerson 1952, Kruskal and Wish 1978, Schiffman et al. 1981). Multidimensional scaling is a technique that attempts to position objects in space according to distance measures rather than classify them as in cluster analysis. The "objects" in this case are the population samples and the distances used are the standardized mean measures of divergence derived with the Freeman-Tukey transformation and using the method of Sofaer and others (1986). A point is usually specified in terms of its coordinate location in reference to a set of axes. An axis defines a direction of movement and the number of axis defines the dimensionality of the space. The reference axes are assumed to be at right angles to one another and can be referred to as a Cartesian Coordinate system (Molto 1983).

The procedure for multidimensional scaling is iterative and the groups are moved around within a space of specified dimensionality in order to find a monotone function expressing the original distances and the distances in the configuration. The fit between the two distances and a monotone function is expressed as a measure referred to as "stress" (Kruskal 1964a and b). The stress is computed as the square root of the sum of the squared deviations of the distances in the configuration space from the monotone function divided by the sum of the squares in the configuration space (Kruskal 1964a and b). This statistic has a theoretical range from 0 to 1 with the larger the value the weaker the fit of the data to a given configuration. After a series of iterations has produced a configuration of minimal stress in some number of dimensions the procedure is terminated. Generally, increasing the number of dimensions improves the fit of the data to a configuration. However, beyond three dimensions, interpretation becomes problematic.

In multidimensional scaling, the position of the objects in space can be described in one dimension (if the objects fall on a line), in two dimensions (if the objects lie on a plane), in three dimensions (if the objects can be represented by points in space), or in a higher number of dimensions (in which case an immediate geometrical representation is not possible). In this study, the representations will be in three dimensions because interpretation of more dimensions is problematic at best.

Principal Component Analysis

In order to assess which dental traits are responsible for most of the variance (and hence population distance) in the population samples, a principal component analysis is performed (Pearson 1901, Daultrey 1976, Manly 1986). The object of the analysis is to take p variables X_1, X_2, ..., X_p and find combinations of these to produce uncorrelated indices Z_1, Z_2,..., Z_p. The lack of correlation is a useful property because it means that the indices are measuring different dimensions in the data. However, the indices are also ordered so that Z_1 displays the largest amount of variation, Z_2 displays the second largest amount of variation, and so forth. The Z_i are called the principal components. When doing a principal component analysis, there is always the hope that the variances of most of the indices will be negligible. In that case, the variation in the data set can be adequately described by the few Z variables with variances that are not negligible.

It should be noted that a principal component analysis does not always work in the sense that a large number of original variables are reduced to a small number of transformed variables. This is often the case when the original variables are uncorrelated. In this situation, the analysis does absolutely nothing. The best results are obtained when the original variables are highly correlated (Manly 1986). With correlated variables it is conceivable that the original variables may be adequately represented by two or three principal components. These components represent underlying "dimensions" in the data. As such, the groups can be plotted along these dimensions in three dimensional space.

Previous Work

The dental morphology of the Santa Catalina and Santa Maria samples has been previously examined (Griffin 1989). As in the present analysis, chi-square statistics, mean measures of divergence, multidimensional scaling, and principal component analysis were used to explore the relationships between the two samples. Overall, there was little difference in trait expression between the two groups. A summary of the findings from this previous research are included here as a prologue to the statistical results from the present study.

Similarities and differences between the two population samples were examined via two-dimensional contingency tables and the Chi-square statistic. Chi-square statistics for each trait are reported in Table 12. Examination of the results of the contingency table analysis reveals that the similarities between the two population samples outweigh the differences. Out of 27 traits examined, seven (double-shoveling, tuberculum dentale, upper first molar hypocone, upper first molar Carabelli's trait, peg-shaped upper third molar, lower second molar groove pattern, and lower first molar protostylid) exhibited differences which were statistically significant ($p<0.05$). However, given $\alpha=0.05$, one expects spurious rejection of the null hypothesis in approximately 5% of the comparisons. The number of statistically significant differences observed in Table 12 exceeds this percentage by five-fold. This suggests a significant difference in expression of dental traits between the Santa Maria and Santa Catalina samples.

Because few studies of nonmetric dental morphology have been done for native American populations of the southeastern United States, population samples from the American Southwest were chosen for comparison. The measurements for this part of the study were collected by Scott (1973). The frequencies of traits for each population

Table 12. Results of Contingency Table Analysis

Dental Trait	Chi-square	D.F.	Significance
shoveling I1	1.586	2	0.452
shoveling I2	0.917	2	0.632
double-shoveling	11.660	2	0.003
interruption groove	3.213	1	0.073
tuberculum dentale	8.010	2	0.018
metacone M3	0.532	2	0.766
hypocone M1	29.414	2	0.000
hypocone M2	5.383	2	0.067
metaconule M1	3.213	1	0.073
Carabelli's trait M1	10.541	2	0.005
parastyle	1.018	1	0.313
peg-shaped incisor	0.630	1	0.427
peg-shaped molar	6.460	1	0.011
anterior fovea	5.519	2	0.063
groove pattern M1	0.021	1	0.885
groove pattern M2	12.402	1	0.000
cusp number M1	2.070	1	0.150
cusp number M2	0.423	1	0.515
deflecting wrinkle	1.104	1	0.293
distal trigonid crest	3.487	1	0.062
protostylid M1	5.233	1	0.022
cusp 5 M1	1.288	1	0.256
cusp 5 M2	1.989	1	0.158
cusp 6 M1	0.865	1	0.352
cusp 6 M2	2.583	1	0.108
cusp 7 M1	0.032	1	0.858
cusp 7 M2	-----	-	-----

are presented in Appendix D. Because Scott's data only included certain dental traits, only those reported in Appendix D were used for this analysis. Obviously, one would expect native American populations from the southwestern and southeastern United States to be different. In this type of analysis however, it is more meaningful to include more than just two population samples.

Mean measures of divergence were calculated as estimates of population distance (Sjovold 1977). Mean measures of divergence (MMD) and standardized mean measures of divergence (MMD/MMD-SD [Sofaer et al. 1986]) were calculated from the dental trait frequencies. Table 13 presents the mean measures of divergence and the standardized mean measures of divergence. The formula suggested by Green and Suchey (1976) was used for all analyses.

In drawing conclusions from the values in Table 13, only the MMD/MMD-SD values were considered. The reason for this is that when one is contrasting populations of different sample sizes, the magnitude of variance tends to vary. As a result, the same MMD value can mean very different things depending upon the nature of the sample sizes being compared. A case in point would be the contrast between Santa Catalina and Navajo (MMD=0.1137) and Santa

Table 13. Measures of Divergence, Guale and Southwest U.S. Dental Samples*

	SCdG	SCdG-SM	PAPAGO	NAVAJO	APACHE	HOPI	ZUNI	YUMA	A WHITE
SCdG	———	0.03416	0.11491	0.11337	0.11715	0.09913	0.12811	0.15491	0.31839
SCdG-SM	2.25256	———	0.08998	0.07520	0. 6616	0.08798	0.09690	0.12193	0.33445
PAPAGO	18.67780	6.18984	———	0.01446	0.00941	0.01526	-0.00951	0.02501	0.34688
NAVAJO	24.20938	5.75664	3.69225	———	-0.01318	0.00193	-0.01862	0.02124	0.37675
APACHE	6.99515	2.64205	0.58611	-0.89953	———	-0.00181	-0.01148	0.00707	0.41356
HOPI	18.23454	6.35563	3.19246	0.59069	-0.11762	———	-0.01594	0.04363	0.36448
ZUNI	3.80899	2.32538	-0.28508	-0.57752	-0.26302	-0.48535	———	-0.02459	0.26103
YUMA	14.05772	6.27165	2.41037	2.37477	0.33477	4.50289	-0.64187	———	0.29033
WHITE	25.34962	16.55775	27.86243	33.88556	19.36280	30.25737	7.01212	17.93135	———

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*Mean measures of divergence above diagonal, standardized mean measures of divergence below diagonal

Catalina and Zuni (MMD=0.12811). From the MMD data alone, it would appear that Santa Catalina is more like the Navajo than it is to the Zuni. However, when the MMD values are divided by the MMD-SD, it is clear that Santa Catalina is much more similar to the Zuni (3.80899) than to the Navajo (24.20938). As would be expected, the Santa Catalina and Santa Maria population samples are more closely correlated with one another than to any of the other population samples (MMD/MMD-SD=2.25256).

The next procedure used to estimate population distances was multidimensional scaling (Kruskal and Wish 1978). Multidimensional scaling is a technique that is designed to construct a "map" showing the relationships between a number of objects, given a table of distances between them. The "objects" in this case are populations and the distances used were the MMD/MMD-SD values derived with the Freeman-Tukey transformation reported in Table 13. The "map" constructed from these distances is presented in Figure 7. As with the MMD/MMD-SD values discussed previously, the results of the multidimensional scaling indicate that the Santa Catalina and Santa Maria population samples are more closely related to each other than to any of the other samples.

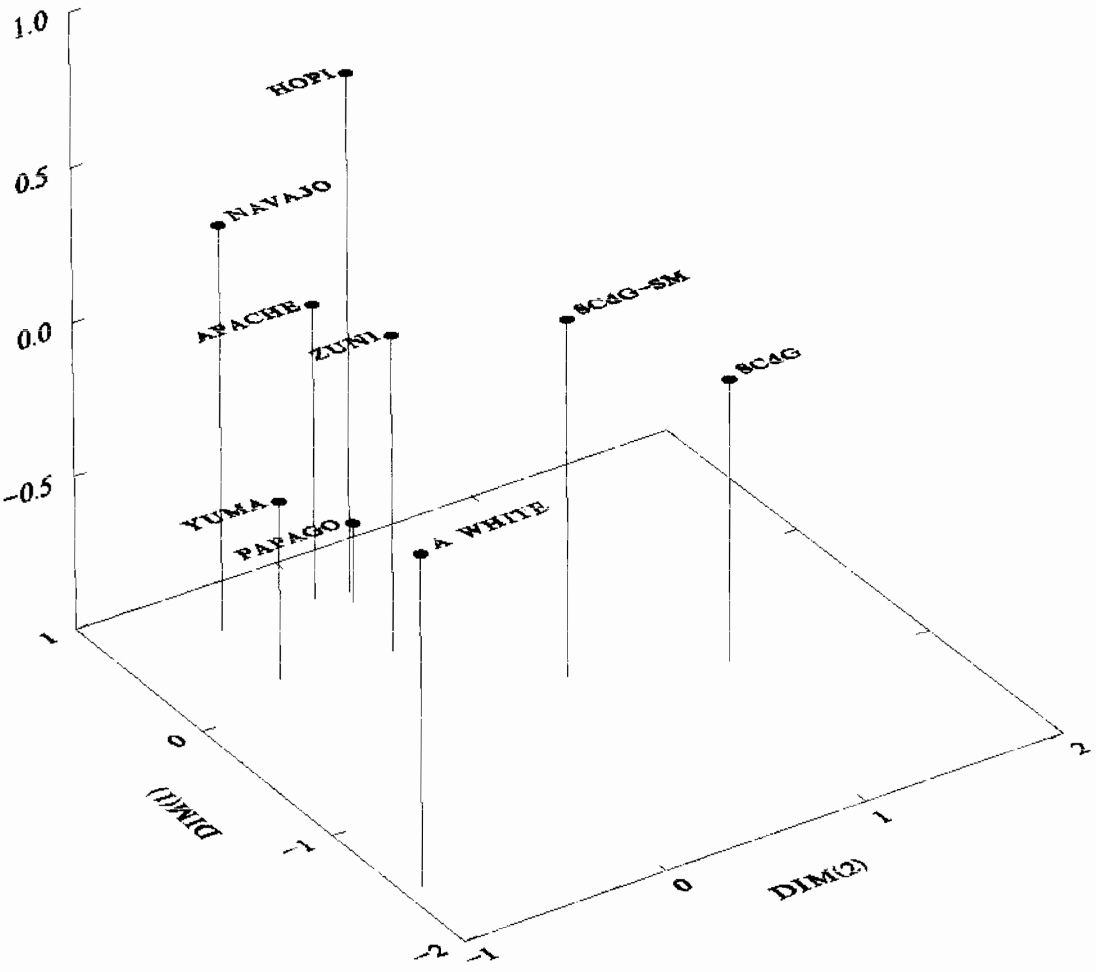

Figure 7. Multidimensional Scaling Analysis, Pilot Study.

In order to assess which dental traits were responsible for most of the variance (and hence population distance) in the population samples, a principal component analysis was performed (Manly 1986). Table 14 presents the unrotated component loadings and the variance explained by each of the principal components. As can be seen, the first three components explain 90.204% of the total variance. These data indicate clearly that the Santa Catalina and Santa Maria samples are quite distinct from the southwestern samples, and all of these native American samples are distinct from American Whites. It can also be observed from the results presented in Table 14 that the traits upper central and lateral incisor shoveling, upper first molar hypocone and Carabelli's trait, lower first and second molar cusp number, lower first molar cusp 6, and lower second molar cusp 7 provide valuable parameters for differentiating these three regional clusters.

Figure 8 presents a "map" of the principal component analysis. The results are the same as reported for the previous analyses of population distances. It is interesting to note, however, that the Santa Maria sample occupies a more central position with respect to the southwestern groups and the American Whites than does the Santa Catalina sample. This result cannot be fully explained by smaller sample size. That is, if this was

Table 14. Component Loadings from Principal Component Analysis

shoveling I1	0.739	0.580	-0.005	0.258
shoveling I2	0.936	0.315	-0.046	0.007
tuberculum dentale	-0.068	0.844	-0.269	-0.207
hypocone M1	0.491	-0.729	-0.033	0.225
hypocone M2	0.699	0.188	0.172	0.238
metaconule M1	0.594	-0.271	0.497	-0.300
Carabelli's trait M1	-0.819	-0.182	0.319	-0.359
groove pattern M1	0.196	-0.641	0.673	0.197
groove pattern M2	-0.097	-0.521	-0.440	0.714
cusp number M1	0.955	0.129	0.128	0.039
cusp number M2	0.899	-0.334	-0.022	-0.137
cusp 6 M1	0.798	0.328	0.146	0.190
cusp 6 M2	0.746	-0.287	0.005	-0.531
cusp 7 M1	-0.157	0.157	0.653	0.284
cusp 7 M2	-0.753	0.162	0.538	0.260

Percent of total variance explained:

1	2	3	4
44.875	21.827	12.350	9.796

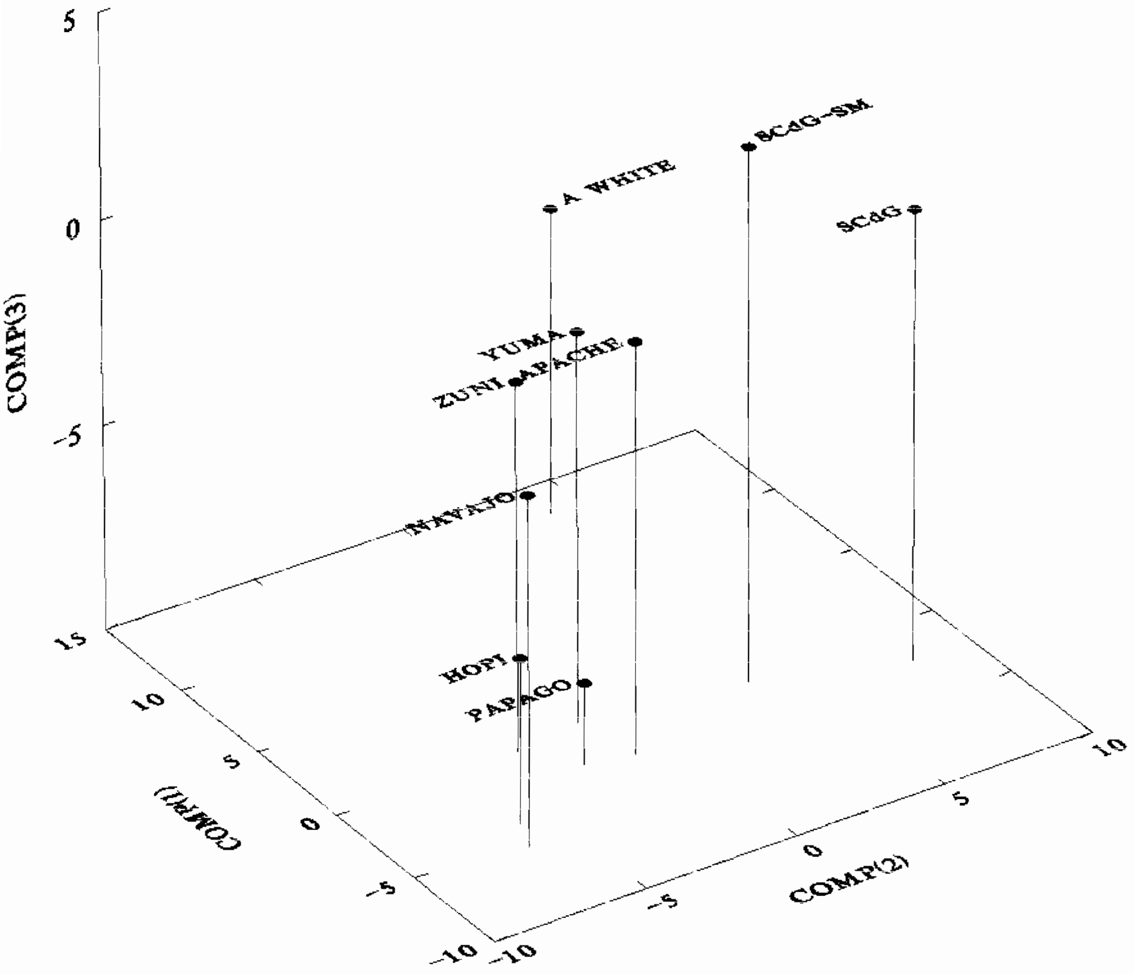

Figure 8. Principal Component Analysis, Pilot Study.

simply a matter of small sample size, then one would expect the Zuni and Apache to occupy much more central positions than they do.

The results of this study indicate that although there are some significant differences in the expression of nonmetric dental traits between the population samples from Santa Catalina and Santa Maria the populations themselves are likely closely genetically affiliated. There also appears to be little or no change in the dental morphology of the Guale after their move from Santa Catalina to Santa Maria.

Morphological Traits

Dental morphological traits were scored along a continuum of expression in each population sample using the methodology provided by Turner and others (1990). Cranial morphological traits were recorded as present or absent, with present representing any degree of trait expression. The dental morphological traits were dichotomized for the statistical analyses involving angular transformations using the criteria suggested by Turner (1987a). Dental and cranial morphological trait frequencies are presented in Tables 15 and 16. Dichotomized dental and cranial trait frequencies as well as trait frequencies from the comparative Amerindian (Dodo and Ishida 1987, Konigsberg et

Table 15. Dental Trait Frequencies

		Frequency (%)					
Dental Trait	Grade	Irene	SCdG	SCdG-SM	SMdY	NC	Ledford
shoveling I1	0	0 (0.0)	1 (1.6)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
	1	1 (1.4)	5 (8.1)	3 (6.9)	2 (5.7)	1 (20.0)	0 (0.0)
	2	25 (36.2)	34 (54.8)	20 (46.5)	10 (28.6)	2 (40.0)	22 (28.9)
	3	29 (42.0)	19 (30.6)	14 (32.6)	17 (48.6)	1 (20.0)	28 (36.8)
	4	14 (20.3)	2 (3.2)	5 (11.6)	4 (11.4)	1 (20.0)	20 (26.3)
	5	0 (0.0)	1 (1.6)	1 (2.3)	2 (5.7)	0 (0.0)	5 (6.6)
	6	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (1.3)
shoveling I2	0	0 (0.0)	1 (1.2)	5 (11.9)	0 (0.0)	0 (0.0)	0 (0.0)
	1	1 (1.5)	11 (12.8)	4 (9.5)	2 (6.1)	3 (27.3)	1 (1.4)
	2	5 (7.5)	33 (38.4)	16 (38.1)	13 (39.4)	2 (18.2)	12 (16.7)
	3	18 (26.9)	18 (21.0)	10 (23.8)	8 (24.2)	3 (27.3)	28 (38.9)
	4	22 (32.8)	15 (17.4)	5 (11.9)	4 (12.1)	1 (9.1)	26 (36.1)
	5	18 (26.9)	4 (4.6)	0 (0.0)	3 (9.1)	1 (9.1)	4 (5.6)
	6	2 (3.0)	2 (2.3)	0 (0.0)	3 (9.1)	1 (9.1)	1 (1.4)
	7	1 (1.5)	1 (1.1)	2 (4.7)	0 (0.0)	0 (0.0)	0 (0.0)
	8	0 (0.0)	1 (1.1)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
double shoveling	0	2 (2.9)	8 (12.3)	11 (22.9)	5 (15.1)	2 (40.0)	3 (3.9)
	1	0 (0.0)	8 (12.3)	7 (14.6)	2 (6.1)	0 (0.0)	2 (2.6)
	2	9 (13.2)	15 (23.1)	11 (22.9)	9 (27.3)	1 (20.0)	7 (9.1)
	3	10 (14.7)	19 (29.2)	2 (4.2)	8 (24.2)	0 (0.0)	20 (26.0)
	4	20 (29.4)	8 (12.3)	13 (27.1)	3 (9.1)	1 (20.0)	28 (36.4)
	5	19 (27.9)	7 (10.8)	4 (8.3)	5 (15.1)	0 (0.0)	14 (18.2)
	6	8 (11.7)	0 (0.0)	0 (0.0)	1 (3.0)	1 (20.0)	3 (3.9)
interruption groove	0	41 (62.1)	28 (41.8)	15 (34.1)	15 (51.7)	0 (0.0)	36 (58.1)
	1	5 (7.6)	22 (32.8)	8 (18.2)	9 (31.0)	3 (27.3)	17 (27.4)
	2	19 (28.9)	11 (16.4)	13 (29.6)	4 (13.8)	6 (54.6)	2 (3.2)
	3	1 (1.5)	2 (2.9)	0 (0.0)	0 (0.0)	2 (18.2)	7 (11.3)
	4	0 (0.0)	4 (5.9)	8 (18.2)	1 (3.4)	0 (0.0)	0 (0.0)

(continued)

Table 15, continued

		Frequency (%)											
Dental Trait	Grade	Irene		SCdG		SCdG-SM		SMdY		NC		Ledford	
metacone M3	0	1	(1.6)	3	(2.6)	0	(0.0)	2	(9.5)	0	(0.0)	0	(0.0)
	1	0	(0.0)	1	(0.8)	0	(0.0)	1	(4.7)	0	(0.0)	0	(0.0)
	2	3	(4.8)	3	(2.6)	2	(5.9)	2	(9.5)	2	(16.7)	0	(0.0)
	3	11	(17.7)	23	(19.8)	7	(20.6)	2	(9.5)	1	(8.3)	7	(18.9)
	3.5	27	(43.5)	34	(29.3)	12	(35.3)	11	(52.4)	5	(41.7)	17	(46.0)
	4	20	(32.2)	48	(41.4)	10	(29.4)	3	(14.3)	3	(25.0)	13	(35.1)
	5	0	(0.0)	4	(3.4)	3	(8.8)	0	(0.0)	1	(8.3)	0	(0.0)
hypocone M1	3	0	(0.0)	1	(0.6)	1	(1.9)	0	(0.0)	0	(0.0)	1	(1.1)
	3.5	2	(2.1)	11	(6.3)	4	(7.8)	4	(8.7)	2	(12.5)	1	(1.1)
	4	39	(41.0)	68	(39.3)	40	(78.4)	33	(71.7)	8	(50.0)	78	(86.7)
	5	54	(56.8)	93	(53.7)	6	(11.7)	9	(19.6)	6	(37.5)	10	(1.1)
hypocone M2	0	0	(0.0)	1	(0.7)	0	(0.0)	1	(2.8)	0	(0.0)	0	(0.0)
	1	0	(0.0)	7	(4.7)	2	(5.3)	1	(2.8)	1	(7.1)	0	(0.0)
	2	7	(8.6)	5	(3.3)	2	(5.3)	3	(8.3)	0	(0.0)	0	(0.0)
	3	12	(14.8)	29	(19.5)	8	(21.0)	8	(22.2)	5	(35.7)	19	(28.8)
	3.5	25	(30.8)	74	(49.7)	11	(28.9)	15	(41.7)	5	(35.7)	25	(37.9)
	4	35	(43.2)	30	(20.1)	15	(39.5)	8	(22.2)	2	(14.3)	22	(33.3)
	5	2	(2.5)	3	(2.0)	0	(0.0)	0	(0.0)	1	(7.1)	0	(0.0)
metaconule M1	0	62	(72.9)	83	(73.4)	30	(88.2)	26	(65.0)	4	(25.0)	35	(42.2)
	1	8	(9.4)	7	(6.2)	0	(0.0)	4	(10.0)	6	(37.5)	27	(32.5)
	2	8	(9.4)	5	(4.4)	0	(0.0)	3	(7.5)	4	(25.0)	17	(20.5)
	3	2	(2.3)	9	(7.9)	3	(8.8)	6	(15.0)	2	(12.5)	4	(4.8)
	4	0	(0.0)	9	(7.9)	1	(2.9)	1	(2.5)	0	(0.0)	0	(0.0)
	5	5	(5.8)	0	(0.0)	0	(0.0)	0	(0.0)	0	(0.0)	0	(0.0)

(continued)

Table 15, continued

		Frequency (%)					
Dental Trait	Grade	Irene	SCdG	SCdG-SM	SMdY	NC	Ledford
metaconule M2	0	68 (94.4)	78 (77.2)	24 (96.0)	30 (96.8)	9 (64.3)	49 (84.5)
	1	0 (0.0)	4 (3.9)	0 (0.0)	0 (0.0)	3 (21.4)	7 (12.1)
	2	0 (0.0)	3 (2.9)	0 (0.0)	1 (3.2)	0 (0.0)	2 (3.4)
	3	0 (0.0)	3 (2.9)	0 (0.0)	0 (0.0)	1 (7.1)	0 (0.0)
	4	1 (1.3)	8 (7.9)	0 (0.0)	0 (0.0)	1 (7.1)	0 (0.0)
	5	3 (4.1)	5 (4.9)	1 (4.0)	0 (0.0)	0 (0.0)	0 (0.0)
Carabelli's trait M1	0	33 (35.8)	23 (23.7)	18 (58.1)	22 (55.0)	5 (33.3)	11 (13.1)
	1	8 (8.7)	14 (14.4)	5 (16.1)	5 (12.5)	6 (40.0)	11 (13.1)
	2	24 (26.0)	20 (20.6)	4 (12.9)	6 (15.0)	3 (20.0)	17 (20.2)
	3	10 (10.8)	14 (14.4)	4 (12.9)	1 (2.5)	0 (0.0)	14 (16.7)
	4	11 (11.9)	11 (11.3)	0 (0.0)	4 (10.0)	0 (0.0)	23 (27.4)
	5	3 (3.2)	13 (13.4)	0 (0.0)	2 (5.0)	0 (0.0)	4 (4.8)
	6	0 (0.0)	1 (1.0)	0 (0.0)	0 (0.0)	1 (6.7)	1 (1.2)
	7	3 (3.2)	1 (1.0)	0 (0.0)	0 (0.0)	0 (0.0)	3 (3.6)
Carabelli's trait M2	0	74 (94.8)	71 (98.6)	23 (95.8)	29 (96.7)	13(100.0)	57 (95.0)
	1	2 (2.5)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (1.7)
	2	1 (1.2)	1 (1.4)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
	3	1 (1.2)	0 (0.0)	1 (4.2)	0 (0.0)	0 (0.0)	2 (3.3)
	4	0 (0.0)	0 (0.0)	0 (0.0)	1 (3.3)	0 (0.0)	0 (0.0)
parastyle	0	62(100.0)	88 (92.6)	36 (97.3)	20 (95.2)	12(100.0)	36 (97.3)
	1	0 (0.0)	2 (2.1)	0 (0.0)	1 (4.8)	0 (0.0)	0 (0.0)
	2	0 (0.0)	1 (1.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (2.7)
	3	0 (0.0)	2 (2.1)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
	4	0 (0.0)	1 (1.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
	5	0 (0.0)	1 (1.7)	1 (2.7)	0 (0.0)	0 (0.0)	0 (0.0)
peg-shaped incisor	0	67(100.0)	79 (98.7)	50(100.0)	32(100.0)	11(100.0)	73(100.0)
	2	0 (0.0)	1 (1.2)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)

(continued)

Table 15, continued

		Frequency (%)					
Dental Trait	Grade	Irene	SCdG	SCdG-SM	SMdY	NC	Ledford
peg-shaped molar	0	61 (98.4)	82 (81.2)	40 (97.6)	22 (91.7)	13(100.0)	39(100.0)
	1	0 (0.0)	19 (18.2)	1 (2.4)	0 (0.0)	0 (0.0)	0 (0.0)
	2	1 (1.6)	0 (0.0)	0 (0.0)	2 (8.3)	0 (0.0)	0 (0.0)
anterior fovea	0	0 (0.0)	3 (3.6)	3 (11.1)	2 (8.3)	0 (0.0)	0 (0.0)
	1	0 (0.0)	4 (4.9)	2 (7.4)	2 (8.3)	0 (0.0)	1 (1.2)
	2	0 (0.0)	6 (7.3)	5 (18.5)	1 (4.2)	0 (0.0)	1 (1.2)
	3	2 (3.2)	12 (14.6)	9 (33.3)	16 (66.7)	9 (81.8)	19 (22.6)
	4	61 (96.8)	57 (69.5)	8 (29.6)	3 (12.5)	2 (18.2)	63 (75.0)
groove pattern M1	1	78 (95.1)	126 (88.7)	27 (87.1)	26 (76.5)	13 (92.9)	78 (90.7)
	2	0 (0.0)	3 (2.1)	1 (3.2)	1 (2.9)	0 (0.0)	0 (0.0)
	3	4 (4.9)	13 (9.1)	3 (9.7)	7 (20.6)	1 (7.1)	8 (9.3)
groove pattern M2	1	9 (11.8)	22 (15.7)	11 (45.8)	12 (44.4)	1 (9.1)	4 (6.8)
	2	4 (5.3)	12 (8.6)	10 (41.7)	1 (3.7)	0 (0.0)	4 (6.8)
	3	63 (82.9)	106 (75.7)	3 (12.5)	14 (51.8)	10 (90.9)	51 (86.4)
cusp number M1	4	1 (1.3)	0 (0.0)	1 (2.8)	0 (0.0)	0 (0.0)	0 (0.0)
	5	56 (70.9)	92 (70.8)	21 (58.3)	27 (77.1)	7 (50.0)	54 (61.4)
	6	20 (25.3)	35 (26.9)	14 (38.9)	8 (22.9)	7 (50.0)	32 (36.4)
	7	2 (2.5)	3 (2.3)	0 (0.0)	0 (0.0)	0 (0.0)	2 (2.2)
cusp number M2	4	6 (8.3)	8 (6.8)	4 (14.8)	5 (20.0)	1 (9.1)	0 (0.0)
	5	54 (75.0)	68 (58.1)	16 (59.3)	14 (56.0)	6 (54.5)	45 (76.3)
	6	12 (16.7)	41 (35.0)	7 (25.9)	6 (24.0)	4 (36.4)	14 (23.7)
deflecting wrinkle	0	9 (34.6)	5 (8.9)	6 (27.3)	11 (57.9)	4 (80.0)	14 (25.4)
	1	2 (7.7)	11 (19.6)	3 (13.6)	4 (21.0)	1 (20.0)	6 (10.9)
	2	8 (30.8)	35 (62.5)	11 (50.0)	2 (10.5)	0 (0.0)	30 (54.6)
	3	7 (26.9)	5 (8.9)	2 (9.1)	2 (10.5)	0 (0.0)	5 (9.1)

(continued)

Table 15, continued

		Frequency (%)					
Dental Trait	Grade	Irene	SCdG	SCdG-SM	SMdY	NC	Ledford
distal trigonid crest	0	35 (87.5)	55 (67.1)	21 (94.4)	21(100.0)	5 (83.3)	58 (86.6)
	1	5 (12.5)	27 (32.9)	1 (4.6)	0 (0.0)	1 (16.7)	9 (13.4)
protostylid M1	0	3 (3.7)	6 (8.4)	3 (14.3)	17 (50.0)	8 (57.1)	16 (18.2)
	1	34 (41.5)	29 (40.8)	14 (66.7)	17 (50.0)	5 (35.7)	51 (57.9)
	2	45 (54.9)	36 (50.7)	4 (19.0)	0 (0.0)	1 (7.2)	21 (23.9)
protostylid M2	0	5 (6.9)	14 (24.1)	6 (66.7)	12 (50.0)	10 (90.9)	13 (21.3)
	1	35 (48.6)	25 (43.1)	1 (11.1)	12 (50.0)	1 (9.1)	39 (63.9)
	2	32 (44.4)	19 (32.7)	2 (22.2)	0 (0.0)	0 (0.0)	9 (14.7)
cusp 5 M1	0	1 (1.3)	0 (0.0)	1 (2.9)	0 (0.0)	0 (0.0)	0 (0.0)
	2	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (1.1)
	3	6 (7.6)	18 (14.1)	1 (2.9)	3 (8.8)	0 (0.0)	20 (22.7)
	4	28 (35.4)	58 (45.3)	27 (77.1)	20 (58.8)	9 (64.3)	32 (36.4)
	5	44 (55.7)	52 (40.6)	6 (17.1)	11 (32.4)	5 (35.7)	35 (39.8)
cusp 5 M2	0	7 (9.7)	9 (7.9)	4 (16.7)	5 (20.0)	1 (9.1)	0 (0.0)
	1	0 (0.0)	2 (1.7)	0 (0.0)	2 (8.0)	0 (0.0)	0 (0.0)
	2	3 (4.2)	6 (5.3)	0 (0.0)	2 (8.0)	2 (18.2)	6 (10.2)
	3	13 (18.0)	32 (28.1)	2 (8.3)	4 (16.0)	2 (18.2)	20 (33.9)
	4	34 (47.2)	59 (51.7)	15 (62.5)	11 (44.0)	5 (45.4)	23 (39.0)
	5	15 (20.8)	6 (5.3)	3 (12.5)	1 (4.0)	1 (9.1)	10 (16.9)
cusp 6 M1	0	59 (74.7)	92 (71.9)	17 (56.7)	26 (76.5)	7 (50.0)	55 (62.5)
	1	1 (1.3)	6 (4.7)	3 (10.0)	1 (2.9)	1 (7.1)	1 (1.1)
	2	5 (6.3)	12 (9.4)	6 (20.0)	4 (11.7)	4 (28.6)	10 (11.4)
	3	12 (15.2)	6 (4.7)	4 (13.3)	3 (8.8)	2 (14.3)	13 (14.8)
	4	2 (2.5)	12 (9.4)	0 (0.0)	0 (0.0)	0 (0.0)	8 (9.1)
	5	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (1.1)

(continued)

Table 15, continued

		Frequency (%)					
Dental Trait	Grade	Irene	SCdG	SCdG-SM	SMdY	NC	LEDFORD
cusp 6 M2	0	60 (88.3)	76 (66.7)	17 (80.9)	19 (76.0)	7 (63.6)	44 (74.6)
	1	0 (0.0)	2 (1.7)	1 (4.8)	1 (4.0)	0 (0.0)	0 (0.0)
	2	1 (1.4)	10 (8.8)	1 (4.8)	2 (8.0)	0 (0.0)	4 (6.8)
	3	5 (6.9)	7 (6.1)	1 (4.8)	1 (4.0)	2 (18.2)	7 (11.9)
	4	6 (8.3)	17 (14.9)	0 (0.0)	1 (4.0)	2 (18.2)	4 (6.8)
	5	0 (0.0)	2 (1.7)	1 (4.8)	1 (4.0)	0 (0.0)	0 (0.0)
cusp 7 M1	0	75 (94.9)	123 (96.0)	31(100.0)	34(100.0)	14(100.0)	87 (98.9)
	1	0 (0.0)	3 (2.3)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
	2	4 (5.0)	1 (0.8)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
	3	0 (0.0)	1 (0.8)	0 (0.0)	0 (0.0)	0 (0.0)	1 (1.1)
cusp 7 M2	0	71 (98.6)	114(100.0)	23(100.0)	24 (96.0)	11(100.0)	59(100.0)
	2	1 (1.4)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
	4	0 (0.0)	0 (0.0)	0 (0.0)	1 (4.0)	0 (0.0)	0 (0.0)

Table 16. Cranial Trait Frequencies

				N (% present)		
Cranial Trait	Irene	SCdG	SCdG-SM	SMdY	NC	Ledford
ossicle at lambda	70 (34.3)	0 (0.0)	63 (31.7)	18 (5.5)	68 (17.6)	29 (27.6)
lambdoid ossicle	70 (62.9)	0 (0.0)	63 (42.9)	19 (31.6)	67 (32.8)	30 (36.7)
ossicle at asterion	62 (37.1)	0 (0.0)	62 (32.3)	20 (30.0)	67 (13.4)	25 (12.0)
parietal notch bone	64 (15.6)	0 (0.0)	64 (6.2)	20 (10.0)	65 (6.1)	29 (6.9)
epipteric bone	51 (19.6)	0 (0.0)	36 (2.8)	18 (0.0)	56 (0.0)	26 (11.5)
bregmatic bone	67 (0.0)	0 (0.0)	62 (1.6)	21 (0.0)	69 (0.0)	32 (0.0)
coronal ossicle	67 (4.5)	0 (0.0)	62 (1.6)	21 (0.0)	67 (4.5)	32 (3.1)
metopism	69 (0.0)	0 (0.0)	70 (0.0)	21 (0.0)	69 (0.0)	32 (0.0)
fronto-temporal art.	50 (2.0)	0 (0.0)	38 (0.0)	18 (0.0)	60 (0.0)	28 (0.0)
supraorbital foramen	67 (17.9)	0 (0.0)	66 (18.2)	20 (25.0)	67 (43.3)	32 (12.5)
frontal foramen	66 (56.1)	0 (0.0)	65 (36.9)	20 (60.0)	68 (69.1)	32 (50.0)
auditory torus	69 (0.0)	0 (0.0)	66 (0.0)	21 (0.0)	69 (0.0)	32 (0.0)
foramen of Huschke	69 (24.6)	0 (0.0)	68 (32.3)	21 (33.3)	65 (12.3)	32 (15.6)
condylar facet double	48 (0.0)	0 (0.0)	36 (0.0)	16 (0.0)	45 (0.0)	19 (0.0)
precondylar tubercle	44 (0.0)	0 (0.0)	33 (12.1)	16 (0.0)	47 (17.0)	18 (11.1)
foramen ovale	48 (2.1)	0 (0.0)	53 (1.9)	16 (0.0)	62 (11.3)	25 (4.0)
foramen spinosum	44 (29.5)	0 (0.0)	55 (21.8)	16 (18.7)	60 (26.7)	25 (8.0)
accessory palatine for.	45 (75.6)	0 (0.0)	42 (78.6)	12 (41.7)	45 (60.0)	21 (42.9)
palatine torus	57 (80.7)	0 (0.0)	57 (77.2)	18 (83.3)	54 (31.5)	29(100.0)
maxillary torus	59 (3.4)	0 (0.0)	58 (27.6)	18 (11.1)	51 (0.0)	31 (25.8)
parietal foramen	67 (31.3)	0 (0.0)	65 (44.6)	21 (19.0)	69 (56.5)	32 (50.0)
posterior condylar can.	39 (33.3)	0 (0.0)	32 (18.7)	7 (57.1)	38 (63.2)	18 (16.7)
mastoid foramen abs.	61 (16.4)	0 (0.0)	63 (12.7)	16 (18.7)	67 (10.4)	24 (8.3)
ant. condylar canal dbl	48 (14.6)	0 (0.0)	33 (18.2)	14 (42.9)	50 (16.0)	20 (10.0)
zygomatico-facial for.	61 (60.7)	0 (0.0)	56 (66.1)	18 (83.3)	64 (32.8)	29 (75.9)
accs. infraorbital for.	47 (6.4)	0 (0.0)	49 (6.1)	12 (0.0)	46 (28.3)	27 (18.5)

al. 1993, Turner 1985) and Sinodont (Dodo and Ishida 1987, 1990, Ishida and Dodo 1993, Turner 1987a) population samples are presented in Appendix E.

Dental Morphology

The major features of the three Guale population samples can be summarized as follows:

(1) Maxillary anterior teeth in all three samples exhibit light to moderate lingual and labial shoveling. Interruption grooves on the upper lateral incisors occur in less than 40% of the individuals from Irene Mound and are more frequently observed in the Santa Catalina and Santa Maria samples (58.2% and 65.9% respectively). Mesio- and distolingual grooves are the predominant types found in all three samples.

(2) Maxillary molars in all three samples tend to be morphologically conservative. Upper first molars have large or very large hypocones and upper second molars exhibit only slightly diminished hypocones. The hypocone is frequently missing on the upper third molars although the metacone is commonly intermediate to large.

(3) The metaconule is infrequently observed on upper first molars for all three samples (<30%). The metaconule occurred rarely on the upper second molars of the Irene Mound and Santa Maria samples (5.6% and 4%

respectively) but was more frequent in the Santa Catalina sample (22.%).

(4) Carabelli's trait occurred in appreciable frequencies on the upper first molars of the Irene mound and Santa Catalina samples but occurred less frequently in the Santa Maria sample. In all three samples, Carabelli's trait was predominantly expressed as pits and grooves rather than fully formed cusps. For all three samples, Carabelli's trait is particularly rare on the upper second molars (<6%).

(5) Morphological reduction of the upper lateral incisors and upper third molars occurs infrequently in all three samples (<2% and <18% respectively).

(6) As with their isomeres, the mandibular molars tend to be morphologically conservative. The Y-groove is the predominant pattern on the lower first molars and the "+" pattern is most frequent on the lower second molars. The hypoconulid is present in over 90% of all lower first, second, and third molars although it tends to be somewhat reduced on the second molars. The entoconulid occurs in appreciable frequencies on the lower first molar (>25%) and occurs less frequently on the lower second molars of the Irene Mound and Santa Maria samples (<20%). The Santa Catalina sample exhibits a higher frequency of lower second molar entoconulids (32.3%).

(7) The three Guale samples show quite low frequencies of the metaconulid on the first and second lower molars. The protostylid is ubiquitous but is predominantly expressed as pits and grooves.

Cranial Morphology

Observation of cranial morphological traits was possible for only two of the three Guale samples due to the extremely fragmentary nature of the *Santa Catalina de Guale* population sample. The primary cranial morphological features of the Irene Mound and Santa Maria population samples can be summarized as follows:

(1) Sutural bones of the posterior cranial vault are common with frequencies ranging from 31 to 63%. Sutural bones of the anterior cranial vault are quite rare in both samples.

(2) Metopic sutures were not present in either sample. Fronto-temporal articulation was observed in only one individual.

(3) Frontal notches or foramina are common in both samples (56.1% and 36.9% respectively). Supraorbital foramina occur in much lower frequencies (<18%).

(4) Positive expressions for variations of the cranial base and maxilla are particularly rare with the notable exceptions of the foramina of Huschke (>24%), accessory palatine foramina (>75%), and palatine tori

(>75%). Accessory palatine foramina and palatine tori occur in quite high frequencies although the palatine tori are limited exclusively to the weakest expression of the trait.

(5) Emissary foramina exhibit a wide range of variation. Parietal foramina occur in appreciable frequencies (>30%); the posterior condylar canal is frequently patent (>32%); the mastoid foramen is infrequently exsutural (<10%); the anterior condylar canal is rarely divided to form a double foramen (<18%); and zygomatico-facial foramina occur quite frequently (>60%).

Summary of Statistical Results

Dental Analysis

Elimination of dental morphological traits due to the biases discussed in Chapter III resulted in a battery of 19 uncorrelated traits of the maxillary and mandibular dentition. The traits included in the distance analysis are summarized in Table 17.

Chi-Square Analysis

Each variable was tested for differences in frequencies of the morphological grades (1) between the primary (Guale)

Table 17. Dental Morphological Traits Included in Distance Analysis

Trait		Teeth Observed	References
shoveling	[SHOV2]	upper lateral incisors	Hrdlicka 1920; Dahlberg 1956; 1963; Moorrees 1957; Scott 1973
double-shoveling	[DSHOV]	upper central incisors	Dahlberg 1956; Turner 1967
interruption groove	[IGROV]	upper lateral incisors	Turner 1967
metacone	[METAC]	upper 3rd molars	Turner et al. 1991
hypocone	[HYPO2]	upper 2nd molars	Larson 1970; 1978; Scott 1973; Turner et al. 1991
metaconule	[M1C5]	upper 1st molars	Harris 1977; Harris and Bailit 1980
Carabelli's trait	[CARAM1] [CARAM2]	upper 1st and 2nd molars	Dahlberg 1956; 1963; Scott 1973; 1980
parastyle	[PARA]	upper 3rd molar	Katich 1975; Turner et al. 1991
peg-shaped incisor	[PSI]	upper lateral incisor	Turner et al. 1991
peg-shaped molar	[PSM]	upper 3rd molar	Turner et al. 1991
groove pattern	[GPM1] [GPM2]	lower 1st and 2nd molars	Gregory 1916; Hellman 1929; Jorgensen 1955
cusp number	[CNM1]	lower 1st molars	Gregory 1916; Hellman 1929; Turner 1967
protostylid	[PM1]	lower 1st molars	Dahlberg 1950; 1956; 1963; Turner 1967; Scott 1973
cusp 5	[C5M2]	lower 2nd molars	Turner 1970; Scott and Dahlberg 1982; Turner et al. 1991
cusp 6	[C6M2]	lower 2nd molars	Turner 1970; Scott 1973; Scott and Dahlberg 1982; Turner et al. 1991
cusp 7	[C7M1] [C7M2]	lower 1st and 2nd molars	Turner 1970; Turner et al. 1991

and non-Guale samples, and (2) among the primary (Guale) and non-Guale samples. These comparisons will (1) delineate trait frequency differences between the Guale and non-Guale samples, and (2) delineate trait frequency differences among the Guale and non-Guale samples. Tau-b statistics were also computed for all of the traits for each sample comparison in order to determine the strength of differences. Chi-square and Tau-b statistics are reported in Table 18.

Examination of the Chi-square and Tau-b statistics reveals a considerable number of differences between the entire group of samples and among the Guale samples. Overall, there are 95 (33.3%) statistically significant differences ($p<0.05$) out of 285 comparisons. Considering only the Guale samples, there are 21 (36.8%) statistically significant differences out of 57 comparisons. Of the significant differences across all groups 33 out of 95 (34.7%) were strong correlations. This represents 11.6% of all comparisons. Among the Guale samples, 7 of the 21 significant differences (33.3%) were strong correlations. This represents 12.3% of the comparisons among the Guale samples. All of the traits differed significantly in at least one of the comparisons.

Among the Guale samples, there are a number of traits which seem to define the major differences between groups.

Table 18. Dental Chi-square Analysis

		IRENE - SCdG					IRENE - SCdG-SM					IRENE - SMdY					IRENE - CALGONQ			
Trait	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p
SHOV2	153	-0.404	44.214	8	0.000	109	-0.486	51.072	7	0.000	100	-0.298	23.370	6	0.001	78	-0.244	13.483	6	0.036
DSHOV	133	-0.417	41.391	6	0.000	116	-0.424	42.338	6	0.000	101	-0.339	20.918	6	0.002	73	-0.157	10.093	5	0.073
IGROV	133	0.130	22.056	4	0.000	110	0.271	22.425	4	0.000	95	0.027	12.311	4	0.015	77	0.408	21.200	3	0.000
METAC	178	0.096	10.831	7	0.146	96	0.070	8.503	6	0.204	83	-0.157	8.928	6	0.178	74	0.021	6.722	6	0.347
HYPO2	230	-0.164	24.225	6	0.000	119	-0.082	7.217	5	0.205	117	-0.201	11.054	6	0.087	95	-0.148	12.431	5	0.029
M1C5	198	0.007	24.071	5	0.000	119	-0.140	19.485	5	0.002	125	0.082	12.727	5	0.026	101	0.305	18.158	4	0.001
CARAM1	189	0.120	13.525	7	0.060	123	-0.226	15.616	6	0.016	132	-0.167	9.732	6	0.136	107	-0.111	19.184	7	0.008
CARAM2	150	-0.103	3.981	3	0.264	102	-0.016	2.269	3	0.518	108	-0.035	5.173	4	0.270	91	-0.087	1.263	3	0.738
PARA	157	0.173	7.245	5	0.203	99	0.131	1.986	1	0.159	83	0.190	2.785	1	0.095	74	*	*	*	*
PSI	147	0.076	1.223	1	0.269	117	*	*	*	*	99	*	*	*	*	78	*	*	*	*
PSM	163	0.249	21.399	2	0.000	103	0.028	2.859	2	0.239	86	0.164	2.022	1	0.155	75	-0.053	0.384	1	0.536
GPM1	224	0.106	4.307	2	0.116	113	0.136	3.510	2	0.173	116	0.275	8.952	2	0.011	96	0.036	0.114	1	0.736
GPM2	216	0.079	1.621	2	0.445	100	-0.577	41.531	2	0.000	103	-0.325	11.804	2	0.003	87	0.067	1.221	2	0.543
CNM1	209	0.023	2.005	3	0.571	115	0.085	3.869	3	0.276	114	-0.047	2.390	3	0.495	93	0.161	3.941	3	0.268
PM1	153	-0.059	1.627	2	0.443	103	-0.255	10.207	2	0.006	116	-0.600	58.506	2	0.000	96	-0.455	27.362	2	0.000
C5M2	186	-0.150	13.545	5	0.019	96	-0.020	5.183	4	0.269	97	-0.229	11.595	5	0.041	83	-0.113	3.043	4	0.551
C6M2	186	0.167	12.230	5	0.032	93	0.014	9.879	5	0.079	97	0.067	8.580	5	0.127	83	0.166	2.696	3	0.441
C7M1	207	-0.029	7.516	3	0.057	110	-0.122	2.707	1	0.100	113	-0.126	2.926	1	0.087	93	-0.089	1.337	1	0.248
C7M2	186	-0.093	1.907	1	0.167	95	-0.058	0.558	1	0.455	97	0.082	3.321	2	0.190	83	-0.043	0.286	1	0.593

(continued)

Table 18, continued

	IRENE - LEDFORD					SCdG - SCdG-SM					SCdG - SMdY					SCdG - CALGONQ				
Trait	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p
SHOV2	139	-0.259	16.678	6	0.011	128	-0.109	14.487	8	0.070	119	0.086	6.631	8	0.577	97	-0.001	5.183	8	0.738
DSHOV	145	-0.146	10.522	6	0.104	113	-0.071	16.527	5	0.005	98	0.029	4.120	6	0.660	70	-0.030	12.256	6	0.056
IGROV	128	0.000	28.082	3	0.000	111	0.160	10.284	4	0.036	96	-0.101	2.252	4	0.690	78	0.324	17.498	4	0.002
METAC	99	0.081	4.870	5	0.432	150	-0.016	5.549	6	0.476	137	-0.189	14.328	6	0.026	128	-0.038	6.911	6	0.329
HYPO2	147	-0.091	15.529	4	0.004	187	0.061	9.476	6	0.149	185	-0.049	4.475	6	0.613	163	-0.044	4.332	6	0.632
M1C5	168	0.237	29.409	4	0.000	147	-0.133	8.217	4	0.084	153	0.059	4.351	4	0.361	129	0.251	23.528	4	0.000
CARAM1	176	0.237	19.352	7	0.007	128	-0.316	22.895	7	0.002	137	-0.262	16.593	7	0.020	112	-0.185	16.913	7	0.018
CARAM2	138	-0.001	1.924	3	0.588	96	0.086	3.362	2	0.186	102	0.065	3.152	2	0.207	85	-0.046	0.334	1	0.563
PARA	99	0.131	1.986	1	0.159	132	-0.084	4.437	5	0.488	116	-0.043	2.408	5	0.790	107	-0.093	1.726	5	0.886
PSI	151	*	*	*	*	130	-0.070	0.976	1	0.323	112	-0.060	0.677	1	0.411	91	-0.039	0.259	1	0.611
PSM	101	-0.079	0.982	1	0.322	142	-0.213	8.378	1	0.004	125	-0.093	14.952	2	0.001	114	-0.160	5.064	1	0.024
GPM1	168	0.333	1.264	1	0.261	173	0.018	0.140	2	0.932	176	0.141	3.271	2	0.195	156	-0.036	0.650	2	0.723
GPM2	135	0.053	1.093	2	0.579	164	-0.428	36.750	2	0.000	167	-0.214	10.120	2	0.006	151	0.086	2.446	2	0.294
CNM1	167	0.116	3.732	3	0.292	166	0.059	6.467	3	0.091	165	-0.062	1.764	2	0.414	144	0.124	3.425	2	0.180
PM1	170	-0.336	21.907	2	0.000	92	-0.248	7.108	2	0.029	105	-0.552	45.234	2	0.000	85	-0.424	19.346	2	0.000
C5M2	131	-0.070	14.070	4	0.007	138	0.111	10.193	5	0.070	139	-0.116	6.451	5	0.265	125	-0.020	2.925	5	0.712
C6M2	131	0.088	3.844	3	0.279	135	-0.113	7.870	5	0.164	139	-0.082	3.706	5	0.592	125	0.026	4.137	5	0.530
C7M1	167	-0.113	7.336	2	0.026	159	-0.088	2.208	3	0.530	162	-0.092	2.398	3	0.494	142	-0.063	1.058	3	0.787
C7M2	131	-0.079	1.203	1	0.273	137	*	*	*	*	139	0.182	3.465	1	0.063	125	*	*	*	*

(continued)

Table 18, continued

Trait	N	SCdG - LEDFORD Tau-b	X^2	D.F.	p	N	SCdG-SM - SMdY Tau-b	X^2	D.F.	p	N	SCdG-SM - CALGONQ Tau-b	X^2	D.F.	p	N	SCdG-SM - LEDFORD Tau-b	X^2	D.F.	p
SHOV2	158	0.261	28.378	8	0.000	75	0.199	18.264	7	0.011	53	0.088	12.562	7	0.084	114	0.372	35.609	7	0.000
DSHOV	142	0.338	26.506	6	0.000	81	0.103	14.745	6	0.022	53	0.000	7.870	6	0.248	125	0.333	34.663	6	0.000
IGROV	129	-0.154	16.798	4	0.002	73	-0.253	8.169	3	0.043	55	0.173	18.454	4	0.001	106	-0.284	38.961	4	0.000
METAC	153	-0.025	8.550	6	0.201	55	-0.227	12.178	6	0.058	46	-0.039	2.090	4	0.719	71	0.003	8.063	4	0.089
HYPO2	215	0.075	17.981	6	0.006	74	-0.125	4.656	5	0.459	52	-0.106	7.247	5	0.203	104	0.004	9.450	4	0.051
M1C5	196	0.208	49.419	4	0.000	74	0.231	10.522	4	0.032	50	0.515	31.327	4	0.000	117	0.325	41.744	4	0.000
CARAM1	181	0.109	14.389	7	0.045	71	0.065	9.905	5	0.078	46	0.145	9.282	4	0.054	115	0.434	36.159	7	0.000
CARAM2	132	0.105	5.987	3	0.112	54	-0.018	2.798	2	0.247	37	-0.123	0.881	1	0.348	84	0.016	0.707	2	0.702
PARA	132	-0.088	4.437	5	0.488	58	0.051	2.937	2	0.230	49	-0.082	0.569	1	0.451	74	-0.002	2.773	2	0.250
PSI	153	-0.077	1.303	1	0.254	82	*	*	*	*	61	*	*	*	*	123	*	*	*	*
PSM	140	-0.246	13.526	1	0.000	65	0.140	4.962	2	0.084	54	-0.077	0.557	1	0.456	80	-0.110	1.349	1	0.245
GPM1	228	-0.028	2.865	2	0.239	65	0.140	1.526	2	0.466	45	-0.081	0.854	2	0.653	117	-0.048	2.693	2	0.260
GPM2	199	0.122	3.641	2	0.162	51	0.199	16.137	2	0.000	35	0.602	22.645	2	0.000	83	0.663	42.510	2	0.000
CNM1	218	0.094	2.198	2	0.333	71	-0.147	3.781	2	0.151	50	0.111	1.071	2	0.585	124	0.021	3.928	3	0.269
PM1	159	-0.267	13.018	2	0.001	55	-0.421	13.551	2	0.001	35	-0.406	7.315	2	0.026	109	0.007	0.544	2	0.762
C5M2	173	0.072	17.618	5	0.003	49	-0.241	7.980	5	0.157	35	-0.139	6.033	4	0.197	83	-0.053	21.400	4	0.000
C6M2	173	-0.087	7.708	5	0.173	46	0.059	1.489	5	0.914	32	0.206	8.390	5	0.136	80	0.071	8.884	5	0.114
C7M1	216	-0.081	4.297	3	0.231	65	*	*	*	*	45	*	*	*	*	119	0.055	0.607	1	0.436
C7M2	173	*	*	*	*	48	0.140	1.324	1	0.250	34	*	*	*	*	82	*	*	*	*

(continued)

Table 18, continued

Trait	SMdY - CALGONQ N	Tau-b	X^2	D.F.	p	SMdY - LEDFORD N	Tau-b	X^2	D.F.	p	CALGONQ - LEDFORD N	Tau-b	X^2	D.F.	p
SHOV2	44	-0.075	4.083	5	0.538	105	0.156	16.527	5	0.005	83	0.150	12.909	5	0.024
DSHOV	38	-0.051	7.444	6	0.282	110	0.259	16.715	6	0.010	82	0.119	11.705	6	0.069
IGROV	40	0.524	20.097	4	0.000	91	-0.047	10.937	4	0.027	73	-0.428	26.448	3	0.000
METAC	33	0.193	5.705	6	0.457	58	0.257	13.436	5	0.020	49	0.042	9.500	4	0.050
HYPO2	50	-0.009	6.698	6	0.350	102	0.137	11.911	5	0.036	80	0.114	8.831	4	0.065
M1C5	56	0.244	11.427	4	0.022	123	0.113	17.718	4	0.001	99	-0.134	2.409	3	0.492
CARAM1	55	0.081	11.964	6	0.063	124	0.364	30.017	7	0.000	99	0.293	22.585	7	0.002
CARAM2	43	-0.102	0.730	1	0.393	90	0.034	4.636	3	0.200	73	0.096	1.204	2	0.548
PARA	33	-0.134	0.922	1	0.337	58	-0.051	2.937	2	0.230	49	0.082	0.569	1	0.451
PSI	43	*	*	*	*	105	*	*	*	*	84	*	*	*	*
PSM	37	-0.176	1.793	1	0.181	63	-0.231	3.968	1	0.046	52	*	*	*	*
GPM1	48	-0.186	2.273	2	0.321	120	-0.184	5.364	2	0.068	100	0.026	0.073	1	0.788
GPM2	38	0.357	6.075	2	0.048	86	0.392	16.294	2	0.000	70	-0.041	1.454	2	0.483
CNM1	49	0.266	3.328	1	0.068	123	0.153	3.764	2	0.152	102	-0.071	1.408	2	0.495
PM1	48	-0.032	3.023	2	0.221	122	0.362	22.182	2	0.000	102	0.273	9.202	2	0.010
C5M2	36	0.111	3.078	5	0.688	84	0.207	22.152	5	0.000	70	0.085	5.507	4	0.239
C6M2	36	0.147	6.388	5	0.270	84	0.022	6.476	5	0.263	70	-0.111	2.919	3	0.404
C7M1	48	*	*	*	*	122	0.057	0.657	1	0.418	102	0.040	0.297	1	0.586
C7M2	36	-0.112	0.742	1	0.389	84	-0.169	2.452	1	0.117	70	*	*	*	*

*no variation in trait score

Of the statistically significant differences between Irene Mound and Santa Catalina and between Irene Mound and Santa Maria, there are two which are consistently strong. Upper lateral incisor shoveling and upper central incisor double-shoveling for both comparisons are statistically significant ($p<0.000$) and strongly correlated with population sample ($\tau_b<-0.400$ or $\tau_b>0.400$). Frequency of lower second molar groove pattern is also significantly ($p<0.000$) and strongly ($\tau_b>0.500$) different between the Irene Mound and Santa Maria samples. In comparisons between the Santa Catalina and Santa Maria, there are two traits which have statistically significant ($p<0.005$) and strong ($\tau_b<-0.300$) differences in frequency. These are first molar Carabelli's trait and lower second molar groove pattern.

In comparison of the Guale samples to the *Santa Maria de Yamassee* (SMdY) sample, the contrast between Irene Mound and SMdY is striking. Comparing Irene Mound with SMdY there are 8 out of 19 (42.1%) comparisons which are statistically significant ($p<0.05$), 3 (37.5%) of which are strong ($\tau_b<-0.300$) correlations. The comparisons between Santa Catalina and SMdY and between Santa Maria and SMdY each include 5 out of 19 (26.3%) statistically significant differences. One (20.0%) in each group comparison is strongly correlated with population sample ($\tau_b<-0.400$).

Comparisons of the Guale population samples with the Ledford Island sample all show a large number of differences. The Irene Mound-Ledford Island and the Santa Catalina-Ledford Island comparisons had the most differences which were statistically significant at the $p<0.05$ level (8 out of 19, 42.1%). Only 2 (25.0%) of the differences were strong ($\tau_b<-0.300$ or $\tau_b>0.300$) in the Irene Mound-Ledford Island comparison and one (12.5%) was strong ($\tau_b>0.300$) in the Santa Catalina-Ledford Island comparison. In contrast, the Santa Maria-Ledford Island comparison had 7 out of 19 (36.8%) statistically significant ($p<0.05$) differences, 5 of which (71.4%) were strong ($\tau_b>0.300$).

Comparisons of the Guale samples with the Carolina Algonquian samples showed a range of differences. The largest differences were in the Irene Mound-Carolina Algonquian comparison with 6 out of 19 (31.6%) significant differences ($p<0.05$). Three (50.0%) of these significant differences were strong ($\tau_b<-0.300$ or $\tau_b>0.300$). The Santa Catalina-Carolina Algonquian and Santa Maria-Carolina Algonquian comparisons had 5 out of 19 (26.3%) and 4 out of 19 (21.0%) significant differences respectively, of which 2 (40.0%) and 3 (75.0%) respectively were strong ($\tau_b<-0.300$ or $\tau_b>0.300$).

Thomas has labeled the Chi-square test as "anthropology's most used and abused statistic" (1986:264). Thus, interpretation of the data from Chi-square statistics should proceed cautiously. In this study, given an alpha level of 0.05, one can expect approximately 5% of the significant differences to be due to chance alone. All of the group comparisons exceed this percentage, some by a considerable amount. This suggests a great deal of diversity between all of the samples and most notably among the Guale samples. Given the historical contexts, this is not totally unexpected. Some of the highest percentages of differences occurred between populations that according to ethnographic accounts are closely related. However, the proposition that certain populations are closely related based on Chi-square analysis should be accepted with caution. The Chi-square statistic only tests the probability of rejection of the null hypothesis. In this case, the null hypothesis is that trait frequency and population sample are uncorrelated.

For this study, the Chi-square analysis is also useful if key traits could be identified that improve the discriminatory power of the population comparisons. Nine trait comparisons are both statistically significant and strongly correlated with population. These traits include for the maxillary dentition, lateral incisor shoveling, lateral incisor double shoveling, lateral incisor interruption groove, first molar metaconule, first and second molar Carabelli's trait; and for the mandibular dentition, first and second molar groove pattern, and first molar protostylid.

Following the methodology discussed in Chapter III, the following analyses will utilize all of the uncorrelated dental morphological traits listed in Table 17. This should give a close approximation of genetic affinities between samples. In addition, each analysis will consider the nine key morphological traits given above in order to delineate differences between the southeast U.S. populations. These two approaches taken together should give a fuller picture of relationships between the groups.

Taxonomic Statistics

Analysis of relationships between populations based on contingency tables is a daunting and sometimes deceptive task. It is impossible for the researcher to simultaneously assess the relationships between groups from this type of data. As discussed earlier, it is necessary to quantify these biological relationships in terms of single measures of divergence.

In order to place the Guale population samples in regional and pan-geographic contexts, the dental morphological traits listed in Table 17 were employed in three different multivariate analyses. The nine key traits enumerated in the previous section were also used in separate analyses of the southeast U.S. samples. Prior to multivariate analysis, dichotomized trait frequencies were arcsine transformed in order to stabilize the variance according to the formula recommended by Green and Suchey (1976).

Comparisons between the Guale samples and southeast U.S., Sinodont, and Amerindian samples are treated separately because different trait batteries were available for each comparison. Traits chosen from each comparison group were based on (1) which traits the researchers included in their studies, and (2) which of these traits were included in Table 17. Dental morphological trait frequencies for the comparison groups are summarized in Appendix E.

Cluster Analysis

In the first multivariate method, arcsine transformed trait frequencies were used as input for a cluster analysis program (Cluster, SYSTAT Inc., Wilkinson 1988a). This program is designed to construct dendrograms in euclidean space based upon Ward's Minimum Variance method (Ward 1963). The results of the cluster analyses are reported in Figures 9 and 10. Examination of Figure 9 reveals that the southeast U.S. samples fall into two distinct clusters and one isolate. The isolate, the Carolina Algonquian ossuary samples, is not an unexpected outcome. The Carolina Algonquian should represent a biologically distinct population. The two distinct clusters are, however, somewhat unexpected. According to ethnographic accounts, the Irene Mound, Santa Catalina, and Santa Maria population samples represent a temporally successive and biologically continuous series. Cluster analysis suggests, however, that the Irene Mound sample is more biologically similar to the Creek population sample from Ledford Island than to the Guale samples from Santa Catalina and Santa Maria. The results of cluster analysis also suggest that the Santa Maria and SMdY samples are biologically similar. These results are not totally incongruous with ethnographic data. According to Spencer and Jennings (1965), the Creek and Guale are closely related groups. Likewise, the Yamassee may have been closely affiliated with the Guale.

The results reported in Figure 10 present the outcome of cluster analysis for all of the dental samples included in this study. The three large clusters evident in Figure

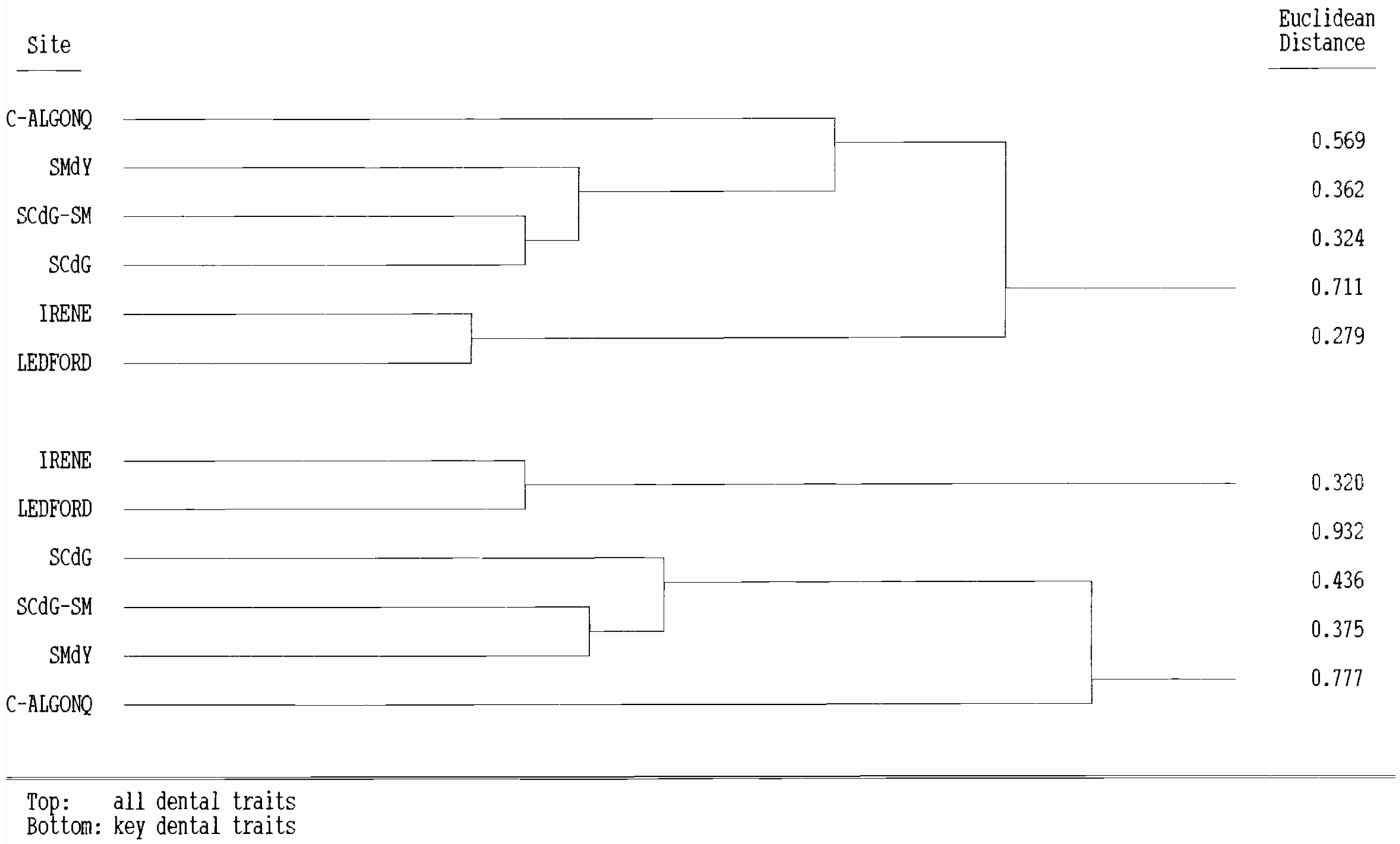

Figure 9. Cluster Analysis, Guale and Southeast U.S. Dental Samples.

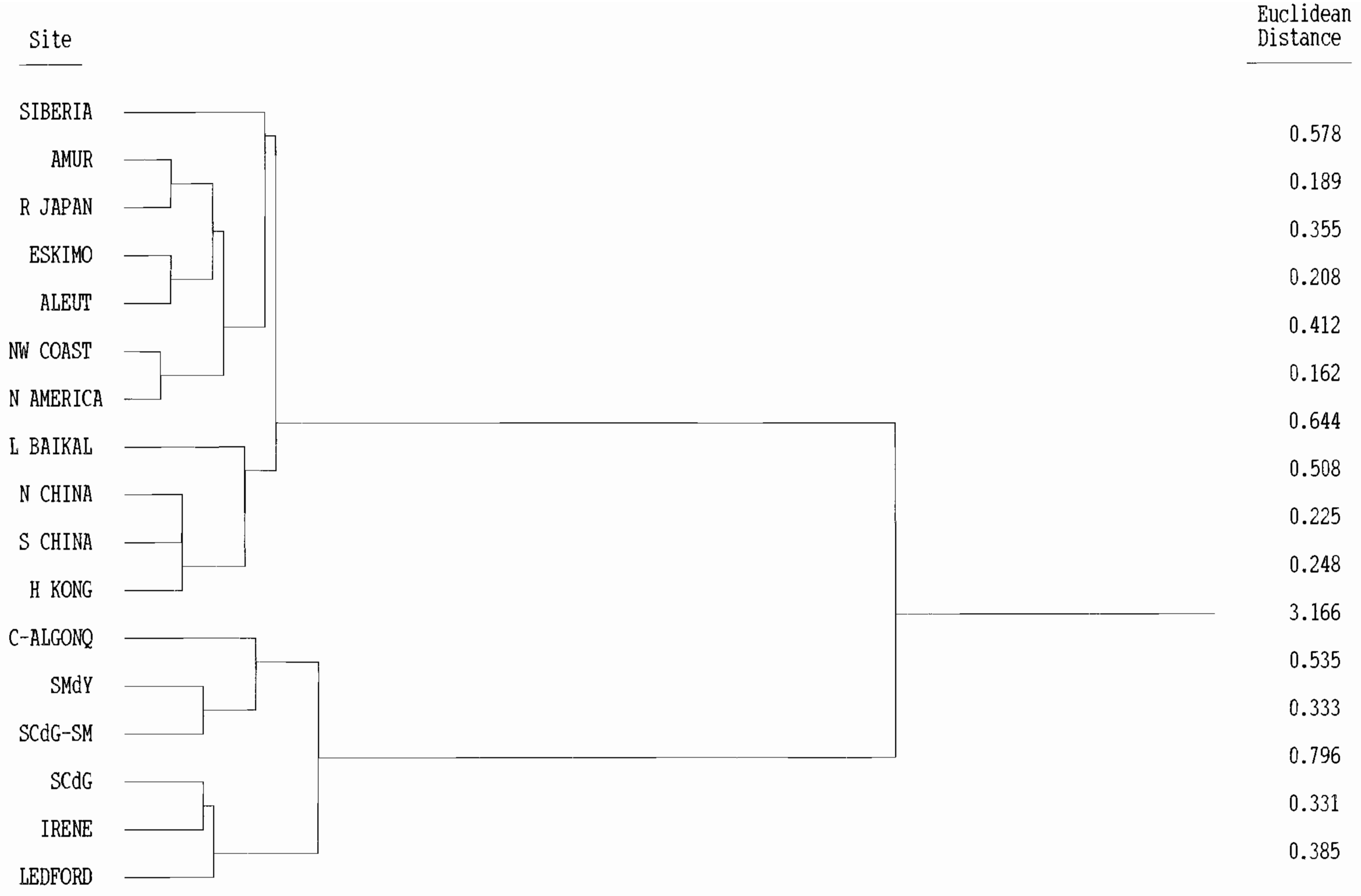

Figure 10. Cluster Analysis, Southeast U.S. and Sinodont Dental Samples.

10 are not unexpected relationships. In effect, the southeast U.S. samples separate from the other samples as a distinct cluster. Because the other samples are clearly not closely related to any of the southeast groups, this result is expected. The two regional clusters for the southeast samples are somewhat different than those described in Figure 9. This result can probably be explained by the fact that two of the traits which contrasted markedly between the Irene Mound sample and the Santa Catalina sample (upper lateral incisor shoveling and interruption groove) were not included in this analysis. Otherwise, the results reported in Figures 9 and 10 are consistent with one another.

Multidimensional Scaling

For the second multivariate technique, multidimensional scaling, arcsine transformed trait frequencies were utilized in a mean measure of divergence analysis. Dissimilarities in trait frequencies were quantified using the formula recommended by Green and Suchey (1976). The variances and standard deviations for this mean measure of divergence were calculated using the method of Sofaer and others (1986). Standardized mean measures of divergence were calculated by dividing each mean measure of divergence by its standard deviation. The standardized mean measures of divergence are more appropriate for comparison of distances among groups of populations with greatly varying sample sizes (Sofaer et al. 1986). In order to be considered statistically significant at the $p<0.05$ level, the mean measure of divergence must be at least twice its standard deviation (i.e., the mean measure of divergence divided by the standard deviation must be greater than 2). Measures of divergence for the dental morphological traits are reported in Tables 19 and 20.

Upon inspection of Tables 19 and 20, it is apparent that an accurate assessment of relationships between groups requires a technique which will visually represent all of the values simultaneously. The technique chosen here is multidimensional scaling (MDS-Guttman, SYSTAT Inc., Wilkinson 1988a). The standardized mean measures of divergence were used as input for the analysis. Guttman's (1968) coefficient of alienation was used. Each analysis was stopped when a level of stress in fitting the coordnate points to the monotonic function dropped below a level of $S=0.0000$. The output from this program results in a table of three-dimensional co-ordinates in euclidean space for each sample. These co-ordinates are then plotted in three-dimensional space giving a representation of the relative distances between populations (Plot, SYGRAPH, Wilkinson 1988b).

Table 19. Measures of Divergence, Guale and Southeast U.S. Dental Samples

	IRENE MD	SCdG	SCdG-SM	SMdY	C-ALGONQ	LEDFORD
IRENE MD	————	1.12283	1.80574	1.98983	3.16032	0.48262
		0.16512	0.38113	0.35539	0.68152	0.07581
SCdG	45.64191	————	0.63304	0.98392	1.60603	1.14602
	14.16579		0.10223	0.17093	0.34948	0.14545
SCdG-SM	38.26937	14.47506	————	0.42781	1.29909	2.30149
	17.72860	4.91168		0.07898	0.35109	0.44902
SMdY	40.59920	21.70832	6.29771	————	1.18966	2.14634
	17.42574	8.68953	2.67148		0.24956	0.28048
C-ALGONQ	30.95110	16.24373	10.84275	9.74059	————	2.01300
	13.65180	7.08506	6.07080	4.33698		0.44209
LEDFORD	15.57970	41.94979	46.20403	41.24629	19.28545	————
	5.99825	12.17316	20.51565	13.52123	8.82359	

Values within each cell represent measures of divergence derived from (1) all dental traits, and (2) key dental traits

Mean measures of divergence above diagonal, standardized mean measures of divergence below diagonal

Table 20. Measures of Divergence, Southeast U.S. and Sinodont Dental Samples*

	IRENE	SCdG	SCdG-SM	SMdY	C-ALGONQ	LEDFORD	NE SIB	AMUR	L BAIKAL
IRENE	--------	0.08697	0.18936	0.24151	0.31436	0.08373	1.06944	0.98294	0.74597
SCdG	8.80964	--------	0.11464	0.14330	0.22609	0.14140	0.76895	0.66718	0.52772
SCdG-SM	9.92627	6.49607	--------	0.04730	0.18350	0.32891	0.49625	0.43343	0.33068
SMdY	12.22804	7.88011	1.73093	--------	0.06446	0.27927	0.50930	0.27626	0.15688
C-ALGONQ	7.25981	5.38084	3.65379	1.26015	--------	0.18523	0.65521	0.43953	0.30576
LEDFORD	6.63946	12.80443	16.34139	13.26747	4.19084	--------	1.17880	0.99175	0.72549
NE SIB	87.08208	69.19240	25.36023	25.25544	14.65075	89.88447	--------	0.15454	0.31768
AMUR	59.98059	44.10854	18.40663	11.31698	9.02598	56.99752	8.58253	--------	0.14015
L BAIKAL	14.68056	10.60326	5.77404	2.74112	3.92047	14.12495	6.11042	2.53853	--------
N CHINA	137.84479	107.57389	28.13083	19.93583	14.20744	122.50520	27.32144	4.53151	1.26698
R JAPAN	113.05551	96.59779	22.42985	12.45145	11.30347	102.58013	27.46532	0.79629	2.39858
H KONG	156.72168	135.53101	35.57380	22.80257	14.98722	134.50395	26.77467	1.99908	2.30436
S CHINA	76.91197	56.30991	15.75559	12.39641	9.94771	75.88757	8.51080	1.69028	1.48727
ESKIMO	100.10619	83.88024	20.03271	11.54196	8.50128	88.21398	14.81360	2.73709	2.26390
ALEUT	85.78832	66.72875	16.38655	12.73340	10.05106	86.24439	11.27221	3.72095	4.00390
NW COAST	97.31140	85.15598	15.10510	10.46800	9.30556	87.86473	21.71253	5.58533	1.36812
N AMER	93.27596	88.08858	14.18057	9.92270	10.11684	85.68176	33.16659	10.83826	1.85476

	N CHINA	R JAPAN	H KONG	S CHINA	ESKIMO	ALEUT	NW COAST	N AMER
IRENE	1.00871	0.78033	1.16155	0.91622	0.78707	0.88177	0.66620	0.56104
SCdG	0.63254	0.52934	0.80782	0.59604	0.54632	0.60119	0.46664	0.40574
SCdG-SM	0.42471	0.33081	0.54244	0.30629	0.31325	0.29132	0.22120	0.19688
SMdY	0.31352	0.19059	0.36097	0.24897	0.18673	0.23504	0.15920	0.14311
C-ALGONQ	0.56051	0.44179	0.59174	0.44014	0.34156	0.42911	0.36422	0.38682
LEDFORD	1.05643	0.83994	1.17460	0.98224	0.79612	0.97925	0.71093	0.62827
NE SIB	0.23610	0.22739	0.23010	0.11497	0.13983	0.13484	0.18214	0.24818
AMUR	0.05739	0.00975	0.02527	0.02946	0.03648	0.05920	0.06864	0.12341
L BAIKAL	0.06043	0.11364	0.10999	0.07689	0.10929	0.20064	0.06482	0.08661
N CHINA	--------	0.07331	0.05723	0.03287	0.13005	0.13188	0.10311	0.15742
R JAPAN	25.02676	--------	0.08696	0.07064	0.05181	0.08001	0.04509	0.05727
H KONG	16.68998	29.18246	--------	0.03480	0.13166	0.16302	0.13997	0.20872
S CHINA	4.08874	9.24994	4.32522	--------	0.06830	0.05469	0.06034	0.12237
ESKIMO	33.14957	14.74533	33.36383	7.81004	--------	0.02807	0.03108	0.07572
ALEUT	20.41499	13.21734	25.27767	4.84879	3.91258	--------	0.07409	0.12653
NW COAST	35.79373	18.38580	48.06028	7.85755	8.73461	12.08830	--------	0.02270
N AMER	77.45623	36.31836	100.11304	18.07190	28.61850	24.28138	14.32049	--------

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*Mean measures of divergence above diagonal, standardized mean measures of divergence below diagonal

Results of the multidimensional scaling of the standardized mean measures of divergence are reported in Figures 11-14. The results of multidimensional scaling confirm the conclusions derived from cluster analysis of the dental traits. As can be seen in Figure 11 and 12, the Santa Maria and Santa Catalina populations are quite similar to one another. The SMdY population sample is most closely related to these two Guale samples. Although the Irene Mound sample and the Ledford Island sample are clearly more similar to one another than to the other samples, they are still somewhat dissimilar to one another. The Carolina Algonquian samples are separate from all other samples.

In Figures 13 and 14 the same patterns as seen in cluster analysis of all dental samples are observed. The southeast U.S. samples separate into two distinct groups: (1) Santa Maria, SMdY, and the Carolina Algonquian, and (2) Ledford Island, Irene Mound, and Santa Catalina. It can also be seen that the SMdY and Santa Maria samples are more similar to Turner's Sinodont groups than are the Santa Catalina and Irene Mound samples.

Principal Component Analysis

Another multivariate technique used to examine group affinities between samples is principal component analysis.

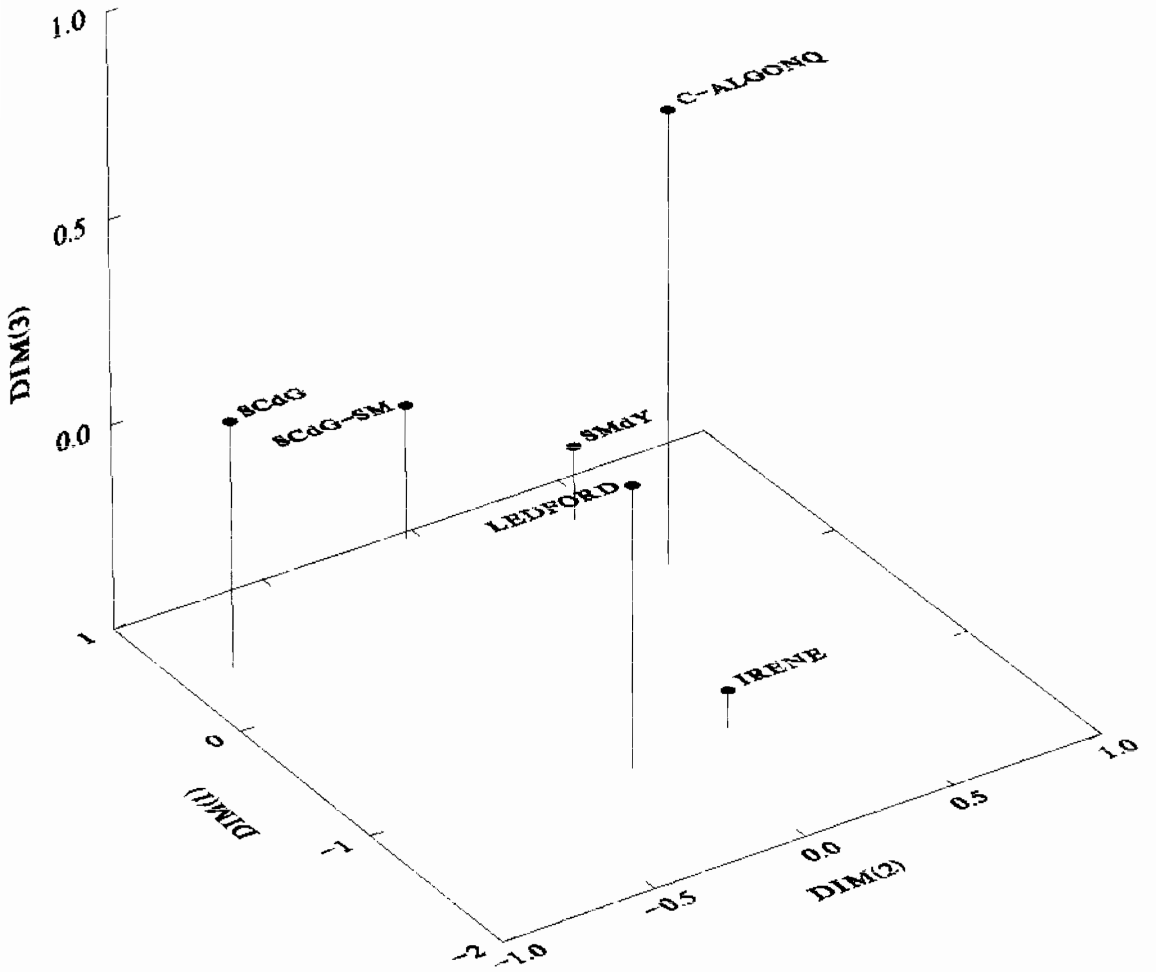


Figure 11. Multidimensional Scaling Analysis, Guale and Southeast U.S. Dental Samples (All Traits).

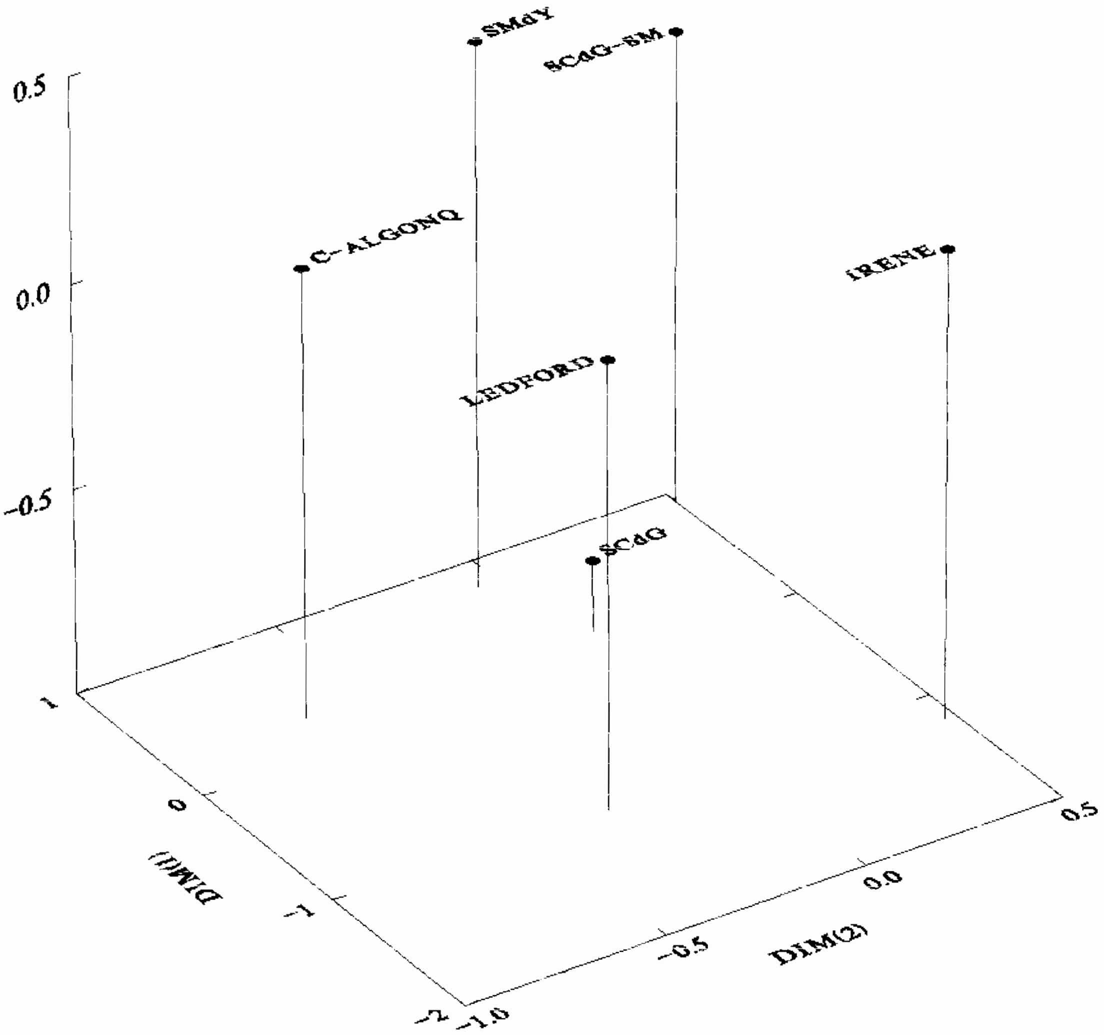


Figure 12. Multidimensional Scaling Analysis, Guale and Southeast U.S. Dental Samples (Key Traits).

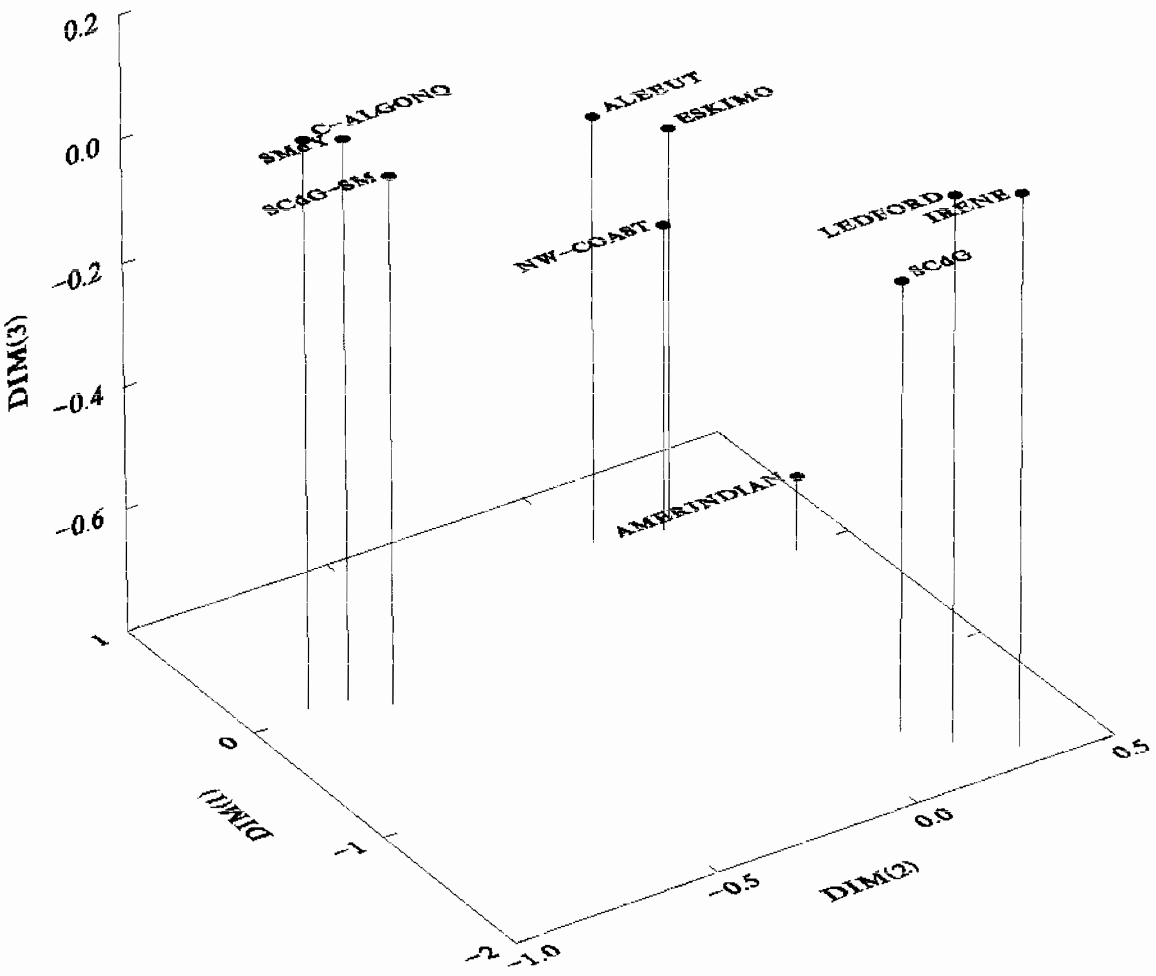


Figure 13. Multidimensional Scaling Analysis, Guale and Amerindian Dental Samples.

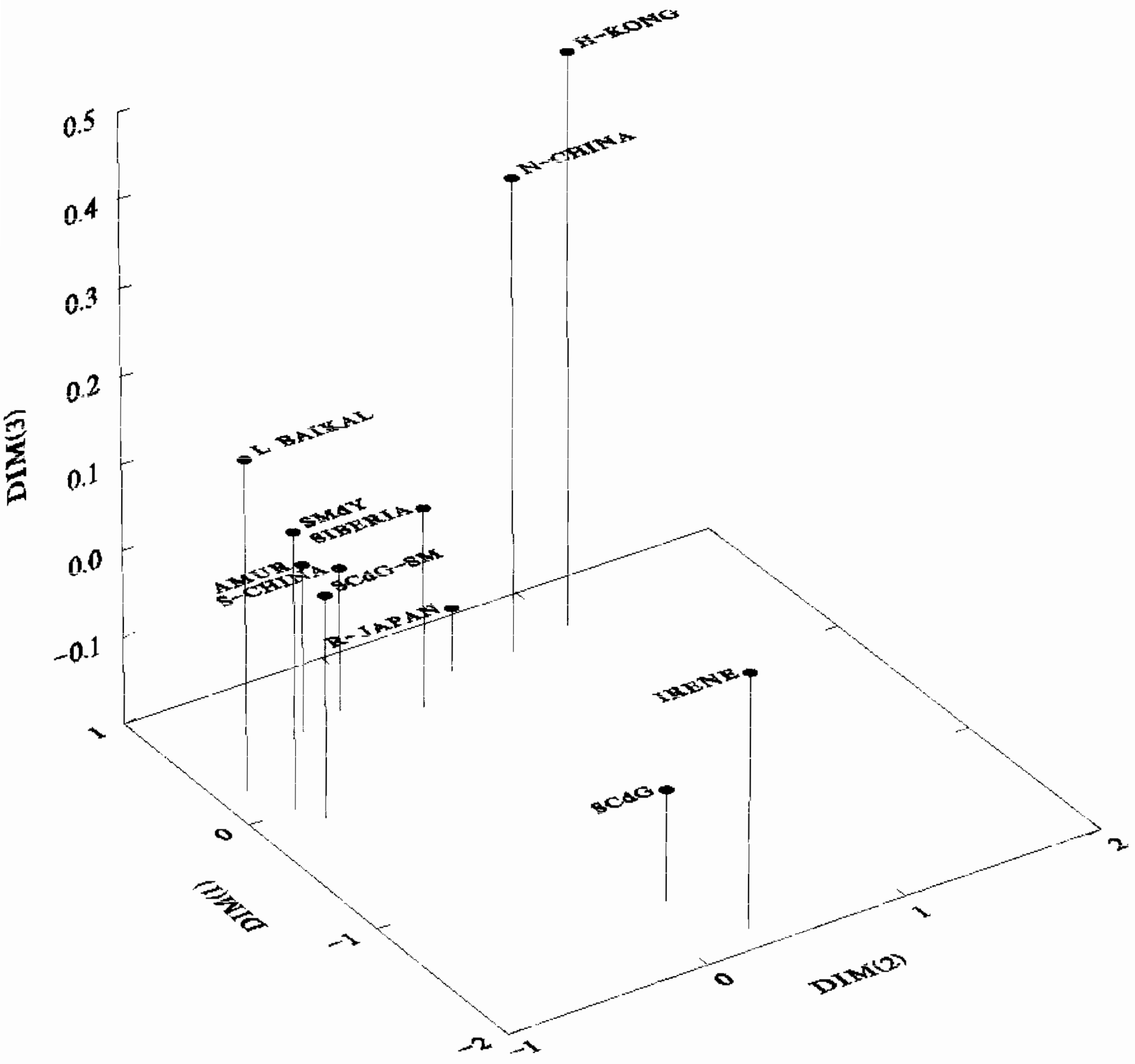


Figure 14. Multidimensional Scaling Analysis, Guale and Sinodont Dental Samples.

For this analysis, arcsine transformed trait frequencies were standardized to have a zero mean and unit variance. Principal components were then derived and varimax rotated to a simpler solution (Factor, SYSTAT Inc., Wilkinson 1988a). Factor score coefficients (eigenvector coefficients) for each variable were then multiplied by the standardized arcsine transformed frequency for each sample. These values were summed for each sample according to the first three principal components. The resulting component scores were plotted in three dimensional space to illustrate the relative position of each sample in multicomponent space (Plot, SYGRAPH, Wilkinson 1988b).

As mentioned previously, a principal component analysis is not always successful when the original variables are uncorrelated. The procedures described in Chapter III were used expressly for the purpose of removing or reducing correlated variables. As such, a principal component analysis may be of limited usefulness here. As can be seen from Tables 21-23, between 74.814% and 91.204% of the total variance can be explained by the first three principal components. The resultant scores are plotted in three dimensional space in Figures 15-17. As can be seen, the results of multidimensional scaling and cluster analysis are generally confirmed.

Table 21. Varimax Rotated Principal Components Analysis of All Dental Traits, Guale and Southeast U.S. Samples

Morphological Trait	Component loadings 1	 2	 3
SHOV2	0.604	-0.438	0.478
DSHOV	0.665	-0.624	0.163
IGROV	-0.405	0.851	0.257
METAC	0.345	0.105	0.690
HYPO2	0.672	-0.622	0.361
M1C5	0.055	0.618	0.477
CARAM1	0.895	-0.184	0.003
CARAM2	-0.514	-0.772	0.056
PARA	-0.174	0.163	-0.750
PSI	-0.047	0.932	-0.316
PSM	0.070	0.160	-0.978
GPM1	-0.705	-0.094	-0.573
GPM2	0.799	0.352	0.434
CNM1	-0.174	0.611	0.707
PM1	0.697	-0.487	-0.064
C5M2	0.715	0.071	0.514
C6M2	0.198	0.939	-0.018
C7M1	0.853	0.010	-0.082
C7M2	-0.646	-0.200	-0.109
Variance explained by rotated components	5.994	5.305	4.080
Percent of variance explained	31.549	27.922	21.475
Total variance explained by first three components:		80.946	

Site	Component Scores 1	 2	 3
IRENE	-0.896	0.965	-0.469
SCdG	-1.044	-0.757	1.449
SCdG-SM	1.047	0.569	-0.235
SMdY	1.097	0.546	1.027
C-ALGONQ	0.526	-1.661	-0.861
LEDFORD	-0.730	0.338	-0.910

Table 22. Varimax Rotated Principal Components Analysis of Key Dental Traits, Guale and Southeast U.S. Samples

Morphological Trait	Component loadings 1	2	3
SHOV2	0.890	0.277	0.056
DSHOV	0.974	0.070	-0.148
IGROV	-0.781	0.387	0.453
M1C5	0.074	0.420	0.895
CARAM1	0.785	0.361	-0.158
CARAM2	0.135	-0.850	-0.246
GPM1	-0.326	-0.835	0.240
GPM2	0.473	0.842	0.226
PM1	0.442	0.259	-0.856
Variance explained by rotated components	3.517	2.732	1.959
Percent of variance explained	39.077	30.358	21.769
Total variance explained by first three components:		91.204	

Site	Component Scores 1	2	3
IRENE	-1.033	-0.545	0.722
SCdG	0.370	-0.731	0.828
SCdG-SM	0.966	0.763	1.085
SMdY	-0.038	1.599	-0.751
C-ALGONQ	1.056	-1.011	-1.315
LEDFORD	-1.321	-0.075	-0.569

Table 23. Varimax Rotated Principal Components Analysis of Dental Traits, Southeast U.S. and Sinodont Samples

	Component loadings		
Morphological Trait	1	2	3
DSHOV	0.813	0.328	0.197
IGROV	0.784	-0.147	0.369
HYPO2	0.261	-0.171	0.920
M1C5	0.794	0.078	0.190
CARAM1	-0.025	-0.750	0.197
PARA	-0.600	-0.403	-0.468
PSM	0.734	0.416	0.345
GPM2	-0.740	0.549	0.176
CNM1	-0.161	-0.805	-0.014
CNM2	0.891	0.221	0.072
PM1	-0.569	0.106	-0.349

Variance explained by rotated components	4.563	2.073	1.594
Percent of variance explained	41.481	18.844	14.489
Total variance explained by first three components:		74.814	

	Component Scores		
Site	1	2	3
IRENE	-2.130	-0.800	0.749
SCdG	-1.567	0.285	0.620
SCdG-SM	-0.729	-0.107	0.361
SMdY	-1.089	1.248	0.082
C-ALGONQ	0.605	-0.916	-2.786
LEDFORD	-1.409	-1.270	-1.447
SIBERIA	1.252	-1.561	1.314
AMUR	1.067	-0.577	0.060
L-BAIKAL	0.260	1.982	-1.498
N-CHINA	0.428	1.390	0.243
R-JAPAN	0.333	-0.071	0.549
H-KONG	0.346	1.227	0.538
S-CHINA	0.577	0.643	0.401
ESKIMO	0.653	-0.347	0.075
ALEUT	0.941	-0.055	0.458
NW-COAST	0.227	-0.496	0.251
N-AMERICA	0.236	-0.576	0.030

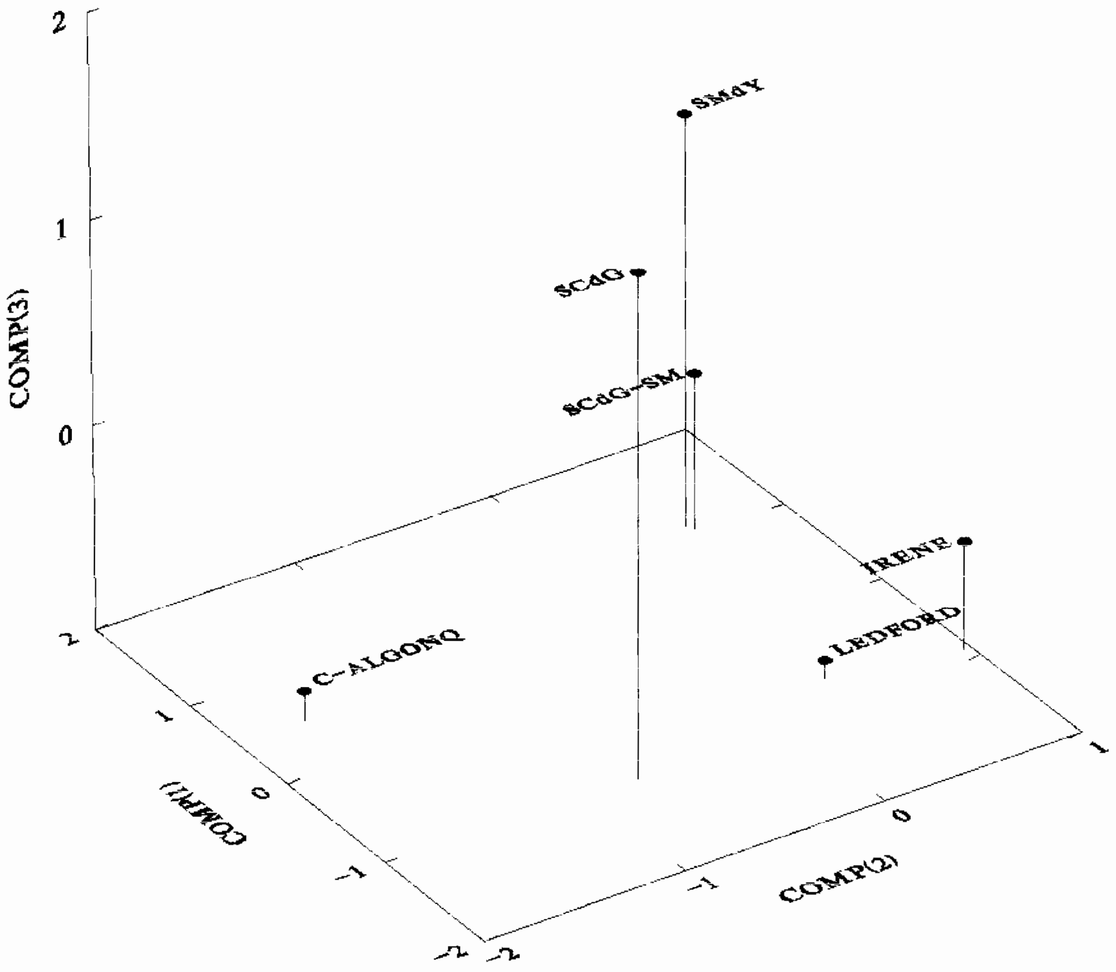


Figure 15. Principal Component Analysis, Guale and Southeast U.S. Dental Samples (All Traits).

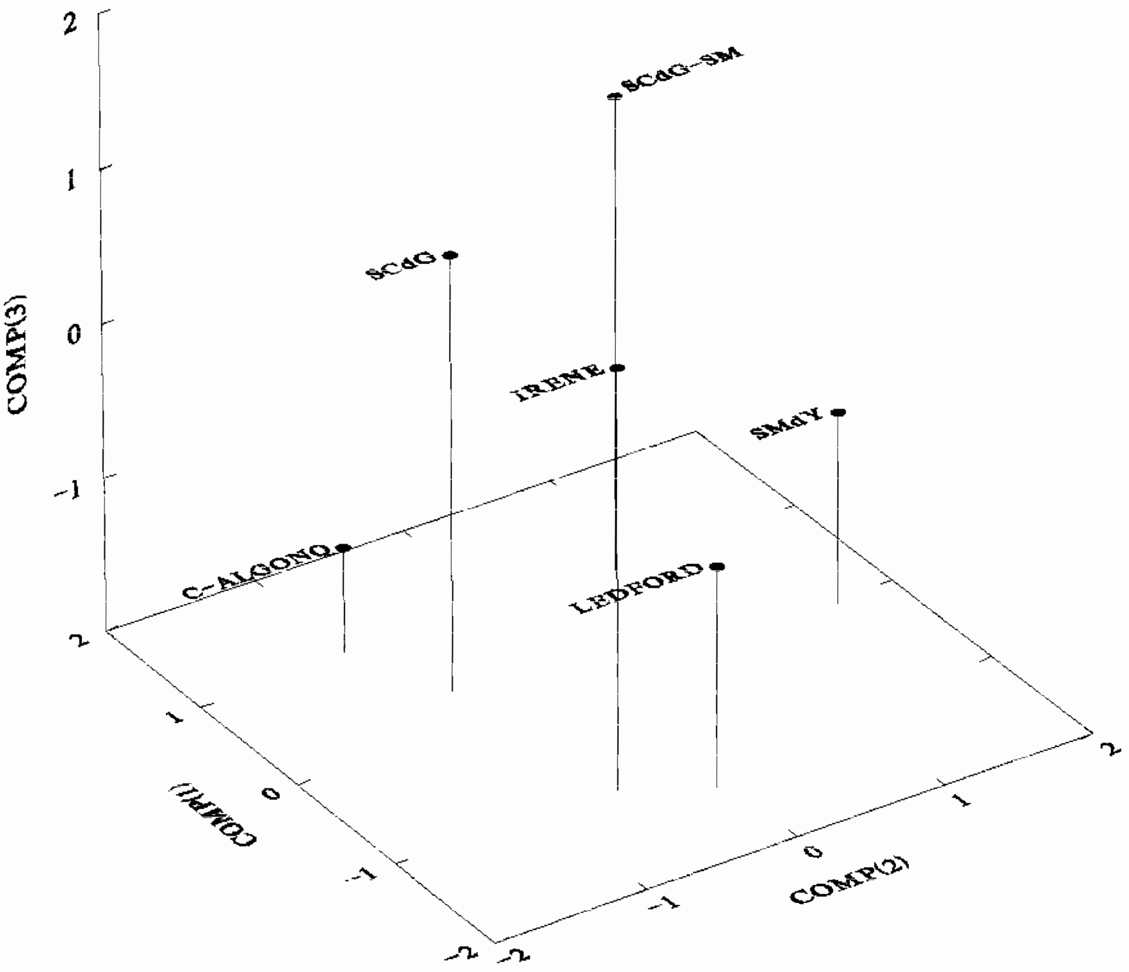


Figure 16. Principal Component Analysis, Guale and Southeast U.S. Dental Samples (Key Traits).

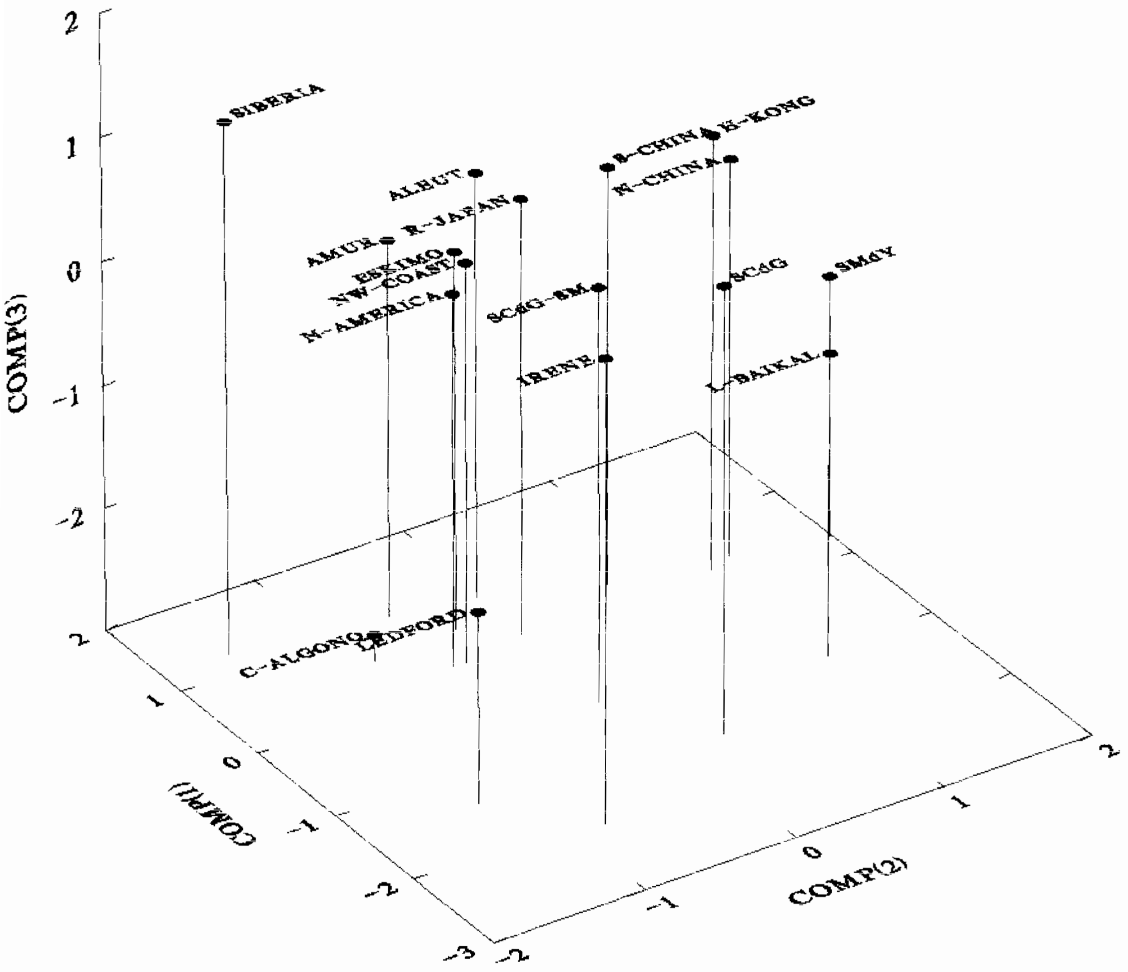


Figure 17. Principal Component Analysis, Southeast U.S. and Sinodont Dental Samples.

From the examination of Figures 15 and 16, the Santa Maria and SMdY samples are clearly similar to one another, as are the Irene Mound and Ledford Island samples. The placement of the Santa Catalina is somewhat more distant from the other samples, and the Carolina Algonquian samples represent a clear isolate from all of the other groups. Figure 17 demonstrates that the southeast U.S. samples form a distinct group with regard to the other Amerindian and Sinodont groups, with the exception of the Lake Baikal sample.

Principal component analysis is also capable of indicating which variables combine to best discriminate between samples. The first principal component in the analysis of all dental traits from the southeast U.S. samples (Table 21) accounts for 31.549% of the total variance. This component features high positive loadings for CARAM1, GPM2, C5M2, and C7M1; moderate positive loadings for SHOV2, DSHOV, and HYPO2; and a high negative loading for GPM1. Trichotomization of sample results (Table 21) reveals that low scorers for this principal component (Irene Mound, Santa Catalina, and Ledford Island) have high frequencies of CARAM1, GPM2, C5M2, and C7M1. These same samples have low frequencies of GPM1. High scorers (Santa Maria and SMdY) have low frequencies of CARAM1, GPM2, C5M2, and C7M1. These same samples have high frequencies of GPM1.

The second principal component in the analysis of all dental traits from the southeast U.S. samples accounts for 27.922% of the total variance. This component has high positive loadings for IGROV, PSI, and C6M2. Trichotomization of sample results (Table 21) reveals that the low scorer for this principal component (Carolina Algonquian) had particularly high frequencies of IGROV, PSI, and C6M2. The high scorer (Irene Mound) had lower scores for these traits.

The third principal component in this analysis accounts for 21.475% of the total variance. This component has a high negative loading for PSM, with moderate to low loadings for the remaining variables. The samples with high scores for this component (Santa Catalina and SMdY) have higher frequencies of PSM than the other samples.

Observing the same relationships high loadings-low score-high frequency, and vice versa, a number of traits can be identified from Tables 22 and 23 which are important discriminators. Among these are SHOV2, DSHOV, CARAM2, GPM2, M1C5, and PM1 for the analysis using key traits for the southeast U.S. samples (Table 22); and DSHOV, CNM2, CNM1, and HYPO2 for the analysis of the southeast U.S. and Sinodont samples (Table 23).

Cranial Analysis

Elimination of cranial morphological traits due to the biases discussed in Chapter III resulted in a battery of 20 uncorrelated traits of the cranial vault and base. The traits included in the distance analysis are summarized in Table 24.

Chi-Square Analysis

Each cranial trait was tested for statistically significant differences in frequencies of presence and absence (1) between the primary (Guale) and non-Guale samples, and (2) among the primary (Guale) and non-Guale samples. These comparisons will (1) delineate trait frequency differences between the Guale and non-Guale samples, and (2) delineate trait frequency differences among the Guale and non-Guale samples. As with the dental morphological traits, Tau-b statistics were computed for all of the traits for each sample comparison in order to determine the strength of differences. Chi-square and Tau-b statistics are reported in Table 25.

Examination of the Chi-square and Tau-b statistics reveals a considerable number of differences between the entire group of samples and among the Guale samples. Overall, there are 50 (23.8%) statistically significant differences ($p<0.05$) out of 210 comparisons. Considering

Table 24. Cranial Morphological Traits Included in Distance Analysis

Trait	Abreviation	References
I. Supernumerary sutures of the cranial vault		
posterior		
(1) lambdoid ossicles	[LO]	Bennett 1965; Berry and Berry 1967; Herzog 1968
(2) ossicle at asterion	[OAA]	Berry and Berry 1967; Suchey 1975; Molto 1983
lateral		
(3) parietal notch bone	[PNB]	Oetteking 1930; Berry and Berry 1967; Ossenberg 1969; Molto 1983
(4) epipteric bone	[EPB]	Wood-Jones 1930; Berry and Berry 1967; Molto 1983
(5) bregmatic bone	[BB]	Wood-Jones 1930; Berry and Berry 1967; Kennedy 1981
(6) coronal ossicle	[CO]	Wood-Jones 1930; Sublett 1966; Berry and Berry 1967
II. Frontal bone observations		
(7) metopism	[MET]	Bolk 1931; Torgersen 1951; Berry and Berry 1967
(8) fronto-temporal articulation	[FTA]	Berry and Berry 1967; Ossenberg 1969
(9) frontal notch	[FN]	Wood-Jones 1930; Berry and Berry 1967
III. Variations of the cranial base and maxilla		
(10) auditory torus	[AT]	Wood-Jones 1930; Berry and Berry 1967
(11) condylar facet double	[CFD]	Anderson 1962; Berry and Berry 1967; Kennedy 1981
(12) precondylar tubercle	[PT]	Inglemark 1947; Berry and Berry 1967; Ossenberg 1967; Molto 1983
(13) foramen ovale	[FO]	Wood-Jones 1930; Berry and Berry 1967
(14) foramen spinosum	[FS]	Berry and Berry 1967; Korey 1970; Suchey 1975
(15) accessory lessor palatine foramen	[APF]	Berry and Berry 1967
(16) palatine torus	[PAT]	Berry and Berry 1967; Turner et al. 1991
IV. Emissary foramina		
(17) parietal foramen	[PF]	Berry and Berry 1967; Ossenberg 1969; Molto 1983
(18) mastoid foramen abs.	[MF]	Berry and Berry 1967
(19) anterior condylar canal double	[ACC]	Berry and Berry 1967; Korey 1970; Ossenberg 1969; Molto 1983
(20) zygomatico-facial foramen	[ZFF]	Berry and Berry 1967; Molto 1983

Table 25. Cranial Chi-square Analysis

	IRENE - SCdG-SM					IRENE - SMdY					IRENE - CALGONQ					IRENE - LEDFORD				
Trait	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p
LO	133	-0.200	5.362	1	0.021	89	-0.258	5.959	1	0.015	137	-0.300	12.557	1	0.000	100	-0.241	5.839	1	0.016
PF	132	0.137	2.478	1	0.115	88	-0.116	1.258	1	0.262	136	0.254	8.848	1	0.003	99	0.180	3.176	1	0.075
BB	129	0.092	1.474	1	0.225	88	*	*	*	*	136	*	*	*	*	99	*	*	*	*
MET	139	*	*	*	*	88	*	*	*	*	138	*	*	*	*	101	*	*	*	*
CO	129	-0.482	0.925	1	0.336	88	-0.105	1.669	1	0.196	134	0.000	0.000	1	1.000	99	-0.032	0.107	1	0.744
EPB	87	-0.249	6.422	1	0.011	69	-0.245	6.624	1	0.010	107	-0.336	15.958	1	0.000	77	-0.102	0.842	1	0.359
FTA	88	-0.093	1.139	1	0.286	68	-0.073	0.620	1	0.431	110	-0.105	1.588	1	0.208	78	-0.085	0.897	1	0.344
PNB	128	-0.150	2.973	1	0.085	84	-0.068	0.421	1	0.516	129	-0.095	3.075	1	0.079	93	-0.121	1.495	1	0.222
OAA	124	-0.051	0.321	1	0.571	82	-0.064	0.339	1	0.560	129	-0.274	9.889	1	0.002	87	-0.248	6.000	1	0.014
AT	135	*	*	*	*	90	*	*	*	*	138	*	*	*	*	101	*	*	*	*
MFE	124	-0.017	0.034	1	0.853	78	0.151	1.832	1	0.176	127	0.193	4.767	1	0.029	85	0.129	1.438	1	0.230
CFD	84	*	*	*	*	64	*	*	*	*	93	*	*	*	*	67	*	*	*	*
PT	77	0.270	7.073	1	0.008	60	*	*	*	*	91	0.300	11.293	1	0.001	62	0.285	5.113	1	0.024
ACC	81	0.048	0.186	1	0.666	62	0.290	4.677	1	0.031	98	0.020	0.038	1	0.846	68	-0.062	0.271	1	0.603
FO	101	-0.007	0.005	1	0.944	64	-0.073	0.581	1	0.446	110	0.176	3.903	1	0.048	73	0.056	0.215	1	0.643
FS	99	-0.088	0.770	1	0.380	60	-0.108	0.735	1	0.391	104	-0.032	0.104	1	0.747	69	-0.251	4.904	1	0.027
APF	87	0.036	0.112	1	0.738	57	-0.297	4.743	1	0.029	90	-0.166	2.512	1	0.113	66	-0.320	6.603	1	0.010
PAT	114	-0.043	0.211	1	0.646	75	0.029	0.064	1	0.801	111	-0.497	28.653	1	0.000	86	0.273	9.852	1	0.002
ZFF	117	0.056	0.369	1	0.544	79	0.201	3.476	1	0.062	125	-0.279	9.862	1	0.002	90	0.150	2.082	1	0.149
FN	131	-0.192	4.852	1	0.028	86	0.034	0.098	1	0.755	134	0.135	2.449	1	0.118	98	-0.057	0.318	1	0.573
AIF	96	-0.005	0.003	1	0.958	59	-0.117	1.405	1	0.236	93	0.290	8.304	1	0.004	74	0.188	2.508	1	0.113

(continued)

Table 25, continued

	SCdG-SM - SMdY					SCdG-SM - CALGONQ					SCdG-SM - LEDFORD					SMdY - CALGONQ				
Trait	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p	N	Tau-b	X^2	D.F.	p
LO	82	-0.097	0.789	1	0.374	130	-0.103	1.390	1	0.238	93	-0.059	0.324	1	0.569	86	0.011	0.011	1	0.918
PF	86	-0.226	4.723	1	0.030	134	0.119	1.903	1	0.168	97	0.051	0.250	1	0.617	90	0.317	9.661	1	0.002
BB	83	-0.064	0.588	1	0.443	131	-0.093	1.505	1	0.220	94	-0.074	0.838	1	0.360	90	*	*	*	*
MET	91	*	*	*	*	139	*	*	*	*	102	*	*	*	*	90	*	*	*	*
CO	83	-0.064	0.588	1	0.443	129	0.083	0.925	1	0.336	94	0.050	0.220	1	0.639	88	0.105	1.669	1	0.196
EPB	54	-0.097	0.820	1	0.365	92	-0.131	1.894	1	0.169	62	0.176	1.927	1	0.165	74	*	*	*	*
FTA	56	*	*	*	*	98	*	*	*	*	66	*	*	*	*	78	*	*	*	*
PNB	84	0.062	0.301	1	0.583	129	-0.002	0.001	1	0.982	93	0.012	0.014	1	0.907	85	-0.064	0.320	1	0.572
OAA	82	-0.021	0.036	1	0.850	129	-0.225	6.656	1	0.010	87	-0.208	4.181	1	0.041	87	-0.185	2.685	1	0.101
AT	87	*	*	*	*	135	*	*	*	*	98	*	*	*	*	90	*	*	*	*
MFE	80	0.163	2.184	1	0.139	129	0.209	5.704	1	0.017	87	0.143	1.802	1	0.180	83	0.006	0.003	1	0.960
CFD	52	*	*	*	*	81	*	*	*	*	55	*	*	*	*	61	*	*	*	*
PT	49	-0.208	3.332	1	0.068	80	0.068	0.372	1	0.542	51	-0.015	0.012	1	0.914	63	0.223	5.072	1	0.024
ACC	47	0.259	2.987	1	0.084	83	-0.029	0.067	1	0.796	53	-0.111	0.684	1	0.408	64	-0.269	4.153	1	0.042
FO	69	-0.067	0.532	1	0.466	115	0.184	4.441	1	0.035	78	0.062	0.284	1	0.594	78	0.160	3.388	1	0.066
FS	71	-0.031	0.071	1	0.789	115	0.056	0.367	1	0.544	80	-0.169	2.552	1	0.110	76	0.075	0.443	1	0.506
APF	54	-0.336	5.686	1	0.017	87	-0.201	3.556	1	0.059	63	-0.357	7.874	1	0.005	57	0.151	1.285	1	0.257
PAT	75	0.064	0.320	1	0.571	111	-0.459	24.303	1	0.000	86	0.301	11.841	1	0.001	72	-0.452	15.429	1	0.000
ZFF	74	0.162	2.103	1	0.147	120	-0.332	13.475	1	0.000	85	0.101	0.883	1	0.347	82	-0.421	15.229	1	0.000
FN	85	0.198	3.308	1	0.069	133	0.323	14.088	1	0.000	97	0.125	1.503	1	0.220	88	0.081	0.569	1	0.451
AIF	61	-0.113	1.352	1	0.245	95	0.296	8.792	1	0.003	76	0.193	2.701	1	0.100	58	0.275	6.946	1	0.008

(continued)

Table 25, continued

Trait	N	SMdY - LEDFORD Tau-b	X^2	D.F.	p	N	CALGONQ - LEDFORD Tau-b	X^2	D.F.	p
LO	49	0.052	0.134	1	0.715	97	0.037	0.135	1	0.714
PF	53	0.312	5.440	1	0.020	101	-0.061	0.374	1	0.541
BB	53	*	*	*	*	101	*	*	*	*
MET	53	*	*	*	*	101	*	*	*	*
CO	53	0.112	1.022	1	0.312	99	-0.032	0.107	1	0.744
EPB	44	0.225	3.307	1	0.069	82	0.286	7.141	1	0.008
FTA	46	*	*	*	*	88	*	*	*	*
PNB	49	-0.056	0.150	1	0.699	94	0.014	0.018	1	0.892
OAA	45	-0.224	2.255	1	0.133	92	-0.019	0.033	1	0.855
AT	53	*	*	*	*	101	*	*	*	*
MFE	41	-0.042	0.071	1	0.790	90	-0.044	0.171	1	0.679
CFD	35	*	*	*	*	64	*	*	*	*
PT	34	0.236	2.655	1	0.103	65	-0.073	0.369	1	0.544
ACC	34	-0.381	4.976	1	0.026	70	-0.077	0.446	1	0.504
FO	41	0.126	1.005	1	0.316	87	-0.114	1.312	1	0.252
FS	41	-0.160	1.024	1	0.312	85	-0.208	4.240	1	0.039
APF	33	0.012	0.004	1	0.947	66	-0.160	1.696	1	0.193
PAT	47	0.331	6.093	1	0.014	83	0.657	46.812	1	0.000
ZFF	47	-0.089	0.379	1	0.538	93	0.400	15.340	1	0.000
FN	52	-0.098	0.497	1	0.481	100	-0.185	3.360	1	0.067
AIF	39	0.256	3.996	1	0.046	73	-0.109	0.895	1	0.344

*no variation in trait score

only the Guale samples, there are 4 (19.0%) statistically significant differences out of 21 comparisons. Of the significant differences across all groups 20 out of 50 (40.0%) were strong correlations. This represents 9.5% of all comparisons. Among the Guale samples, none of the 4 significant differences were strong correlations (τ_b<-0.300 or τ_b>0.300). All of the traits differed significantly in at least one of the comparisons.

Comparison of the two Guale samples in terms of cranial morphological traits shows much fewer differences than for the dental traits. The comparisons between the Irene Mound sample and the Santa Maria sample show 4 out of 21 (19.0%) statistically significant ($p<0.05$) differences, none of which were strong (τ_b<-0.300 or τ_b>0.300).

In comparison with the SMdY sample, the Guale samples showed few differences. For the Irene Mound-SMdY and Santa Maria-SMdY comparisons there were 4 out of 21 (19.0%) and 2 out of 21 (9.5%) differences which were statistically significant ($p<0.05$). None of the statistically significant differences were strong (τ_b<-0.300 or τ_b>0.300) in the Irene Mound-SMdY comparison and one (50.0%) was strong (τ_b<-0300) in the Santa Maria-SMdY comparison.

The contrast with the Ledford Island sample and the Guale samples was slightly stronger. For the Irene Mound-Ledford Island and Santa Maria-Ledford Island comparisons there were 6 out of 21 (28.6%) and 3 out of 21 (14.3%) differences which were significant ($p<0.05$). One of these (16.6%) differences was strong in the Irene Mound-Ledford Island sample comparison. Two (66.6%) of the significant differences in the Santa Maria-Ledford Island comparison were strong ($\tau_b<-0.300$ or $\tau_b>0.300$).

The contrasts of the Guale samples with the Carolina Algonquian sample are more striking. Among the Irene Mound-Carolina Algonquian comparisons there are 10 out of 21 (47.6%) differences which are statistically significant ($p<0.05$), 4 (40.0%) of which are strong ($\tau_b<-0.300$ or $\tau_b>0.300$). In the Santa Maria-Carolina Algonquian comparisons there are 7 out of 21 (33.3%) differences which are statistically significant, 3 (42.8%) of which are strong ($\tau_b<-0.300$ or $\tau_b>0.300$).

As with the dental morphological traits, given an alpha level of 0.05, one can expect approximately 5% of the significant differences to be due to chance alone. All of the group comparisons exceed this percentage, some by a considerable amount. Again, this suggests a great deal of diversity between all of the samples.

Nine trait comparisons are both statistically significant and strongly correlated with population. These traits include lambdoid ossicle, parietal foramen, epipteric bone, precondylar tubercle, anterior condylar canal, accessory palatine foramen, palatine torus, zygomatico-facial foramen, and frontal notch or foramen.

Following the methodology discussed in Chapter III, the following analyses will utilize all of the uncorrelated cranial morphological traits listed in Table 24. This should give a close approximation of genetic affinities between samples. In addition, each analysis will consider the nine key cranial morphological traits given above in order to delineate differences between the southeast U.S. populations. These two approaches taken together should give a fuller picture of relationships between the groups.

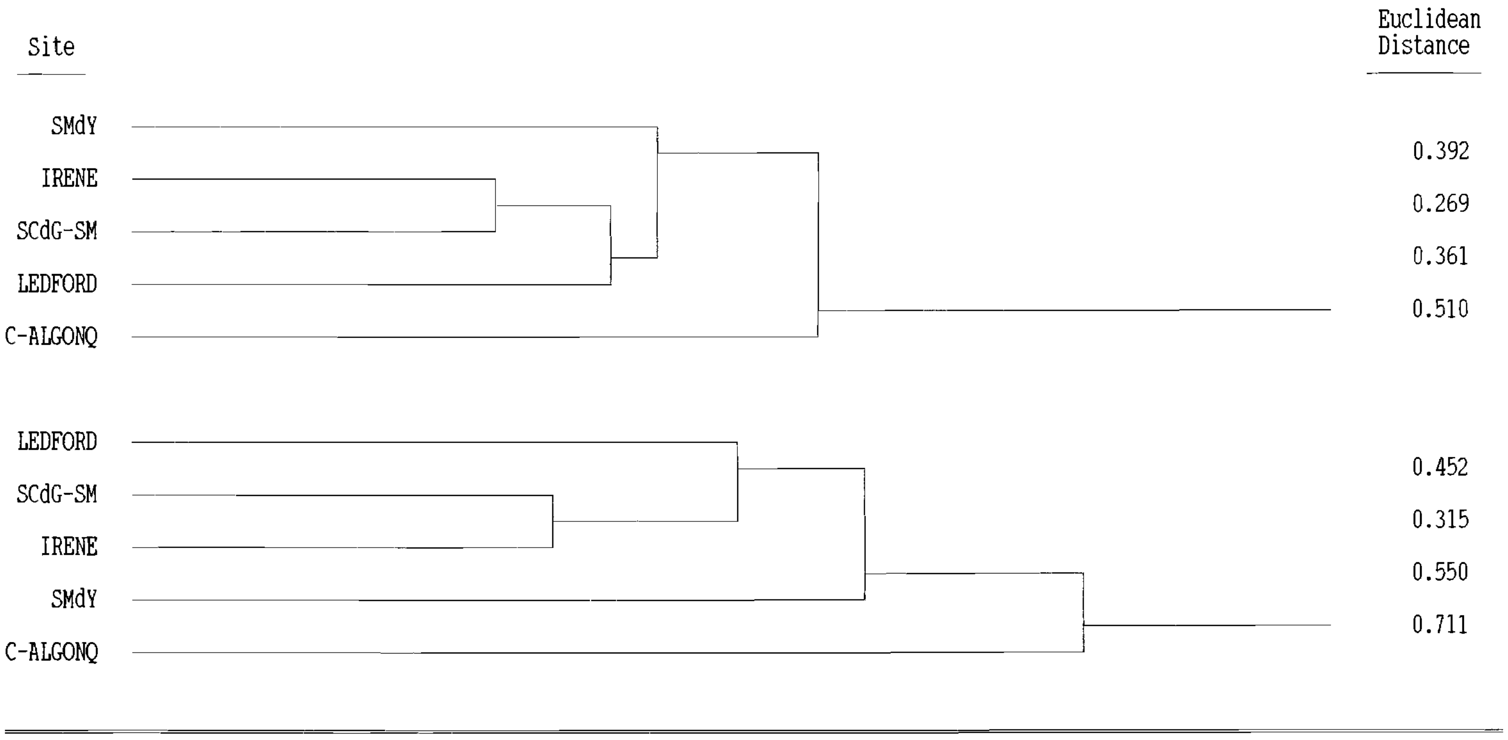
Taxonomic Statistics

As with the dental traits, in order to place the Guale population samples in regional and pan-geographic contexts, the cranial morphological traits listed in Table 24 were employed in three different multivariate analyses. The nine key traits enumerated in the previous section were also used in separate analyses of the southeast U.S. samples. Prior to multivariate analysis, trait frequencies were arcsine transformed in order to stabilize the variance according to the formula recommended by Green and Suchey (1976).

Comparisons between the Guale samples and southeast U.S., Sinodont, and Amerindian samples are treated separately because different trait batteries were available for each comparison. Traits chosen from each comparison group were based on (1) which traits the researchers included in their studies, and (2) which of these traits were included in Table 24. Cranial morphological trait frequencies for the comparison groups are summarized in Appendix E.

Cluster Analysis

In the first multivariate method, arcsine transformed trait frequencies were used as input for a cluster analysis program (Cluster, SYSTAT Inc., Wilkinson 1988a). The results of the cluster analyses are reported in Figures 18-20. Examination of Figure 18 reveals that the southeast U.S. samples fall into one cluster and two isolates. As with the dental cluster analyses, the Carolina Algonquian represent a distinct isolate from the other samples. Unlike the dental analyses, cranial cluster analysis separates the SMdY as a distinct isolate from the other samples, although



Top: all cranial traits
Bottom: key cranial traits

Figure 18. Cluster Analysis, Guale and Southeast U.S. Cranial Samples.

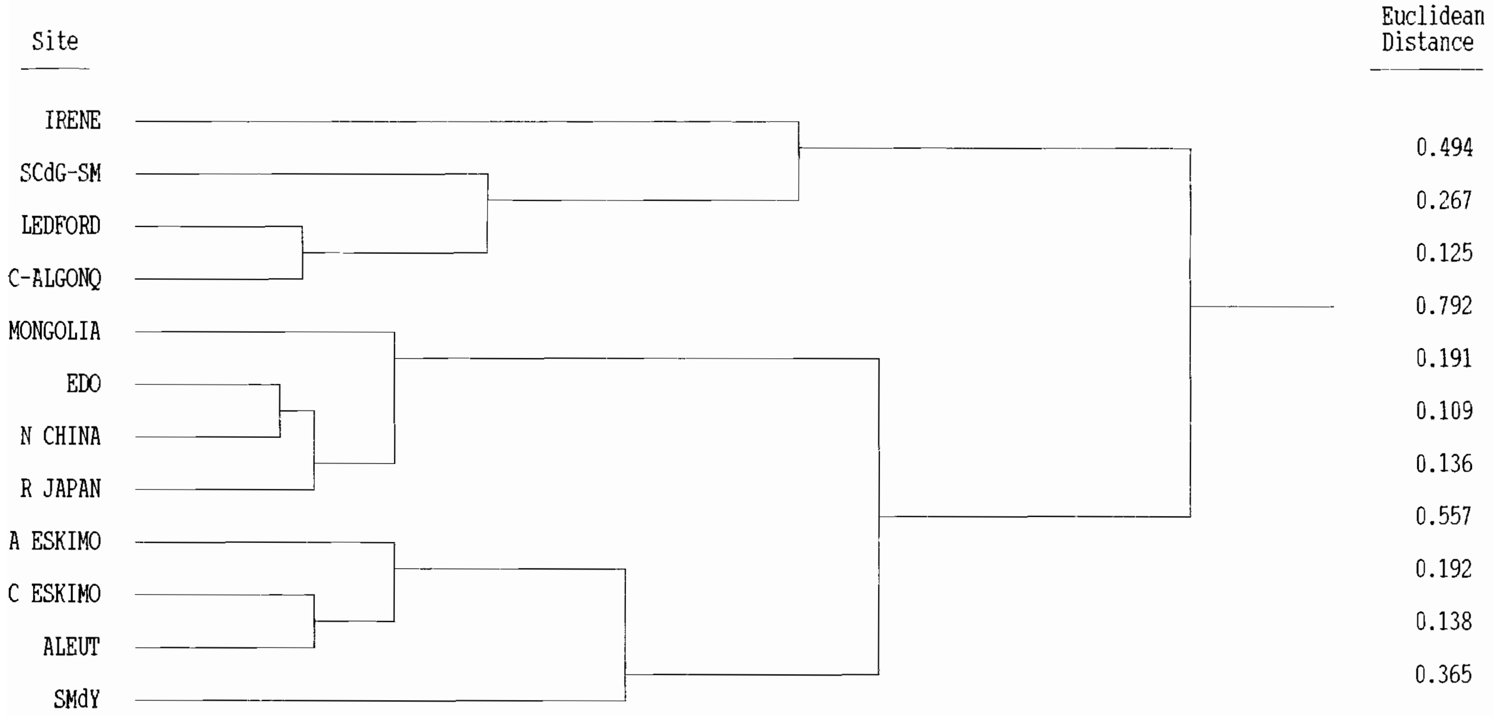


Figure 19. Cluster Analysis, Southeast U.S. and Sinodont Cranial Samples.

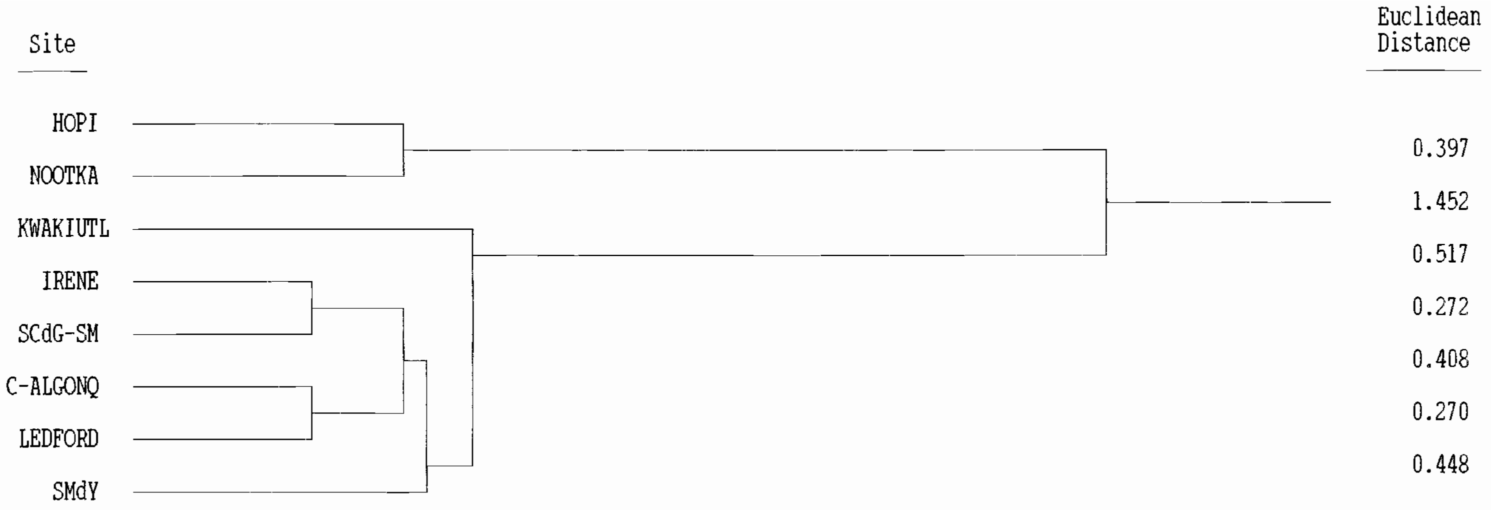


Figure 20. Cluster Analysis, Southeast and Southwest U.S. Cranial Samples.

it is clearly more closely affiliated with the Guale and Ledford Island samples than with the Carolina Algonquian. In contrast to the dental cluster analysis, the Irene Mound, Santa Maria, and Ledford Island samples form a cluster. The Irene Mound and Santa Maria samples are clearly more similar to one another than either is to the Ledford Island sample.

The results reported in Figures 19 and 20 present the outcome of cluster analysis for southeast U.S. and Sinodont samples and the southeast U.S. and southwest U.S. samples respectively. As with the dental cluster analysis, the southeast U.S. samples generally separate as a distinct cluster from the other groups of samples. One notable exception can be seen in Figure 19 with the SMdY sample. This sample is placed as an isolate close to the cluster of subarctic Amerindian populations. This is not to suggest that the SMdY sample is derived from subarctic populations, but rather emphasizes the degree of dissimilarity in terms of cranial morphology compared to the other southeast U.S. samples. Similarly, the Kwakiutl sample is shown as an isolate of the southeast U.S. cluster. This is only an expression of the dissimilarity of the Kwakiutl in comparison to the Hopi and Nootka samples.

Multidimensional Scaling

For the second multivariate technique, multidimensional scaling, arcsine transformed trait frequencies were utilized in a mean measure of divergence analysis. The methodology for the cranial multidimensional scaling analysis is identical to that of the dental analysis described earlier. Measures of divergence for the dental morphological traits are reported in Tables 26-28.

As in the dental analysis, the standardized mean measures of divergence were used as input for a multidimensional scaling program (MDS-Guttman, SYSTAT Inc., Wilkinson 1988a). The output from this program results in a three-dimensional representation of the relative distances between populations in euclidean space. Guttman's (1968) coefficient of alienation was used. Each analysis was stopped when a level of stress in fitting the coordnate points to the monotonic function dropped below a level of S=0.0000.

Results of the multidimensional scaling of the standardized mean measures of divergence are reported in Figures 21-24. The results of multidimensional scaling are somewhat different from that derived from cluster analysis of the cranial traits. As can be seen in Figures 21 and 22, the Santa Maria and SMdY are particularly similar to one

Table 26. Measures of Divergence, Guale and Southeast U.S. Cranial Samples

	IRENE MD	SCdG-SM	SMdY	C-ALGONQ	LEDFORD
IRENE MD	———	0.03496 0.05959	0.06515 0.16187	0.15400 0.30691	0.07650 0.12654
SCdG-SM	2.97180 3.13519	———	0.03593 0.16076	0.10264 0.19968	0.04082 0.10529
SMdY	2.81405 4.46355	1.51223 4.23541	———	0.17033 0.34436	0.05886 0.15976
C-ALGONQ	14.25336 18.06953	8.95009 10.65169	7.45014 9.55410	———	0.18014 0.45315
LEDFORD	4.41780 4.62900	2.27009 3.61457	2.00698 3.44794	10.58255 16.72561	———

Values within each cell represent measures of divergence derived from (1) all dental traits, and (2) key dental traits
Mean measures of divergence above diagonal, standardized mean measures of divergence below diagonal

Table 27. Measures of Divergence, Southeast U.S. and Sinodont Cranial Samples*

	IRENE	SCdG-SM	SMdY	C-ALGONQ	LEDFORD	N CHINA	EDO	R JAPAN	MONGOLIA	ALEUT	A ESKIMO	C ESKIMO
IRENE	———	0.10437	0.08729	0.12729	0.10294	0.18496	0.16697	0.22905	0.20662	0.12068	0.15826	0.18288
SCdG-SM	4.51189	———	0.02001	0.02249	-0.01422	0.08987	0.08251	0.15922	0.06995	0.09159	0.07149	0.13779
SMdY	2.02148	0.44596	———	0.12156	0.07660	0.08847	0.07090	0.15465	0.12795	0.01709	0.03361	0.02871
C-ALGONQ	6.19720	1.00716	2.87082	———	-0.04229	0.08421	0.09105	0.15681	0.05756	0.07033	0.09158	0.12891
LEDFORD	2.95917	-0.38875	1.35504	-1.24508	———	0.03115	0.01873	0.07935	0.00898	0.04201	0.03569	0.07743
N CHINA	13.05919	5.64892	2.45892	6.31293	1.13008	———	-0.00040	0.00420	0.00405	0.02534	0.01811	0.03847
EDO	11.66962	5.13803	1.96277	6.75684	0.67563	-0.05600	———	0.00576	0.01874	0.03236	0.01347	0.03000
R JAPAN	16.46671	10.16689	4.32862	11.98319	2.90484	0.62040	0.83585	———	0.03030	0.07049	0.04194	0.06489
MONGOLIA	14.82994	4.45882	3.57899	4.39153	0.32831	0.59767	2.71354	4.64350	———	0.05809	0.05892	0.09340
ALEUT	7.70856	5.27368	0.45614	4.74140	1.44615	2.97336	3.74208	8.52449	7.01117	———	0.02530	0.00340
A ESKIMO	11.67357	4.66632	0.94995	7.19337	1.32330	2.82896	2.06350	6.82033	9.55586	3.19902	———	0.01366
C ESKIMO	12.50493	8.41260	0.78767	9.34172	2.76219	5.15481	3.95057	8.99985	12.92320	0.37904	1.99396	———

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*Mean measures of divergence above diagonal, standardized mean measures of divergence below diagonal

Table 28. Measures of Divergence, Southeast and Southwest U.S. Cranial Samples*

	IRENE	SCdG-SM	SMdY	C-ALGONQ	LEDFORD	HOPI	NOOTKA	KWAKIUTL
IRENE	———	0.03651	0.13875	0.10622	0.07339	0.49416	0.40939	0.17778
SCdG-SM	2.35567	———	0.04031	0.05584	0.04685	0.64699	0.53106	0.17888
SMdY	4.39524	1.25456	———	0.07726	0.06408	0.74643	0.68094	0.26167
C-ALGONQ	7.38380	3.72131	2.48522	———	0.01900	0.52764	0.40294	0.15285
LEDFORD	3.21807	1.99988	1.62472	0.85203	———	0.48656	0.36016	0.06863
HOPI	42.25756	52.45314	26.34916	47.12124	24.79951	———	0.12297	0.57584
NOOTKA	23.34739	29.15238	20.07639	23.60277	14.20857	8.40352	———	0.32576
KWAKIUTL	15.20610	14.45183	9.25898	13.63831	3.50529	66.26738	21.98709	———

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*Mean measures of divergence above diagonal, standardized mean measures of divergence below diagonal

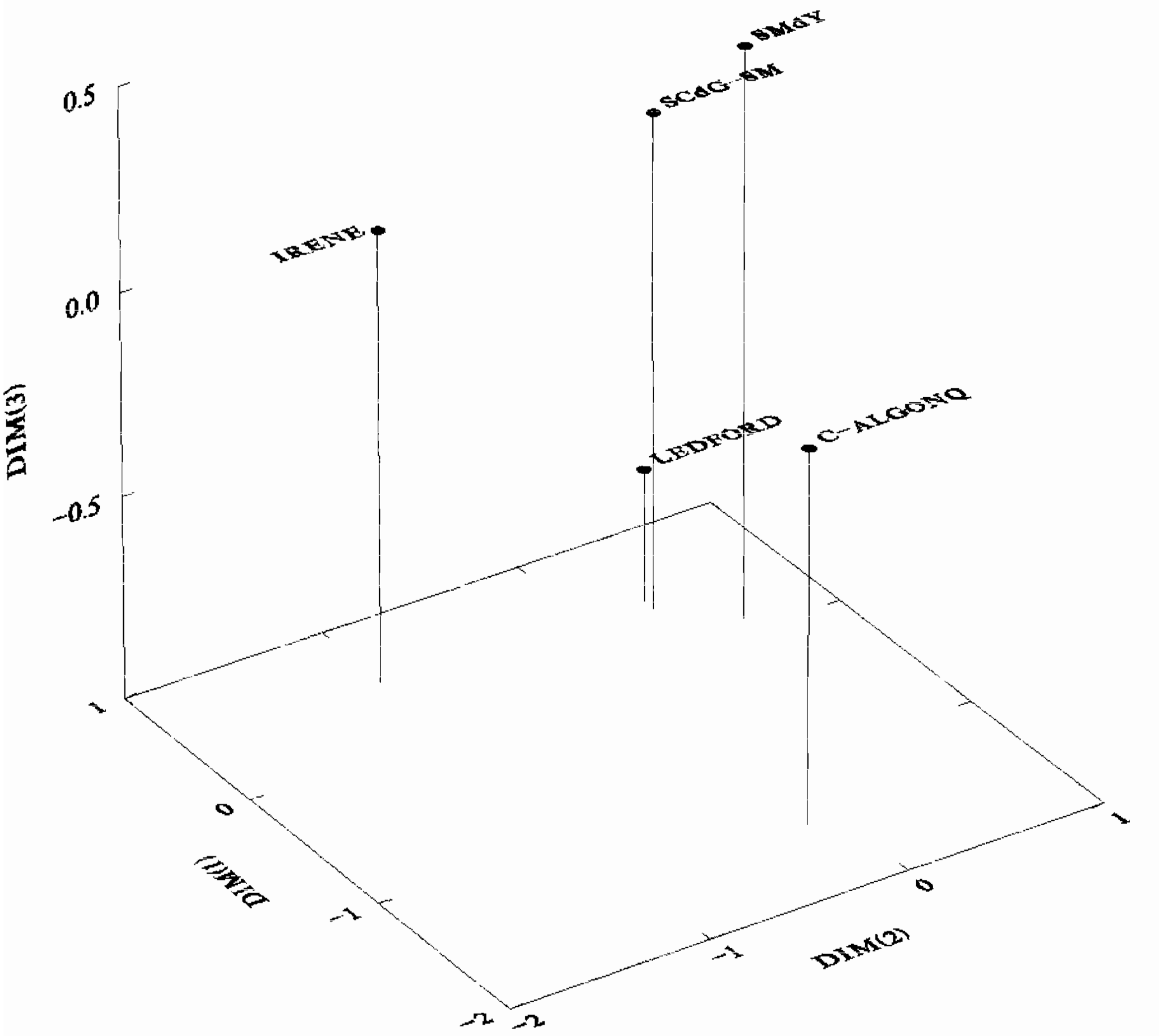

Figure 21. Multidimensional Scaling Analysis, Guale and Southeast U.S. Cranial Samples (All Traits).

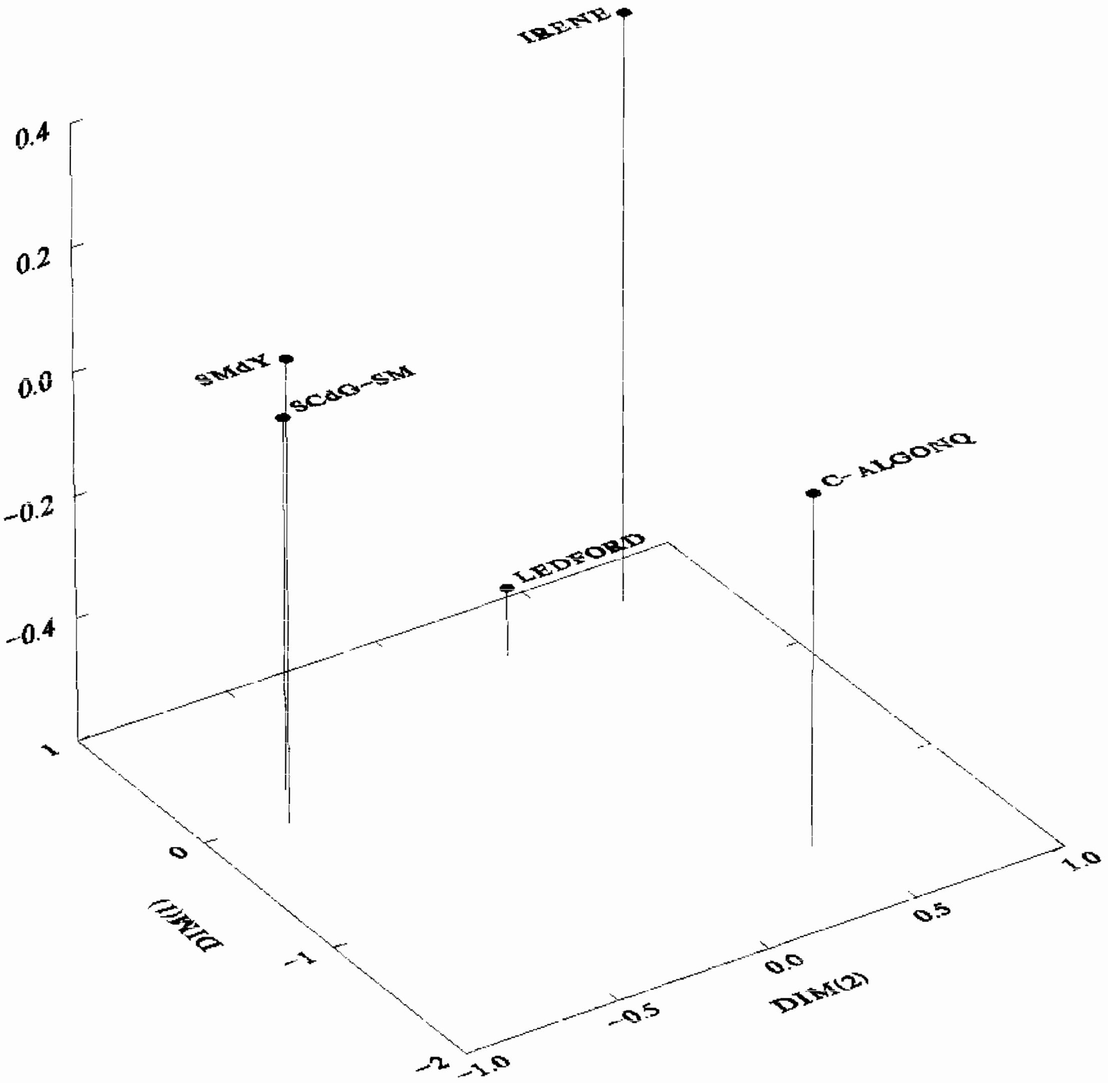

Figure 22. Multidimensional Scaling Analysis, Guale and Southeast U.S. Cranial Samples (Key Traits).

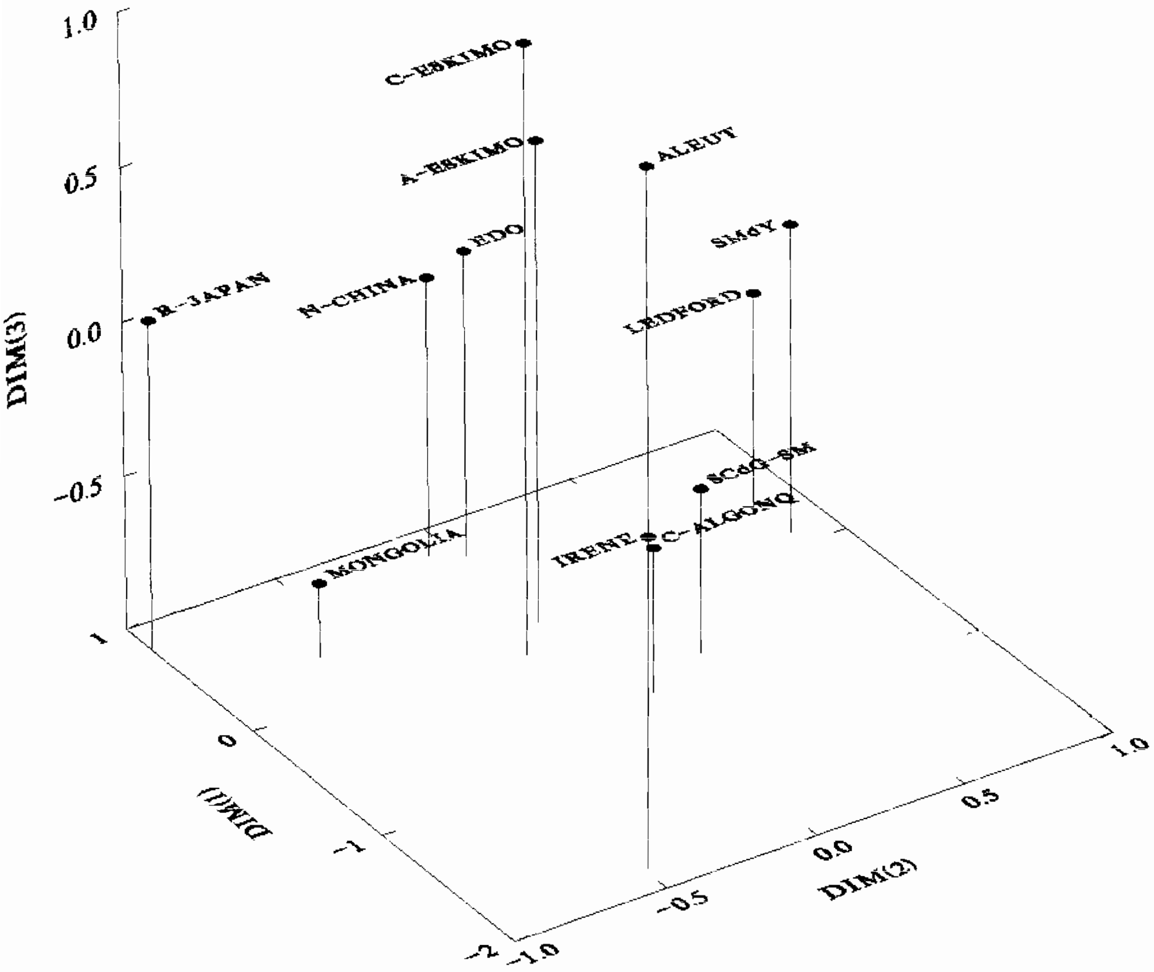

Figure 23. Multidimensional Scaling Analysis, Southeast U.S. and Sinodont Cranial Samples.

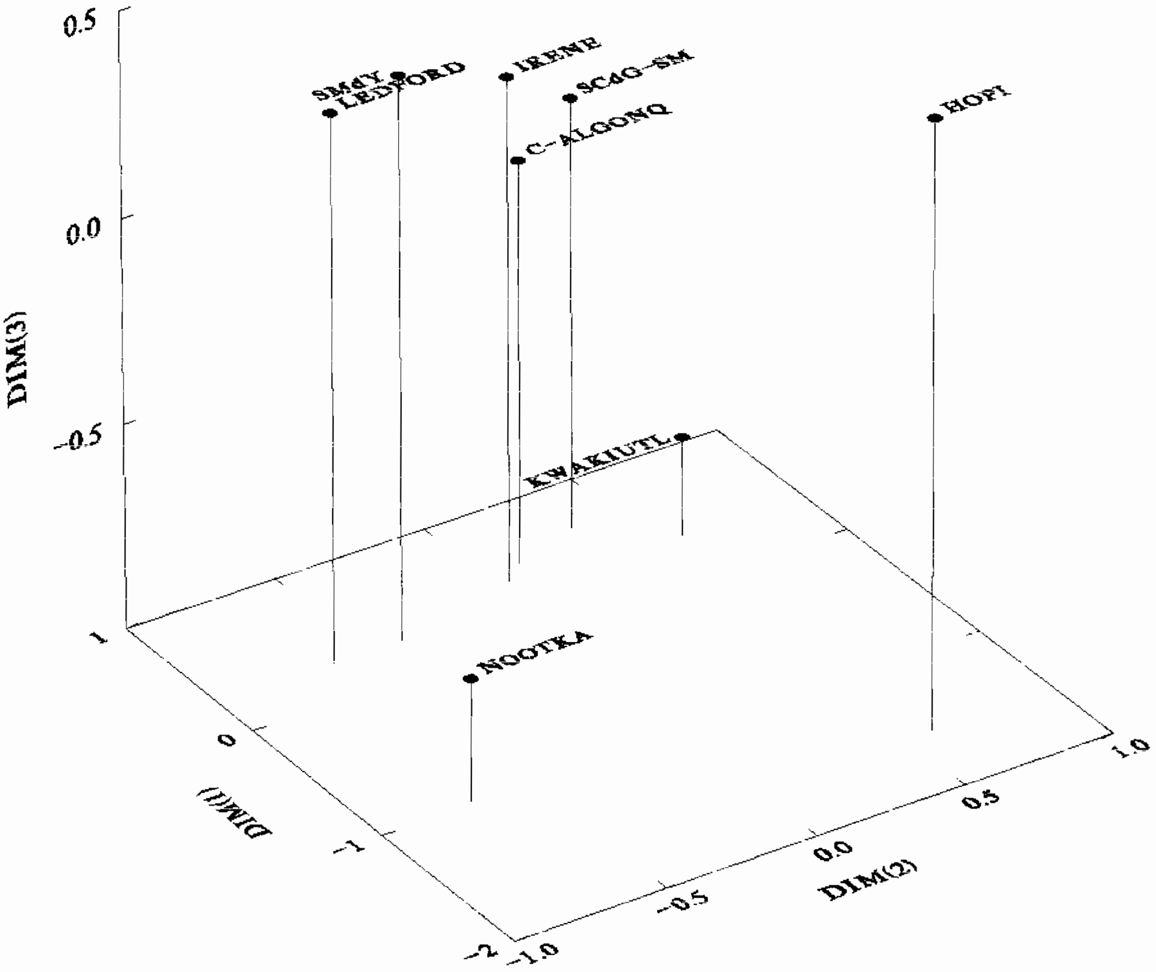

Figure 24. Multidimensional Scaling Analysis, Southeast and Southwest U.S. Cranial Samples.

another. In Figure 21, it appears that the Ledford Island sample is somewhat similar to the Santa Maria and SMdY samples. However, Figure 22 shows the Ledford Island sample as quite distinct from the Santa Maria and SMdY samples. In both Figure 21 and Figure 22, the Irene Mound sample and the Carolina Algonquian sample are quite dissimilar to all of the other groups as well as to each other.

The results reported in Figures 23 and 24 mirror the results obtained from cluster analysis of the southeast U.S., Amerindian, and Sinodont samples. The southeast U.S. samples are clearly distinct from the other samples and form clusters in one plane contrasted to all of the other groups. As would be expected, the southeast U.S. samples are generally more similar to the Amerindian samples than to the other Sinodont samples.

Principal Component Analysis

The last multivariate technique used to examine group affinities between samples is principal component analysis. As with the dental analysis, arcsine transformed trait frequencies were standardized to have a zero mean and unit variance. Principal components were then derived and varimax rotated to a simpler solution (Factor, SYSTAT Inc., Wilkinson 1988a). Factor score coefficients (eigenvector coefficients) for each variable were then multiplied by the standardized arcsine transformed frequency for each sample. These values were summed for each sample according to the first three principal components. The resulting component scores were plotted in three dimensional space to illustrate the relative position of each sample in multicomponent space (Plot, SYGRAPH, Wilkinson 1988b).

As can be seen from Tables 29-32, between 79.119% and 89.261% of the total variance can be explained by the first three principal components. The resultant scores are plotted in three dimensional space in Figures 25-28. As can be seen, the results of multidimensional scaling and cluster analysis are generally confirmed.

From the examination of Figures 25 and 26, the SMdY is generally separated from the rest of the population samples. None of the population samples are markedly similar to one another in terms of cranial morphology. Figures 27 and 28 demonstrate that although the southeast U.S. samples form a diverse group, they all fall on one side of a plane in comparison to all other groups of samples.

Using the same methodology described in the principal component analysis of dental traits, key traits can be identified for the analysis of cranial morphology. As

Table 29. Varimax Rotated Principal Components Analysis of All Cranial Traits, Guale and Southeast U.S. Samples

	Component loadings		
Morphological Trait	1	2	3
LO	0.861	-0.050	0.500
OAA	0.105	0.881	0.115
PNB	0.137	0.913	-0.011
EPB	0.562	0.383	0.586
BB	-0.346	-0.029	0.518
CO	0.802	-0.310	-0.153
MET	-0.902	0.170	0.193
FTA	0.260	0.893	0.135
FN	-0.124	-0.024	-0.840
AT	-0.910	0.168	0.209
CFD	-0.880	0.013	0.381
PT	0.095	-0.971	0.003
FO	0.821	0.198	-0.332
FS	0.436	0.461	-0.690
APF	0.770	0.232	-0.020
PAT	-0.192	0.174	0.904
PF	0.459	-0.888	-0.034
MFA	-0.383	0.897	-0.175
ACC	-0.815	0.464	-0.258
ZFF	-0.584	0.409	0.697
AIF	0.387	-0.819	-0.259

Variance explained by rotated components	7.364	6.635	3.903
Percent of variance explained	35.069	31.594	18.584
Total variance explained by first three components:		85.247	

	Component Scores		
Site	1	2	3
IRENE	-1.169	-1.262	0.062
SCdG-SM	-0.262	0.219	-0.677
SMdY	1.569	-0.803	0.308
C-ALGONQ	-0.286	0.996	1.456
LEDFORD	0.149	0.849	-1.150

Table 30. Varimax Rotated Principal Components Analysis of Key Cranial Traits, Guale and Southeast U.S. Samples

	Component loadings		
Morphological Trait	1	2	3
LO	-0.314	0.904	-0.289
EPB	0.163	0.675	-0.569
FN	0.099	-0.381	0.663
PT	-0.958	-0.129	0.125
APF	0.040	0.865	0.286
PAT	0.111	0.003	-0.985
PF	-0.963	0.189	0.179
ACC	0.676	-0.655	0.108
ZFF	0.458	-0.302	-0.822
Variance explained by rotated components	2.661	2.739	2.633
Percent of variance explained	29.571	30.433	29.257
Total variance explained by first three components:		89.261	

	Component Scores		
Site	1	2	3
IRENE	-0.935	-1.325	-0.103
SCdG-SM	0.343	-0.583	0.226
SMdY	-1.191	1.315	0.066
C-ALGONQ	0.865	0.309	-1.494
LEDFORD	0.917	0.284	1.305

Table 31. Varimax Rotated Principal Components Analysis of Cranial Traits, Southeast U.S. and Sinodont Samples

	Component loadings		
Morphological Trait	1	2	3
OAA	0.650	0.374	-0.296
PNB	-0.921	0.265	0.079
MET	-0.865	-0.191	0.132
PT	-0.029	-0.963	0.149
FO	0.304	0.109	-0.860
ACC	0.094	0.698	0.612
Variance explained by rotated components	2.121	1.673	1.247
Percent of variance explained	35.344	27.882	20.788
Total variance explained by first three components:		84.014	

	Component Scores		
Site	1	2	3
IRENE	-0.502	-1.439	2.686
SCdG-SM	-1.626	0.646	-0.515
SMdY	-1.106	-1.587	-1.416
C-ALGONQ	-1.071	1.241	0.507
LEDFORD	-0.738	1.210	0.263
N-CHINA	0.918	0.334	-0.115
EDO	0.799	0.153	-0.167
R-JAPAN	1.698	0.247	0.254
MONGOLIA	0.639	1.143	0.011
ALEUT	0.332	-0.701	-0.065
A-ESKIMO	0.119	-0.290	-0.701
C-ESKIMO	0.540	-0.957	-0.763

Table 32. Varimax Rotated Principal Components Analysis of Cranial Traits, Southeast and Southwest U.S. Samples

	Component loadings		
Morphological Trait	1	2	3
LO	0.475	0.772	-0.084
OAA	-0.168	-0.323	-0.709
PNB	-0.250	0.873	0.031
EPB	0.548	0.571	-0.255
BB	0.865	0.048	0.225
CO	0.113	0.932	0.292
MET	0.885	0.033	0.332
FO	0.947	0.001	0.096
FS	-0.604	-0.301	-0.610
APF	0.044	0.202	-0.856
ACC	-0.668	-0.114	0.222
AIF	0.627	0.500	0.440
Variance explained by rotated components	4.264	3.053	2.178
Percent of variance explained	35.531	25.442	18.146
Total variance explained by first three components:		79.119	

	Component Scores		
Site	1	2	3
IRENE	0.105	-0.430	1.908
SCdG-SM	0.202	0.483	1.254
SMdY	1.251	1.086	-0.708
C-ALGONQ	0.488	0.641	-0.352
LEDFORD	0.143	0.197	-0.604
HOPI	-1.832	0.832	-0.370
NOOTKA	-1.101	-1.009	-0.465
KWAKIUTL	0.745	-1.800	-0.653

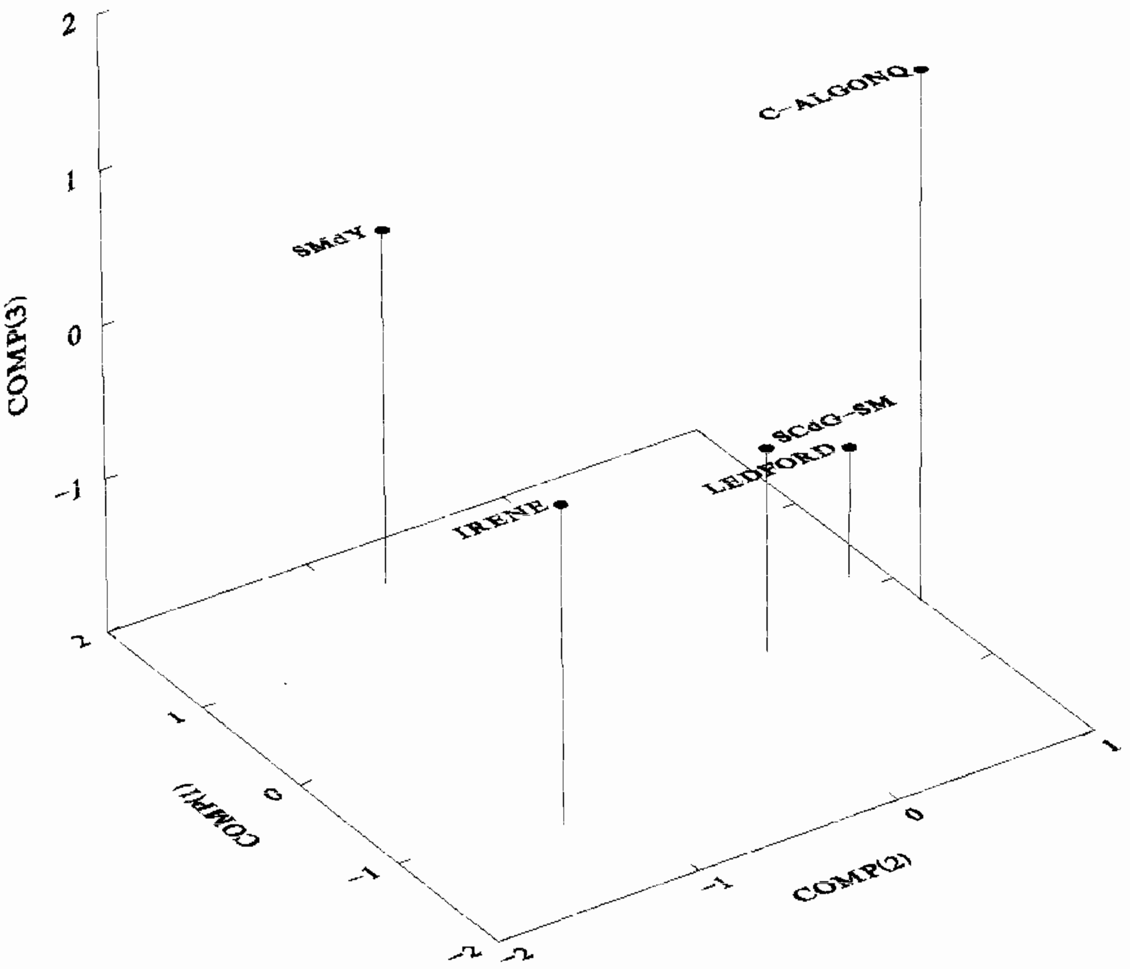

Figure 25. Principal Component Analysis, Guale and Southeast U.S. Cranial Samples (All Traits).

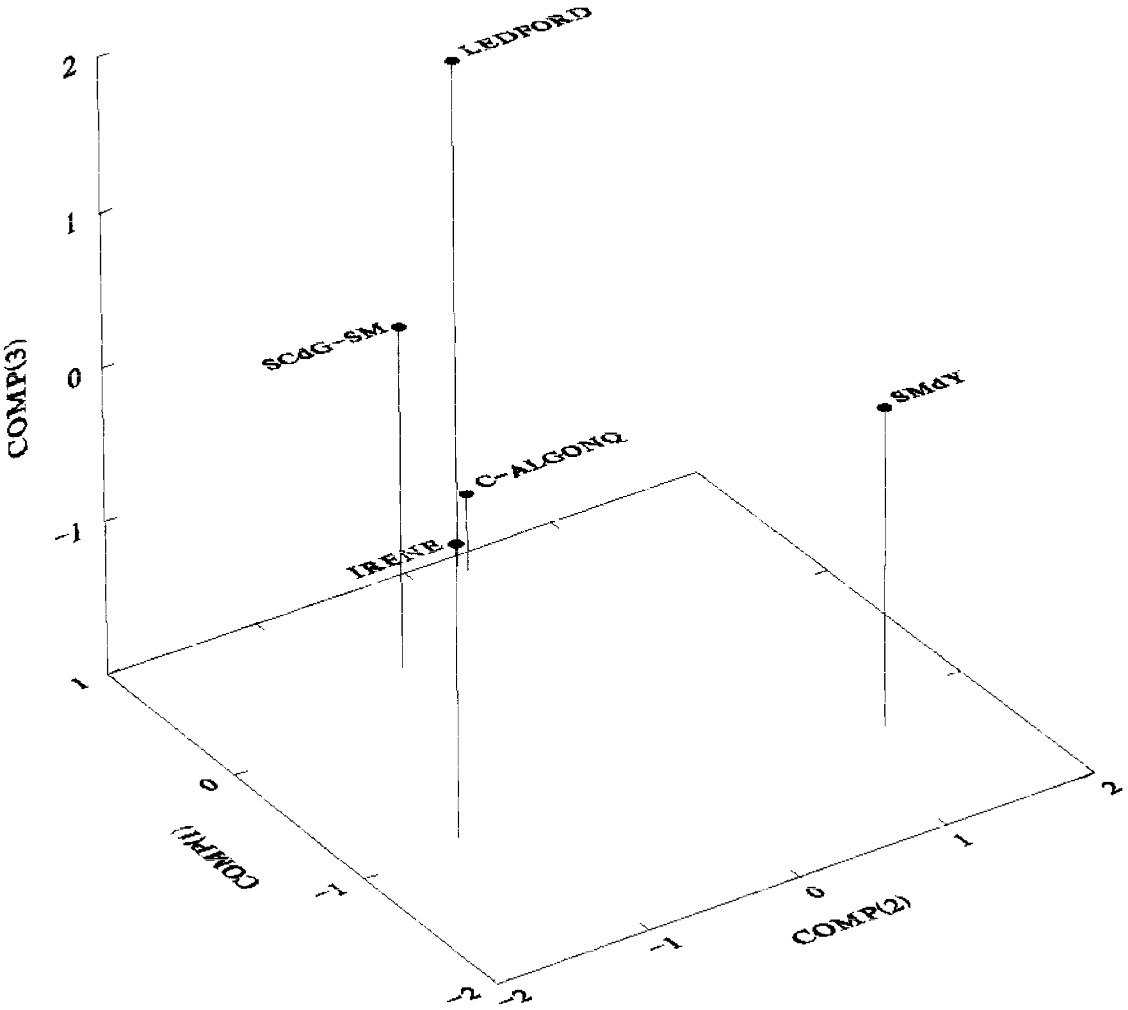

Figure 26. Principal Component Analysis, Guale and Southeast U.S. Cranial Samples (Key Traits).

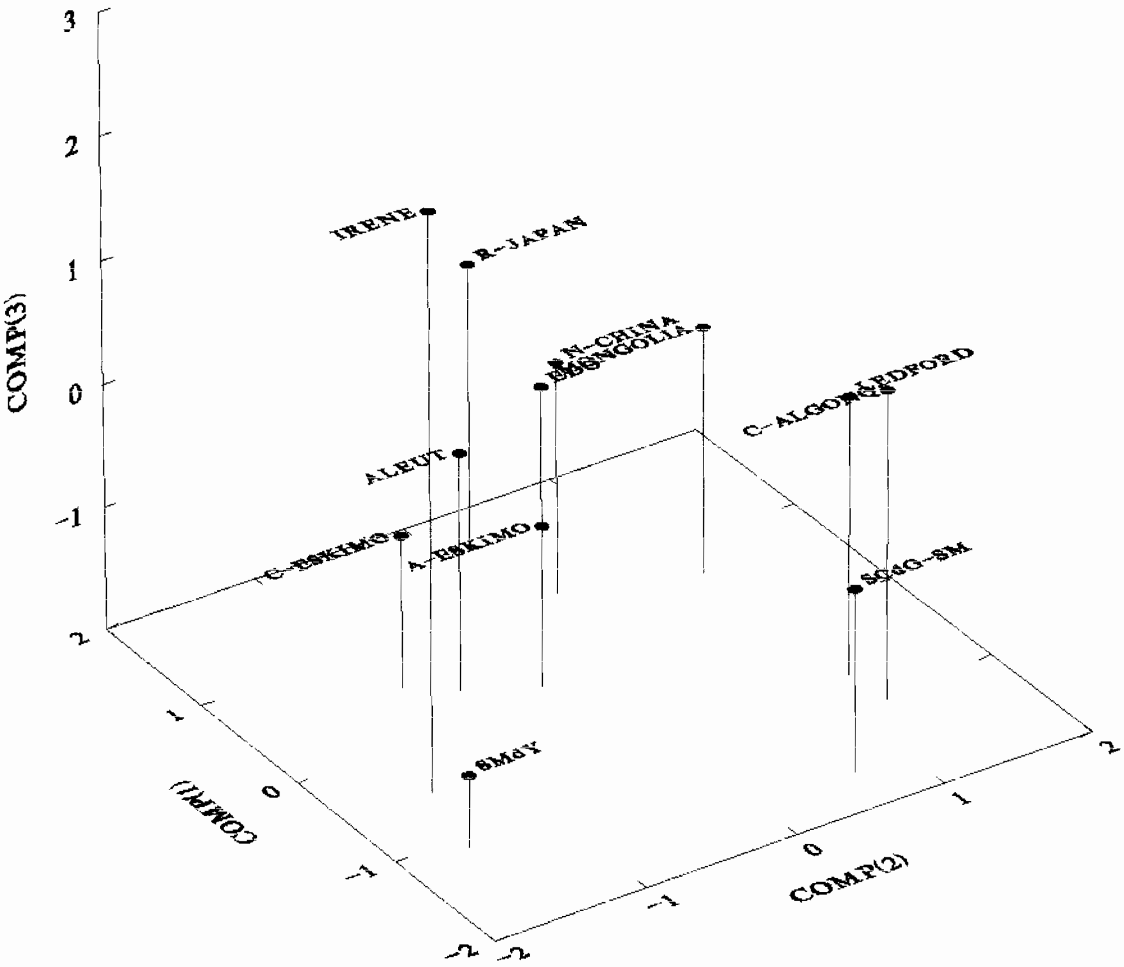

Figure 27. Principal Component Analysis, Southeast U.S. and Sinodont Cranial Samples.

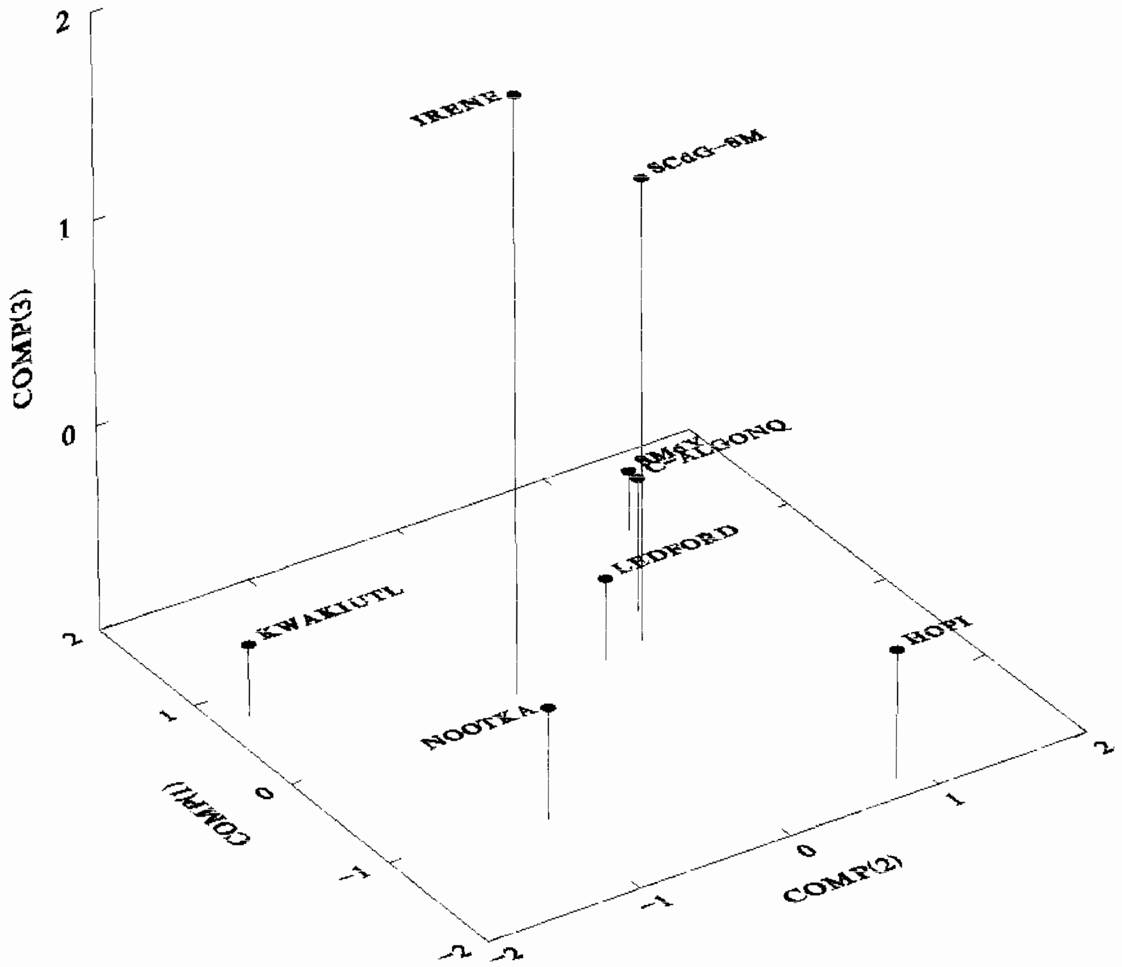

Figure 28. Principal Component Analysis, Southeast and Southwest U.S. Cranial Samples.

mentioned previously, a principal component analysis is not always successful, in the sense that a large number of original variables are reduced to a small number of transformed variables. This is often the case when the original variables are uncorrelated. The methodology described in Chapter III was used expressly for the purpose of removing or reducing correlated variables. Thus, the identification of major discriminators here offers little to the analysis. Upon inspection of Tables 29-32, it can be seen that virtually all of the variables have high component loadings at some point.

CHAPTER V - DISCUSSION AND CONCLUSIONS

The results of this study can be discussed in relation to a number of specific issues. Among these are (1) the reliability of statistical results obtained from analyses of two disparate types of traits, (2) the likely biological relationships between the population samples which have been culturally and linguistically identified as Guale, (3) the biological affinity of the Guale to other groups from the southeast United States which have been ethnographically identified as culturally and linguistically distinct from the Guale, and (4) the biological relationship between southeast United States Native American groups and other Amerindian and Asian groups.

Addressing the first issue, the results of statistical analyses here are tenable. Results obtained from multivariate analyses of dental and cranial morphological data are generally consistent with one another. Because these two classes of traits likely share very different etiological backgrounds, the consistency of results indicates that the outcomes are not spurious. Furthermore, the three multivariate analyses employed here derived similar solutions via different methods. This also indicates that the results of this study are well founded. The minor inconsistencies found in the analyses of cranial traits may simply reflect a more complex etiology and higher proportion of nongenetic influences on expression for these traits.

Secondly, according to the results reported here, the Guale do not represent a continuous population. The Santa Maria population is probably a derivative from the Santa Catalina population. However, the Irene Mound population is distinct, in terms of dental and cranial morphology, from either of these two later groups. The *Santa Catalina de Guale* and *Santa Catalina de Guale de Santa Maria* samples were consistently placed close to one another in multivariate analyses of dental and cranial data. Given the ethnographic record, provided in part by the records of the Spanish mission effort in *La Florida*, it is not unexpected that the Santa Catalina and Santa Maria samples would be placed close together in a biological distance analysis. This is indeed the case, although there are significant differences in trait frequencies. These differences may best be explained by genetic drift. The considerably differing demographic profiles for the two population samples (Larsen and Russell 1989, Larsen et al. 1990, Russell et al. 1990) may suggest that a segment of the population is underrepresented at Santa Maria (20-35 years of age). Considering the relatively short duration of the cemetery at Santa Maria (about 16 years) and the dismal social climate at the mission, it is a distinct possibility that individuals in this age class migrated, voluntarily or involuntarily, from Santa Maria. Such a selective removal could account for genetic drift. Considering the volatile social circumstances at the time, many other possible explanations for genetic drift exist (e.g., warfare, circumscription, and elevated mortality).

Another alternative explanation for the significant differences between Santa Catalina and Santa Maria may be inferred from the differing degrees of diversity observed among each sample. The Santa Catalina sample exhibits a great deal more variability in terms of trait expression than that observed for the Santa Maria sample. The diversity observed at Santa Catalina could reflect the likely aggregation of diverse populations at this mission. Because Santa Catalina was one of the early missions in the area and may have been characterized by the mixture of diverse gene pools, one might expect that this sample would exhibit a wide range of trait variability. Given that (1) in terms of biological distance the Santa Catalina and Santa Maria samples are quite close, (2) the Santa Catalina sample temporally preceded the Santa Maria sample, and (3) the population of Santa Maria most likely derived from that of Santa Catalina, the evidence suggests a population "bottleneck" between the two temporal periods. That is, the gene pool was sharply restricted between the temporal period of Santa Catalina and that of Santa Maria. Any of the previously mentioned factors could cause such a "bottleneck" (e.g., differential mortality, migration, warfare).

The placement of the Irene Mound sample is more problematic. Separate multivariate analyses of dental and cranial morphological traits consistently placed this sample relatively far from the other Guale samples and closer to the Creek sample from Ledford Island. This result is especially notable in regard to the placement of the other Guale samples quite far from the Ledford Island sample and distinct from the Irene Mound sample. This is not to suggest that inhabitants of Irene Mound migrated from Tennessee. It does however cast suspicion on the contention that the Irene Mound sample and the later Guale samples are a continuous population. The results of previous studies that have assumed biological continuity for the Guale should therefore be accepted cautiously.

It has been inferred from the ethnographic record that the Guale were a derivative group from the inland Creek (Spencer and Jennings 1965). That the Guale sample from

Irene Mound and the Creek sample from Ledford Island are quite similar in terms of dental and cranial morphology suggests a close biological connection between these groups. While the results of multivariate analyses of dental morphology consistently placed the Irene Mound and Ledford samples close to one another, the results obtained from analysis of cranial morphology were less consistent. The somewhat equivocal results of the cranial analyses in regard to the placement of Irene Mound and Ledford Island samples may suggest a less straightforward relationship than that suggested by analyses of dental morphological traits. The interpretation may be that the Irene Mound sample was more closely affiliated with the Creek than with the later Guale from Santa Catalina and Santa Maria. Because populations in this geographic area were in a state of political and social flux between the temporal period of Irene Mound and that of the later Guale samples, this interpretation is plausible. It should also be noted that the term *Guale* was used interchangeably as a geographic location and a cultural/linguistic group (Jones 1978). Therefore, referring to a group as *Guale* may have connoted geographic location and not necessarily linguistic, cultural, or biological affiliation. It may also be the case that while the Guale represented a distinct linguistic and cultural group, they did not represent a distinct biological one. As mentioned previously, the sample from Santa Catalina likely represents an aggregate population. If this is the case, one would hardly expect the prehistoric Irene Mound inhabitants to be closely related to the population sample from Santa Catalina. This is further complicated by the probability that because it was a ceremonial center, Irene Mound likely was also an aggregate population. Regardless of which interpretation one chooses, it is clear from the results presented here that the prehistoric Guale from Irene Mound were significantly dissimilar in terms of dental and cranial morphology from the historic Guale of both Santa Catalina and Santa Maria.

If the historic Guale populations of the Georgia coast derive from the late prehistoric Irene Mound population, quite substantial population changes must have occurred. If this is the case, extensive gene flow from other populations was likely involved because of the relatively brief time interval between the occupation of Irene Mound and that of *Santa Catalina de Guale* (≈100 years). Given the particularly unstable political and social conditions among the Guale after European contact and the extensive period of missionization of the native inhabitants, aggregation of local populations could have precipitated such gene flow.

The degree of similarity, based on multivariate analyses of nonmetric traits, between the Santa Catalina and

Santa Maria samples and the *Santa Maria de Yamassee* sample suggests that these population samples may be closely related. This similarity is especially marked between the Santa Maria and *Santa Maria de Yamassee* samples. It is unexpected that the Santa Maria and *Santa Maria de Yamassee* population samples would be consistently placed close together in a population distance analysis. The ethnographic record is unclear as to the cultural and linguistic affiliation of the Guale and Yamassee. However, these two groups are usually distinguished as distinct groups (Mooney 1969, Bushnell 1986). Evidence presented in this analysis may suggest a closer affinity than the ethnographic record indicates. It may be that historically the Guale and Yamassee were distinguished solely by geographic location, and not cultural, linguistic, or biological differences. Given the sketchy ethnographic record for the Yamassee, this interpretation is plausible.

The Carolina Algonquian population samples consistently appear distinct in regard to the other southeast United States samples. This outcome is not unexpected considering the ethnographic identification of the Algonquian as a group with origins far to the north and unlike many of their geographically close neighbors in the southeast United States. It is especially notable however, that the Carolina Algonquian are included in a cluster with other groups from the southeast United States when compared with other Amerindian and Asian populations. This may suggest a noticeable degree of regional gene flow in this geographic area.

Lastly, the population samples from the southeast United States were consistently distinguished from samples from other Amerindian samples and populations from Asia. Because the data were collected by different observers, this could be an artifact of trait recording procedures. However, the consistency of the results from different trait types and differing multivariate methods suggests otherwise. In the case of dental morphological traits, the same methodology was used for all of the samples included here, regardless of observer. It is expected that population samples from these different geographic areas should form distinctly different clusters. However, considering Turner's analyses of Amerindian biological relationships (Greenberg et al. 1986, Turner 1986a, 1989), it is unexpected that populations from the southeast United States should form such a distinct cluster in regard to other Amerindian groups. The results presented here suggest that the populating of the Americas may be more complex than Turner and coworkers have concluded. The suggestion that the New World was populated in three large migrations from Asia (Greenberg et al. 1986) may be overly simplistic, especially considering the biological diversity suggested by recent molecular studies among ancient (Pääbo et al. 1988, 1989, Pääbo 1989) and extant Native American groups (Pääbo et al. 1990, Schanfield et al. 1990, Schurr et al. 1990, Kidd et al. 1991, Ward et al. 1991, Schanfield 1992, Wallace and Torroni 1992, Callegari-Jacques et al. 1993).

As stated in the hypothesis for this study, there are at least two alternatives which the results could support. The first possibility is that the precontact Guale of the Georgia coast and the postcontact Guale of the Georgia and Florida coasts represent a single temporally and biologically continuous population. If this were indeed the case, the results of this study should have indicated a homogeneous population over all of the temporal periods with few significant differences in frequency for the dental and cranial morphological traits. Likewise, if the population samples in this study represented a temporally continuous population, it would be expected that the biological distance between the Guale samples would be small in comparison to those from other non-Guale groups. In this case, comparison with the non-Guale population samples should reveal a significant difference in trait frequencies and in biological distance. It would be expected that the differences would be greater for those groups that are geographically more distant from the Guale (e.g., Algonquian and Creek) than for the closer populations (e.g., Yamassee) which have a greater opportunity for gene flow.

The second possibility is that the results of this study could have indicated a heterogeneous population with differing degrees of diversity between the temporal periods. This being the case, large biological distances between the Guale samples would suggest the presence of discontinuous populations. The possibilities for such an apparent lack of continuity include: (1) high levels of genetic drift occurring between generations of an in situ population, (2) significant amounts of gene flow from other populations altering the composition of the gene pool, or (3) the samples were drawn from different populations. Any one of these processes or a combination of them could cause significant changes in composition of the gene pool between temporal periods.

The results of this study support the later alternative. The Guale samples examined here represent a diverse series of population samples in terms of both dental and cranial morphology. These results contradict, in part, earlier assumptions of population relationships on the Georgia coast. Although biological continuity may be argued for the postcontact Guale from Santa Catalina and Santa Maria, the same argument does not seem to hold true for the relationship between the precontact Irene Mound sample and the postcontact Guale groups. The marked similarity between the Creek population sample from Ledford Island and the Guale sample from Irene Mound may suggest a biological connection between these populations. According to ethnographic sources, the Guale are a derivative group from the Creek (Spencer and Jennings 1965). The similarity between the Ledford Island and Irene Mound samples may therefore reflect the retention of ancestral Muskhogean traits in both samples. This contention cannot be fully explored without further comparative studies of other Muskhogean groups.

The findings of this study, obtained from two genetically independent lines of evidence (dental and cranial morphology) can be summarized as follows:

(1) Cranial and dental morphological traits provide complementary and consistent measures of biological distance for the population samples examined here. Because these two classes of traits share quite different etiological backgrounds, the consistency of results suggests that the conclusions of this study are well founded.

(2) Trait by trait analysis suggests a degree of diversity between the Guale samples which cannot be fully

explained by sampling error. The numbers of statistically significant differences for each population comparison exceed by a substantial margin the number of expected differences, given an alpha level of 0.05.

(3) The degree of dissimilarity between the Santa Catalina and Santa Maria samples, although significant, is relatively small in consideration of the other sample distances. This degree of dissimilarity can best be explained by genetic drift. This contention is additionally supported by the comparatively smaller sample size observed at Santa Maria, which represents the temporally later sample.

(4) The degree of dissimilarity observed between the Irene Mound sample and the other Guale samples cannot be adequately explained by random genetic drift. Other mechanisms must be invoked to explain this difference.

(5) The population sample from *Santa Maria de Yamassee* was consistently placed close to the Santa Maria sample in multivariate analyses. This outcome may suggest a close biological affiliation between these two populations. The relationship between the Santa Catalina sample and the *Santa Maria de Yamassee* sample was less clear, but may also suggest a biological affiliation between the two groups.

(6) The Carolina Algonquian population samples are consistently identified as a distinct isolate from the other southeast United States samples. However, when compared to other Amerindian populations, the Algonquian are clustered with other samples from the southeast United States. This may suggest a detectable level of regional gene flow.

(7) The population samples from the American southeast form a distinct cluster when compared to other Amerindian samples and Asian samples from Turner's Sinodont classification. As expected, the southeast Amerindian samples are clearly more biologically similar to Amerindian groups than to Asian Sinodont groups. However, the samples from the southeast United states are distinctly dissimilar to other Amerindian groups.

In conclusion, univariate and multivariate analyses have demonstrated that the Guale population samples examined here are particularly diverse in terms of expression of dental and cranial morphological traits. This diversity cannot be fully explained in terms of in situ genetic drift. Thus, the argument for biological continuity of native populations from the Georgia and Florida coasts cannot be fully supported, at least with regard to comparison of the

Guale from Irene Mound with the later mission period Guale from Santa Catalina and Santa Maria.

This study presents a preliminary picture of population relationships in the protohistoric southeastern United States. Although the results presented here may be incongruous with past assumptions of population relationships in the area, this study should offer new avenues to be explored in future research. Biological distance is a relatively untapped source of information pertaining to populations in this geographic area, which were among the first to be impacted by European exploration of the New World. Future research should help delineate relationships between groups of populations in this geographic area which is vital to our understanding of interactions between the colonizers and the colonized.

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APPENDICES

Appendix A - Coding Forms and Format

NONMETRIC DENTAL TRAITS (ASU SYSTEM)

locality______________________________
site__________________________________(1-3)
burial________________________________(4-6)
individual____________________________(7-8)
unit__________________________________(9-11)
collection____________________________(12-13)

sex____________(14) criteria_______________________
____
____(15-21)

age__________(22-24) criteria_______________________
____
____(25-31)

age category__________________________________(32)

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32

END CARD 1 | 0 | 1 | 79-80

comments______________________________________
____
____
____

ADULT DENTITION

Left maxilla

14	15	16	17	18	19	20	21
M3	M2	M1	P4	P3	C	I2	I1

Right maxilla

22	23	24	25	26	27	28	29
I1	I2	C	P3	P4	M1	M2	M3

M3	M2	M1	P4	P3	C	I2	I1
30	31	32	33	34	35	36	37

Left mandible

I1	I2	C	P3	P4	M1	M2	M3
38	39	40	41	42	43	44	45

Right mandible

DECIDUOUS DENTITION

Left maxilla

46	47	48	49	50
dM2	dM1	dC	dI2	dI1

Right maxilla

51	52	53	54	55
dI1	dI2	dC	dM1	dM2

dM2	dM1	dC	dI2	dI1
56	57	58	59	60

Left mandible

dI1	dI2	dC	dM1	dM2
61	62	63	64	65

Right mandible

END CARD 2 | 0 | 2 | 79-80

winging	____________		14
shoveling	____________		15-18
curvature	____________		19
double-shoveling	____________		20-21
interruption groove	____________		22-23
tuberculum dentale	____________		24-25
canine mesial ridge	____________		26-27
canine d.a.r.	____________		28-29
metacone	____________		30-33
hypocone M1	____________		34-37
hypocone M2	____________		38-41
cusp 5 (metaconule)	____________		42-45
Carabelli's trait	____________		46-49
parastyle	____________		50
enamel extensions	____________		51-54
premolar root number	____________		55-56
molar root number	____________		57-58
peg-shaped incisor	____________		59-60
peg-shaped molar	____________		61-62
odontome - upper	____________		63-66
odontome - lower	____________		67-70
lower P3 variation	____________		71-72
lower P4 variation	____________		73-74
END CARD 3		0 3	79-80

anterior fovea	________		14-15
groove pattern	________		16-19
cusp number	________		20-23
deflecting wrinkle	________		24-25
distal trigonid crest	________		26-27
protostylid	________		28-31
cusp 5	________		32-35
cusp 6	________		36-39
cusp 7	________		40-43
Canine root number	________		44-45
Tomes' root	________		46-47
first molar root number	________		48-49
second molar root number	________		50-51
torsomolar angle	________		52-53
palatine torus	________		54
mandibular torus	________		55
dental wear	________		56-57
abcessing and periodontal disease	________		58-59
END CARD 4		0 4	79-80

NONMETRIC CRANIAL TRAITS

locality______________________________
site______________________________(1-3)
burial______________________________(4-6)
individual______________________________(7-8)
unit______________________________(9-11)
collection______________________________(12-13)

sex______________(14) criteria______________________________

______________________________(15-21)

age____________(22-24) criteria______________________________

______________________________(25-31)

age category______________________________(32)

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32

END CARD 1 0 1 79-80

highest nuchal line	____________		14-15
ossicle at lambda	____________		16
lambdoid ossicle	____________		17-18
parietal foramen	____________		19-20
bregmatic bone	____________		21
metopism	____________		22
coronal ossicle	____________		23-24
epipteric bone	____________		25-26
fronto-temporal art.	____________		27-28

parietal notch bone			29-30
ossicle at asterion			31-32
auditory torus			33-34
foramen of Huschke			35-36
mastoid foramen exs.			37-38
mastoid foramen abs.			39-40
post. condylar canal pa.			41-42
condylar facet double			43-44
precondylar tubercle			45
ant. condylar canal dbl			46-47
foramen ovale			48-49
foramen spinosum			50-51
accs. palatine foramen			52-53
palatine torus			54
maxillary torus			55-56
zygomatico-facial for.			57-58
supraorbital foramen			59-60
frontal notch or for.			61-62
ant. ethmoid foramen ex.			63-64
post. ethmoid foramen ab.			65-66
accs. infraorbital for.			67-68
cranial deformation			69-70
END CARD 2		0 2	79-80

IDENTIFICATION

The individual identification comprises columns 1-32 of the first card for each form (Card 1). For each subsequent card of each form, the individual identification consists of only columns 1-13. The codes for each component of the individual identification are found on the following pages. The locations for each component are as follows:

Site	1-3
Burial Number	4-6
Individual Number	7-8
Collection	12-13
Sex	14
Sex Criteria	15-21
Age (specific)	22-24
Age Criteria	25-31
Age Category	32

IDENTIFICATION CODES

Site

(214)	Irene Mound
(301)	*Santa Catalina de Guale* - Quad IV, Structure 1 (St. Catherines Island)
(303)	*Santa Catalina de Guale de Santa Maria* (Amelia Island)
(304)	Mission Santa Maria (Amelia Island)
(801)	Baum Site, Burial 1
(802)	Baum Site, Burial 5
(803)	Baum Site, Burial 7
(804)	Piggot Site
(805)	Flynt Site
(900)	Ledford Island

Burial and Individual

The burial number corresponds to the actual burial number assigned in the field (i.e. 1,2,3 etc.). The individual number indicates which individual within the burial. For example Burial 4B would be Burial 4, Individual 2.

Collection

(1)	The American Museum of Natural History
(3)	National Museum of Natural History, Smithsonian Institution
(8)	Purdue University
(9)	Savannah Science Museum
(10)	Garrow and Associates, Inc.
(20)	McClung Museum, University of Tennessee - Knoxville

Sex

(1) Indeterminate
(2) Female
(3) Male

Age

Records the actual number in years (with one decimal place).

Age Category

(1) Infant (0-2)
(2) Child (2.1-12.0)
(3) Adolescent (12.1-16.0)
(4) Adult (16.1-43.0)
(5) Senile Adult (43.1+)
(6) Unknown

Sex Criteria

(1) Phenice (1969)
(2) overall pelvic morphology (sciatic notch, subpubic angle, symphysis orientation, size of obturator foramen and acetabulum, preauricular sulcus, parturition scars) (Bass 1987)
(3) gracile skull (small mastoids, supraorbitals, nuchal area) (Bass 1987)
(4) gracile mandible (Bass 1987)
(5) gracile postcranial (small skeletal elements, reduced size of muscle markings) (Bass 1987)
(6) robust skull (large mastoids, supraorbitals, nuchal area) (Bass 1987)
(7) robust mandible (Bass 1987)
(8) robust postcranial (large skeletal elements, markedly roughened areas of muscle attachment) (Bass 1987)

Age Criteria

(1) epiphyseal union (Krogman and Iscan 1986)
(2) dental calcification and eruption (Ubelaker 1984)
(3) general thickness of cortical bone and overall size of skeletal elements
(4) tooth wear -- functional age (Choi 1986, Miles 1963, Russell and Choi 1987)
(5) pubic symphyseal face metamorphosis (Todd 1920, Meindl et al. 1985)
(6) ossified spheno-occipital synchrondrosis (Bass 1987)
(7) auricular surface (Lovejoy et al. 1985)

DENTITION CODING FORMAT

This is a 1 (one) character format, each character corresponding to one of the deciduous or permanent teeth. If there is no information on a tooth (ie. maxilla or mandible is missing or partially missing), the space should be left blank indicating 'missing data'. For both deciduous and permanent dentitions:

0 = absent antemortem
1 = present

2 = absent postmortem
3 = present but not articulated
4 = tooth missing, alveolus not fully resorbed
5 = present but unerupted
6 = not erupted (no information on presence)
8 = crown destroyed by caries
9 = congenital absence

Example:
The following dentition was recorded for SCI-SCDG Individual 71.

Mandibular Left I2,C,PM3,PM4,M1,M2
Mandibular Right I2,PM4,M1,M2
Maxillary Left I1,C,PM3,M1
Mandibular Right PM3

This has been properly encoded on the following page.

Note:
Because this individual is an adult, it is assumed that the deciduous dentition erupted properly and the teeth were lost antemortem. Therefore, '0's were recorded for the deciduous dentition, not blanks (which would indicate missing data).

ADULT DENTITION

Left maxilla

/	/	1	/	1	1	/	1
M3	M2	M1	P4	P3	C	I2	I1

Right maxilla

/	/	/	1	/	/	/	/
I1	I2	C	P3	P4	M1	M2	M3

M3	M2	M1	P4	P3	C	I2	I1
/	1	1	1	1	1	1	/

Left mandible

I1	I2	C	P3	P4	M1	M2	M3
/	1	/	/	1	1	1	/

Right mandible

DECIDUOUS DENTITION

Left maxilla

46	47	48	49	50
0	0	0	0	0
dM2	dM1	dC	dI2	dI1

Right maxilla

51	52	53	54	55
0	0	0	0	0
dI1	dI2	dC	dM1	dM2

dM2	dM1	dC	dI2	dI1
0	0	0	0	0
56	57	58	59	60

Left mandible

dI1	dI2	dC	dM1	dM2
0	0	0	0	0
61	62	63	64	65

Right mandible

END CARD 2 | 0 | 2 | 79-80

Appendix B - Discrete Dental Trait Observations

```
21440201---033-------300-------4----------------------------------------------01
21440201---0311111111111111111111111121111----00000000000000000000-------------02
21440201---03322750330200----353540403535--------00022----0000--------0-0-----03
21440201---03--------------------------------------0-105500-------------------04
21440301---033-------200-------4----------------------------------------------01
21440301---03---1111111111111111111111111111100000000000000000000-------------02
21440301---03322330220000------35--50--40-0-0-2-00-0-0----00-0000000000002----03
21440301---034411115655--001111555500000200--------00103300-------------------04
21440401---031-------050-------24040004400-4-1-5-0-1-1-5-0-022----------------01
21440401---0363-33333-33333-6661666666666336333333333332133333313-------------02
21440401---03-3-4404-0000----------4020---00--00---2------00--0000------------03
21440401---034411-355-5330011-155-300-000-0-----------0-100-------------------04
21440501---032-------200-------4----------------------------------------------01
21440501---03--------12222111121112222211111100000000000000000000-------------02
21440501---033-2--0-4----------35--40--20-3-4-0-00-2-2-------0----00000000----03
21440501---034411-366-6--1111-144-422-200-0--------11103300-------------------04
21440601---033-------300-------4----------------------------------------------01
21440601---032011112322101031--------2221111100000000000000000000-------------02
21440601---03-2---02-----------3050----------0---02----------00-0--0-0-0-0----03
21440601---03---1-3-5-5-----1-1-4-4-0-0-0-0---------0105550-------------------04
21440801---033-------200-------4----------------------------------------------01
21440801---031111112111110111112211211111111100000000000000000000-------------02
21440801---033-4550-433------303050--35350-00000002-22----00000000-0-0-0-0----03
21440801---034411336666----2222444433330000--------00103300-------------------04
21440901---032-------150-------3----------------------------------------------01
21440901---031111221111111111111111121111111100000000000000000000-------------02
21440901---03333-3044-0------4040404035355555000000000-----00000-000000000----03
21440901---034411335555----2222555500000000--------00103300-------------------04
21441301---031-------020-------140--0-3-0-44116622001133440011----------------01
21441301---03-----------------------------------------------------------------02
21441301---03-----------------------------------------------------------------03
21441301---03-----------------------------------------------------------------04
21441601---033-------250-------4----------------------------------------------01
21441601---03-33113111111111-----------------00000000000000000000-------------02
21441601---03444550552000--------5050404000000000-1122----00------------------03
21441601---03----------------------------------------0-4-0--------------------04
21441701---032-------250-------4----------------------------------------------01
21441701---0321---------22111---------121111100000000000000000000-------------02
21441701---03------------------20--404040-000-0000-022-------0-----0-0-0-0----03
21441701---03---1-3-5-5-----1-1-4-4-0-0-0-0---------0104400-------------------04
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21441801---03--11--55------22--55--00--00------------103300-------------------04
21442101---032-------190-------4----------------------------------------------01
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21442101---031--5----1---------355050----00--22--022------0--00--000000000----03
21442101---034411335555----0000554400000000--------00203332-------------------04
21442201---032-------230-------4----------------------------------------------01
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21442201---0332233055-2--------35--403535-000-0000-222-----0-0000000000000----03
21442201---03--11335555----1111554400000000--------00104410-------------------04
21442301---031-------130-------3----------------------------------------------01
21442301---0333-33333------3-632221222211222600000000000000000000-------------02
21442301---03-1-2-03---------4-------3030--00--000--11----0-0-0-0-00--00------03
21442301---03----3---5-------1---0---0---2------------02200-------------------04
21442501---032-------190-------4----------------------------------------------01
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21442501---03---5----2-------35--40--35--0-5-4-3-02-2-----0-0-000000000000----03
```

```
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21442701---03-3---0----------3035505040400000330002222------00----------------03
21442701---034-1-116-55--0-22224-443-000000------------33---------------------04
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21443001---03113333333--33---111111222222211100000000000000000000-------------02
21443001---03-223-0330-0-----30--50--35--2-0-4-0-02-2-----0-0-00000-0-0-0-----03
21443001---03441133555500002222554400000000--------11-033-0-------------------04
21443101---031-------050-------2--40-0-4-044115522000055000022----------------01
21443101---036626666363666166665666666666656600000000000000000000-------------02
21443101---03-33330332222----------4035---00--42----------00------------------03
21443101---0344113-555-220022--444-000-000-----------001100-------------------04
21443102---031-------050-------24040004400------------------22----------------01
21443102---036336663363666156-------------3--1222222221-----------------------02
21443102---03-33330332222--------4040--3500-044-----------00------------------03
21443102---03-4-1---5---2-0-2---5---0---0------------1-110--------------------04
21443103---031-------250-------4----------------------------------------------01
21443103---03--------22222111---------------------00000-----------------------02
21443103---03------------------35--50--40-0-0-4-00-0-0-------0----------------03
21443103---03------------------------------------------3-0--------------------04
21443401---031-------030-------2--40-0-4-0-0-1-5-0-0-2-5-0-0-2----------------01
21443401---03--3--3--3-3--3---------------3-----------3---------3-------------02
21443401---03--4--0-3------------4040----22-----------------------------------03
21443401---03-4-1---5---2-0-1---5---0---0--------------11---------------------04
21443701---033-------200-------4----------------------------------------------01
21443701---032111111212111111111111222221111000000000000000000000-------------02
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21443701---034411336544--000011440000002000--------00103300-------------------04
21443801---032-------290-------4----------------------------------------------01
21443801---03-111111---33333-----------111-1100000000000000000000-------------02
21443801---03---5----0-0---------50504040---------0022----0---0000-0-0-0-0----03
21443801---03------------------------------------------5500-------------------04
21444001---032-------190-------4----------------------------------------------01
21444001---032111121111111111111112121111111900000000000000000000-------------02
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21444001---034411335555----1111554400000000--------0-003300-------------------04
21444202---031-------080-------2--50-0-1-1---1-5-----1-5-0-044----------------01
21444202---03-3--3--------3---33-3------3333----------3-3------33-------------02
21444202---03----------------------4035---10--40---10----------0--00-000-0----03
21444202---034411335665--111111554400200200------------22---------------------04
21444801---032-------250-------4----------------------------------------------01
21444801---03-33--333-33----3-------33-------00000000000000000000-------------02
21444801---03-3-3303-0000------3550--50--0-0-0-0-0--------00-0----------------03
21444801---03------------------------------------------44---------------------04
21445201---032-------250-------4----------------------------------------------01
21445201---031111112122111111111211122112112100000000000000000000-------------02
21445201---0332---04---------3030505040000000000000022------00000000--00------03
21445201---03--113-555-----222-555-000-000---------00104400-------------------04
21445301---033-------250-------4----------------------------------------------01
21445301---032111211211111112221111121111111100000000000000000000-------------02
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21445801---033-------250-------4----------------------------------------------01
21445801---03-------33---------3--------1110100000000000000000000-------------02
21445801---03333--055---------------------------------------------------------03
21445801---034411--66------22--33--33--00--------------44-0-------------------04
21446001---033-------160-------4----------------------------------------------01
21446001---032111111222112111--3-------------00000000000000000000-------------02
21446001---03---4----0-0-------00404020200000220000022----0--20000------------03
21446001---033-3---4---0-0-1---0---0---0-------------1-220--------------------04
21446101---032-------250-------4----------------------------------------------01
21446101---031111113333333333111111222321111100000000000000000000-------------02
21446101---03-33660440000----353540403535000022000002211330000000000000000----03
```

```
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21446601---031-------040-------2505000330044116611001133110022----------------01
21446601---036636666636666366663666666666636611222222111122222211-------------02
21446601---03--3--0-4------------5050----00--55-------------------------------03
21446601---034411--55--110022--55--00--00------------101100-------------------04
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30111400---01--1-2-5-5---------5-4-0-0-0-0-------------44---------------------04
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30115000---01------------------------------------------4----------------------04
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30122800---01----33-------------------------------------4---------------------04
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30123000---01------------------3----------33-00000000000000000000-------------02
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30123300---01------------------------------------------3----------------------04
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30124200---011000000034000040004----------------------------------------------01
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30127100---01--11--55----------44--00--00---------------55---------------------04
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30127200---01----------------333333---------3000000000000000000000-------------02
30127200---01------------------------------------------------------------------03
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30128300---01-2-2302-0000-------40------0---0------------00----------0------03
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30128900---01-3333----------------------------------------------------------02
30128900---01-------------------40--30--0-0-2-0--------------0-0------------03
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30129100---01----3------------------------------------44--------------------04
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30129200---01---------------------------33330000000000000000000-------------02
30129200---01---------------------------------------------------------------03
30129200---01---3-3-5----------5---0---0---------------5--------------------04
30129300---011000000007002000002--------------------------------------------01
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30129300---01----2----1--0022----4040353500001300---------0--00000003300----03
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30130400---01-----------------------------------------------------------------03
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30130500---01333333--------3333333-------333300000000000000000000-------------02
30130500---01--------------3-404050--35350-000-000----------110-0-0-000-00----03
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30130600---01-33333333333333--33-333---33333-3-------33-----------------------02
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30130800---01-------------------33-3-3--333--00000000000000000000-------------02
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30131100---01------------------333-------33--00000000000000000000-------------02
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30131100---01--33--66----------33--44--00---------------3---------------------04
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30131300---01---------------2--30------35---0---00-----------00--0---0---2----03
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30131500---01-----3-------------------------------------4---------------------04
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30133000---01-------------0-3------50--40-0-0-1-0-----------------------------03
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30134800---01------------------------------------------11---------------------04
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30134900---01-----------------------------------------------------------------03
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30135700---01----------------33-------------300000000000000000000-------------02
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30135700---01--------5----------------------------------4---------------------04
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30136000---01-------------------------------------------7---------------------04
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30136300---01------------------------------------------2----------------------04
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30136400---01------------------------------------------4----------------------04
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30136500---01------------3-33----------------00000000000000000000-------------02
30136500---01------------------35------35-------------------------------------03
30136500---01------------------------------------------4----------------------04
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30136600---01---------3---3---------------------------3-----------------------02
30136600---01----1-----------------50-----------------------------------------03
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30136600---01-------------------------------------------1---------------------04
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30136700---01------------------------------------------4----------------------04
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30136800---01------------------3-------------------------3--------------------02
30136800---01-----------------------------------------------------------------03
30136800---014-3---6---2-0-----4---1---0----------------1---------------------04
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30136900---01-----------333-3----------------00000000000000000000-------------02
30136900---01------------------40--40-----1------0-----------0-0-0------------03
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30408101---08-----1---5-------0---4---0---0----------003202-------------------04
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30408201---08331111665500000011334433000000----------002200-------------------04
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30408501---08-----------------------------------------------------------------03
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30408901---08-----------------------------------------011-0-------------------04
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30409601---08--------------------------------00000000000000000000-------------02
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30409601---08-----------------------------------------------------------------04
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30410401---08----------------------------------------105744-------------------04
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30411001---08--------------------4040----00--00---22-----------0--------------03
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80100141---202-------250-------4----------------------------------------------01
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80100141---20----------------4040505050000000000001133-----0000000------------03
80100141---20----------------------------------------0-4-0--------------------04
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80100147---201111111111111111111111121111111100000000000000000000-------------02
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80100156---201111112222211111011111111111111100000000000000000000-------------02
80100156---20----------------3535505040352100110000000------00000000000000----03
80100156---203311335544----0000440000000000---------0102200-------------------04
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80100501---203333336666----0000444433330000--------00104400-------------------04
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80400113---20----------------6566666666666656----------1122222211-------------02
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80400121---20------------------------------------------6-0--------------------04
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80400131---203311115555----1111554400000000----------101100-------------------04
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80400143---20------------------35353530--110-000-0-----------0----------------03
80400143---20331133555500000004422000000000----------101100-------------------04
80400146---203-------350-------4----------------------------------------------01
80400146---201111221222221111----------------0000000000-----------------------02
80400146---20---1----1-0-----5050505050402233110000000----0-00--00------------03
80400146---20----------------------------------------1-4-0--------------------04
80400151---203-------200-------4----------------------------------------------01
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80400151---20---4----3-------404040--35--2-0-----0--------0-000-0-------------03
80400151---20-3-1-3-5-5-0-0-0-0-5-5-0-0-0-0----------102200-------------------04
80400161---202-------160-------3----------------------------------------------01
80400161---20----------------1111111111------00000000000000000000-------------02
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80400161---203-1-3-6-6-----1-0-5-4-2-4-0-0------------0-1-0-------------------04
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90000201---21-----------------------------------------------------------------03
90000201---21-----------------------------------------------------------------04
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90000401---210----0-3-2------4040404030300000110000000----0000000000002322----03
90000401---21441133------111111--------------------00104300-------------------04
90000501---212-------250-------4----------------------------------------------01
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90000501---21-4-4-03-1-0-------30------40---0---00---2----0--0-----000-400----03
90000501---214411335555----1111442200000000--------00-12200-------------------04
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90000601---21--366633336666--6636666666666366313333333-1233333331-------------02
90000601---21-55-4044--------------40-----2---3-----------00------------------03
90000601---213333--66--220000--44--33--00--------------0000-------------------04
90000701---213-------150-------3----------------------------------------------01
90000701---219111122333211119911222222222211900000000000000000000-------------02
90000701---21-33-4033-1-0--------4040404022002200-000011---0--0000------------03
90000701---213311315555----1111555500000000--------00002200-------------------04
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90001201---21--166611216661----16661111666156111000011-1110000211-------------02
90001201---21-4-3306-1111--------4040----22--22---02------00------------------03
90001201---214411-255-5000000-044-200-000-0----------101100-------------------04
90001302---211-------030-------240--0-2---4-1-6-2-0-0-3-4-0-1-----------------01
90001302---21-----------------------------------------------------------------02
90001302---21--------------------40------0---2--------------------------------03
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90001401---213-------250-------4----------------------------------------------01
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90001401---2102-3303-1100----40--505040401000220000011----000-000000000000----03
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90001601---21-----------------------------------------------------------------03
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90001701---21-----------------------------------------------------------------03
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90002501---21-----------------------------------------------------------------04
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90002701---21--------------------4040----00--44-------------------------------03
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90002901---21-----------------------------------------------------------------03
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90003401---21--1--35--5----1--15--50--00--0--------11002215-------------------04
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90003601---21--------------------4040----11--12-------------------------------03
90003601---213333-355-5000011-155-300-000-0------------11---------------------04
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90004201---214411335565--110000553300440000----------101100-------------------04
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90006601---216111111111111111661111111111211160000000000000000000-------------02
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90008001---21-----------------------------------------------------------------03
90008001---21-----------------------------------------------------------------04
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90008301---21-----------------------------------------------------------------03
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90009001---21-4---05---------------40-----1---3----0--------------------------03
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90009301---21-----------------------------------------------------------------03
90009301---21-----------------------------------------------------------------04
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90010101---211-------030-------240401155--44115511001155000011----------------01
90010101---21--3----333---3--66566333333--3--33333333111333333333-------------02
90010101---21-5533066------------4040----22--77------------0------------------03
90010101---214411--55--110011--55--00--00-------------01100-------------------04
90010201---213-------180-------4----------------------------------------------01
90010201---211111111111111111111111111111111100000000000000000000-------------02
90010201---21033330443111----303040403535112233000002222330000000000003322----03
90010201---21441133666622001111444422220000--------00201100-------------------04
90010301---211-------005-------1----------4-1-5-0-0-1-5-0-0-11----------------01
90010301---21-----------------------------------------------------------------02
90010301---21-----------------------------------------------------------------03
90010301---21-----------------------------------------------------------------04
90010401---212-------250-------4----------------------------------------------01
90010401---210000011111112213333011122211100000000000000000000000-------------02
90010401---21044440330000----3535--40--40-1-1-3--0-0-2-1-100-0----------------03
90010401---21----------------------------------------203355-------------------04
90010501---211-------005-------1----------44116622111144110011----------------01
90010501---21-----------------------------------------------------------------02
90010501---21-----------------------------------------------------------------03
90010501---21-----------------------------------------------------------------04
90010601---213-------130-------3----------------------------------------------01
90010601---216111111111111116611111111111111600000000000000000000-------------02
90010601---211224403300000000----5050353500002200-1100----00--000000002211----03
90010601---214411336655--001171334444000000----------101100-------------------04
90010701---212-------250-------4----------------------------------------------01
90010701---211---------1--111----22222212111100000000000000000000-------------02
90010701---21----------------3030--40--40-0-0-4-00-0-1-2-3--00----------------03
90010701---214411225555----1111444400000000---------0203300-------------------04
90011401---212-------250-------4----------------------------------------------01
90011401---211111111111111111811111111111111010000000000000000000-------------02
90011401---21122220330000----404040403535000044000002211330000000000000000----03
90011401---214411--555---00111-554-000-000---------00202303-------------------04
90011501---212-------350-------4----------------------------------------------01
90011501---211100111111111100001111111111100000000000000000000000-------------02
90011501---21022220220100----35----4035---00--00-0-00-----000-00-000000000----03
90011501---214-3---5-----0-1---4---0---0-------------105455-------------------04
90011801---213-------130-------3----------------------------------------------01
90011801---212211111121111115511111222111111500000000000000000000-------------02
90011801---2103-3304-0022------304040--4011-022-0022-0----00-0000000002222----03
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90011801---214411336666--000000332244330000----------102200-------------------04
90012101---213-------200-------4----------------------------------------------01
90012101---2111111111111221111111111111111111110000000000000000000000-------------02
90012101---210222-0330-0-----353550404035220022000111111330-00000000000000----03
90012101---214411226655----1111334433000000--------00002200-------------------04
90012301---213-------250-------4----------------------------------------------01
90012301---2111111112-------3111222222222011100000000000000000000-------------02
90012301---21---3----0-0-----404050--40--1-1-4-0-00-1-1-3-0-000-0-------------03
90012301---21441133666622002222444433220000--------00103301-------------------04
90012601---213-------350-------4----------------------------------------------01
90012601---2181111111111111--101122222211088100000000000000000000-------------02
90012601---21033330550000--------404035-----------002-113-00------------------03
90012601---21--------------------------------------00206655-------------------04
90012701---212-------250-------4----------------------------------------------01
90012701---2111111333331113333333333-3-33111130000000000000000000-------------02
90012701---21-22441003300----353540403030000044002220011110000000000000022----03
90012701---214411115555----111155550000000011--221100-04400-------------------04
90013001---213-------200-------4----------------------------------------------01
90013001---21118111111111111111111111112111110000000000000000000000-------------02
90013001---211443304400------3535--403035-100-40002222----0000000000002200----03
90013001---214411335555----1111554400000000--------00203300-------------------04
90013101---213-------200-------4----------------------------------------------01
90013101---21-11111212211111-111111111211201100000000000000000000-------------02
90013101---2113---03-------------4040353533113300-0000------0000000000001-----03
90013101---214-1-336-552-0-1-113-444-000-00--------11203303-------------------04
90013201---212-------250-------4----------------------------------------------01
90013201---212111113333333-33111333332211110100000000000000000000-------------02
90013201---21044440550100------3540--40400-000-0000-22112200-0000000002200----03
90013201---2144113-555-2211111-555-000-000---------00104403-------------------04
90013501---212-------300-------4----------------------------------------------01
90013501---212110000000101111000003000010000000000000000000000000-------------02
90013501---21------------------40--40--40-2-1-4-00-1-1-------0----------------03
90013501---21----------------------------------------004555-------------------04
90013601---212-------300-------4----------------------------------------------01
90013601---21--------11111019001111122111011000000000000000000000-------------02
90013601---210-4-40-6-0-0--------------40---0---0----------0---0-000000000----03
90013601---214-1--35--50-0-1--14--40--00--0---------0105435-------------------04
90013801---211-------050-------23030003400441155--110044000022----------------01
90013801---216656663366666566665666666666656611111111111111111111-------------02
90013801---21-3-4-04-2-0---------3030----00--33---00------0-------------------03
90013801---214411--66--220022--33--22--00------------101100-------------------04
90013901---211-------040-------2404011000033115500112244000022----------------01
90013901---21-33666333666633-633666666666663361111111111111111111-------------02
90013901---21-445-0440-0---------4040303011003300-02------0-------------------03
90013901---2133113-5-5-2200222-444-000-000-----------101100-------------------04
90014101---212-------250-------4----------------------------------------------01
90014101---219211111111111119211111111111210100000000000000000000-------------02
90014101---21122220330000--------4040--3000-000-0-00-0----00--0000000-110-----03
90014101---214-----5-------1---4---0---0-------------204403-------------------04
90014201---212-------250-------4----------------------------------------------01
90014201---219112220000000119111133333331111100000000000000000000-------------02
90014201---21--------------------4040404000000000-0000-------------000-000----03
90014201---214411335555----1111444400000000--------01104430-------------------04
90014401---211-------010-------1-----------4-1-6-2-1-2-3-3-0-1----------------01
90014401---21-----------------------------------------------------------------02
90014401---21-----------------------------------------------------------------03
90014401---21-4-1---5---1-1-2---4---0---0---------------1---------------------04
90014501---211-------030-------240401133--44117722002233440011----------------01
90014501---216636663333666366663666666666636611111111111122222211-------------02
90014501---21-3333044------------5050----33--44-----------00------------------03
90014501---214411--66--220022--34--43--00------------101100-------------------04
90014701---21--------180-------4----------------------------------------------01
90014701---211111111111111111112111111111111100000000000000000000-------------02
90014701---21122220443300----353540403535000055330000011330000000000000011----03
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90014701---21-3-133-555-2-0-110-533-000-00011---22200102200-------------------04
90015201---211-------070-------24040113300-4-1-5-3-1-2-5-0-033----------------01
90015201---21--33---3---------33-----666661--32222222232222222211-------------02
90015201---21-3---04-------------40------1---3----0---------------------------03
90015201---2144333-555-3311222-555-000-000------------022-0-------------------04
90015601---211-------040-------2404011330033116622002244220022----------------01
90015601---216656666366666566665666666666665661111111111122222211-------------02
90015601---21-3---01-------------4040----11--33---22--------------------------03
90015601---213311--66--110022--44--22--00------------101100-------------------04
90015701---211-------010-------140--0-0---------------------1-----------------01
90015701---21-----------------------------------------------------------------02
90015701---21--------------------40------0---4--------------------------------03
90015701---21------------------------------------------1----------------------04
90015801---213-------220-------4----------------------------------------------01
90015801---219812111111121189910111111111101900000000000000000000-------------02
90015801---21144740440300--------4040353500005000-0000----10--0---00000000----03
90015801---21----33--55------11--33--00--00----------202203-------------------04
90016201---211-------080-------240400033--441155----0044000044----------------01
90016201---21-515553--355515--33555------51--30000000033000000003-------------02
90016201---21---22---0000--------4040353511004400-2200----00--000000000011----03
90016201---2133113-555-0000020-333-000-000-----------001100-------------------04
90016301---213-------180-------4----------------------------------------------01
90016301---2151111112-33333335111111111111115000000000000000000000-------------02
90016301---21---44---0000----203540403030110022110000011110000000000000000----03
90016301---2144113366662200111133333333000011--221100-02200-------------------04
90016601---211-------030-------2404000000044116622110022440011----------------01
90016601---216636663333666366665666666666665661111111111111111111-------------02
90016601---21-4433055------------4040----00--00-----------00------------------03
90016601---214411--66--220000--22--44--00------------101100-------------------04
90016801---211-------030-------240--0-3---4-1-6-2-0-0-3-2-0-33----------------01
90016801---21-----------------------------------------------------------------02
90016801---21--------------------4040----00--33-------------------------------03
90016801---21-4-1---6---2-0-2---3---2---0--------------11---------------------04
90017101---213-------200-------4----------------------------------------------01
90017101---21-----33333333333---3333333333---00000000000000000000-------------02
90017101---21-33330110000------40--40--30-2-0-0-00-0-211-300-0-0-000002211----03
90017101---21------------------------------------------33---------------------04
90018001---211-------090-------2404011000044115522--1155000033----------------01
90018001---216616632233366166651666111166615611000000111100000011-------------02
90018001---21--2-10-5-3-0--------3535----11--00---11-------0------------------03
90018001---21441111555522111111553300000000----------101100-------------------04
90018101---211-------050-------2353500120044116622112233330022----------------01
90018101---21--3--3-3-333-3---3333--------33-3--------333------33-------------02
90018101---21-5--402-------------4040----11--22---00-------0------0-0-0-1-----03
90018101---21441133666622112222333333330000------------11---------------------04
90018701---213-------200-------4----------------------------------------------01
90018701---21-----3333-333333110123112333-38-00000000000000000000-------------02
90018701---21-222-0440-0-------405050--4022-032-00-0-011-30--0-0-0-0-0-0-0----03
90018701---21---12--55------22--55--00--00---------0--033-3-------------------04
90019001---211-------020-------140401144---------------------1----------------01
90019001---21-----------------------------------------------------------------02
90019001---21-33--044------------4040----33--55-------------------------------03
90019001---21----------------------------------------1------------------------04
90019101---211-------040-------2404022220044115522002255000022----------------01
90019101---21--3--333333--3----3---3333---3--333333333333------33-------------02
90019101---21-3344033------------4040----22--33-----------00------------------03
90019101---214411--55--220022--55--00--00--------------11---------------------04
90019801---211-------015-------140--1-2---44115522001155000011----------------01
90019801---21-----------------------------------------------------------------02
90019801---21--------------------4040----22-----------------------------------03
90019801---214411--55--220011--55--00--00--------------11---------------------04
90020001---213-------250-------4----------------------------------------------01
90020001---213113333333333333----------------00000000000000000000-------------02
90020001---21-44440220000----303040403030--------0-2--12-200000000------------03
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90020001---21------------------------------------------44---------------------04
90020201---213-------300-------4----------------------------------------------01
90020201---210011112122111110111111122111101100000000000000000000-------------02
90020201---21-4---04-------------4040--30-2--------2-1--------000000000000----03
90020201---21--------------------------------------00105533-------------------04
90020601---211-------090-------2----------------------------------------------01
90020601---21--3--3333333-3---33333-333---3-----------------------------------02
90020601---21-33440333344--------4040----11--33---22------00---0--0-0-0-0-----03
90020601---214411-366-6--1111-133-344-400-0------------22---------------------04
90023401---211-------040-------2--40-1-4-044115522111155000022----------------01
90023401---21--3----------3--6656666666666566-3333333331122222211-------------02
90023401---21--------------------4040----11--44---00--------------------------03
90023401---2144113-555-2200111-555-000-000------------011-0-------------------04
90025401---211-------030-------2--40-1-3-044115522111155000022----------------01
90025401---21------333----3----3----------3----3-3-33-333------33-------------02
90025401---21-222-033--------------50-----1---3-----------0-------------------03
90025401---214411--66--220011--44--22--00--------------11---------------------04
90030601---213-------250-------4----------------------------------------------01
90030601---211111111121111111111111111111118100000000000000000000-------------02
90030601---2102-3304-3030----3535404030301100220002022----0000000000000000----03
90030601---2144333-555---00111-555-000-000---------00104400-------------------04
90034601---212-------200-------4----------------------------------------------01
90034601---211811111111111111111111111111118100000000000000000000-------------02
90034601---21033440550022----40404040--3522-0440001111----0000000000001100----03
90034601---2133113366----0022--33--44--00----------11103333-------------------04
90034701---211-------080-------2404022330044116633001133330033----------------01
90034701---21-3333333--33-33--3366663333361563-3----3-31322222231-------------02
90034701---21-5-4-05-0-3---------4040403511112200-00------0---000--0---3------03
90034701---2144113-666-3300111-333-333-000------------022-0-------------------04
90035601---211-------080-------2404011220044115522001155000033----------------01
90035601---216316663323666136--3666522566613611000000011110000011-------------02
90035601---21-3-4404-1122--------4040303011000000-0000----00------------------03
90035601---214411-355-6220011-155-400-200-0----------102200-------------------04
90035701---211-------080-------2404000000044115511001144000033----------------01
90035701---216316663333666136651666333366615611300003111130000311-------------02
90035701---21-33220331122--------4040353500000000-0000----00------------------03
90035701---21441133555511001111444400000000----------102200-------------------04
90035901---213-------250-------4----------------------------------------------01
90035901---211111111111111111111111111111111100000000000000000000-------------02
90035901---21022330440020----4040505040402200550002222----0000000000003311----03
90035901---214411335555----1111554400000000--------00104400-------------------04
90041501---211-------070-------2404011220044115522001155000022----------------01
90041501---216616665115666166651666111166615611100001111100000011-------------02
90041501---210333-0550-2---------4040----11--24---00------0-------------------03
90041501---21441133555522001111554400000000----------101100-------------------04
90041901---211-------030-------2404011440044115511002255000011----------------01
90041901---21--3---333----3--665666666666656633---3--331132222311-------------02
90041901---21-443-055------------4040----11--44---00------0-------------------03
90041901---214411--55--110022--44--00--00-------------011-0-------------------04
90042301---211-------090-------240401133004-1-6-----1-3-0-0-33----------------01
90042301---216516661111666156651666111100015611000000111110000000-------------02
90042301---21444330551122--------4040303022003300-0000----00------------------03
90042301---21441133665522001111333333000000----------101104-------------------04
90042401---213-------250-------4----------------------------------------------01
90042401---211111111111111111111111111111111100000000000000000000-------------02
90042401---21333330440000----4035404030300000440000000----0000000000001100----03
90042401---21441133555522002222444400000000--------00204400-------------------04
```

Appendix C - Discrete Cranial Trait Observations

```
21440501---032-------200-------4-----------------------------------------------01
21440501---0311000110000--------0000-----------------11-0---0-1------00--------02
21440601---033-------300-------4-----------------------------------------------01
21440601---0311111000000000000011000011000000000000001111100011----0000--------02
21440801---033-------200-------4-----------------------------------------------01
21440801---031111-0-000-----0-0-0-0-0-0-1100000-----111001-0-0-----0-10--------02
21440901---032-------150-------3-----------------------------------------------01
21440901---0300000000000-----01100000000110000000000001000-1-1-----0010--------02
21441001---032-------400-------4-----------------------------------------------01
21441001---03000000000000000000000000000--------000011200110000----0000--------02
21441201---032-------300-------4-----------------------------------------------01
21441201---0311000100000----000000000100-0-0--0-0-1-0----1-----------00--------02
21441601---033-------250-------4-----------------------------------------------01
21441601---031101--1-0------00000000------------------000110011------00--------02
21442101---032-------190-------4-----------------------------------------------01
21442101---0311011110000-----0-100-1----0000000-------2001-0010------00--------02
21442201---032-------230-------4-----------------------------------------------01
21442201---0311111110000--------0011----000001000---00100110011----0010--------02
21442201---033-------410-------4-----------------------------------------------01
21442201---03000110000000000000000001100000000000----1110011001100000110--------02
21442201---033-------200-------4-----------------------------------------------01
21442201---0311011000000000000000000110000000000000011100110011----0000--------02
21444301---032-------350-------4-----------------------------------------------01
21444301---0311000000000000000110000-0-01100000-----------10011------00--------02
21444001---032-------190-------4-----------------------------------------------01
21444001---030000100000000000000000000-0--------000011000000011----0000--------02
21445201---032-------250-------4-----------------------------------------------01
21445201---03000110000000000001100001100--------000011100010011----0000--------02
21445301---033-------250-------4-----------------------------------------------01
21445301---0311011000000----000000001100--0-00-0011--2001------------00--------02
21445501---032-------300-------4-----------------------------------------------01
21445501---03111000000000000110000001100--00000------0--00-0010----0010--------02
21446001---033-------160-------4-----------------------------------------------01
21446001---0311111000000----0-0-00001100--00000----00100-------------10--------02
21446201---032-------350-------4-----------------------------------------------01
21446001---031100111000001000000001100001100-00-----------10011-----110--------02
21446701---032-------300-------4-----------------------------------------------01
21446701---030000010000000000001111001011000000000----100110010----0000--------02
21447301---033-------300-------4-----------------------------------------------01
21447301---03000001100000000000000110000000000000010--200000011------00--------02
21447401---032-------400-------4-----------------------------------------------01
21447401---03110000000000000000000001100--00000------------0011------00--------02
21448401---032-------150-------3-----------------------------------------------01
21448401---0311100010000000000110000-----------------11-0-10001-----000--------02
21448901---033-------250-------4-----------------------------------------------01
21448901---0311000110000000000001100011000100000000111200110011----0000--------02
21449501---033-------250-------4-----------------------------------------------01
21449501---03111110000000000001100001000-------------------00--------10--------02
21449601---032-------200-------4-----------------------------------------------01
21449601---030001101000000000100011110010000000000011100000110011000010--------02
21449701---032-------350-------4-----------------------------------------------01
21449701---0311111000000-0-011010000110001000110000112000000000----0000--------02
21449801---032-------300-------4-----------------------------------------------01
21449801---031100000000000000000000000011--00000000000020011010011000000--------02
21449901---033-------400-------4-----------------------------------------------01
21449901---0311000000000--------00001100010000000000--20000001111000000--------02
21450101---032-------250-------4-----------------------------------------------01
21450101---0311000000000000000000000-------00001-0-1--100110000------10--------02
21450201---032-------200-------4-----------------------------------------------01
21450201---03111111000000000000000-1----0000000-------100--0011------00--------02
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21450401---033-------250-------4----------------------------------------------01
21450401---031100010000000000000----110000000110-----200110101----0010--------02
21450601---032-------300-------4----------------------------------------------01
21450601---030000011001110000011000000000000010001111100000000----0000--------02
21450801---033-------250-------4----------------------------------------------01
21450801---0311011000000000000--00001100-------0000-1200000111----0000--------02
21451501---032-------400-------4----------------------------------------------01
21451501---0311011010011000000000000010001000000---11-00-10000----0000--------02
21451601---032-------350-------4----------------------------------------------01
21451601---0300001000000-0-00000001000111000000000100100--00-1-----000--------02
21451701---033-------350-------4----------------------------------------------01
21451701---0300111000000-1-0-0-0-0-0-0-1--------0-011100010011-0-0-000--------02
21452001---033-------300-------4----------------------------------------------01
21452001---03000000000000000000000101100-------0-0-00200000011------00--------02
21452301---032-------350-------4----------------------------------------------01
21452301---03111111100100000111100110000-----------------00000------00--------02
21452901---032-------350-------4----------------------------------------------01
21452901---031101100000000000000000000001000000000000200110100----0000--------02
21453201---032-------300-------4----------------------------------------------01
21453201---0311101000000000000000100100010000000-0-1-100110011----0000--------02
21453301---033-------200-------4----------------------------------------------01
21453301---031110000000001000100000010011000010000011200010111----0000--------02
21453401---032-------400-------4----------------------------------------------01
21453401---03110001100000000000000000000-1-00-0-0-0-0100-01110-----000--------02
21453601---032-------200-------4----------------------------------------------01
21453601---0311011000000-0-0-0-00000-1-0-------0000-12001100-0----0000--------02
21453801---032-------200-------4----------------------------------------------01
21453801---0311000---0----------00001-0-0-00010----11100110011----1100--------02
21454001---032-------200-------4----------------------------------------------01
21454001---03111110100001100001100000100000000000100110011-000----0010--------02
21454201---033-------200-------4----------------------------------------------01
21454201---0311011000000000000--00001100--000000011-1211000001----0010--------02
21454201---032-------250-------4----------------------------------------------01
21454201---0311001-----------1000011110001000000000111000-10-0----0000--------02
21455001---032-------200-------4----------------------------------------------01
21455001---0300110110000----000000000011000000000-0-----00010-------00--------02
21455201---033-------200-------4----------------------------------------------01
21455201---03001011100000-0-1111001111000000000000011100110000----0000--------02
21455301---032-------200-------4----------------------------------------------01
21455301---0300111-000100100000000110000-----------00200000000----1010--------02
21455601---032-------300-------4----------------------------------------------01
21455601---0311011000000000000110000000000000011-1---0-0110101------10--------02
21455801---032-------250-------4----------------------------------------------01
21455801---03000001100000-0-001100110000-000010----01100000000----0000--------02
21456101---033-------250-------4----------------------------------------------01
21456101---0311111000000-0-0-0-100000011-0-00-1-0-011100110011-----000--------02
21456501---032-------200-------4----------------------------------------------01
21456501---03--1110000001-0-1-0-0-0-0-0---000000-0---200110000------00--------02
21456801---032-------200-------4----------------------------------------------01
21456801---03111110000001100-0-0-0-1-0-1000001100-11100000001100000010--------02
21457001---032-------300-------4----------------------------------------------01
21457001---0300111--00110011011000110011--00000---------000100------10--------02
21457701---032-------300-------4----------------------------------------------01
21457701---03110111100001100001100110000110000000001100011001111000010--------02
21457801---033-------450-------5----------------------------------------------01
21457801---03111111110000000001100001100-------0000--000110011------00--------02
21458501---032-------250-------4----------------------------------------------01
21458501---03001100000000100000000000100--------0-0110000-000011000000--------02
21458901---033-------400-------4----------------------------------------------01
21458901---0311111110000----000000001001------------------0000------10--------02
21459401---033-------450-------5----------------------------------------------01
21459401---031100000000000000000000011001-0--0-0000--100110000-----000--------02
21459501---033-------150-------3----------------------------------------------01
21459501---03110001-00000---0-0-0-0-0-1-----------------0-0011------00--------02
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21460301---0300010000000-----0-100110000-0-0--1------100000-0-----0000--------02
21460501---033-------450-------5----------------------------------------------01
21460501---03110110000000000101100001100110000000001100011001111000000--------02
21461501---033-------150-------3----------------------------------------------01
21461501---0311011000000--------00001-0--------0-0-110001-0001----0-00--------02
21461601---033-------450-------5----------------------------------------------01
21461601---0300011000000----111100010110--------001--100---0-1------00--------02
21462001---032-------250-------4----------------------------------------------01
21462001---03--011100000----0---0-0----------------11100110000----0000--------02
21462201---033-------250-------4----------------------------------------------01
21462201---0311011000000------1100001-0--------0-0-1-100-0-0-1------10--------02
21462701---033-------250-------4----------------------------------------------01
21462701---03110011000001-000011000001000000000001111200--01-1-----000--------02
21463301---032-------250-------4----------------------------------------------01
21463301---0300011000000-0-010000000------------0-1------00000-----010--------02
38564101---032-------300-------4----------------------------------------------01
38564101---030010011000011000000-0-0-----1-00-0000011000000000----0000--------02
38564601---032-------250-------4----------------------------------------------01
38564601---0300--10100001100----0010----110000000000000110000000000000--------02
38565001---033-------350-------4----------------------------------------------01
38565001---03-----1-00001000001100001100--000000-000-00001000001100000--------02
38565101---032-------250-------4----------------------------------------------01
38565101---03111111100011100000100000011100000000000000000000011110000--------02
38565401---033-------400-------4----------------------------------------------01
38565401---03110111100000000000110000110010000000111110011000011000000--------02
38565501---032-------350-------4----------------------------------------------01
38565501---03000110000000000--000-0------------000111000110000----0000--------02
38565601---033-----------------4----------------------------------------------01
38565601---030011100000001001111001011001100010001111000110000----0000--------02
38566001---032-----------------4----------------------------------------------01
38566001---03000111100000100001000000000000000000101100010000011110000--------02
38566201---033-----------------4----------------------------------------------01
38566201---03000000000000110000000000000-----------------10000------00--------02
30300301000082123450041500045074----------------------------------------------01
30300301000081101101000000000000000000000-------0010-------0100-------00000000002
30300302000083000067854400040005----------------------------------------------01
303003020000811000110000----000000011100010000000011--100001001-----000000000002
30300401000082123050041700045074----------------------------------------------01
303004010000811---01-0--0000----00001100--------0-0------11100-------00000000002
30300402000082123450039400040074----------------------------------------------01
3030040200008-------0000--------0000---------------------------------00000000002
30300612000083000067844700040005----------------------------------------------01
30300612000081111110000000001000000000000-0-------010100000000-----1000000000002
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30300801000081100000-0--------1000111100---------0---1001-1111-------11000000002
30300901000083120067818800045074----------------------------------------------01
30300901000081101-100000000000001111001000000000000111001100011----1100000000002
30301001000083120067835400045074----------------------------------------------01
303010010000811000110000----0-1-0-0-0-0-------------------0000-------00000000002
30301101000083120067837200045074----------------------------------------------01
30301101000081111110000000000011000-1001--000000001--100010001-----0000000000002
30301401000083120067836400045074----------------------------------------------01
303014010000811000110000-----01100000011--------0-0--111-10000-----0-01000000002
30301501000083120067839000045074----------------------------------------------01
303015010000811000110000----001000000110-----------11100110000-----0-00000000002
30301701000083000067850000040005----------------------------------------------01
303017010000811100000000----00000-0-1100------------------0011-------00000000002
30301801000083120067840900045074----------------------------------------------01
30301801000081100-00-0------0-1-0-0-1-0-------------------1111-------00000000002
30302001000082023450025400040074----------------------------------------------01
30302001000080000000000000000000-0-0-0-0--------00011100100000000000000000000002
30302101000082023450051700045075----------------------------------------------01
3030210100008111111000000000001100001000-------00001--111-0000----0--10000000002
```

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30302201000083120067837000045074----------------------------------------------01
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30302301000083120067840100045074----------------------------------------------01
303023010000811001010000-----001000010000000000001011111100011-----0000000000002
30302401000082003450040000040004----------------------------------------------01
303024010000811111000000----100100000000-------0-0-11100001011-----0000000000002
30302601000083020067853000045075----------------------------------------------01
303026010000811000000000----0000000011000000011000011111000000-----0000000000002
30302701000082123450035900045074----------------------------------------------01
3030270100008111011000000000001100000000--000010000---10011001011110000000000002
30302801000083020067847100040075----------------------------------------------01
303028010000811000100000000001100000000000000000000---100110000----0100000000002
30302901000083120067817800045074----------------------------------------------01
303029010000811000100000----00100001-----------00000-100-10000-----0001000000002
30303001000082023450039500040074----------------------------------------------01
3030300100008111000000000000110100000110000000000101-100010000-----0000000000002
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303031010000811011000000000000000000001100-------00001-100100000-----0000000000002
30303201000082023450043100000075----------------------------------------------01
30303201000080011100000000000000--11-----------0011--000-00000-------01000000002
30303301000082123450030200045074----------------------------------------------01
303033010000811111100000----0000000000000000000000001100000010-----0000000000002
30303401000083120067845500005075----------------------------------------------01
303034010000811111000000----0011001100000000000000011100110011110000100000000002
30303402000083120067825600045074----------------------------------------------01
303034020000811000--00000000000111100000000000000001-100110011----0-000000000002
30303501000082123450049300005075----------------------------------------------01
303035010000800011010001000011100000000000000000000-------0000------100000000002
30303601000082003450043900040075----------------------------------------------01
30303601000081111101000000000011001111000000001000011111111111100001000000000002
30303602000082003000036700040004----------------------------------------------01
303036020000811000110000000000001110000000000000000-1100110011------1-0000000002
30303701000081000000013012000003----------------------------------------------01
3030370100008-----010000-----0---0-0-0-0------------1100------------0-0000000002
30303801000082023450043000040005----------------------------------------------01
3030380100008110001000000000000000011000000000000001-111111101----0-110000000002
30303901000083023450048100040005----------------------------------------------01
30303901000081100101000000000001001-1100-------0011-0111--0000-----0100000000002
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303040010000811-11110000000000000000011011000011111001001100 01----1-100000000002
30304003000082023450049400000075----------------------------------------------01
303040030000811---00-0------00--00000011-------0000-------1100------100000000002
30304101000081000000009012000002----------------------------------------------01
30304101000080000011000000000011001100000000000000011100000000000000000000000002
30304301000083120067834800045074----------------------------------------------01
303043010000811000101000000000000000000000000100000110001100000----0000000000002
30304401000083120067846900045075----------------------------------------------01
30304401000081100011000000001000001110010000100000011111110011----0000000000002
30304501000083000067827300040004----------------------------------------------01
30304501000081100000000000000011000011000000000000011100010000110000000000000002
30304601000083020067843900045075----------------------------------------------01
303046010000811000000000000000--00001100001100000100011111000000110000000000000002
30304801000083120067840800045074----------------------------------------------01
303048010000811---01-0------0001000011000000000------000--1100------000000000002
30305001000082123450044800045075----------------------------------------------01
30305001000081101010000001001100000001001110000000011111010000----00100000000002
30305002000082123450052000045075----------------------------------------------01
30305002000081100011000000000000000000000000000001100111110000----0-000000000002
30305103000082023450031800040074----------------------------------------------01
3030510300008111110100000-0-00000011-----------1011--0001-0011------100000000002
30305104000083000067847000040005----------------------------------------------01
3030510400008--------0----------0011-----0-0--0000011100110000----00100000000002
30305201000082123450047000045075----------------------------------------------01
3030520100008001111000000-0-101100111100-------0010--00-1-0-1-----0-000000000002
```

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303054010000800111000000-0-0-0-1-----1-0---00-000001111100001011110000000000000002
30305601000083120067855000045075----------------------------------------------01
303056010000811000100000000000000000011000000--000000011000001----00000000000002
30305701000082123450052200045075----------------------------------------------01
30305701000080010000000000000-0-00000-1--------0-0-0-11100000011--00100000000002
30305801000082123450042200045074----------------------------------------------01
303058010000811000100000--00000000001100----------------101011----0-000000000002
30305901000082123450048100045075----------------------------------------------01
3030590100008111000000000000000100111100-------000011100110011----10000000000002
30305902000083120067819812045074----------------------------------------------01
303059020000800000011000000000000000-1-0--------0-01110011011111--00100000000002
30306001000082123450039200045074----------------------------------------------01
303060010000800000100000----00000-0-1-0--------0001-----001100----0-000000000002
30306101000082123450038000040074----------------------------------------------01
303061010000811111110000----001100000000-------0011111001-0011------100000000002
30306201000083020067846500040075----------------------------------------------01
303062010000811000100000000000011000010011100000000-1100110000----00000000000002
30306301000081000000003012000002----------------------------------------------01
303063010000800011---0------10000011-0-000-----------0001-00--11--00000000000002
30306501000083120067829100040074----------------------------------------------01
303065010000811010000000----000000001100-1-00-00011-1100110000------000000000002
30306601000082123450019012005074----------------------------------------------01
303066010000800000100000----000000110000-------------100--0000------000000000002
30306901000083120067841100045074----------------------------------------------01
303069010000800000110000-----0-----0--------------------------------130000000002
30307301000083120067842100045074----------------------------------------------01
303073010000811011100000----000000001100000010000000-----1-1101------100000000002
30307401000083000067813012000003----------------------------------------------01
30307401000082-1----0000-----------------------------000--0000------0-0000000002
30307402000083000060844000040005----------------------------------------------01
303074020000811---01---------1---0-0-1-0------------------0000------000000000002
30307601000081000000010012000002----------------------------------------------01
303076010000800111000000--00000000000100--00---0000-000011011000--00000000000002
30307701000083120067838300045074----------------------------------------------01
30307701000081101010-0------000000000000-------0-0-001111-1000----00000000000002
30307801000083120067825000045074----------------------------------------------01
303078010000800011000000----000000001100--0010000111-000000000----00000000000002
30308001000081000000003012000002----------------------------------------------01
30308001000080010-11000------------------------------000110000----0-000000000002
30308701000081000000008012000002----------------------------------------------01
30308701000081101---0000----00000-1--1-0-------------10011---------0000000000002
30309101000082123450045000045075----------------------------------------------01
303091010000811011010000001000110000000000000000100001-111000010----0-000000000002
30309201000082123450037500045074----------------------------------------------01
303092010000811000100000000000000000000000000000000111001100001---00100000000002
30309401000082020450032100040074----------------------------------------------01
303094010000811011000000----00000011-1-0-------------000------------0-0000000002
30400101---082-------250-------4----------------------------------------------01
30400101---0800000000000000000000000001001--000000011--100110011------10--------02
30400501---083-------350-------4----------------------------------------------01
30400501---0811000000000000000110000110011000110000111001100000----0000--------02
30401201---082-------200-------4----------------------------------------------01
30401201---08110110000000000000000011000000000000000100111111----0000--------02
30401601---082-------250-------4----------------------------------------------01
30401601---08000000000000000000100111100000001100110010011 0000----0000--------02
30404201---082-------180-------4----------------------------------------------01
30404201---08000000000000000000000111100---00-00000--100000010----0010--------02
30404301---083-------300-------4----------------------------------------------01
30404301---08-----1000000000000000001100--000--0000-------0111------00--------02
30404601---083-------300-------4----------------------------------------------01
30404601---081101100000000000000000000----000110000000000000000----0000--------02
30404701---082-------180-------4----------------------------------------------01
30404701---0800001010000----000000111100--00000000011000110011------00--------02
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30405101---083-------350-------4----------------------------------------------01
30405101---08110000000000000001100101100--00011100011100110011------00--------02
30405501---082-------250-------4----------------------------------------------01
30405501---08110000000000000000000111100--00011----00100110001----0000--------02
30406501---083-------350-------4----------------------------------------------01
30406501---08110000000000000001100000000--00000----00100111011----0010--------02
30407201---083-------400-------4----------------------------------------------01
30407201---0811000100000000000110000001111000--0000--100000001-----000--------02
30407801---081-------050-------2----------------------------------------------01
30407801---0800000100000000000000011----1100000000011100110011------00--------02
30408401---083-------350-------4----------------------------------------------01
30408401---08110001100000000000000000011---00-0000000111110011----0010--------02
30408501---082-------350-------4----------------------------------------------01
30408501---0800011110000-0-000000000-1-0-------------000110010------00--------02
30409101---081-------090-------2----------------------------------------------01
30409101---080000000000000001-0-00111-0-11-00-1------1001-0000----0000--------02
30409401---081-------060-------2----------------------------------------------01
30409401---08-----0000000000----0011-----------000011100110011-1-00000--------02
30409501---083-------400-------4----------------------------------------------01
30409501---0811000000000-----0-00000-1-0-------0-1-------11100------10--------02
30409701---082-------200-------4----------------------------------------------01
30409701---0800-11110000----00000000-----------------100------------00--------02
30410301---083-------300-------4----------------------------------------------01
30410301---081100000000000000011000001000000000000000111--1111------00--------02
30410401---083-------350-------4----------------------------------------------01
30410401---0800111000000000001000000-----------0-0------111100-----010--------02
80100101---202-------350-------4----------------------------------------------01
80100101---201100011000000000000000011001100000001100000001111--001100--------02
80100102---201-------060-------2----------------------------------------------01
80100102---20001110000----0000--0000110011--000--0000000001111----0000--------02
80100103---202-------200-------4----------------------------------------------01
80100103---200011111000000001100000000001100011000011000001100----1100--------02
80100104---203-------350-------4----------------------------------------------01
80100104---20110001100000000000000001100110001100001100000000011000000--------02
80100105---203-------400-------4----------------------------------------------01
80100105---20110111100000000--000000--0011000000000000000000001111----00--------02
80100106---203-------350-------4----------------------------------------------01
80100106---201101100000000000000000011111100000000011-00001111----1100--------02
80100107---203-------350-------4----------------------------------------------01
80100107---201101111001100000000000011001100000110011000001111----0000--------02
80100108---203-------400-------4----------------------------------------------01
80100108---20110--0000000000001100001100-------11000000000111111--0000--------02
80100109---202-------350-------4----------------------------------------------01
80100109---20110111100110000000000001100--00000000011000001111----1100--------02
80100110---202-------350-------4----------------------------------------------01
80100110---2000111000000000000000011000011---111100--0--0011111100--00--------02
80100111---202-------400-------4----------------------------------------------01
80100111---20110000000000000000000001100110010011--1110011111111----00--------02
80100112---203-------350-------4----------------------------------------------01
80100112---20110001100000000000000000000-------0000--0----11001111--00--------02
80100113---203-------350-------4----------------------------------------------01
80100113---20000011000000000000000001100110001100001100000111111000000--------02
80100114---203-------400-------4----------------------------------------------01
80100114---200001111000000--00000000110011--000111111000000011----0000--------02
80100115---202-------350-------4----------------------------------------------01
80100115---2011000110000--00000000001100110000000001100000110011001100--------02
80100116---202-------160-------3----------------------------------------------01
80100116---20000110000000000000000--00001100000001100000001111------00--------02
80100117---203-------300-------4----------------------------------------------01
80100117---20110001100000000000000--11001100000000011-00000000----1100--------02
80100118---202-------400-------4----------------------------------------------01
80100118---20110001100110000000000001100110001100001100000001111000000--------02
80100119---202-------400-------4----------------------------------------------01
80100119---20000000000000000000000001100--000--000011000001100----1100--------02
```

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80100120---203-------400-------4----------------------------------------------01
80100120---20110001100000000000000001100--00000000011000000011------00--------02
80100121---203-------350-------4----------------------------------------------01
80100121---20001111100000000000000001100--000110000--000000011------00--------02
80100122---203-------400-------4----------------------------------------------01
80100122---20110000000000000000000001111--000000011--000001100----0000--------02
80100123---202-------350-------4----------------------------------------------01
80100123---20110110000000000000000001100--000000011---00--1100------00--------02
80100124---203-------350-------4----------------------------------------------01
80100124---20111001100000000000000001100-------0000-----001111----1100--------02
80100125---203-------400-------4----------------------------------------------01
80100125---201101111000000000000000011000000000000011000000011----0000--------02
80100126---203-------250-------4----------------------------------------------01
80100126---2000100110000000000110000000000000000000--000001111----1100--------02
80100127---203-------400-------4----------------------------------------------01
80100127---2011111110000000000000000110011-----110011000001111--000000--------02
80100128---202-------300-------4----------------------------------------------01
80100128---20110001100000000--000000000110000000000--000000011------00--------02
80100129---202-------250-------4----------------------------------------------01
80100129---2011000110000000000000000110011---000011--000000011------00--------02
80100130---202-------300-------4----------------------------------------------01
80100130---20110110000000000001100001100--000000011--000110011----0000--------02
80100131---203-------400-------4----------------------------------------------01
80100131---20111001100000000000000001100110000000111100000111111--0000--------02
80100132---203-------250-------4----------------------------------------------01
80100132---20111001100000000000000001111110000000000000000--11------00--------02
80100133---203-------350-------4----------------------------------------------01
80100133---20000001100000000000000001100--000110000-------1100------00--------02
80100134---203-------200-------4----------------------------------------------01
80100134---201101100000000000000000011001100000000011000000011----0000--------02
80200501---203-------250-------4----------------------------------------------01
80200501---2011000000000-0-0000000000000-----0-000000100010011----0000--------02
80200502---203-------350-------4----------------------------------------------01
80200502---2011000110000000000110000110000001000000--100110011----0000--------02
80200503---203-------400-------4----------------------------------------------01
80200503---2011000000000-0-0000000000000-----0-000000100010011----0000--------02
80200504---203-------300-------4----------------------------------------------01
80200504---20110001100000000001000001100-------0000-------0011------00--------02
80200505---202-------450-------5----------------------------------------------01
80200505---2011000000000----000000000000-------------0--110000------00--------02
80200506---202-------400-------4----------------------------------------------01
80200506---2011000110000----000000111100-----------111--110011----1100--------02
80200508---202-------350-------4----------------------------------------------01
80200508---2000000000000------10000011000000100000000000111111----0000--------02
80300701---203-------300-------4----------------------------------------------01
80300701---2000000110000----000000001100-------00----00000001-------00--------02
80300702---203-------200-------4----------------------------------------------01
80300702---20110001000000000000000001100-------000011000110000------00--------02
80300703---203-------300-------4----------------------------------------------01
80300703---2011000000000--00000100000100--00100000011-00000111------00--------02
80300704---202-------350-------4----------------------------------------------01
80300704---2011111000000----001000000100----------------000010------00--------02
80300705---203-------400-------4----------------------------------------------01
80300705---2011000000000000000000000------0000000--11---000100----0000--------02
80300706---203-------350-------4----------------------------------------------01
80300706---2011011000000----000100001001-------0000--0--01--------0000--------02
80300707---203-------350-------4----------------------------------------------01
80300707---2011001000000----000000000000-------0-0---000111100----0000--------02
80300708---203-------400-------4----------------------------------------------01
80300708---2011---0000----------00001-0------------00000011001----0000--------02
80300709---203-------450-------5----------------------------------------------01
80300709---2011111010000--00001100001100-------000011000001000------00--------02
80300710---203-------450-------5----------------------------------------------01
80300710---20111101100000000000000--1100-------0000-----001111------00--------02
```

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80300711---203-------300-------4----------------------------------------------01
80300711---2011001010000--0000000000011000000000011---00000101------00--------02
80300712---202-------200-------4----------------------------------------------01
80300712---20110000000000000001000--0100--00000-------00110001--000000--------02
80300713---202-------400-------4----------------------------------------------01
80300713---201101011000000000100000001001-0-00-0110100001100111-0-1100--------02
80400111---203-------450-------5----------------------------------------------01
80400111---201100111000000000000000000000000000000000100010001----0100--------02
80400112---203-------400-------4----------------------------------------------01
80400112---20110001000000000000000111100--00000001100100100011----0000--------02
80400121---202-------350-------4----------------------------------------------01
80400121---200001001000000001000000000110000000000011---000011----1000--------02
80400131---202-------150-------3----------------------------------------------01
80400131---2011000100000000000010000000010000000000111--100000----0000--------02
80400141---203-------350-------4----------------------------------------------01
80400141---2011000110000000000000000110000001000001001--000001----0000--------02
80400142---203-------180-------4----------------------------------------------01
80400142---20110001100000000000000111100-0-00-00011001--011100----0000--------02
80400143---202-------150-------3----------------------------------------------01
80400143---201100000000000000000000000001000110001100100011100----0000--------02
80400144---201-------050-------2----------------------------------------------01
80400144---20000011000000000000000110000-------0011001--000001----0000--------02
80400145---203-------350-------4----------------------------------------------01
80400145---201101111000000000111000100000000111001111100010001----0100--------02
80400146---203-------250-------4----------------------------------------------01
80400146---2011000000000000000000000-----------000011100100000----0000--------02
80400151---203-------200-------4----------------------------------------------01
80400151---201101000000000000000000011001100100------1---10000----1000--------02
80400161---202-------160-------3----------------------------------------------01
80400161---2011000110000000000000000-1-01100001010---00-100-1------00--------02
80511001---203-------350-------4----------------------------------------------01
80511001---20110101100000000000000111100-------0000-------0011------00--------02
80521501---203-------350-------4----------------------------------------------01
80521501---201100000000000001000001100000000000000001-1000-0000----0-00--------02
80522701---202-------350-------4----------------------------------------------01
80522701---200000000000000001101000001100000000000011100110011----1000--------02
90000401---212-------280-------4----------------------------------------------01
90000401---21---0-1-00001-0-0-0-0-0-0-1--------1-1-1--0-0100101-0-1-10--------02
90001801---212-------150-------3----------------------------------------------01
90001801---211111101000000000000000011000000000----00111110000----0010--------02
90001901---213-------400-------4----------------------------------------------01
90001901---21110001000000000000000001100-------------2001-0000----0-00--------02
90002101---213-------350-------4----------------------------------------------01
90002101---21110000000000000000000001100-------0000001000010-1------00--------02
90002201---212-------300-------4----------------------------------------------01
90002201---21111110000000000100000001100-------0011--100110000----0010--------02
90002301---212-------250-------4----------------------------------------------01
90002301---21110000000000000000000000000-------------200-00011-----010--------02
90004201---211-------120-------2----------------------------------------------01
90004201---211111101000000000001000011000000000000000100110000000001010--------02
90006101---212-------200-------4----------------------------------------------01
90006101---2111111000000----00--0000----0000000000000200110-0-----0010--------02
90006202---212-------300-------4----------------------------------------------01
90006202---2111000100000000000000000-----------000000100110000----0010--------02
90006301---213-------420-------4----------------------------------------------01
90006301---2111100110000000000000000000011---00000010211110001----0000--------02
90007301---211-------100-------2----------------------------------------------01
90007301---210011110000000000000001100001000000000011100000000----0010--------02
90009701---212-------300-------4----------------------------------------------01
90009701---21110111000010000110000111001000000000000020010011100000000--------02
90010401---212-------250-------4----------------------------------------------01
90010401---21110001000000000000000001100-------0000--200110010-----010--------02
90010601---213-------130-------3----------------------------------------------01
90010601---2111000000000000000--00111100-------000011100110000----0010--------02
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90010701---212-------250-------4----------------------------------------------01
90010701---21000000100000000000000111100--00100000000200110100-0-11110--------02
90011201---213-------300-------4----------------------------------------------01
90011201---2111000110000--------0000----0000000----11211110000----1100--------02
90011401---212-------250-------4----------------------------------------------01
90011401---21-----000000000000--0000----000000100000110011010111000010--------02
90011501---212-------350-------4----------------------------------------------01
90011501---211100011000011000000000011000000000000000111000011--000000--------02
90012001---212-------400-------4----------------------------------------------01
90012001---2111000000000--------0000----0000000---------000111----0000--------02
90012401---213-------350-------4----------------------------------------------01
90012401---211101111000000000000000011001100000000000211110011----0000--------02
90012901---213-------200-------4----------------------------------------------01
90012901---21111110000000000000000001100--0001000001121111001111000000--------02
90013501---212-------300-------4----------------------------------------------01
90013501---2111000110000--0000000000-0-000000000000---00110000----1110--------02
90013701---213-------350-------4----------------------------------------------01
90013701---2100000110000--------00001-0-------------11-1--0010------00--------02
90014001---212-------300-------4----------------------------------------------01
90014001---21110000010000000000000001100-------0000--100110011-1-0-010--------02
90014101---212-------250-------4----------------------------------------------01
90014101---2111011000000000010000011----1000-000000--200010011----0010--------02
90014201---212-------250-------4----------------------------------------------01
90014201---21111000100001100111100001100000001100001010011001111001000--------02
90015601---212-------450-------5----------------------------------------------01
90015601---211101100000000000000000000000000000------100100010------10--------02
90015801---213-------220-------4----------------------------------------------01
90015801---21-----0000000-000---0-0-1-0-0000110000011200110011----0000--------02
90015901---212-------300-------4----------------------------------------------01
90015901---21110001000000000000000001100-------000011111--0011------10--------02
90020201---213-------300-------4----------------------------------------------01
90020201---21110010000000000000000000000000000000001010011001111001110--------02
90030601---213-------250-------4----------------------------------------------01
90030601---2111000000000--00-0-00000-----------0000--10011-0-1-----010--------02
90041401---213-------350-------4----------------------------------------------01
90041401---2111000110000000000110000----11000000000--100--0000------10--------02
91000101---082-------200-------4----------------------------------------------01
91000101---08--00-010000----0-0-00001-0-0000101-----------0000------00--------02
91000201---081-------110-------2----------------------------------------------01
91000201---08--000010000-0-0-0-0-0-0-1-01100000-0-000100000000-----000--------02
91000301---082-------500-------5----------------------------------------------01
91000301---0800000010000-----------------------------100--0000------00--------02
91000801---083-------180-------4----------------------------------------------01
91000801---0811000010000000000000000011001-00101000000000110000----0000--------02
91001401---081-------070-------2----------------------------------------------01
91001401---0800---11-1----------0000---------------------10-0-------00--------02
91001601---081-------090-------2----------------------------------------------01
91001601---0800011100000--------0000----00--000001100100110000------00--------02
91001801---083-------500-------5----------------------------------------------01
91001801---08110--000100--------0000----0000000000000100001100------00--------02
91002101---082-------200-------4----------------------------------------------01
91002101---0800011110000------0000001100010000000000-000110000----0000--------02
91002301---083-------400-------4----------------------------------------------01
91002301---08000001101000000101100001100-----------00000000010----0000--------02
91002501---083-------450-------5----------------------------------------------01
91002501---08000--000000--------0000------------------0011-0-0------00--------02
91002601---082-------300-------4----------------------------------------------01
91002601---0800011000000----0-0-0-0-1-0-----------------------------00--------02
91002701---083-------550-------5----------------------------------------------01
91002701---080000010000000--1100000000110000000000-----000111-----000--------02
91002801---083-------450-------5----------------------------------------------01
91002801---0800000111100---------------------------00100010011----0000--------02
91002901---082-------250-------4----------------------------------------------01
91002901---0800000110000--------0000-----------0000--000110011------00--------02
```

Appendix D - Southwest U.S. Discrete Dental Traits

For the following data, to be considered a positive manifestation of a trait (pres.), the following standards were used (from Scott 1973):

shoveling I1 (SHOV1)	>2
shoveling I2 (SHOV2)	>2
tuberculum dentale (TD)	>0
hypocone M1 (HYPO1)	<4
hypocone M2 (HYPO2)	<4
metaconule M1 (M1C5)	>0
Carabelli's trait M1 (CARAM1)	>2
cusp number M1 (CNM1)	>4
cusp number M2 (CNM2)	>4
cusp 6 M1 (C6M1)	>1
cusp 6 M2 (C6M2)	>1
cusp 7 M1 (C6M1)	>0
cusp 7 M2 (C7M2)	>0

Population	Trait	Pres.	N	Frequency
Santa Catalina	SHOV1	21.0	61.0	0.34426
	SHOV2	42.0	86.0	0.48837
	TD	25.0	62.0	0.40323
	HYPO1	12.0	173.0	0.06936
	HYPO2	115.0	149.0	0.77181
	M1C5	30.0	113.0	0.26549
	CARAM1	41.0	97.0	0.42268
	GPM1	125.0	142.0	0.88028
	GPM2	21.0	140.0	0.15000
	CNM1	130.0	130.0	1.00000
	CNM2	109.0	109.0	1.00000
	C6M1	32.0	128.0	0.25000
	C6M2	36.0	114.0	0.31579
	C7M1	5.0	128.0	0.03906
	C7M2	0.0	114.0	0.00000
Santa Maria	SHOV1	20.0	43.0	0.46512
	SHOV2	18.0	42.0	0.42857
	TD	25.0	42.0	0.59524
	HYPO1	5.0	51.0	0.09804
	HYPO2	23.0	38.0	0.60526
	M1C5	4.0	34.0	0.11765
	CARAM1	5.0	31.0	0.16129
	GPM1	27.0	31.0	0.87097
	GPM2	11.0	24.0	0.45833
	CNM1	35.0	35.0	1.00000
	CNM2	23.0	23.0	1.00000
	C6M1	10.0	30.0	0.33333
	C6M2	3.0	21.0	0.14286
	C7M1	1.0	31.0	0.03226
	C7M2	0.0	23.0	0.00000

Population	Trait	Pres.	N	Frequency
Papago	SHOV1	144.0	171.0	0.84211
	SHOV2	86.0	168.0	0.51190
	TD	72.0	133.0	0.54135
	HYPO1	8.0	178.0	0.04494
	HYPO2	119.0	147.0	0.80952
	M1C5	28.0	126.0	0.22222
	CARAM1	54.0	160.0	0.33750
	GPM1	83.0	90.0	0.92222
	GPM2	16.0	95.0	0.16842
	CNM1	175.0	175.0	1.00000
	CNM2	98.0	140.0	0.70000
	C6M1	54.0	135.0	0.40000
	C6M2	16.0	129.0	0.12403
	C7M1	53.0	158.0	0.33544
	C7M2	22.0	128.0	0.17188
Navajo	SHOV1	324.0	376.0	0.86170
	SHOV2	232.0	386.0	0.60104
	TD	226.0	324.0	0.69753
	HYPO1	18.0	462.0	0.03896
	HYPO2	223.0	291.0	0.76632
	M1C5	72.0	339.0	0.21239
	CARAM1	122.0	434.0	0.28111
	GPM1	213.0	267.0	0.79775
	GPM2	27.0	185.0	0.14595
	CNM1	404.0	404.0	1.00000
	CNM2	180.0	252.0	0.71429
	C6M1	118.0	362.0	0.32597
	C6M2	36.0	230.0	0.15652
	C7M1	76.0	414.0	0.18357
	C7M2	15.0	279.0	0.05376

Population	Trait	Pres.	N	Frequency
Apache	SHOV1	30.0	31.0	0.96774
	SHOV2	16.0	26.0	0.61538
	TD	14.0	24.0	0.58333
	HYPO1	0.0	43.0	0.00000
	HYPO2	14.0	20.0	0.70000
	M1C5	6.0	39.0	0.15385
	CARAM1	10.0	48.0	0.20833
	GPM1	34.0	41.0	0.82927
	GPM2	3.0	17.0	0.17647
	CNM1	48.0	48.0	1.00000
	CNM2	12.0	19.0	0.63158
	C6M1	19.0	48.0	0.39583
	C6M2	5.0	19.0	0.26316
	C7M1	4.0	49.0	0.08163
	C7M2	0.0	22.0	0.00000
Hopi	SHOV1	206.0	251.0	0.82072
	SHOV2	157.0	271.0	0.57934
	TD	149.0	210.0	0.70952
	HYPO1	4.0	287.0	0.01394
	HYPO2	170.0	232.0	0.73276
	M1C5	34.0	180.0	0.18889
	CARAM1	98.0	279.0	0.35125
	GPM1	87.0	105.0	0.82857
	GPM2	3.0	82.0	0.03659
	CNM1	278.0	280.0	0.99286
	CNM2	148.0	184.0	0.76289
	C6M1	77.0	215.0	0.35814
	C6M2	40.0	166.0	0.24096
	C7M1	68.0	277.0	0.06335
	C7M2	14.0	221.0	0.06335

Population	Trait	Pres.	N	Frequency
Zuni	SHOV1	47.0	57.0	0.82456
	SHOV2	18.0	40.0	0.45000
	TD	30.0	38.0	0.78947
	HYPO1	0.0	44.0	0.00000
	HYPO2	7.0	7.0	1.00000
	M1C5	1.0	34.0	0.02941
	CARAM1	18.0	47.0	0.38298
	GPM1	30.0	40.0	0.75000
	GPM2	0.0	7.0	0.00000
	CNM1	46.0	46.0	1.00000
	CNM2	4.0	7.0	0.57143
	C6M1	16.0	42.0	0.00000
	C6M2	0.0	7.0	0.00000
	C7M1	10.0	45.0	0.22222
	C7M2	0.0	5.0	0.00000
Yuma	SHOV1	61.0	67.0	0.91045
	SHOV2	30.0	61.0	0.49180
	TD	33.0	60.0	0.55000
	HYPO1	0.0	63.0	0.00000
	HYPO2	23.0	26.0	0.88462
	M1C5	7.0	56.0	0.12500
	CARAM1	23.0	63.0	0.36508
	GPM1	50.0	61.0	0.81967
	GPM2	9.0	38.0	0.23684
	CNM1	67.0	68.0	0.98529
	CNM2	17.0	36.0	0.47222
	C6M1	9.0	68.0	0.13235
	C6M2	2.0	36.0	0.05556
	C7M1	12.0	66.0	0.18182
	C7M2	1.0	37.0	0.02703

Population	Trait	Pres.	N	Frequency
Amer White	SHOV1	1.0	94.0	0.01064
	SHOV2	2.0	102.0	0.01961
	TD	68.0	104.0	0.65385
	HYPO1	0.0	108.0	0.00000
	HYPO2	59.0	104.0	0.56731
	M1C5	9.0	71.0	0.12676
	CARAM1	70.0	111.0	0.63063
	GPM1	9.0	11.0	0.81818
	GPM2	2.0	19.0	0.10526
	CNM1	91.0	95.0	0.95789
	CNM2	18.0	101.0	0.17822
	C6M1	0.0	67.0	0.00000
	C6M2	2.0	102.0	0.01961
	C7M1	21.0	92.0	0.22826
	C7M2	22.0	86.0	0.25581

Appendix E - Discrete Trait Frequencies Used for Distance Analysis

Any degree of expression for the cranial data was considered present. For the dental discrete data, to be considered a positive manifestation of a trait (pres.), the following standards were used (from Turner 1987a):

shoveling I2 (SHOV2)	>2
double shoveling I1 (DSHOV)	>1
interuption groove I2 (IGROV)	>0
metacone M3 (METAC)	>1
hypocone M2 (HYPO2)	>1
metaconule M1 (M1C5)	>0
Carabelli's trait M1 (CARAM1)	>1
Carabelli's trait M2 (CARAM2)	>1
cusp number M1 (CNM1)	>4
parastyle M3 (PARA)	>0
peg-shaped incisor (PSI)	>0
peg-shaped molar (PSM)	>0
groove pattern M1 (GPM1)	>1
groove pattern M2 (GPM2)	>1
cusp number M1 (CNM1)	>5
cusp number M2 (CNM2)	>4
protostylid M1 (PM1)	>0
cusp 5 M2 (C5M2)	>1
cusp 6 M2 (C6M2)	>1
cusp 7 M1 (C7M1)	>0
cusp 7 M2 (C7M2)	>0

Population	Trait	Pres.	N	Frequency
Irene Mound	SHOV2	61	67	0.9104
	DSHOV	66	68	0.9706
	IGROV	25	66	0.3788
	METAC	61	62	0.9839
	HYPO2	81	81	1.0000
	M1C5	23	85	0.2706
	CARAM1	51	92	0.5543
	CARAM2	2	78	0.0256
	PARA	0	62	0.0000
	PSI	0	67	0.0000
	PSM	1	62	0.0161
	GPM1	4	82	0.0488
	GPM2	67	76	0.8816
	CNM1	22	79	0.2785
	CNM2	6	72	0.0833
	PM1	79	82	0.9634
	C5M2	65	72	0.9028
	C6M2	12	72	0.1667
	C7M1	4	79	0.0506
	C7M2	1	72	0.0139
SCDG	SHOV2	41	86	0.4767
	DSHOV	49	65	0.7538
	IGROV	39	67	0.5821
	METAC	112	116	0.9655
	HYPO2	141	149	0.9463
	M1C5	30	113	0.2655
	CARAM1	60	97	0.6185
	CARAM2	1	72	0.0139
	PARA	7	95	0.0737
	PSI	1	80	0.0125
	PSM	19	101	0.1881
	GPM1	16	142	0.1127
	GPM2	118	140	0.8428
	CNM1	38	130	0.2923
	CNM2	8	117	0.0684
	PM1	65	71	0.9155
	C5M2	103	114	0.9035
	C6M2	36	114	0.3158
	C7M1	5	128	0.0391
	C7M2	0	114	0.0000

Population	Trait	Pres.	N	Frequency
SCDG-SM	SHOV2	17	42	0.4047
	DSHOV	30	48	0.6250
	IGROV	29	44	0.6591
	METAC	34	34	1.0000
	HYPO2	36	38	0.9474
	M1C5	4	34	0.1176
	CARAM1	8	31	0.2581
	CARAM2	1	24	0.0417
	PARA	1	37	0.0270
	PSI	0	50	0.0000
	PSM	1	41	0.0244
	GPM1	4	31	0.1290
	GPM2	13	24	0.5417
	CNM1	14	36	0.3889
	CNM2	4	27	0.1481
	PM1	18	21	0.8571
	C5M2	20	24	0.8333
	C6M2	3	21	0.1428
	C7M1	0	31	0.0000
	C7M2	0	23	0.0000
SMDY	SHOV2	18	33	0.5454
	DSHOV	26	33	0.7879
	IGROV	14	29	0.4827
	METAC	18	21	0.8571
	HYPO2	34	36	0.9444
	M1C5	14	40	0.3500
	CARAM1	13	40	0.3250
	CARAM2	1	30	0.0333
	PARA	1	21	0.0476
	PSI	0	32	0.0000
	PSM	2	24	0.0833
	GPM1	8	34	0.2353
	GPM2	15	27	0.5555
	CNM1	8	35	0.2286
	CNM2	5	25	0.2000
	PM1	17	34	0.5000
	C5M2	18	25	0.7200
	C6M2	5	25	0.2000
	C7M1	0	34	0.0000
	C7M2	1	25	0.0400

Population	Trait	Pres.	N	Frequency
Carolina Algonquian	SHOV2	6	11	0.5454
	DSHOV	3	5	0.6000
	IGROV	11	11	1.0000
	METAC	12	12	1.0000
	HYPO2	13	14	0.9286
	M1C5	12	16	0.7500
	CARAM1	4	15	0.2667
	CARAM2	0	13	0.0000
	PARA	0	12	0.0000
	PSI	0	11	0.0000
	PSM	0	13	0.0000
	GPM1	1	14	0.0714
	GPM2	10	11	0.9091
	CNM1	7	14	0.5000
	CNM2	1	11	0.0909
	PM1	6	14	0.4286
	C5M2	10	11	0.9091
	C6M2	4	11	0.3636
	C7M1	0	14	0.0000
	C7M2	0	11	0.0000
Ledford Island	SHOV2	59	72	0.8194
	DSHOV	72	77	0.9351
	IGROV	26	62	0.4193
	METAC	37	37	1.0000
	HYPO2	66	66	1.0000
	M1C5	48	83	0.5783
	CARAM1	62	84	0.7381
	CARAM2	2	60	0.0333
	PARA	1	37	0.0270
	PSI	0	73	0.0000
	PSM	0	39	0.0000
	GPM1	8	86	0.0930
	GPM2	55	59	0.9322
	CNM1	34	88	0.3864
	CNM2	0	59	0.0000
	PM1	72	88	0.8182
	C5M2	59	59	1.0000
	C6M2	15	59	0.2542
	C7M1	1	88	0.0114
	C7M2	0	59	0.0000

Population	Trait	Pres.	N	Frequency
NE Siberia[1]	DSHOV	6	24	0.2500
	IGROV	36	67	0.5373
	HYPO2	105	138	0.7609
	M1C5	2	63	0.0317
	CARAM1	20	109	0.1835
	PARA	1	104	0.0096
	PSM	56	256	0.2187
	GPM2	18	89	0.2022
	CNM1	23	46	0.5000
	CNM2	3	86	0.0388
	PM1	19	87	0.2184
	C7M1	50	96	0.5208
Amur[1]	DSHOV	8	18	0.4444
	IGROV	8	27	0.2963
	HYPO2	43	52	0.8269
	M1C5	9	42	0.2143
	CARAM1	16	60	0.2667
	PARA	0	27	0.0000
	PSM	42	98	0.4286
	GPM2	9	56	0.1607
	CNM1	22	44	0.5000
	CNM2	6	52	0.1154
	PM1	4	53	0.0755
	C7M1	4	55	0.0727
Lake Baikal[1]	DSHOV	5	10	0.5000
	IGROV	5	14	0.3571
	HYPO2	24	24	1.0000
	M1C5	2	3	0.6667
	CARAM1	3	10	0.3000
	PARA	2	15	0.1333
	PSM	5	32	0.1562
	GPM2	1	21	0.0476
	CNM1	3	9	0.3333
	CNM2	4	18	0.2222
	PM1	4	13	0.3077
	C7M1	4	21	0.1905

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[1] Turner 1987a

Population	Trait	Pres.	N	Frequency
N China-Mongolia[1]	DSHOV	64	213	0.3005
	IGROV	98	210	0.4667
	HYPO2	367	406	0.9039
	M1C5	83	295	0.2813
	CARAM1	114	374	0.3048
	PARA	12	131	0.0916
	PSM	201	380	0.5289
	GPM2	22	338	0.0651
	CNM1	79	211	0.3744
	CNM2	44	258	0.1705
	PM1	100	332	0.3012
	C7M1	32	341	0.0938
Recent Japan[1]	DSHOV	176	267	0.6592
	IGROV	134	301	0.4452
	HYPO2	417	482	0.8651
	M1C5	77	390	0.1974
	CARAM1	143	458	0.3122
	PARA	4	234	0.0171
	PSM	212	504	0.4206
	GPM2	46	352	0.1307
	CNM1	134	314	0.4267
	CNM2	47	345	0.1362
	PM1	75	353	0.2125
	C7M1	25	382	0.0654
Hong Kong[1]	DSHOV	85	299	0.2843
	IGROV	121	283	0.4276
	HYPO2	270	299	0.9030
	M1C5	60	276	0.2174
	CARAM1	113	301	0.3754
	PARA	5	145	0.0345
	PSM	89	238	0.3739
	GPM2	17	228	0.0746
	CNM1	90	267	0.3371
	CNM2	72	296	0.2432
	PM1	12	227	0.0529
	C7M1	26	295	0.0881

Population	Trait	Pres.	N	Frequency
S China[1]	DSHOV	8	33	0.2424
	IGROV	12	44	0.2727
	HYPO2	80	93	0.8602
	M1C5	10	62	0.1613
	CARAM1	25	99	0.2525
	PARA	3	68	0.0441
	PSM	31	124	0.2500
	GPM2	10	80	0.1250
	CNM1	24	60	0.4000
	CNM2	15	77	0.1948
	PM1	21	85	0.2470
	C7M1	9	85	0.1059
Eskimo[2]	DSHOV	54	91	0.59341
	HYPO2	205	257	0.79766
	M1C5	42	182	0.23077
	CARAM1	37	211	0.17535
	PARA	13	219	0.05936
	PSM	97	472	0.20551
	GPM2	43	214	0.20551
	CNM1	71	178	0.39888
	CNM2	8	209	0.03828
	PM1	37	224	0.16518
	C7M1	32	248	0.12903
Aleut[2]	DSHOV	19	38	0.50000
	HYPO2	80	117	0.68376
	M1C5	13	108	0.12037
	CARAM1	7	112	0.06329
	PARA	5	79	0.06329
	PSM	55	212	0.25943
	GPM2	28	143	0.19580
	CNM1	45	104	0.43269
	CNM2	12	112	0.10714
	PM1	30	116	0.25862
	C7M1	11	131	0.08397

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[2] Turner 1985

Population	Trait	Pres.	N	Frequency
NW Coast[2]	DSHOV	90	156	0.57692
	HYPO2	414	451	0.91796
	M1C5	80	376	0.21276
	CARAM1	96	386	0.24870
	PARA	10	354	0.02825
	PSM	105	566	0.18551
	GPM2	54	491	0.10998
	CNM1	165	406	0.40640
	CNM2	20	471	0.04246
	PM1	151	450	0.33555
	C7M1	40	467	0.08565
N America[2]	DSHOV	597	796	0.75000
	HYPO2	1245	1358	0.91679
	M1C5	214	1161	0.18432
	CARAM1	456	1282	0.35569
	PARA	37	897	0.04125
	PSM	271	1551	0.17472
	GPM2	174	1631	0.10668
	CNM1	683	1388	0.49207
	CNM2	129	1597	0.08078
	PM1	703	1679	0.41870
	C7M1	182	1788	0.10179
Irene Mound	LO	24	70	0.3428
	OAA	23	62	0.3710
	PNB	10	64	0.1562
	EPB	10	51	0.1961
	BB	0	67	0.0000
	CO	3	67	0.0447
	MET	0	69	0.0000
	FTA	1	50	0.0200
	FN	37	66	0.5606
	AT	0	69	0.0000
	CFD	0	48	0.0000
	PT	0	44	0.0000
	FO	10	48	0.0208
	FS	13	44	0.2954
	APF	34	45	0.7555
	PAT	46	57	0.8070
	PF	21	67	0.3234
	MFA	10	61	0.6065
	ACC	7	48	0.1458
	ZFF	37	61	0.6065
	AIF	3	47	0.0638

Population	Trait	Pres.	N	Frequency
SCDG-SM	LO	20	63	0.3175
	OAA	20	62	0.3226
	PNB	4	64	0.0625
	EPB	1	36	0.0278
	BB	1	62	0.0161
	CO	1	62	0.0161
	MET	0	70	0.0000
	FTA	0	38	0.0000
	FN	24	65	0.3692
	AT	0	66	0.0000
	CFD	0	36	0.0000
	PT	4	33	0.1212
	FO	1	53	0.0189
	FS	12	55	0.2182
	APF	33	42	0.7857
	PAT	44	57	0.7719
	PF	29	65	0.4461
	MFA	8	63	0.1269
	ACC	6	33	0.1818
	ZFF	37	56	0.6607
	AIF	3	49	0.0612
SMDY	LO	1	18	0.0556
	OAA	6	20	0.3000
	PNB	2	20	0.1000
	EPB	0	18	0.0000
	BB	0	21	0.0000
	CO	0	21	0.0000
	MET	0	21	0.0000
	FTA	0	18	0.0000
	FN	12	20	0.6000
	AT	0	21	0.0000
	CFD	0	16	0.0000
	PT	0	16	0.0000
	FO	0	16	0.0000
	FS	3	16	0.1875
	APF	5	12	0.4167
	PAT	15	18	0.8333
	PF	4	21	0.1905
	MFA	3	16	0.1875
	ACC	6	14	0.4286
	ZFF	15	18	0.8333
	AIF	0	12	0.0000

Population	Trait	Pres.	N	Frequency
Carolina Algonquian	LO	12	68	0.1765
	OAA	9	67	0.1343
	PNB	4	65	0.0615
	EPB	0	56	0.0000
	BB	0	69	0.0000
	CO	3	67	0.0448
	MET	0	69	0.0000
	FTA	0	60	0.0000
	FN	47	68	0.6912
	AT	0	69	0.0000
	CFD	0	45	0.0000
	PT	8	47	0.1702
	FO	7	62	0.1129
	FS	16	60	0.2667
	APF	27	45	0.6000
	PAT	17	54	0.3148
	PF	39	69	0.5652
	MFA	7	67	0.1045
	ACC	8	50	0.1600
	ZFF	21	64	0.3281
	AIF	13	46	0.2826
Ledford Island	LO	8	29	0.2758
	OAA	3	25	0.1200
	PNB	2	29	0.0689
	EPB	3	26	0.1154
	BB	0	32	0.0000
	CO	1	32	0.0312
	MET	0	32	0.0000
	FTA	0	28	0.0000
	FN	16	32	0.5000
	AT	0	32	0.0000
	CFD	0	19	0.0000
	PT	2	18	0.1111
	FO	1	25	0.0400
	FS	2	25	0.0800
	APF	9	21	0.4286
	PAT	29	29	1.0000
	PF	16	32	0.5000
	MFA	2	24	0.0833
	ACC	2	20	0.1000
	ZFF	22	29	0.7586
	AIF	5	27	0.1852

Population	Trait	Pres.	N	Frequency
N Chinese[3]	OAA	22	163	0.1349
	PNB	43	159	0.2704
	MET	11	167	0.0658
	PT	20	164	0.1219
	FO	5	166	0.0301
	ACC	35	166	0.2108
Edo[3]	OAA	18	146	0.1233
	PNB	38	160	0.2375
	MET	10	194	0.0515
	PT	10	154	0.0649
	FO	2	151	0.0132
	ACC	26	155	0.1677
Recent Japan[4]	OAA	20	172	0.1163
	PNB	62	172	0.3605
	MET	16	180	0.0889
	PT	16	178	0.0889
	FO	3	180	0.0167
	ACC	26	180	0.1444
Mongolian[4]	OAA	26	176	0.1477
	PNB	32	175	0.1829
	MET	16	178	0.0899
	PT	31	174	0.1782
	FO	6	177	0.0339
	ACC	28	176	0.1591
Aleut[4]	OAA	14	114	0.1228
	PNB	22	112	0.1964
	MET	4	114	0.0351
	PT	6	116	0.0517
	FO	9	115	0.0783
	ACC	40	117	0.3419
Alaskan Eskimo[4]	OAA	29	199	0.1457
	PNB	55	198	0.2778
	MET	1	200	0.0050
	PT	15	198	0.0757
	FO	3	200	0.0150
	ACC	51	199	0.2563

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[3] Ishida and Dodo 1993
[4] Dodo and Ishida 1987

Population	Trait	Pres.	N	Frequency
Canada Eskimo[4]	OAA	12	150	0.0800
	PNB	38	149	0.2550
	MET	3	152	0.0020
	PT	4	141	0.0284
	FO	4	144	0.0278
	ACC	48	138	0.3478
Hopi[5]	LO	39	93	0.4193
	OAA	25	101	0.2475
	PNB	6	105	0.0571
	EPB	7	74	0.0946
	BB	22	93	0.3441
	CO	3	84	0.0357
	MET	31	95	0.3263
	FO	87	95	0.9158
	FS	3	102	0.0294
	APF	50	108	0.4630
	ACC	9	95	0.0947
	AIF	35	105	0.3333
Nootka[5]	LO	15	36	0.4167
	OAA	5	44	0.1136
	PNB	8	50	0.1600
	EPB	5	24	0.2083
	BB	16	48	0.3333
	CO	5	24	0.2083
	MET	10	50	0.2000
	FO	31	50	0.6200
	FS	3	50	0.0600
	APF	32	50	0.6400
	ACC	9	49	0.1837
	AIF	31	49	0.6326
Kwakiutl[5]	LO	55	95	0.5789
	OAA	19	110	0.1727
	PNB	28	118	0.2373
	EPB	4	53	0.0755
	BB	0	87	0.0000
	CO	20	64	0.3125
	MET	2	121	0.0165
	FO	6	118	0.0508
	FS	8	119	0.0672
	APF	60	116	0.5172
	ACC	25	115	0.2174
	AIF	37	117	0.3162

[5] Konigsberg et al. 1993