Cranial morphological structure of North and South American populations: Implication for discussions about the early human occupation of the American continents

Research Thesis

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By

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Abstract

The biological and morphological diversity of Native American populations has been a topic of intense scrutiny over the past decades, with recent studies demonstrating that the process of human dispersion across the American continents was complex and non-linear. Despite this, the two continents are often combined into one macro-continent in studies about past and present biological diversity, and the differences in human history and occupation between them are largely ignored or oversimplified. In this study, we contribute to the debate about past human dispersion in the Americas by analyzing the cranial morphological variation of 39 population samples from both North and South America. Cranial morphology was represented through 18 linear craniometric variables, and their morphological affinities were explored using multidimensional scaling (MDS) and k-means clusters based on Mahalanobis distances. The MDS results show that North and South American populations overlap considerably in their morphological affinities. However, the k-means results plotted over the geographic location of the series show strong similarities between high-latitude North and South American populations and high affinities among Andean South American populations and most North American series. Eastern South American groups differentiate themselves from other populations, highlighting the biological impacts of different population histories across the southern continent. These results contrast with previous perspectives of grouping the settlement of the two continents into a single large dispersion event. The high degree of cranial diversity seen in the American continents reinforces the need to discuss North and South American human occupation separately by considering their unique histories.

Introduction

North and South America hold a unique place in the topic of early human migration. As the last two large land masses occupied by humans, North and South America have been a topic of debate for centuries, with hundreds of articles dedicated to the topic in the last two decades alone. Current consensus based on genetic and archaeological evidence supports that the dispersion of humans into the American continents across the Bering Strait started at the earliest 30,000 years ago, with the majority of the evidence supporting later arrival dates (between 15,000 and 13,500 years ago) (16). However, there exist many contradictions to this time frame which challenge this scenario, suggesting more complex histories of human occupation of the continents. Some archaeological sites in South America date back to 32,000 years ago (19). Recently, 40,000-year-old potential human footprints in volcanic ash have been reported in Mexico (44), and even a site dated to 130,000 years BP has been proposed in North America (22). This lack of conclusive evidence has continued to motivate the desire to better understand early human migration into the American continents.

North and South America have a lot to offer in terms of diverse environments and histories. During the end of the Pleistocene, around the time of the initial human occupation of the continents, the last glacial maximum ended by the retreat of the continental ice sheets around 15,000 years ago, creating rapidly changing environments overlapping with early human occupation (33). The Pleistocene, defined as a time of glaciation, allowed for early human migration over the Bering Strait into North America, but presented challenges for human dispersion after the initial crossing, due to the cold environments and icesheets covering the northern portion of North America (40). Given the tight window of climatic opportunity, some authors have suggested an extremely rapid dispersion into South America, with some models calculating the process in as little as 300 years (33). These debates sometimes lead to questioning of the original entry date of humans into the continents (33). These rapid climate changes influenced the flow of human migration through the continents (49). Environmental changes resulted in diversity of plant and animal species, megafaunal extinction events, and a variety of wet vs. dry regions, which highlight the ecological diversity within the two continents during the time of early human settlement (10). Hubbe et al. (2009) describe the influence certain climate parameters have on cranial morphology diversity in human populations (26), suggesting that climatic diversity seen in late Pleistocene North and South America would have contributed to the biological diversity in the continents. The climatic changes occurring in the two continents that overlap with human arrival in North America is a unique phenomenon, unlike what is observed in other regions of the globe (46).

After the initial arrival of humans into North America, there was a rapid dispersion and radiation within the different ecological regions on both North and South America. Despite the wealth of discussions about how humans crossed from Asia into North America, information on how humans migrated from North America to South America are sparce (10). The diverse environments of North and South America most likely would result in changes in human populations while traveling between the two continents, given climatic and regional ecological diversity. Many of the studies done on human dispersion in the two continents group them into

one topic of discussion and refer to the scope of their conclusions as pertaining to “the Americas” or the “New World”. In doing that, the complexity and variety in the two unique continents, in reference to population specific dispersion events and, by consequence, the biological variation of the human groups in each continent, are overlooked and ignored when generalized models of human settlement are created. The studies which dispute the timing of the initial entrance of humans into North America, extrapolate those conclusions south by stating findings that are generalized to all of America (12, 30, 34). Research that does focus on South American timing and models also extrapolate their conclusions to North American migration models (18). This extrapolation and generalization of models creates a framework that restricts what kinds of questions are being asked, and in turn what kind of answers are then being produced.

Key aspects of the entire picture of early human migration may be overlooked when the two continents are grouped into one. Even earlier studies that highlight morphological diversity and that are in favor of considering population’s specific contexts and histories are still constrained by the idea of interchangeable North and South American human dispersion processes (41, 49, 29). For example, Stone’s study (2019) about the first peoples to enter Beringia from Siberia mentions the genetic and cultural diversity of the high latitude North American populations due to gene flow and regional climatic changes (49). The acknowledgement of the regional diversity present and complexity of migrations moves us toward more accurate frameworks for investigating population settlements. The sample populations used in the study are arctic North American populations. However, the study extrapolates these findings to explain processes in more than just arctic North America with the phrase “the Americas”, disregarding the importance of regional and population histories. Hubbe et al. (2021) present evidence for high morphological variation in early human populations in Quintana Roo, Mexico, and address the oversimplification of current models. However, the restrictive framework of referring to “the Americas” is still in use (29). In addition to Hubbe et al. (2021), there have been a few articles addressing the need to reframe the conceptual models in use (36, 10). We continue to add to this discussion and highlight the problematic use of phrases like “New World” or “the Americas”, which simplifies by nature that which is a complex process and fail to capture the dynamic actions of human dispersion through the two continents.

The settlement and early human dispersion through North and South America are a topic with no clear consensus to date. Multiple forms of evidence, including archaeological (11, 49, 22), linguistic (20, 38), and genetic (6, 43, 51), yield differing results (17, 40). The settlement of the two continents has been unclear since the early 1900’s (25) and is still debated in archaeology and biological anthropology today. Current models of settlement include a single migration into the continent, two discrete migrations, three dispersion events, continuous gene-flow with Asia, and varying combinations of these scenarios (29). The inconclusiveness of our models represents the limitations our field has faced in properly reconstructing past dispersion, as different forms of evidence support different models. In addition to the limitations that are intrinsic to the samples available and methods to reconstruct population affinities and dispersion models, there also exist constraints that we place around our conceptualization of settlement processes. Contextual and regional specific evidence found is often concluded as an

explanation for all of North and South America. By consequence, those generalizations halt the possibilities of further explanations of dispersion across the continents when it is perceived that both North and South America migration has been explained. Broadly applied models can blind us to the intricacy of population specific histories that result in biological variation within both continents

The habits of generalizing models of human settlement in North and South America are likely due to the colonial view of the settlement of *the Americas.* The large scholarly interest surrounding *the Americas* has developed within the historical context of European colonialization. Alongside the European efforts to colonize the continents came the efforts to understand the origins of the people occupying the land. The motivation to study the origins of Native American populations came from a desire to understand and, in turn, control a group that was unfamiliar to colonial Europe. The first official scientific excavation in the history of archaeology was an excavation of a Native American mound in Virginia led by Thomas Jefferson in 1784 (37). The context of this excavation situates a white man in power attempting to 'discover' the culture and origins of Native American populations, reflecting the European point of view engrained in the origins of this research. North American academia led the research on the peopling of the Americas in the early 20th century (1, 3, 7, 15, 24, 25, 47), continuing to lay the foundations of how we frame the two continents.

The colonial influence in bioarcheology is evident in early literature on the peopling of North and South America. Early articles on the settlement of the "New World" were not only guided by a structure which generalizes across regions, but in some cases also argued for biological and morphological homogeneity within Native American populations. The 1960 article by Stewart, for example, argues that the initial arrival of humans across the Bering Strait isolated the population resulting in both phenotypic and genotypic homogeneity in Native Americans across all of America (48). This statement of homogeneity, regardless of its accuracy, encourages research to stop after investigation on the initial entrance into North America. In contrast, Genové (1967) does acknowledge issues with views on the peopling of the Americas, including but not limited to the presuppositions scholars have of biological homogeneity in Native American populations (14). However, this article is an outlier in the literature of the 20th century *peopling of the Americas* and continues to group the continents into one topic of discussion. The 1932 article by Barbeau, while acknowledging diversity and arguing multiple migration waves into North America, continues to refer to "America", while the majority of references only pertain to the North American continent (3). While scholars began focusing on the topic of human origins in the Americas, they were influenced by the historic colonial framework from which the subject evolved, by making generalizable claims across geographic regions with phrases like "New World" and "the Americas" and overlooking the unique regional climatic, ecological, and historical contexts. It is necessary that we look at the origins of research on the settlement of North and South America with a critical eye to redefine how we frame our models of migration and dispersion. To create the most accurate and representative models of human settlement we must think reflexively to see how the field of Anthropology's own historical contexts shape our understanding of the origins of Native American populations.

Here, we aim to contribute to the discussion of the settlement of North and South America with the analysis of craniometric data from multiple prehistoric human populations from South and North America. The null hypothesis we test is the historical assumption that there is little population diversity present between the continents and therefore North and South America may be grouped into one topic of discussion.

Materials and Methods

Our sample comprises of 2,117 male human crania representing 39 geographic populations. A list of the populations used, sample sizes, geographic region, and the source for the measurements is presented in Table 1. The crania included were measured by two observers (Tsunehiko Hanihara and Walter Neves). The data includes 18 linear measurements of individuals crania, as detailed in Table 2. Only population samples with more than five individuals and individuals with less than 10 missing variables in the raw dataset were included in the analysis. Variables that showed significant inter-observer error (OCC) were also removed. Females were excluded because the sample size from Hanihara's dataset was too small to allow for reliable comparisons between continents.

Missing values were replaced using multiple regression estimations. The values added are estimates of the expected values predicted from the variables present for the individual, following the approach detailed in Hubbe et al 2011 (27). Multiple regressions were conducted in R (42).

To test for morphological affinities among series, morphological distances were represented by multi-dimensional scaling (MDS) analysis based on Mahalanobis squared distances (31). Mahalanobis distances (D^2) represent the morphological distance among groups, scaled by the inverse of the pooled within-group covariance matrix. The MDS analyses were run with three data sets: all variables, just variables of the face, and just variables of the neurocranium. Interorbital-breadth (DKB) was excluded from the face analysis as it is one of the measurements subject to inter-observer error, and its inclusion on the facial analysis was producing results that were significantly affected by this measurement. Variables identified as part of face or neurocranium are listed in Table 2.

Our second objective was to explore the ways in which series can be grouped based on their morphological affinities, and how these groupings are reflected in space based on their geographic location. To do so, we performed the k-means clustering analysis for each distance matrix. The k-means analysis takes the groups available in the distance matrix and classifies them into k clusters, based on the nearest distances. Several k-means analyses were done on the data, with k ranging from 2 to 10. Analyses were done with the three datasets, as before. The k-means cluster results were then mapped for k = 2, 3 and 7 groups to show geographic representation of the morphological clusters calculated. K-means analyses, and geographic maps were generated in R, using package FCPS (50) and functions developed by Daniel Fidalgo and Mark Hubbe. Geographic coordinates of sites were collected from previous publications with this dataset (26, 28).

Population	Population code	Sample Size	Region	Source
Eskimo Asia	AESK	22	NNAME	TH
Alaska	ALAS	35	NNAME	TH
Arizona	ARIZ	40	NAME	TH
Arkansas	ARKA	28	NAME	TH
Botocudos	BBCE	17	SAME	WN
CA British Columbia	BCOL	53	NNAME	TH
Cabeçuda	CABE	23	SAME	WN
Cabeçudas	CBS	8	SAME	WN
Eskimo Canada	CESK	29	NNAME	TH
Chile	CHIL	20	SAME	TH
Aleut 2	EALE	44	NNAME	TH
Enseada	ENSE	11	SAME	WN
Florida	FLOR	95	NAME	TH
Forte Marechal Luz	FMLUZ	6	SAME	WN
Eskimo Greenland	GESK	103	NNAME	TH
Guaraguaçu	GUARAGACU	10	SAME	WN
Illinois	ILLI	117	NAME	TH
Kentucky	KENT	37	NAME	TH
Maryland	MARY	52	NAME	TH
Mexico	MEXI	67	NAME	TH
Eskimo Alaska 3	NALA	63	NAME	TH
California 1	NCAL	59	NAME	TH
New Mexico	NMEX	54	NAME	TH
Eskimo Alaska 2	NWAL	106	NNAME	TH
Venezuela	NWSA	21	SAME	TH
New York	NYOR	27	NAME	TH
Ontario	ONTA	30	NNAME	TH
Patagonia	PATA	55	SAME	TH
Peru	PERU	221	SAME	TH
Piaçaguera	PIAÇA	10	SAME	WN
California 2	SCAL	163	NAME	TH
Dakota South 1	SDAK	118	NAME	TH
Sumidouro	SUMID	9	SAME	WN
Eskimo Alaska 1	SWAL	130	NNAME	TH
US Alaska Tlingit	TLIN	28	NNAME	TH
Tupi North Brazil	TUPINORTH	14	SAME	WN
Utah	UTAH	58	NAME	TH
Virginia	VIRG	57	NAME	TH
Aleut 1	WALE	77	NNAME	TH

Table 1. Populations included in this study (NNAME= north North America, NAME= North America, SAME= South America; TH = Data collected by Dr. Tunehiko Hanihara, WN = Data Collected by Dr. Walter Neves)

Variables	Grouping
Maximum cranial length (GOL)	Neurocranium
Nasion-opisthocranion (NOL)	Neurocranium
Cranial base length (BNL)	Neurocranium
Maximum cranial breadth (XCB)	Neurocranium
Maximum frontal breadth (XFB)	Neurocranium
Biauricular breadth (AUB)	Neurocranium
Biasterionic breadth (ASB)	Neurocranium
Basion-bregma height (BBH)	Neurocranium
Nasion-bregma chord (FRC)	Neurocranium
Bregma-lambda chord (PAC)	Neurocranium
Basion prosthion length (BPL)	Face
Bizygomatic breadth (ZYB)	Face
Nasion prosthion height (NPH)	Face
Interorbital breadth (DKB)	N/A
Orbital height (OBH)	Face
Nasal breadth (NLB)	Face
Nasal height (NLH)	Face
Palate breadth (MAB)	Face

Table 2. Linear measurements included in this study —measurement definitions according to Howells (1973, 1989) (23).

Results

Multi- Dimensional Scaling Analysis

Cranium

The morphological affinities of the series from the MDS analysis based on the D2 distance matrix are represented in Figure 1, coded by region. The MDS analysis shows structured morphological groups, with some overlaps and outliers between continents, rejecting the null hypothesis that both continents are similar enough to be grouped together in one single macro-region or continental-wide morphological pattern. The MDS results present the eastern Brazilian populations, Tupi North Brazil and Sumidouro as outliers, as they are not grouping closely with any region. The structured groupings do not separate themselves from each other completely as the regional morphologies overlap each other to some degree. Particularly, high latitude North American Populations (NNAM) and the high latitude South American series from Patagonia show overlap.

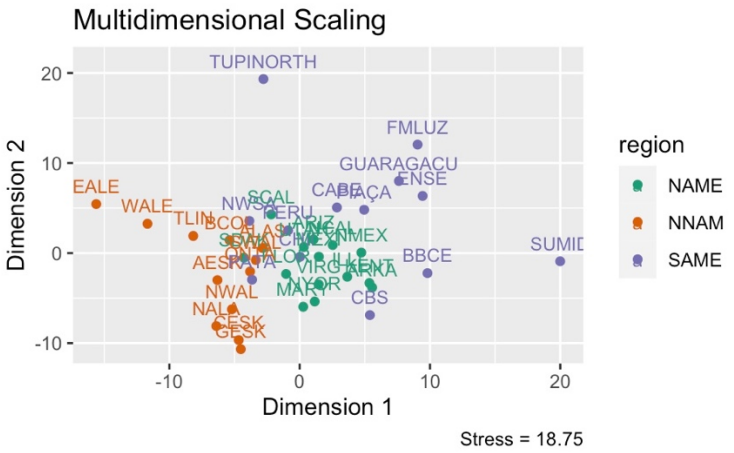

Figure 1. Multi-dimensional scaling analysis based on the D2 distance matrix including all variables of the cranium coded by geographic region (NAME= North America, NNAME= north North America, SAME= South America)

Face

The results of the MDS analysis based on only face variables is shown in Figure 2. When only face variables are analyzed a similar structure of regional affinities is observed, with overlap still presents. However, there is more spread of the South American series, in particular the populations Sumidouro and Tupi North Brazil, which appear as outlier groups in this analysis. The high latitude association seen between Patagonia and north North American (NNAME) series seen for the whole skull is still present here.

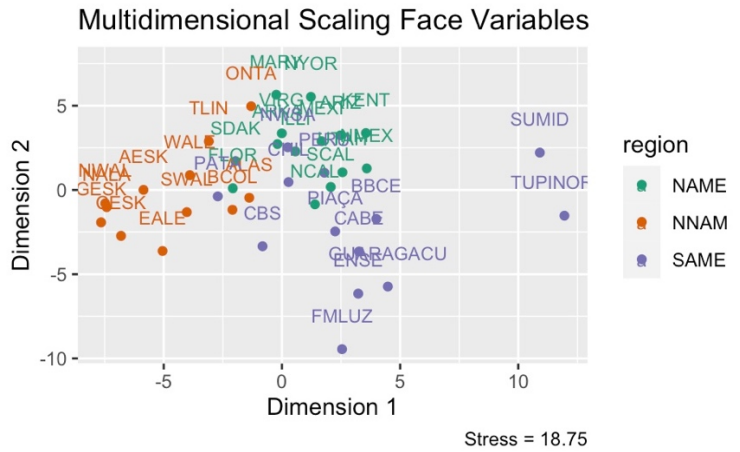

Figure 2. Multi-dimensional scaling analysis based on the D2 distance matrix including variables of the face coded by geographic region (NAME= North America, NNAME= north North America, SAME= South America)

Neurocranium

The MDS analysis results based on only neurocranium variables, coded by region, is shown in Figure 3. The regional groupings show significant overlap compared to the entire cranium and face variables, implying less regional differentiation in neurocranium variables, supporting currently accepted ideas that neurocranium morphology is less influenced by the environment. The eastern South American population, Tupi North Brazil, continues to appear as an outlier. Although not as distinct as in the previous analyses, the high latitude SAME series Patagonia continue to show high morphological affinities with series from the NNAM region.

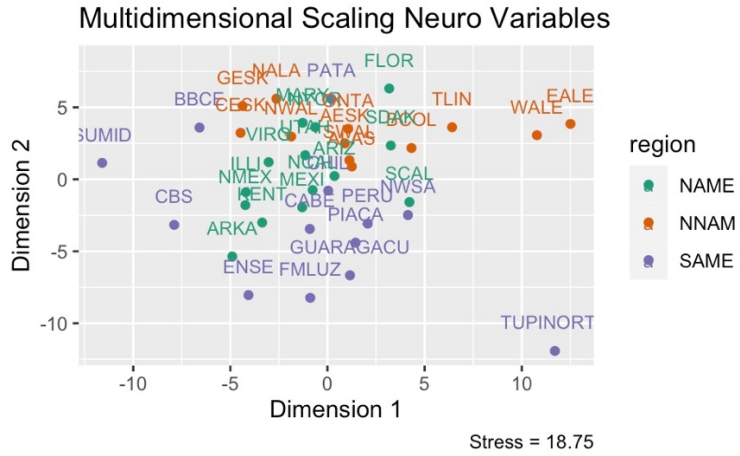

Figure 3.Multi-dimensional scaling analysis based on the D2 distance matrix including all variables of the neurocranium coded by geographic region (NAME= North America, NNAME= north North America, SAME= South America)

K-means Clustering Analysis

Cranium

The results of the k-means clustering analysis, for k = 2, 3, and 7 groups are shown in Figure 4, superimposed to the geographical location of the series. High latitude North and South American populations show strong affinities with each other. Andean South American populations group themselves with most North American series. Eastern South America Brazilian populations differentiate themselves from the other series in the southern continent beginning in the k = 3 group analysis, and the Aleut populations (Islands south of Alaska) separate themselves in the k=7 analysis. The k-means clustering results for the entire cranium for k-groupings 2-10 are shown in Table 3.

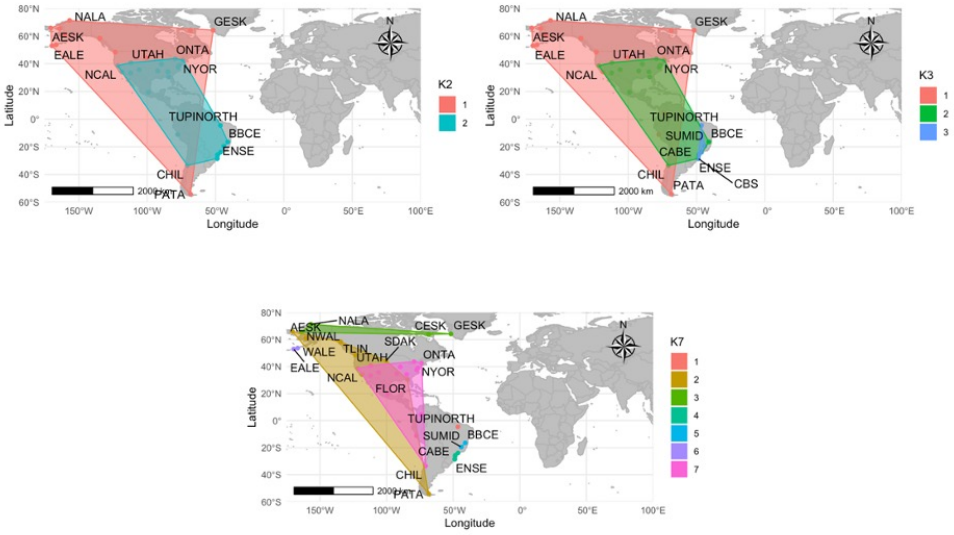

Figure 4. K-means clustering analysis including all variables of the cranium for k=2, 3, and 7 superimposed to the geographical location of the series.

Population	Region	K2	K3	K4	K5	K6	K7	K8	K9	K10
AESK	NNAM	1	1	4	1	5	2	7	7	7
ALAS	NNAM	1	1	2	3	5	2	7	7	7
ARIZ	NAME	2	2	3	5	2	7	4	9	1
ARKA	NAME	2	2	3	5	2	7	3	5	6
BBCE	SAME	2	2	3	4	4	5	1	2	1
BCOL	NNAM	1	1	2	3	5	2	7	7	7
CABE	SAME	2	3	1	2	6	4	6	8	9
CBS	SAME	2	2	3	2	6	4	3	5	6
CESK	NNAM	1	1	4	1	1	3	2	6	10
CHIL	SAME	2	2	3	5	2	7	7	4	2
EALE	NNAM	1	1	2	3	5	6	8	3	4
ENSE	SAME	2	3	1	2	6	4	6	8	9
FLOR	NAME	2	2	3	5	5	2	7	7	7
FMLUZ	SAME	2	3	1	2	6	4	6	8	9
GESK	NNAM	1	1	4	1	1	3	2	6	10
GUARAGACU	SAME	2	3	1	2	6	4	6	8	9
ILLI	NAME	2	2	3	5	2	7	3	5	6
KENT	NAME	2	2	3	5	2	7	3	5	6
MARY	NAME	2	2	3	5	2	7	4	9	5
MEXI	NAME	2	2	3	5	2	7	4	9	2
NALA	NNAM	1	1	4	1	1	3	2	6	10
NCAL	NAME	2	2	3	2	6	7	3	5	6
NMEX	NAME	2	2	3	5	2	7	4	9	1
NWAL	NNAM	1	1	4	1	1	3	2	6	10
NWSA	SAME	2	1	2	3	2	7	7	4	2
NYOR	NAME	2	2	3	5	2	7	4	9	5
ONTA	NNAM	2	2	3	5	2	7	4	9	5
PATA	SAME	1	1	4	1	5	2	7	7	7
PERU	SAME	2	1	2	3	2	7	7	4	2
PIAÃ‡A	SAME	2	3	1	2	6	4	6	8	9
SCAL	NAME	2	1	2	3	5	2	7	4	2
SDAK	NAME	1	1	3	5	5	2	7	7	7
SUMID	SAME	2	3	1	4	4	5	1	2	8
SWAL	NNAM	1	1	4	1	5	2	7	7	7
TLIN	NNAM	1	1	2	3	5	2	7	7	7
TUPINORTH	SAME	2	3	2	3	3	1	5	1	3
UTAH	NAME	2	2	3	5	2	7	4	9	1
VIRG	NAME	2	2	3	5	2	7	3	5	6
WALE	NNAM	1	1	2	3	5	6	8	3	4

Table 3. K-means clustering analysis values for K=2-10 for all variables of the cranium

Face Variables

The k-means clustering analysis of only face variables, for k = 2, 3, and 7 groups are shown in Figure 5, superimposed on the geographic coordinates of the series. High latitude North and South American populations continue to show strong morphological affinities, creating a wide-spread cluster in the continents. The northern continent eastern series distinguish themselves from the NAME region in k=7 clusters. Eastern south America, while still showing considerable unique identities, are grouping with the North American series and some western SAME populations, in the k=3 and k=7 clusters, showing a less clear separation of eastern South America from North America in this analysis. The Aleut populations that previously distinguished themselves in the k=7 clusters in Figure 4, are now grouped with high latitude SAME population Patagonia and North American Florida. The k-means clustering results for only face variables for k = 2-10 are shown in Table 4.

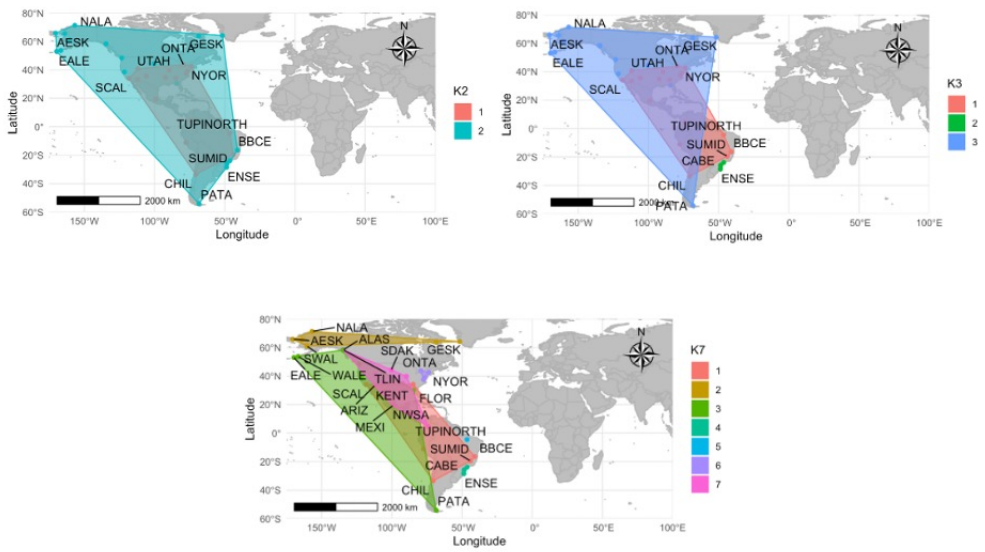

Figure 5.K-means clustering analysis including variables of the face for k=2, 3, and 7 superimposed to the geographical location of the series.

Population	Region	K2	K3	K4	K5	K6	K7	K8	K9	K10
AESK	NNAME	2	3	3	5	2	2	4	4	7
ALAS	NNAME	2	3	3	5	2	7	4	4	7
ARIZ	NAME	1	1	1	3	5	7	2	6	6
ARKA	NAME	1	1	1	3	5	7	2	6	6
BBCE	SAME	2	1	1	1	6	1	5	8	9
BCOL	NNAME	2	3	3	5	2	3	4	4	7
CABE	SAME	2	2	2	1	6	4	5	8	2
CBS	SAME	2	2	2	1	6	4	6	7	2
CESK	NNAME	2	3	3	5	4	2	4	2	10
CHIL	SAME	1	1	1	4	1	1	8	3	1
EALE	NNAME	2	3	3	5	2	3	1	5	5
ENSE	SAME	2	2	2	1	6	4	6	7	2
FLOR	NAME	2	3	3	5	2	3	1	5	5
FMLUZ	SAME	2	2	2	1	6	4	6	7	3
GESK	NNAME	2	3	3	5	4	2	4	2	10
GUARAGACU	SAME	2	2	2	1	6	4	5	8	9
ILLI	NAME	1	1	1	3	5	7	2	6	6
KENT	NAME	1	1	1	4	1	1	8	3	1
MARY	NAME	1	1	1	3	5	6	7	9	4
MEXI	NAME	1	1	1	3	5	7	2	6	6
NALA	NNAME	2	3	3	5	4	2	4	4	7
NCAL	NAME	2	3	3	1	6	3	5	8	9
NMEX	NAME	1	1	1	4	1	7	2	6	6
NWAL	NNAME	2	3	3	5	4	2	4	2	10
NWSA	SAME	1	1	1	3	5	7	2	6	6
NYOR	NAME	1	1	1	3	5	6	7	9	4
ONTA	NNAME	1	1	1	3	5	6	7	9	4
PATA	SAME	2	3	3	5	2	3	1	5	5
PERU	SAME	1	1	1	4	1	1	8	3	1
PIAÃ‡A	SAME	2	2	2	1	6	4	5	8	9
SCAL	NAME	1	1	1	4	1	1	8	3	1
SDAK	NAME	2	3	3	5	2	7	2	6	6
SUMID	SAME	1	1	1	4	1	1	8	3	1
SWAL	NNAME	2	3	3	5	2	2	4	4	7
TLIN	NNAME	2	3	3	5	2	3	1	5	5
TUPINORTH	SAME	1	1	4	2	3	5	3	1	8
UTAH	NAME	1	1	1	4	1	7	2	6	6
VIRG	NAME	1	1	1	3	5	6	7	9	4
WALE	NNAME	2	3	3	5	2	3	1	5	5

Table 4. K-means clustering analysis values for K=2-10 for variables of the face

Neurocranium

The k-means clustering analysis of only neurocranium variables, for k = 2, 3, and 7 groups are presented in Figure 6, superimposed to the geographic coordinates of the series. The k=2 cluster for the neurocranium distinguishes itself from face and entire cranium by grouping everyone except northern South America and the Aleut populations in north North America. The Aleut series continues to separate themselves again, similar to the cranium k=7 clusters. However, the eastern South American populations no longer show significant individuality and the arctic NNAME series no longer separates itself in k=7 clusters. The k-means clustering results for only neurocranium variables for k-groupings 1-10 are shown in Table 5.

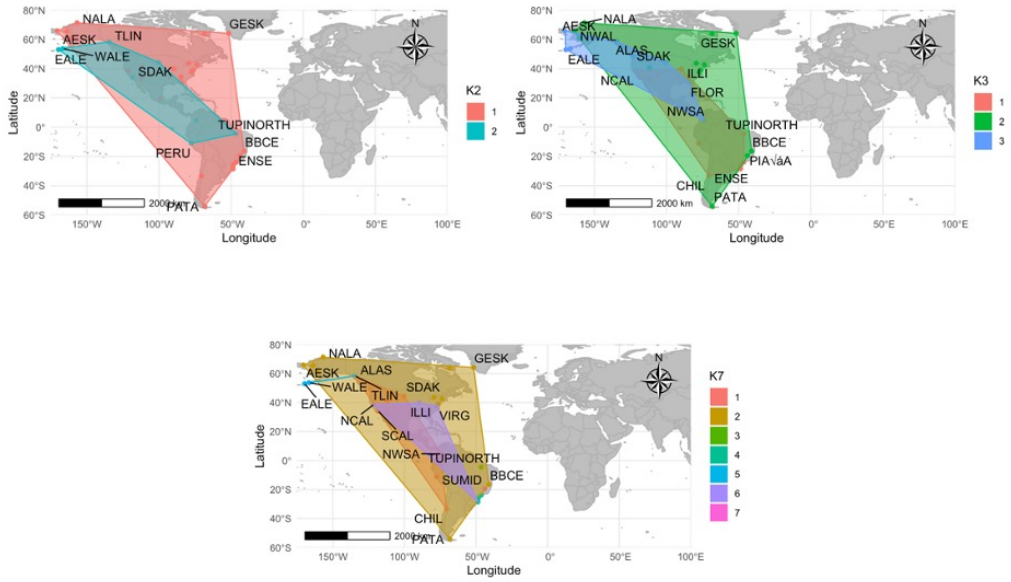

Figure 6.K-means clustering analysis including all variables of the neurocranium for k=2, 3, and 7 superimposed to the geographical location of the series.

Population	Region	K2	K3	K4	K5	K6	K7	K8	K9	K10
AESK	NNAME	1	3	1	2	3	2	6	1	9
ALAS	NNAME	1	3	1	5	3	1	4	4	1
ARIZ	NAME	1	1	3	5	1	1	4	9	2
ARKA	NAME	1	1	3	1	2	6	8	8	8
BBCE	SAME	1	2	2	4	4	2	2	5	7
BCOL	NNAME	2	3	1	2	3	1	6	4	1
CABE	SAME	1	1	3	5	1	6	4	3	4
CBS	SAME	1	1	3	1	2	6	8	8	8
CESK	NNAME	1	2	2	4	4	2	7	5	7
CHIL	SAME	1	1	3	5	1	1	4	3	4
EALE	NNAME	2	3	1	2	6	5	1	6	10
ENSE	SAME	1	1	3	1	2	4	5	2	3
FLOR	NAME	1	3	1	2	3	6	6	4	1
FMLUZ	SAME	1	1	3	1	1	4	5	2	3
GESK	NNAME	1	2	2	4	4	2	7	5	7
GUARAGACU	SAME	1	1	3	5	1	4	4	3	4
ILLI	NAME	1	1	3	1	2	6	8	8	8
KENT	NAME	1	1	3	1	2	6	8	8	8
MARY	NAME	1	2	2	4	4	2	7	1	9
MEXI	NAME	1	1	3	5	1	1	4	9	4
NALA	NNAME	1	2	2	4	4	2	7	1	7
NCAL	NAME	1	1	3	5	1	6	4	3	4
NMEX	NAME	1	1	3	1	1	1	2	9	2
NWAL	NNAME	1	2	2	4	3	2	7	1	9
NWSA	SAME	2	3	1	5	1	1	4	4	4
NYOR	NAME	1	2	2	4	3	2	7	1	9
ONTA	NNAME	1	2	2	4	3	2	7	1	9
PATA	SAME	1	2	2	4	3	2	7	1	9
PERU	SAME	2	1	3	5	1	1	4	9	4
PIAÃ‡A	SAME	1	1	3	5	1	4	4	3	4
SCAL	NAME	2	1	4	5	3	1	4	9	2
SDAK	NAME	2	3	1	2	3	1	6	4	1
SUMID	SAME	1	2	2	4	4	7	2	5	6
SWAL	NNAME	1	2	2	5	3	2	4	4	1
TLIN	NNAME	2	3	1	2	3	5	1	4	1
TUPINORTH	SAME	2	1	4	3	5	3	3	7	5
UTAH	NAME	1	2	2	4	3	1	2	9	2
VIRG	NAME	1	2	2	4	2	6	8	8	8
WALE	NNAME	2	3	1	2	6	5	1	6	10

Table 5. K-means clustering analysis values for K=2-10 for variables of the neurocranium

Discussion and Conclusions

The results in this paper show structured cranial morphological diversity, rejecting the null hypothesis that human processes occurring in North and South America are similar, and therefore can be grouped together. In addition to population series separating by geographic region, there exist complex patterns of affinity. These complex patterns suggest there are additional factors at play influencing the morphological affinities shown. High latitude North American populations and high latitude South American populations show strong affinities. High latitude South American populations, like Patagonia, separating from other South American series support previous studies (39) that other factors, for example responses to climate (26), influence morphological variation and complicate the previous perspectives of a homogenous American population and history. Furthermore, South American groups show different degrees of association with North America depending on whether they are east or west of the Andes Mountain range, implying an impact of geographic barriers on morphological affinities as well. In addition, eastern South American populations, as well as arctic North American populations often separate themselves from other series in the continent. Overall, the populations group together in geographic patterns, showing separation dependent on unique factors for that population's historical and environmental context. The exceptions to the patterns shed as much light as the patterns themselves. Tupi North Brazil and Sumidouro often appear separate from the rest of the populations in the distance matrices plots, which correlate with the eastern Brazilian populations grouping together outside of the other regional groups in the k-means analysis maps. These complex patterns of morphological affinities between population series dismiss the idea of a uniform North and South America. Therefore, we can reject the null hypothesis that discussing the Americas as a whole is an accurate way to describe the biological variation in the continents and in turn describe models of early human dispersion.

Many studies on human settlement and dispersion models of North and South America group the two continents together, frequently presenting the continents under the labels of *The Americas* (2, 6, 8, 13, 16, 17, 18-21, 29-30, 32, 34, 36, 40, 45, 49, 51) and *New World* (9, 27, 34, 35, 38, 41, 47-48). Studies that highlight the time frame of the first entrance into "the Americas" extend the same relevance of the implications of their conclusions to both continents, without accurate representation from both North and South America. For example, McGowan (2016) investigates the initial entry across the ice-free corridor from Siberia into Beringia. The evidence of the initial entrance into North America is extrapolated to explain processes on both continents by stating early humans migrated into "the Americas" (33). In accordance with initial entrance evidence being drawn across both continents, models that are representative of North America are extrapolated to include South American dispersion events (12, 30, 43). For example, Raff and Bolnick (2014) create a hypothetical scenario for settlement of the continents shown in their Figure 1. However, the caption states "peopling of the Americas" with only North America shown in the image, completely disregarding South America in the inclusion of "the Americas" (43). Similarly, South American models are also extrapolated to North America (11, 18). For example, Dillehay et al. (2015) uses new archaeological evidence from Monte Verde, Chile to explain processes in 'the Americas' and the 'New World' (11). While

the complexity of dispersion processes is acknowledged, these phrases generalize regionally specific evidence across the two continents. The details and complexities of multiple within-continent dispersions are erased when models are generalized between the continents. Our results show geographical patterns of morphological affinities that get overlooked and blended when statements of dispersion are made for both continents simultaneously. By reassessing how wide of a net we cast for what the evidence available can explain, more attention can be given to the variation present.

Even though the settlement of the two continents is researched through many different methodologies (genetic, linguistic, archeological, and morphological), there continues to exist debate over a consensus for the model of settlement. The fault does not lie only in limitations specific to the various methodologies, but in the overall framework of which the studies of the settlement of North and South America are molded. Although previous models are not inaccurate in their results given their framework and methods, the structured morphological diversity among the populations in North and South America counters the previous interpretations of the process of early human movement across the continent. Previous interpretations expand the reaches of their evidence to both continents by the consequence of habit and shared jargon in the field of study on the settlement of North and South America. Geographical patterns and different morphological affinity groupings shown in our results support that generalizing claims across continents and regions are inaccurate when these patterns of morphological similarities exist. Moving away from processes in the north continent being extrapolated into the south continent, and vice versa will help avoid broad generalized models of human dispersion into *the* Americas.

An explanation of these morphological patterns and outliers shown in our results require investigation of their own; however, to do so each series deserves to be analyzed within the region's eco-geographical and historical realities. Given the cranial morphological diversity present, we argue that future studies would benefit from moving away from grouping the two continents together, and at the very least encourage research to reevaluate the validity of extrapolations made in the past. The previous generalizations oversimplify the processes and therefore fall short on explaining the origins of Native American biological diversity. The tradition of one large arrow entering North America and continuing, seemingly unaffected, into South America must be changed. Instead, we suggest a perspective of multiple smaller arrows within both continents, allowing for the individuality of population's experiences to be more accurately represented.

Given that our sample was sourced from two observers, our conclusions are based on the assumptions that there was not significant observer differences or biases. We attempted to remove bias by excluding variables that generated extreme separation between observers (OCC). The results were placed in a context heavily focused on arguing for the individuality of North and South American migration discussions. However, we also want to acknowledge our lack of emphasis on Central American populations in our study, given that our sample populations lacked proper representation from Central American series. Our argument can be

strengthened through the addition of central American populations in our sample to show the most accurate patterns of morphological affinities.

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