

**Paleoamerican morphology's
dispersion in the New World and its
implications for the settlement
of the Americas.**

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Abstract

During most of the 19th and 20th centuries, the best accepted paradigm for the settlement of the New World suggested that all Native American populations, past and present, derived from only one biological population, coming from Northeast Asia. However, craniometric analyses of early South and Mesoamerican skulls questioned this model by showing that the oldest populations known in the New World did not share the same morphological pattern with late Amerindian groups. The morphological pattern of these early populations is now known as Paleoamerican, and has been found widespread across South and Meso America, in population samples as well as in isolated specimens. Here we analyze for the first time the morphological affinities of all known Early American skulls from South and Meso America. Morphological affinities were assessed through Principal Components Analysis, and two tests were carried out. In the first the Early Americans were separated according to their geographic region while in the second they were considered as one same population. The results confirm previous analyses done by Neves and collaborators, showing high morphological affinities among the Early Americans samples as well as between these and Australo-Melanesian series. Late Amerindians always appear opposite from Early Americans in the morphospace. These results indicate that groups presenting the Paleoamerican morphology were widespread across South and Meso America, suggesting a relatively high population density, which facilitated gene flow among regional groups.

In the beginning of the XX century, Hrdlicka (1912, 1917) published his vision that Native American diversity could be accommodated in one single biological stock. His vision of a high homogeneity among American populations, past and present, was later adopted as a paradigm for the settlement of the New World, together with (and probably helped by) the discovery of Clovis and Folsom points in 1927 (Figgins 1927) that till very recently were seen as the archetype of the first human groups to arrive in the Americas (see Roosevelt et al. 1996 and Waters & Stafford 2007 for strong evidence against the Clovis First paradigm). Yet, Hrdlicka's view of the settlement of the Americas could hardly be accepted by many of his contemporaries. Rivet (1908), Imbelloni (1938) and Dixon (1923), to name a few, argued against the biological homogeneity of Native American populations. In the cases of Rivet (1908, 1942) and Imbelloni (1938) it was suggested that some of these populations did not share a common ancestor in East Asia, as defended by Hrdlicka, and advocated for the necessity of at least one more migration, probably coming from Melanesia, to explain this diversity.

Despite the views of Rivet and Imbelloni, Hrdlicka's view prevailed, establishing already in early XX century the idea that America's settlement was very monotonous in terms of human biology. Between the 1940s and most of 1960s there was a general abandonment of craniometric studies as potential sources of information about human micro-evolution (Armelagos et al. 1982; Harper & Laughlin, 1982). The relation between anthropometrical studies and the racial controversy that peaked in the years after World War II helped to discredit the attempts to analyze the cranial variation of early Americans under a comparative perspective.

During the 1970s, advances in the quantitative and computational techniques allowed for the craniometric studies to move beyond the typological description of early decades, reassuming its role as an important tool to investigate human biological relationships. Howells (1973) pivoted the new era of craniometric studies, with his worldwide analysis of human morphological diversity. Together with two further publications (1989, 1995), Howells showed that human groups within each geographic region shared similar morphological patterns, thus demonstrating the validity of craniometrics to infer human biological affinities. Yet, despite efforts to understand human biological diversification through craniometrics, little attention was given to the American case. Even though Howells measured 30 samples around the world only 4 were measured in America, all showing clear relationship with East Asians and consequently supporting the homogeneity of Native Americans.

This lack of interest in America is hard to explain, since during the same period craniometric analyses were being used to infer human microevolutionary trajectories in other regions of the globe. According to Jantz and Owsley (2001), one possibility is that the question of Native American origins was already solved in the eyes of the North American Anthropological community since the time of Hrdlicka. In South America, craniometric studies did not receive much attention as well, mainly because classical and typological physical anthropology survived until very late in the sub-continent (see Mello e Alvim et al., 1977 for an example).

In the late 1980s, early human skeletal remains from South America were finally analyzed through multivariate methods of quantitative analysis (see Neves and Pucciarelli 1989, 1990, 1991 for the first contributions). The results obtained clearly suggested that these remains had stronger morphological affinity with Australo-Melanesians and Africans than with late Amerindians or East Asians. Upon the (re)discovery that early South Americans did not share high affinities with Native Americans, Neves and collaborators started analyzing early South American skeletal remains available in museum collections in Brazil and elsewhere. These further studies confirmed their initial impressions (Neves & Pucciarelli 1998; Neves et al. 1998, 1999a, 1999b, 1999c). This allowed for the suggestion that the arrival of

mongoloid groups in the New World was preceded by the entrance of groups showing a quite distinct morphological pattern, later named as the Paleoamerican morphology (Jantz & Owsley 1997; Steele & Powell 1999; Powell and Neves 1999). While the typical Native American morphology is very similar to East Asian morphology (classically known as Mongoloid) and shows a central tendency towards short and wide skulls, with high and flat faces and high orbit and noses, the Paleoamerican morphology has a very distinct tendency defined by long and narrow skulls, with low and projected faces and low orbits and noses (Neves & Hubbe 2005; Neves et al, 2007). The model suggested by Neves and collaborators is now known as the "Two Main Biological Components Model" (Neves et al. 2003).

However, despite the growing evidence towards a widespread presence of the Paleoamerican morphology in the Americas, these results were largely ignored until very recently by the North American anthropological community. Early critics to the model argued that it was based on a small number of skulls, and thus the Paleoamerican morphological pattern could be just a local extreme of the mongoloid morphological variation (Brace et al. 2001; Dillehay 2000, Roosevelt et al. 2002, van Vark et al. 2003).

Early human skeletons are rare in the continent, but especially so in North America, where no more than a few skeletons older than 8 kyr are known (Jantz and Owley 2001). In South America, the situation is less dramatic. As a result of 20 years of effort by Neves to generate an acceptable chronological contextualization for the potential Late Pleistocene/Early Holocene human remains which sat in storage in many South American institutions, a collection of early remains surpassing one hundred skulls from distinct regions of South and Meso America are now known. Without exception, all skulls older than 7.5 thousand years analyzed to date share the Paleoamerican morphological pattern. This morphological pattern has been found in Lagoa Santa, Central Brazil (Neves & Hubbe, 2005), where 81 skulls were analyzed; in the Bogotá Savannah, Colombia (Neves et al, In Press), a sample composed of 17 skulls; in Central México (González-José et al., 2003), represented by 5 skulls; and in isolated skulls from Southeastern Brazil (Capelinha; Neves et al., 2005), Central Brazil (Toca das Onças; Hubbe et al., 2004), Northeastern Brazil (Toca dos Coqueiros; Hubbe et al. In Press) and in Southern Chile (Palli Aike; Neves et al., 1999c). Thus, in the last five years the study of the South and Mesoamerican oldest human remains have successfully contested the criticisms that the peculiar cranial morphology of the first Americans would be a result of sampling only a few early skeletal remains.

However, the idea of two very different human populations entering the New World is not confirmed by molecular biology. In general, molecular studies of recent native populations favor one single migration (see Zegura et al., 2004, for a review on the subject), reinforcing Hrdlicka's ideas that all Native Americans (past and present) share a common ancestor in northeast Asia. At first, those espousing the dual-origin model defended the idea that Paleoamerican groups were largely, if not totally, replaced by mongoloids without genetic exchange between them (Munford et al., 1995; Neves et al., 1999d). Accordingly, the lack of molecular evidence for a bipartite model could be explained by the lack of molecular signature of the first population in present biological variation. Yet, recent craniometric studies have shown a late survival of Paleoamerican morphology in different regions of South and Meso America. In some cases, the survival occurred in isolated regions, where the mongoloids were unable to reach. This is the case of Tierra del Fuego (Lahr, 1995) and the Baja California peninsula (Gonzalez-José et al. 2003). But, in other regions, the Paleoamerican morphology survived unchanged side by side with Mongoloid groups. Such coexistence has been found in the Bogota Savannah, Colombia (Neves et al. In Press), among the central Brazil Botocudo Indians (Atui 2005), and in South Brazil, among the Umbu tradition (Neves et al. 2004b). These findings make it hard to reconcile the molecular and the morphological data.

The studies of early American skulls carried out so far have assessed these remains in relation to the worldwide morphological diversity as separate samples. Despite the fact that the results are very convergent, regardless of the region the samples come from, the South and Mesoamerican early human skeletal remains have never been assessed as a whole. Here we demonstrate that all early human specimens from South and Mesoamerica known so far share a high morphological affinity. Accordingly, they can be considered as part of one major single population.

MATERIAL AND METHODS

The Early Americans sample analyzed here is composed by 107 individuals, 56 males and 51 females. Together they represent three major regions (Lagoa Santa, Bogota Savannah and Central Mexico) and some isolated specimens (Toca dos Coqueiros, Capelinha and Palli Aike). All specimens are dated to between 11.5 and 6.0 thousand radiocarbon years BP. Table 1 details the number of individuals in each sample, their chronology and geographic region. Figure 1 illustrates their geographic location.

In each skull, 46 linear measurements were taken (Tables 2 and 3) by one of us (WN), following the protocol of W. W. Howells. To assess the morphological affinities of these early specimens, they were compared to 30 Howells samples, which describe the human morphological variation around the globe. To increase the number of late Amerindian samples, two Brazilian coastal series (Base Aérea and Tapera) were added to the analyses. Names, size and geographic origin of the comparative samples can be seen in Table 4.

Morphological affinities were assessed through Principal Components Analysis. Two different analyses were conducted: the first considered the early Americans separated according to their respective regions; the isolated specimens were grouped together. The second analysis considered all Paleoindians together, as one sample. The objective of the first analysis was to demonstrate that early Americans from different regions have a high morphological affinity among themselves. The second analysis explored their intra and extra continental morphological affinities as a group.

Principal Components were extracted from the covariance matrices of the group centroids. Males and females were analyzed separately and in each case analyses were run on the raw database and on databases where the size effect of the skulls was corrected. Such correction was achieved by dividing each variable by the geometric mean of the individual, following the method proposed by Darroch and Mosimann (1985). To minimize the number of variables represented by a few individuals, the first approach was based on 41 variables for males and 39 for females, while the second was based on 46 variables for males and 39 for females (Tables 2 and 3). All analyses were performed on databases without missing values.

RESULTS

Figure 2 shows the morphological affinities represented by the first two principal components (PCs) of the male centroids, without size correction, when the Early Americans were considered as separated samples, according to their region. In this case, both PCs resume 86.06% of the original variance. As can be seen, there is a close affinity between Lagoa Santa, Colombia, the isolated specimens and Australo-Melanesian series. The Paleomexican sample appears associated to Easter Island and Eskimo. With the exception of Eskimos, the late Amerindian samples appear in the opposite side of the graph, closely associated with East Asians.

In Figure 3 the same analysis is represented, but now size effect was removed from the samples. Here the PCs summarize 46.91% of the original data. In this analysis Lagoa Santa and Colombia are again closely associated with Australo-Melanesians. With the removal of size effect, there is a clear approximation between Paleomexicans and the other Early American series, while the isolated skulls appear as outliers to all series. The late Amerindian samples, with the exception of Eskimos, occupy the opposite side of the graph together with East Asians, mainly when the first component is considered.

Figure 4 shows the morphological affinities for females, when both size and shape information is considered, still considering the Early Americans as separate samples according to region. The two PCs in this analysis represent 64.39% of the original variation. In this case, only Lagoa Santa and Colombia were included in the analysis, since there are no female isolated skulls and the only Paleomexican female skull is too fragmented to be considered. Nonetheless, the association between Early Americans and Australo-Melanesians is evident, while the late Amerindian samples appear on an opposite position, associated to East Asians.

When size effect is removed, the morphological affinities among females are as showed in Figure 5. The PCs used in this analysis resume 48.57% of the original variance. Again, the Early American samples appear closely associated between themselves and with Australo-Melanesians, especially Tolai. Following the pattern previously observed, the late Amerindian samples appear on an opposite position in relation to Early Americans.

Figure 6 represents the morphological affinities among the male series, without size correction, when Early Americans are considered as one series. The first two PCs in this case resume 66.81% of the original variation. There is no doubt about the close association between them and Australo-Melanesians, in contraposition to the late Amerindian samples, closely associated to East Asians. The exception to this rule is Eskimo, which appears more associated to Polynesians.

Exactly the same relationship is seen in Figure 7, where size effect has been removed. The first two PCs in this case condense 49.81% of the original variation.

In Figure 8 the morphological affinities of females, with size and shape considered, are shown. The two PCs used to construct this graph resume 64.85% of the original variation. The relationships seen here are exactly the same presented in the previous analyses. Early Americans are closely associated to Australo-Melanesians, while late Amerindians appear associated to East Asians in an opposite position on the second component.

Figure 9 shows the morphological affinities of female centroids with only shape information considered. Here, the first two PCs resume 51.63% of the original variation. Again, Early Americans appear associated to Australo-Melanesians, but especially to Tolai. Late Amerindians appear distant from Early Americans and closely associated to East Asians.

DISCUSSION AND CONCLUSIONS

The results presented here clearly demonstrate that the Early Americans analyzed do not share any morphological affinities with the later Native American groups represented in the study. As stated before, the idea that Early Americans present a distinctive morphological pattern from recent Amerindians is not new. It has been proposed in the 19th and early 20th centuries by many scholars (Lacerda & Peixoto, 1876; Rivet 1908; Dixon 1923; Imbelloni 1938), and continuously restated through modern quantitative analysis for almost 20 years now (Neves & Pucciarelli 1989, 1990, 1991, 1998; Neves et al. 1999a, b, c, 2003, 2004a, 2007; Powell & Neves 1999; Steele and Powell 1999; Neves & Hubbe 2005). In this context, the results presented here help to demonstrate that the Paleoamerican morphology is not a sampling anomaly, but a real morphological entity, or bauplan, that characterized the pristine populations of the New World.

The craniometric analysis of Early Americans groups does not contribute much to our knowledge about the time or the route of entry of these populations in the New World. Since the proposition of the bipartite model, Neves and collaborators have systematically argued that the first biological component to enter the New World did so around 14 kyr and that they arrived from Northeast Asia through the Bering Strait. Rather than a conclusion derived from the craniometric analyses of the first South Americans, this view is based primarily on a parsimonious reading of the archaeological data available so far. Many authors have interpreted these results as suggesting a trans-pacific route to South America directly from Australo-Melanesia. However, Paleoamerican groups share high morphological affinities with Late Pleistocene skulls in East Asia, such as Upper Cave 01 (Neves & Pucciarelli 1998), which have been shown to present a generalized morphology (Kamminga & Wright 1988; Wright 1995). The strong morphological affinity between them supports the view that Paleoamericans and Australo-Melanesians shared a common ancestor in Southeast Asia.

The results presented here suggest that Paleoamericans were as able as the later mongoloid groups to disperse throughout the entire New World, occupying many different ecosystems. The idea that these populations would have been completely replaced by mongoloid groups with minimum genetic exchange between them, as initially argued by defendants of the bipartite model (Munford et al. 1995; Neves et al. 1999d), has been revised in the light of new results (Lahr 1995; Gonzalez-José et al. 2003; Neves et al. 2004b, 2007; Atui 2005). The fact that Paleoamerican late survival is not as rare as previously thought suggests a relatively high population density for these groups. Again, this is supported by the results obtained here.

Independent evidence for a higher population density for Paleoamericans comes from their morphological identity across the continent. Genetic drift is expected to have larger magnitudes in the differentiation of small groups scattered in large areas. Thus, if the Paleoamericans were characterized by small groups with a small degree of contact among them, it would be expected a high variance between them. The results present here clearly demonstrate that Early American groups shared one same skull architecture, i.e. low interregional

variance, despite the fact that they were, in some cases, located thousand of kilometers apart (Figure 1). This is especially true between Lagoa Santa and Colombia, which appear together in all analyses performed. Even Paleomexicans, which appear somewhat separated in the Size and Shape analysis, appears perfectly associated with the other early samples when size factor is corrected.

On the other hand, assuming that Paleoamericans had a relatively high population density prior to the arrival of the mongoloid groups, makes it harder to explain the apparent lack of miscegenation between both biological components. As already mentioned, molecular studies of modern Amerindians suggest a relative homogeneity among these populations (Bonatto & Salzano 1997; Zegura et al. 2004; Schurr 2004).

In conclusion, the results of the analyses based on the totality of human skulls older than 6 kyr BP from South and Meso America demonstrate that Paleoamericans were wide-spread across the continent and suggest that these pristine Americans had a relatively high population density which facilitated gene flow among regional groups. Future research will have to focus on the period of

Table 1 - Number of individuals, chronology and geographic location for the Early American samples used in the study.

<i>Early American Series</i>	<i>N Males</i>	<i>N Females</i>	<i>N Total</i>	<i>Chronology (kyr BP)</i>	<i>Geographic Location</i>
Lagoa Santa	43	39	82	11.0 - 7.5	Minas Gerais, Brazil
Colombia	6	11	17	10.0 – 6.0	Sabana de Bogotá, Colombia
Paleomexicans	4	1	5	~ 6.0	Mexico Basin, Mexico
Toca dos Coqueiros	1	0	1	~ 10.0	Piaui, Brazil
Capelinha	1	0	1	~ 8.5	São Paulo, Brazil
Palli Aike	1	0	1	~ 8.0	Patagonia, Chile
Total	56	51	107		

Table 2 – Variables measured and their values in millimeters (males).

<i>Variable name</i>	<i>Lagoa Santa</i>	<i>Colombia</i>	<i>Paleomexicans</i>	<i>Isolated specimens</i>	<i>All Early Americans</i>
labello-occipital length (GOL)	184,45	186,50	198,50	183,00	186,01
Nasio-occipital length (NOL)	180,84	183,17	196,25	180,67	182,67
Basion-nasion length (BNL) ¹	-	-	-	-	100,69
Basion-bregma height (BBH) ¹	-	-	-	-	135,00
Maximum cranial breadth (XCB)	129,86	129,50	137,50	130,67	130,60
Maximum frontal breadth (XFB)	110,70	107,50	116,33	114,33	110,90
Zygomaxillare breadth (ZYB)	132,00	136,50	142,50	128,00	133,78
Biauricular breadth (AUB)	122,04	122,00	127,75	119,00	122,41
Biasterionic breadth (ASB)	110,17	109,17	114,00	109,33	110,15
Nasion-prosthion height (NPH)	63,75	68,83	67,00	71,00	65,33
Nasal height (NLH)	47,89	50,17	49,33	48,25	48,44
Orbit height (OBH)	33,15	32,92	37,00	35,00	33,43
Orbit breadth (OBB)	39,77	38,67	43,50	40,00	39,80
Bijugal breadth (JUB)	116,62	115,50	122,00	113,00	116,64
Nasal breadth (NLB)	24,71	25,25	25,67	24,50	24,89
Alate breadth, external (MAB)	62,93	59,50	67,00	61,00	62,89
Bimaxillary breadth (ZMB) ¹	-	-	-	-	99,71
Zygomaxillary subtense (SSS) ¹	-	-	-	-	21,89
Bifrontal breadth (FMB)	101,05	98,00	105,33	95,00	100,60
Nasio-frontal subtense (NAS)	14,96	13,83	15,67	14,00	14,81
Biorbital breadth (EKB)	97,71	96,83	101,00	96,00	97,70
Dacryon subtense (DKS)	8,09	8,17	12,00	5,00	8,16
Interorbital breadth (DKB)	24,47	22,50	26,33	23,00	24,25
Simotic cord (WNB)	7,94	8,67	10,67	4,00	8,25
Malar length, inferior (IML)	40,00	36,60	38,00	35,00	38,52
Malar length, maximum (XML)	54,79	54,80	52,00	45,50	53,64
Malar subtense (MLS)	11,63	10,40	10,50	7,00	10,79
Cheek height (WMH)	24,46	25,50	24,00	21,50	24,43
Oramen magnum length (FOL) ¹	-	-	-	-	36,09
Frontal cord (FRC)	110,88	110,25	117,50	107,00	111,12
Frontal subtense (FRS)	23,82	23,00	22,25	26,00	23,72
Nasion-subtense fraction (FRF)	49,48	47,83	49,50	47,33	49,11
Parietal cord (PAC)	115,29	115,75	119,50	122,67	116,29
Parietal subtense (PAS)	25,04	24,00	23,75	29,67	25,10
Zygoma-subtense fraction (PAF)	60,21	60,33	60,25	65,67	60,63
Occipital cord (OCC)	99,28	99,30	103,00	95,67	99,17
Occipital subtense (OCS)	30,10	31,80	35,00	26,33	30,33
Lambda-subtense fraction (OCF)	48,43	51,40	45,50	42,33	48,12
Nasion radius (NAR)	95,27	96,00	95,25	96,17	95,47
Subspinale radius (SSR)	97,00	101,00	98,33	91,00	97,85
Prosthion radius (PRR)	102,92	103,40	109,67	108,00	104,18
Dacryon radius (DKR)	83,56	84,67	88,00	82,00	84,32
Zygoorbitale radius (ZOR)	83,44	86,17	85,33	84,67	84,36
Frontalmalare radius (FMR)	81,25	83,17	84,33	79,00	81,77
Ectoconchion radius (EKR)	75,31	76,00	76,67	74,00	75,52
Zygomaxillare radius (ZMR)	77,40	78,00	75,33	77,33	77,27

¹ Variables not used in the analyses that considered the Early Americans as separated groups because they were absent in at least one of the samples.

Table 3 – Variables measured and their values in millimeters (females).

<i>Variable name</i>	<i>Lagoa Santa</i>	<i>Colombia</i>	<i>All Paleoamericans</i>
Glabello-occipital length (GOL)	178,92	180,78	179,61
Nasio-occipital length (NOL)	175,48	179,44	176,80
Basion-nasion length (BNL)	95,63	98,60	96,42
Basion-bregma height (BBH)	130,50	130,40	130,40
Maximum cranial breadth (XCB)	127,70	130,56	128,51
Maximum frontal breadth (XFB)	108,17	108,00	108,22
Biauricular breadth (AUB)	113,95	115,13	114,68
Biasterionic breadth (ASB)	104,57	109,50	105,97
Nasion-prosthion height (NPH)	58,40	65,80	62,14
Nasal height (NLH)	44,71	48,70	46,50
Orbit height (OBH)	32,40	34,10	33,15
Orbit breadth (OBB)	37,35	37,80	37,56
Nasal breadth (NLB)	24,58	24,45	24,50
Palate breadth, external (MAB)	59,88	62,00	60,59
Bimaxillary breadth (ZMB)	95,75	93,00	94,75
Bifrontal breadth (FMB)	95,58	97,11	96,27
Nasio-frontal subtense (NAS)	13,14	14,22	13,55
Interorbital breadth (DKB)	22,53	22,78	22,70
Simotic cord (WNB)	8,25	9,57	8,75
Malar length, inferior (IML)	31,58	34,50	33,50
Malar length, maximum (XML)	47,67	50,63	49,67
Malar subtense (MLS)	9,08	9,75	9,46
Cheek height (WMH)	22,38	22,73	22,64
Foramen magnum length (FOL)	33,96	33,00	33,97
Frontal cord (FRC)	107,41	107,80	107,74
Frontal subtense (FRS)	24,78	24,09	24,54
Nasion-subtense fraction (FRF)	46,76	46,18	46,58
Parietal cord (PAC)	112,57	109,50	112,08
Parietal subtense (PAS)	24,52	21,50	23,84
Bregma-subtense fraction (PAF)	60,04	57,63	59,66
Occipital cord (OCC)	96,72	99,00	97,19
Occipital subtense (OCS)	28,72	30,50	29,26
Lambda-subtense fraction (OCF)	45,67	48,38	46,30
Nasion radius (NAR)	90,78	93,88	91,81
Subspinale radius (SSR)	91,06	95,00	92,90
Zygoorbitale radius (ZOR)	80,29	81,14	80,71
Frontalmalare radius (FMR)	79,53	79,25	79,44
Ectoconchion radius (EKR)	73,21	71,71	72,46
Zygomaxillare radius (ZMR)	73,25	74,14	73,67

Table 4 – Sample size and geographic location of the reference series included in the study.

Series	Geographic Region	N Males	N Females
BASE AÉREA	Late Archaic America	12	12
TAPERA	Late Archaic America	28	30
ESKIMO	North America	53	55
ARIKARA	North America	42	27
SANTA CR	North America	51	51
PERU	South America	55	55
TEITA	Africa	33	50
DOGON	Africa	47	52
ZULU	Africa	55	46
EGYPT	Africa	58	53
BUSHMAN	Africa	41	49
N JAPAN	Asia	55	32
S JAPAN	Asia	50	41
AINU	Asia	48	38
BURIAT	Asia	55	54
ANYANG	Asia	42	-
HAINAN	Asia	45	38
AUSTRALI	Australo-Melanesia	52	49
TASMANIA	Australo-Melanesia	45	42
TOLAI	Australo-Melanesia	56	54
NORSE	Europe	55	55
ZALAVAR	Europe	53	45
BERG	Europe	56	53
S MAORI	Polynesia	10	-
N MAORI	Polynesia	10	-
MOKAPU	Polynesia	51	49
EASTER I	Polynesia	49	37
MORIORI	Polynesia	57	51
ANDAMAN	South Asia	35	35
PHILLIPI	Western Pacific	50	27
GUAM	Western Pacific	30	-
ATAYAL	Western Pacific	29	18
Total		1417	1198



Figure 1 – Geographic location and approximate chronology of the Early American samples analyzed.

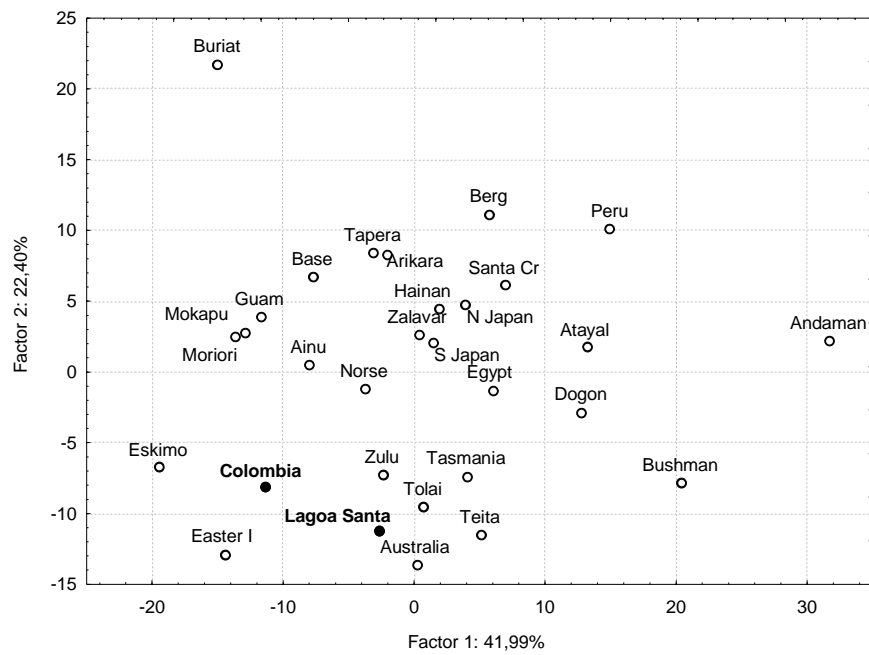


Figure 4 - Morphological affinities among the series centroids (females, size and shape) seen through the first two principal components. In this analysis the Early Americans were separated in groups according to their geographic origin. The percentages associated to each axis are the amount of the original information condensed by each principal component.

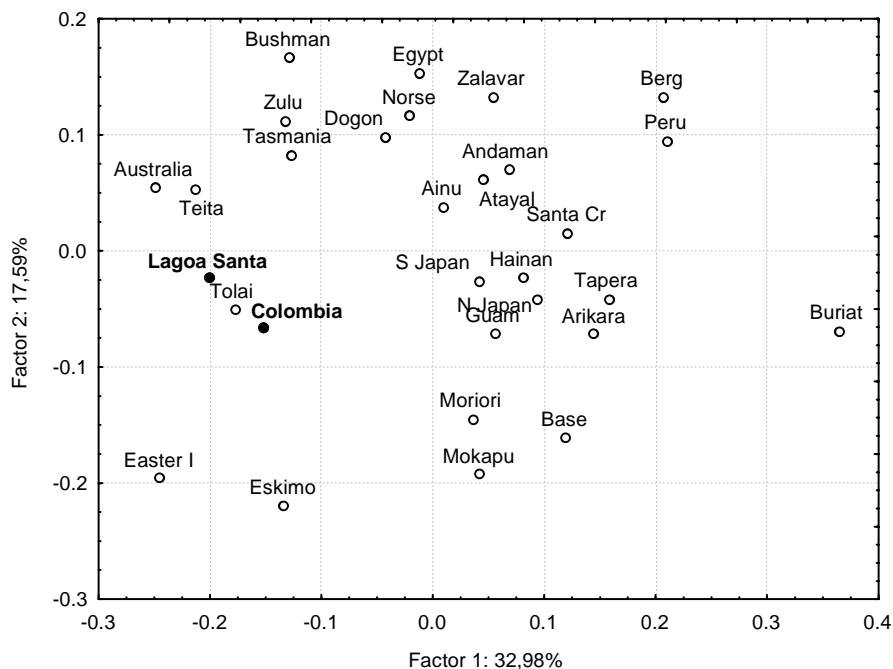


Figure 5 - Morphological affinities among the series centroids (females, shape alone) seen through the first two principal components. In this analysis the Early Americans were separated in groups according to their geographic origin. The percentages associated to each axis are the amount of the original information condensed by each principal component.

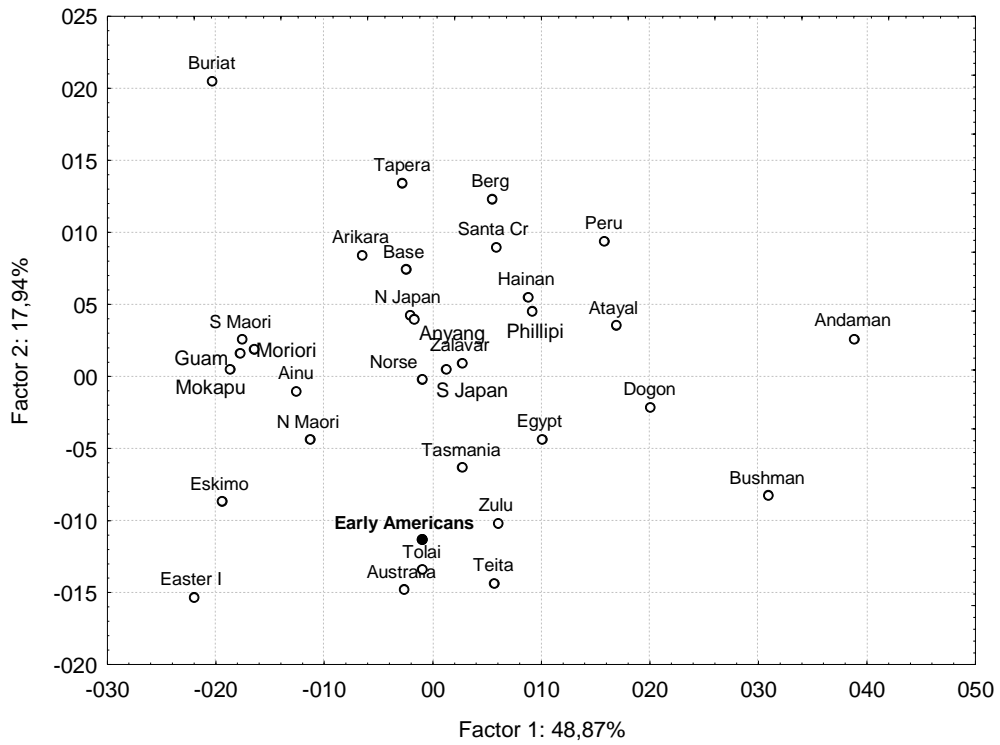


Figure 6 - Morphological affinities among the series centroids (males, size and shape) seen through the first two principal components. In this analysis the Early Americans were grouped in one single series. The percentages associated to each axis are the amount of the original information condensed by each principal component.

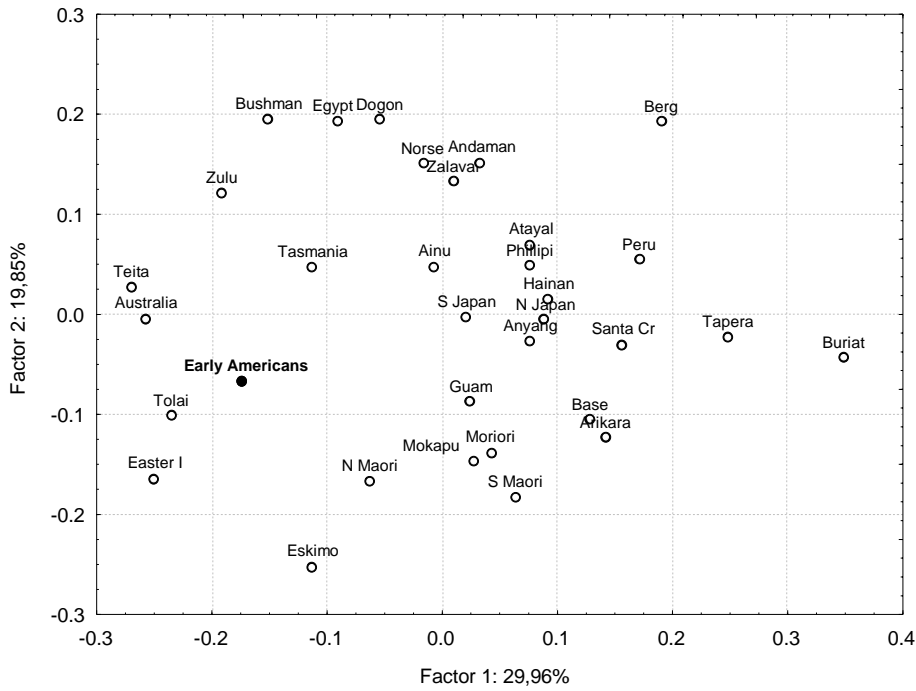


Figure 7 - Morphological affinities among the series centroids (males, shape alone) seen through the first two principal components. In this analysis the Early Americans were grouped in one single series. The percentages associated to each axis are the amount of the original information condensed by each principal component.

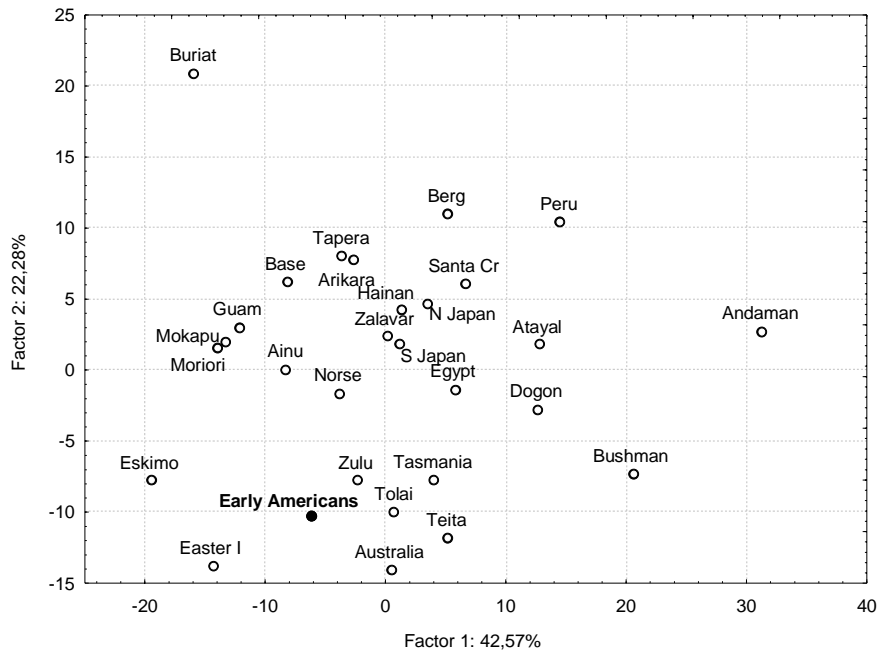


Figure 8 - Morphological affinities among the series centroids (females, size and shape) seen through the first two principal components. In this analysis the Early Americans were grouped in one single series. The percentages associated to each axis are the amount of the original information condensed by each principal component.

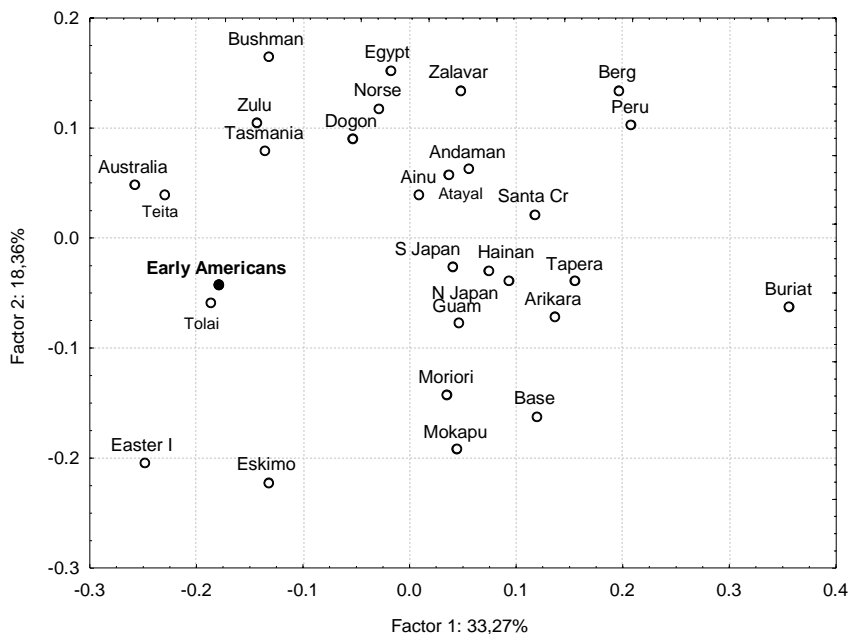


Figure 9 - Morphological affinities among the series centroids (females, shape alone) seen through the first two principal components. In this analysis the Early Americans were grouped in one single series. The percentages associated to each axis are the amount of the original information condensed by each principal component.

arrival of Mongoloid groups in Meso and South America and consequently in the process of transition or replacement of Paleoamericans by the newcomers.

FOOTNOTES

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