BIOCULTURAL DYNAMICS OF POSTCRANIAL SKELETAL VARIATION: A FOCUS ON ONTOGENY, SOCIOECONOMIC STATUS, AND POPULATION HISTORY

By

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ABSTRACT

My dissertation investigates how biology and culture impact human skeletal morphology. The human skeleton offers insights into an individual's lived experience, which can be quantified as morphological changes brought about by intrinsic (e.g., hormones, genetics, nutrition) and extrinsic (e.g., climate, socioeconomic impacts, political decisions) forces acting on aspects of human variability. The result is patterned (and thus predictable) skeletal variation. Forensic anthropologists utilize this patterned morphological variation to estimate the components of the biological profile (i.e., age, sex, stature, and population affinity). In more general terms, this patterned variability results from the inherently plastic nature of the human body, which responds to external forces but only in a limited number of ways. The malleability of the human skeleton underscores the complexity of this phenotypic expression.

This research considers the potential contributory forces of 11 postcranial macromorphoscopic (MMS) traits, investigated at various stages of growth and development throughout childhood and well into adulthood, and within a number of quantifiable biocultural contexts that may account for skeletal differences. Previously, the timing and causes of postcranial variation were poorly understood. However, I identify potential factors influencing morphological change and assess the biological (intrinsic) and cultural (extrinsic) factors influencing and potentially generating postcranial skeletal morphology across the life course. This research offers a novel perspective beyond the skull, using under-researched, but quantifiable variations in the cervical vertebrae, scapulae, sternum, humeri, femora, patellae, and calcanei. Focusing on implications for forensic anthropology, while accounting for biological-cultural interactions, this study investigates postcranial morphology within four theoretical frameworks: 1) human variation and population history, 2) secular change, 3) growth and development, and 4) biocultural

evolution.

Employing these frameworks, I explore the utility of cranial and postcranial MMS traits—in tandem—in machine learning models to estimate population affinity and generate likelihood estimates for group membership as a measure of biological distance. Next, I focus on spinous process morphologies in cervical vertebrae to identify and quantify levels of secular change. I then consider growth rates and timing, particularly relative to developmental processes and puberty, using a model designed to capture, measure, and quantify the age-of-appearance/age-of-stability of these morphological variants. Finally, I model sociocultural impacts—social race, socioeconomic status, and education— on postcranial MMS traits to determine whether these factors influence skeletal morphology. These efforts are each designed to shed light on the nuanced relationship between biology, culture, and social dynamics within the context of forensic anthropology.

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"As a construct, race is decidedly nonbiological, is malleable across time and space, and is reflective of historical, social, political, economic, and cultural contexts. As experiential and embodied, race may be understood as sensed experiences that can have measurable impacts on the body" (Benn Torres, 2019, p. 75).

INTRODUCTION

The purpose of this dissertation is to investigate postcranial macromorphoscopic (MMS) traits within multiple frameworks. The aim is to understand whether postcranial MMS traits can be used to inform forensic anthropological practice *and* to explore the biological-cultural interaction between the skeleton and social dynamics. The frameworks used to explore postcranial morphology include: 1) human variation and population history; 2) secular change; 3) growth and development; and 4) biocultural evolution. These schemata coincide with the four manuscripts generated for this dissertation. Below, are outlined the theoretical components of each framework, while also providing context for the associated manuscript.

* * *

Human variation significantly influences research in biology and anthropology. While biologists focus on variation related to microscopic and macroscopic elements of the human body, anthropologists study variation in a wide array of aspects centered on the human experience. For example, they might study differences in social constructs, belief systems within communities, or concentrate on characteristic differences in material culture. Morphology, the study of form and structure, is researched across multiple subdisciplines of biological anthropology—from primatology and paleoanthropology to bioarchaeology and forensic anthropology. Morphological studies can be used to answer a plethora of questions related to evolution, development, life history, and functionality.

Bone is an excellent proxy to evaluate an individual's lived experience and can serve as an excellent tool to study human morphological variation and measure aspects of biocultural adaptation. As a living tissue, bone constantly adapts throughout an individual's. In anthropology, biocultural models exemplify intrinsic and extrinsic factors emphasizing the dynamic relationships between biological variation and societal structures. This framework does not separate biology from culture but implores us to understand the complex interactions between the two, how they shape one another over time (Gravlee, 2009; Agarwal & Beauchesne, 2010; Blakey, 2020). This interplay can leave imprints on the human skeleton, reflecting environmental adaptation and the embodiment of an individual's social history overtime, especially at their youngest age.

For this dissertation, the growth and development of 11 postcranial MMS traits, from birth through adulthood and across various populations, are explored using a comparative ontogenetic and biocultural framework. Spiros (2019) standardized 11 postcranial MMS traits by creating a consistent scoring method. These traits, usually considered present or absent, had previously been described in the literature typically in isolation or without a structured way to collect the data (Barnes, 2012; Buikstra & Ubelaker, 1994; Donlon, 2000; Duray et al., 1999; Finnegan, 1978; Mathew et al., 2016; Mitchell, 1998; Pietrusewsky & Douglas, 2002; Saunders, 1978; Saunders & Popovich, 1978; Saunders & Rainey, 2008). Spiros' (2019) protocol standardizes a scoring approach and expands a number of binary representations to more accurately capture trait variability and allow for increased usability and applicability in modern forensic anthropology. Spiros (2019) illustrated the significant difference in trait states between groups but lacked a diverse sample. This suite of traits has thus been categorized as macromorphoscopic traits, a nod to the cranial MMS traits currently standardized in forensic anthropology, as well as to distinguish these traits from other, less frequency postcranial variants.

The American National Standards Institute and American Academy of Forensic Sciences Standards Board (ANSI/ASB) have developed consensus-based terminology with the experts in forensic anthropology. When referring to a 'population' in this context, forensic anthropologists are talking about groups with shared factors such as geography, biology, culture, language, etc. A 'reference group' is a sample of a population used within a method. 'Population affinity' is a measure (such as distance or probability of membership) of similarity between an individual and the reference groups, not to the exclusion of ancestry, but as a more inclusive term encompassing the estimation of an individual's similarity to various groupings of populations (ANSI/ASB Standard 132, 2023). The first manuscript uses the word 'ancestry', as it was published three years prior to the publication of these standards. As such, population affinity would have been more apt and is therefore utilized in the subsequent manuscripts.

HUMAN VARIATION AND POPULATION HISTORY

Manuscript One ("Ancestry Estimation Using Cranial and Postcranial Macromorphoscopic Traits") explores postcranial MMS variability among a sample of U.S. Black and White individuals. The objective of this study was to quantify variability in a modern U.S. skeletal cohort to assess the value of postcranial MMS traits, to highlight a combined cranial/postcranial trait approach to population affinity estimation, and to build/test statistical classification models for forensic anthropological application. Morphology in skeletal biology is all about shape differences and how they vary from person to person. This concept is broadly understood to capture human variation, variation that is generally patterned in some form between individuals. This patterning allows forensic anthropologists to estimate biological profile parameters such as age, sex, stature, and population affinity. For example, the ability to utilize biological components to estimate population affinity is due to correlations between population history and social race through

biocultural reciprocity. However, it's crucial to recognize that race itself is not a biological construct but rather a sociocultural one. The intersection of biology and culture is pivotal in this research context. Inherited genetic variation serves as an example of biological diversity rather than evidence of biological races. Unlike race, genetic variants are observable worldwide and can be described using consistent descriptors. Patterned phenotypic variation associated with race may have arisen due to adaptations from geographic variation and/or the embodiment of sociocultural inequalities perpetuated by power structures that parallel population history. However, it's important to understand that race, as a concept, lacks an inherent genetic basis. As a concept it is highly contingent upon temporal and geographical contexts, as evidenced by the diverse descriptors used to describe social race within various societies. This study is the first of its kind to combine cranial and postcranial MMS traits and to place these postcranial variants within a statistical framework, applying machine learning algorithms to test their utility in forensic anthropology for population affinity estimation.

SECULAR CHANGE

Manuscript Two ("A Heuristic Approach to the Duray Method: Validation and Modern Refinement") considers how temporal changes may influence morphological variation, specifically of the cervical vertebrae. The postcranial MMS trait, spinous process bifurcation (SPB) varies by which the extent of the posterior bony projection of the cervical vertebrae is divided. Following Duray and colleagues (1999) and, subsequently, Spiros (2019), this manuscript explores this variation spanning two centuries to explore secular change in the postcranial skeleton. Secular change in skeletal biology is morphological change across a period of time (Jantz & Meadows Jantz, 2000; Jantz, 2001; Katzmarzyk & Leonard, 1998; Relethford, 2004; Sparks & Jantz, 2002). It is crucial to understand whether changes in the skeleton occur continuously across

distinct time periods to grasp the dynamics of evolution, environmental shifts, cultural transformations, and population variabilities over time. In the forensic context, understanding these shifts allows us to recognize the applicability of our methods created on various skeletal assemblages and choose appropriate references for methodological approaches. Postcranial studies have documented secular change in various ways but never for postcranial MMS traits.

ONTOGENY & DEVELOPMENTAL PLASTICITY

Manuscript Three ("Ontogenetic and Puberty Influences on Postcranial Morphological Variation") investigates the developmental timing of postcranial MMS traits and potential influences that may contribute to the presence and manifestation of the traits. Bone ontogeny is a process that occurs throughout life during one of the three postnatal phases: 1) growth/development, 2) modeling, and 3) remodeling (Clarke, 2008). To identify how (and why) postcranial traits are differentially expressed, growth histories are recreated using both standard age cohorts (Buikstra and Ubelaker, 1994) and puberty stages (Risser, 1958). Bone remodeling is a continuous, lifelong process renewing bone strength and maintaining equilibrium in the bony matrix (Clarke, 2008). Thus, beginning around the onset of puberty, certain bony morphologies differentiate following hormonal variations between males and females (Cunningham et al., 2016).

Understanding the ontogeny and structure of bone only goes so far in exploring human variation. Development is viewed through the lens of evolutionary patterns within our species and human developmental trajectories are complex. Determining what is "normal" in growth and developmental timing is highly connected with the environmental influences, biological pathways, and an individual's life course (Agarwal & Beauchesne, 2010). A number of factors can influence an individual's phenotype throughout their life—diet, lifestyle, genetics, hormones, etc. These need to be considered in conjunction with the phenotypic expression to understand the etiology of

the phenotype from an individual, generational, and/or community perspective (Agarwal & Beauchesne, 2011).

In order to take this approach, a developmental systems theory framework (Oyama et al., 2001; Agarwal, 2016) guides this research into the development and variation in the postcranial skeleton. Developmental systems theory (DST) links evolutionary, developmental, political, and economic influences on biology with specific focus on how inequity and privilege can be embodied in humans during development (Duncan et al., 2014; Hicks & Leonard, 2014; Mansfield & Guthman, 2015; Meloni, 2015). As such, postcranial MMS traits are surveyed across various age cohorts, incorporating puberty as a potential intrinsic factor for occurrence, and exploring the influence of social race on as a proxy for understanding if embodied inequity and privilege influence manifestation and/or time of appearance of the traits.

BIOCULTURAL EMBODIMENT

Manuscript Four ("Embodiment of Sociocultural Influences on Postcranial Skeletal Morphology") builds off the theoretical underpinnings of the third manuscript. This research explores the influences of sociocultural factors on modern United States individuals through postcranial morphology. Health encompasses the overall well-being of an individual and reflects how their body copes with stressors. One's health impacts the body, and this is especially prevalent during developmental periods. The exact etiology of postcranial variants is still unknown, and thus they could be associated with an individual's health in various ways (e.g., caused by adequate or lack of nutrition and/or embodied stress responses to external factors). Closely related to health is an individual's socioeconomic status. Socioeconomic status (SES) impacts access to healthcare, quality of living, educational obtainment, financial stability, and safe living environments, all of which are crucial determinants of one's physical and mental health. This dynamic health-wealth

relationship is incorporated within the systemic inequalities that impact marginalized groups at a disproportionate rate, specifically when incorporating social race.

The embodiment of racism, particularly in the U.S., has fostered the intertwining of race and socioeconomic status (LaVeist, 2005). Systemic issues such as segregation, interracial marriage laws, and redlining, which remained legal until relatively recently, have maintained inequities in our society. While these specific overt practices have *technically* been outlawed, their lasting consequences persist, impacting individuals' intergenerational financial, social, and mental well-being. Moreover, covert, and enduring practices— including implicit biases, racial profiling, disproportionate incarceration, environmental racism, and wealth disparities— continue to reinforce systemic racism. These practices are interconnected with biological variation stemming from a shared ancestry and are further perpetuated by ongoing policies and practices of separation and discrimination. Thus, though social race is not biologically determined, the dynamic processes within the human body give rise to biological patterns that can be influenced by racism.

LaVeist (2005) outlines four key issues researchers should consider when exploring the racialization of health disparities: 1) environmental and social risks associated with segregation; 2) research with large datasets lacking psychosocial variables; 3) datasets with psychosocial variables lacking diversity; and/or, 4) the overlap of race and SES complicating the "and/or" question. Williams and colleagues (2016) suggest including race in these discussions, even after SES is considered. They suggest adverse conditions such as poverty, abuse, and trauma vary among different SES and racial groups and health is directly associated with these life course factors. Like the discrepancy in adverse circumstances, SES indicators are also not equivalent across every racial group. The wage gap, for example, shows disproportionate incomes among individuals with the same education level. Institutional and interpersonal racism, expressed in any

number of ways (educational differences, varied employment opportunities, historical segregation, redlining, etc.) can cause very real differences in SES mobility. Interpersonal racism, in particular, has been associated with increased health risks, specifically during childhood (Williams et al., 2016). Additional psychosocial stressors disparities (e.g., underemployment, violence, discrimination, financial strain, toxic environments) between marginalized groups lead to elevated health inequality (Williams et al., 2016). This poses the question; can this embodiment be perpetuated through skeletal variation?

While the embodiment of sociocultural effects are explored in biology (Chen et al., 2006; Duncan et al., 2014; Gravlee, 2009; Hicks & Leonard, 2014; LaVeist, 2005; Meloni, 2015; Oyama et al., 2001; Panter-Brick & Fuentes, 2009; Stotz & Griffiths, 2018; West-Eberhard, 1989), research is scarce regarding quantifying the interaction of SES and the embodiment of social race in the human skeleton (O'Donnell & Edgar, 2021). And, although there are a large number of studies focused on health disparities and stressors on the skeleton, these often confound race and socioeconomic status. This research begins to sparse out the possible sources of postcranial variation manifestation by exploring both biological and cultural impacts on the skeleton.

SUMMARY AND OBJECTIVES

Manuscript One ("Ancestry Estimation Using Cranial and Postcranial Macromorphoscopic Traits") compares the utility of cranial MMS traits and postcranial MMS traits in a population affinity framework, exploring the combination of the two data types in tandem. Manuscript 2 ("A Heuristic Approach to the Duray Method: Validation and Modern Refinement") focuses on the spinous process bifurcation of the cervical vertebrae to assess secular change and its influence on the utility of these features. Manuscript 3 ("Ontogenetic and Puberty Influences on Postcranial Morphological Variation") delves into understanding the development of the traits with

consideration to growth and puberty. Lastly, Manuscript 4 ("Embodiment of Sociocultural Influences on Postcranial Skeletal Morphology") uses a biocultural perspective to identifying the levels of influence social race, socioeconomic status, education, and sex have on postcranial MMS trait manifestations.

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MANUSCRIPT 1. ANCESTRY ESTIMATION USING CRANIAL AND POSTCRANIAL MACROMORPHOSCOPIC TRAITS

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ABSTRACT

Ancestry estimation methods using macromorphoscopic (MMS) traits commonly focus exclusively on cranial morphology. The objective of this study was to demonstrate the value of postcranial MMS traits, highlighting a combined cranial/postcranial trait approach to ancestry estimation using quadratic discriminant function and a variety of machine learning classification models including artificial neural networks (aNN), random forest models, and support vector machine. Eight cranial and eleven postcranial MMS traits were collected from the Terry and Bass Skeletal Collections (American Black = 81; American White = 173). Our classification models using cranial and postcranial traits correctly classified 88–92% of the sample, improving classification accuracies by nearly fifteen percent over models relying exclusively on cranial data. These same results demonstrate the importance of a multivariate statistical framework incorporating cranial and postcranial data and the nearly unlimited potential of machine learning models to improve the accuracy of ancestry estimates over traditional methods of analysis. To facilitate implementation in casework, one of the more robust models (aNN) is incorporated into a web-based application, ComboMaMD Analytical, to facilitate cranial and postcranial MMS traits

analysis for ancestry estimation.

INTRODUCTION

Ancestry classifications in forensic anthropology generally include two methodological approaches—metric and nonmetric, or macromorphoscopic, trait analysis. Macromorphoscopic traits (MMS) are cranial morphological traits differentially expressed between groups and analyzed within a statistical framework for the estimation of ancestry. Standardization of these traits was intended to increase the objective implementation of cranial morphology in forensic anthropological analyses and to ensure their validity in ancestry estimations (Hefner, 2003). Testing and validation of cranial MMS traits suggest standardization has improved the MMS approach for trait analysis (Hefner, 2007, 2009, 2014, 2018; Hefner & Ousley, 2014; Hefner et al., 2015; Kamnikar et al., 2017; Klales & Kenyhercz, 2015; Monsalve & Hefner, 2016; Plemons & Hefner, 2016); however, there remains a significant gap in postcranial MMS trait analyses as they pertain to estimations of ancestry.

Many of the forensic anthropological analyses implemented today reflect a growing concern for method standardization and the pursuit of more accurate, reliable, and demonstrably valid methods of analysis. In 1993, the Daubert decision (Daubert v. Merrell Dow Pharmaceuticals, Inc, 1993) resulted in governance over the admissibility of quantitative evidence provided by expert witnesses. The Daubert decision was clear: an admissible method should identify “known or potential error” (Daubert v. Merrell Dow Pharmaceuticals, Inc, 1993, p. 580). Forensic practitioners responded, revisiting and validating old methods of analysis, and creating more reliable methods of analysis (Christensen et al., 2014; Ousley & Hollinger, 2012). Validating old methods is not sufficient alone to move forward. Developing new methods with known error rates answers the call of Daubert and adds to the growing body of literature concerning ancestry

estimation in forensic anthropology.

The relative dearth of forensic anthropological research on postcranial trait variation for ancestry estimation may be due to the belief that the postcranial skeleton is too susceptible to environmental plasticity to demonstrate any true differences among ancestral groups, an idea rooted in research into the plasticity of long bone proportions, morphology, and overall size in metric applications (Jantz et al., 2016; McIlvaine & Schepartz, 2015; Wescott, 2005). Moreover, the notion that postcranial traits are ineffectual in ancestry estimations may stem from "skull science," the antiquated focus on the cranial, over the postcranial, skeleton (Spradley, 2016). From the late 19th through the mid-20th century researchers focused primarily on the description of skeletal "anomalies" (Cunningham, 1886; Hrdlička, 1932; Macalister, 1900; Topinard, 1885; Trotter, 1934). The genomic revolution in the late 1960s signaled the transition from individual traits (anomalies) to a suite of postcranial traits for measuring population relatedness (Anderson, 1963; Donlon, 2000; Finnegan, 1978; Pietrusewsky & Douglas, 2002; Saunders, 1978; Spiros, 2019). Although the results of that research suggested "infracranial traits are just as 'useful' as cranial traits in nonmetric distance studies" (Saunders, 1978, p. 406), postcranial trait research nearly halted with a few notable exceptions (Donlon, 2000; Spiros, 2019; Duray et al. 1999). Donlon (2000) documented the significance of postcranial trait variation in biological distance studies, using them to weigh in on the debate concerning diversity within and among multiple groups. While individual postcranial trait expressions are variable, Donlon's results indicate they are useful for discriminating groups even when samples are closely related.

Recently, a suite of postcranial traits was devised via definitions, drawings, and, for the first time, an ordinal scoring system (Spiros, 2019). This method reflects not only the call for standardization by the Daubert decision (1993), but also the 2009 National Academy of Sciences

(NAS) report on strengthening forensic sciences (National Research Council, 2009) and the 2016 President's Council of Advisors on Science and Technology (PCAST) report on forensic science in criminal courts (PCAST, 2016). This scoring procedure provides a rigorous data collection protocol for postcranial traits and more accurately defines variations for each character state (i.e., Anterior and Middle Calcaneal Facet & Septal Aperture). Spiros (2019) documented frequency distribution differences between American Black and American White samples; however, the application of her scoring protocol to estimate ancestry has not been confirmed and the incorporation of the protocol with cranial MMS traits has not been assessed or quantified. For clarity, we will refer to the cranial and postcranial variables used in this study as macromorphoscopic (MMS) traits.

MATERIALS AND METHODS

Reference Samples

A matched cranial and postcranial MMS dataset originating from the Robert J. Terry Skeletal (Terry) and the W.M. Bass (Bass) Donated Skeletal Collections is used for this analysis. The complete sample (N = 254) represents American Black (n = 81) and American White (n = 173) individuals (Table 1.1). Ancestry is more complex than simply corresponding skeletal morphology to social constructs like American Black or American White. These classification strategies provide a large-scale proxy that allows us to begin to understand the true range of biological variation. Additional population data will provide more refined ancestry estimations, beyond the two-group exploration that is presented here. To reflect previous cranial macromorphoscopic research, the two collections were combined (Hefner, 2003, 2007, 2009; Hefner & Ousley, 2014; Plemons & Hefner, 2016). Secular change in craniofacial morphology has been noted (Jantz & Meadows Jantz, 2000), but is currently unknown for postcranial MMS traits.

The sample from the Terry Collection represents American Black (n = 20) and American White (n = 20) individuals with 19th century birth years, including females (n = 21) and males (n = 19) ranging in ages between 24 and 80 years. The sample from the Bass Collection represents American Black (n = 61) and American White (n = 153) individuals with 19th and 20th century birth years, including females (n = 101) and males (n = 113) ranging in age between 23 and 99 years. The cranial data were provided by the Macromorphoscopic Databank (MaMD) (Hefner, 2018).

Table 1.1 Sample composition

	Sex		
Sample	Female	Male	*Total*
Terry American Black	7	13	20
Terry American White	14	6	20
Bass American Black	11	50	61
Bass American White	90	63	153
Total	122	132	254

Data Collection

Eight cranial (Hefner, 2009) and eleven postcranial (Spiros, 2019) MMS traits are included in this study (Tables 1.2 and 1.3). We did not pool scores for bilateral traits or the accessory transverse foramina (ATF), resulting in 27 postcranial scores. Nearly eight percent of the data were missing, due to either an absent skeletal element or differences in data collection protocols. For example, spinous process bifurcation (SPB) for only the third and fourth vertebrae were collected from the Terry Collection but SPB was scored for C2 to C7 for the Bass Collection, resulting in very high rates of missing data for SPB (C2–18.2%; C5–21.3%; C6–21.3%; C7–19.8%). Only postbregmatic depression (PBD) had a higher frequency of missing data (32.0%).

Analytical Methods

Missing data imputations were conducted using the "mice" package (van Buuren &

Groothuis-Oudshoorn, 2010) in R 3.6.0 (R Core Team, 2013). Multivariate imputation by chained equations (MICE) is a highly flexible imputation method simultaneously handling binary, categorical, and continuous data (van Buuren, 2018; Schenker & Taylor, 1996; Kenyhercz, et al. 2019). The MICE method generates multiple imputations using predictive mean matching ("pmm"), a hot deck method that pulls complete datasets that are similar to the individual with missing values and pools these data to generate a complete dataset for the individual with missing values (van Buuren, 2018; Schenker & Taylor, 1996). Because "pmm" draws from your dataset, the method rejects impossible or unrealistic values (van Buuren, 2018; Schenker & Taylor, 1996).

Frequency distributions were calculated using the "psych" package (Revelle & Revelle, 2019). To assess the strength of the relationship between cranial and postcranial MMS traits, correlations were calculated using the tetrachoric function in the "psych" package (Revelle & Revelle, 2019) which calculates tetrachoric and polychoric correlations. Correlation coefficients were calculated (i) separately for the American Black and American White samples to identify within-group correlations, and (ii) on the complete sample (pooled ancestry) to identify inter-ancestral trends. The "corrplot" package (Wei et al., 2017) visualized these matrices with correlograms.

Modeling cranial and postcranial MMS traits for ancestry estimation with parametric methods and machine learning algorithms provide measures of trait effectiveness. Methods include quadratic discriminant function analysis (QDA), artificial neural networks (aNN), random forest models (RFM), and support vector machine (SVM). The data were divided uniformly into training and test sets, using 70% of the sample for training and validation and the remainder as a hold-out, or test, sample for subsequent cross-validation of each model. Cross-validation using the test sample avoided overfitting the model. Previous (successful) application of these methods to cranial

MMS analysis led to their selection in the current research (Hefner, 2009, 2014; Hefner & Ousley, 2014; Hefner et al., 2014). We tested each model against three separate datasets: (i) a cranial dataset, (ii) a postcranial dataset, and, (iii) a pooled cranial/postcranial dataset.

Linear discriminant function analysis (LDA) and QDA both assume the data are drawn from a Gaussian (normal) distribution. We chose QDA for this study over LDA because the former does not assume shared correlation structures between the two groups. Although the QDA assumption of normality is not met, Hefner & Ousley (2014) contend QDA may be appropriately applied and can correctly classify at a higher rate than either LDA or logistic regression. Classification models with the QDA for the training and test sets generated cross-validated classification accuracies (CCR, or correct classification rate). A forward– backward stepwise selection was applied to identify the best fitting model and to determine the most parsimonious trait combinations for model goodness-of-fit (41,42).

The research assessed the classification power of several nonparametric data mining techniques (machine learning algorithms) appropriate for categorical data. The aNN model used a search algorithm to assign random weights to each variable, thus creating a feed-forward neural network (Ripley, 1994) with all 35 variables. The inclusion of bias nodes (similar to signal looping in the brain) tunes the model to better fit the data and, in turn, maximizes classification accuracy. The aNN model was calculated using the "nnet" package (Venables & Ripley, 2002) in R.

Random forest models combine a decision tree approach with multiple trees (i.e., an ensemble) and majority voting at each terminal node to classify an unknown individual using a randomly selected subset of the original variables. RFM bootstrap aggregating (or, "bagging", an out-of-bag [OOB] error rate) increases model performance by repeatedly testing randomly drawn samples from the original data, repeating the process and refining the model over n trees. RFMs

do not assume a Gaussian distribution, small sample sizes do not significantly affect classification accuracy, missing data are not an issue, and the method is relatively robust to outliers in the data (Hefner & Ousley, 2014; Ousley, 2016; Hastie et al., 2009; Williams, 2011). Five hundred trees stabilized the OOB error rate using four variables at each node (Hastie et al., 2009). Two variable importance measures (VIMs) are calculated during the analysis: mean decrease in accuracy and mean decrease in Gini (Hefner et al., 2014; Liaw & Wiener, 2002). All RFM analyses were conducted using the "randomForest" package (Liaw & Wiener, 2002).

Support vector machines generate classification rules by maximizing the margin between two a priori groups using data situated at the edges of multivariate space (i.e., the intersection between the two groups). Small sample sizes and outliers do not affect SVMs because the method identifies these support vectors to define a nonlinear classifier that maximizes classification accuracy. The number of support vectors is directly related to model predictability; a larger number of support vectors indicates less separable data (Cortes & Vapnik, 1995). We applied a radial basis function (RBF) kernel because the data are not normally distributed and RBFs are the recommended default kernel due to flexibility over other approaches (Hastie et al., 2009; Williams, 2011; Cortes & Vapnik, 1995). All SVM analyses were conducted using the "e1071" package (Meyer et al., 2015).

Finally, we dichotomized a number of postcranial variables to maximize between group variation to assess their power in distinguishing between the two groups. Threshold values were heuristically determined, and naïve estimators were calculated using the frequency distribution data.

RESULTS

Trait Frequency and Correlation

Tables 1.2 and 1.3 provide frequency distribution data for all cranial and postcranial MMS traits. The American Black (Fig. 1.1) and American White (Fig. 1.2) correlation coefficients indicate a moderately strong negative correlation between cranial and postcranial MMS traits and that the correlation structure differs between groups, indicating models assuming trait independence should be applied cautiously (Fig. 1.3). The American Black sample is more symmetrical (i.e., more inter-trait correlations) than the American White sample. The pooled American Black and White sample resulted in slightly more significant inter-trait correlation coefficients.

Table 1.2 Cranial traits scores and frequencies

Frequencies of Cranial Traits (%)

Trait	Abbreviation	Scores	American Black (*n*=81)	American White (*n*=173)	Trait	Abbreviation	Scores	American Black (*n*=81)	American White (*n*=173)
Anterior Nasal Spine	ANS	1	46%	15%	Nasal Aperture Width	NAW	1	2%	50%
		2	37%	42%			2	63%	48%
		3	17%	43%			3	35%	2%
Postbregmatic Depression	PBD	0	58%	87%	Nasal Overgrowth	NO	0	72%	68%
		1	40%	13%			1	28%	32%
Nasal Bone Contour	NBC	0	30%	3%	Inferior Nasal Aperture	INA	1	21%	1%
		1	36%	12%			2	31%	6%
		2	11%	36%			3	28%	49%
		3	17%	44%			4	17%	31%
		4	6%	6%			5	2%	13%
Malar Tubercle	MT	0	4%	28%	Interorbital Breadth	IOB	1	16%	54%
		1	49%	56%			2	40%	40%
		2	33%	13%			3	44%	6%
		3	14%	3%					

Table 1.3 Postcranial traits scores and frequencies

Frequencies of Postcranial Traits (%)

Trait	Abbreviation	Scores	American Black (*n*=81)	American White (*n*=173)	Trait	Abbreviation	Scores	American Black (*n*=81)	American White (*n*=173)
Atlas Accessory Transverse Foramen	ATLAS ATF	0	59%	62%	C3 Accessory Transverse Foramen	C3 ATF	0	98%	96%
		1	20%	12%			1	2%	4%
		2	21%	26%			2	0%	0%
C4 Accessory Transverse Foramen	C4 ATF	0	89%	83%	C5 Accessory Transverse Foramen	C5 ATF	0	54%	56%
		1	10%	16%			1	31%	30%
		2	1%	2%			2	15%	14%
C6 Accessory Transverse Foramen	C6 ATF	0	42%	27%	C7 Accessory Transverse Foramen	C7 ATF	0	73%	72%
		1	33%	28%			1	20%	18%
		2	25%	45%			2	7%	10%
Posterior Bridging	PB	0	64%	81%	Double Superior Articular Facet	DSAF	0	79%	81%
		1	23%	14%			1	16%	15%
		2	12%	5%			2	5%	4%
C2 Spinous Process Bifurcation	C2 SPB	0	11%	8%	C3 Spinous Process Bifurcation	C3 SPB	0	65%	14%
		1	48%	23%			1	22%	24%
		2	41%	69%			2	12%	62%
C4 Spinous Process Bifurcation	C4 SPB	0	58%	16%	C5 Spinous Process Bifurcation	C5 SPB	0	42%	5%
		1	21%	21%			1	28%	12%
		2	21%	63%			2	30%	83%
C6 Spinous Process Bifurcation	C6 SPB	0	40%	25%	C7 Spinous Process Bifurcation	C7 SPB	0	98%	80%
		1	28%	26%			1	2%	18%
		2	32%	49%			2	0%	2%
Left Suprascapular Foramen	L SSF	0	98%	81%	Right Suprascapular Foramen	R SSF	0	98%	76%
		1	2%	19%			1	2%	24%
Left Supracondyloid Process	L SCP	0	99%	99%	Right Supracondyloid Process	R SCP	0	99%	98%
		1	1%	1%			1	1%	2%
Left Septal Aperture	L SA	0	25%	16%	Right Septal Aperture	R SA	0	30%	18%
		1	49%	62%			1	53%	68%
		2	6%	3%			2	1%	2%
		3	20%	18%			3	16%	11%
Left Third Trochanter	L TT	0	100%	94%	Right Third Trochanter	R TT	0	98%	96%
		1	0%	6%			1	2%	4%
Left Vastus Notch	L VN	0	38%	75%	Right Vastus Notch	R VN	0	37%	70%
		1	62%	25%			1	63%	30%
Left Anterior and Middle Calcaneal Facets	L AMCF	0	5%	4%	Right Anterior and Middle Calcaneal Facets	R AMCF	0	4%	3%
		1	68%	32%			1	69%	36%
		2	21%	39%			2	22%	35%
		3	6%	25%			3	5%	26%
Sternal Aperture	STA	0	83%	90%					
		1	17%	10%					

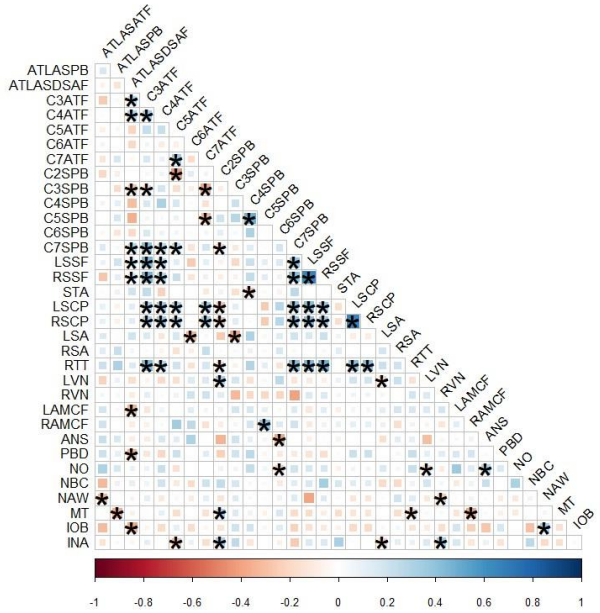

Figure 1.1 Graphical display of the correlation matrix for the American Black dataset. Note: The between trait correlation is indicated by an asterisk when p<0.01

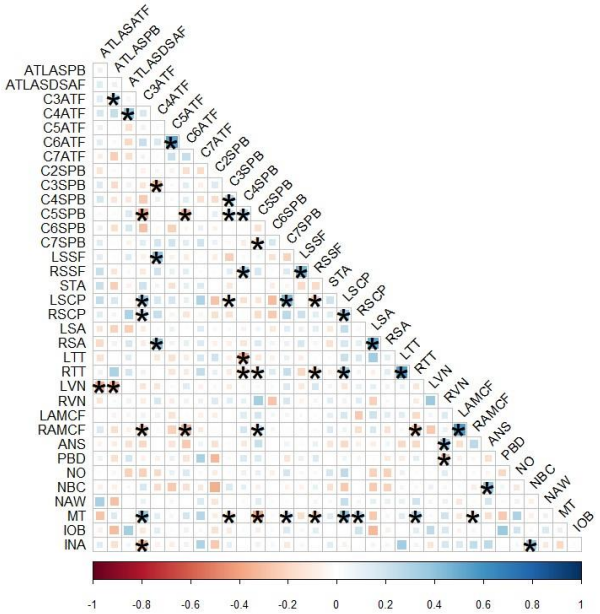

Figure 1.2 Graphical display of the correlation matrix for the American White dataset. Note: The between trait correlation is indicated by an asterisk when p<0.01

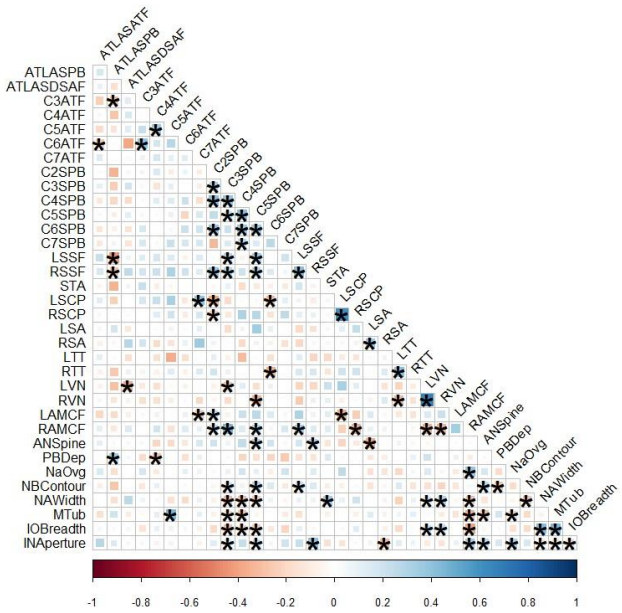

Figure 1.3 Graphical display of the correlation matrix for the pooled dataset. Note: The between trait correlation is indicated by an asterisk when p<0.01

Classification Models

Table 1.4 provides classification accuracies for test samples only, by the individual models. Models using only the cranial MMS trait data correctly classified 80.0–85.0% of the samples while the models developed using only postcranial MMS traits correctly classified 77.6–81.6% of the samples. Combining the cranial and postcranial MMS traits generated classifications between 89.5% and 92.1%, improving accuracies by thirteen percent (Table 1.4).

Table 1.4 Correct classification rates for combined, cranial, and postcranial test samples

Combined Dataset					
ANN			**QDA**		
Group	American Black	American White	**Group**	American Black	American White
American Black	100.0%	0.0%	American Black	95.8%	4.2%
American White	13.5%	86.5%	American White	11.5%	88.5%
% Correct	90.8%		*% Correct*	90.8%	
RFM			**SVM**		
Group	American Black	American White	**Group**	American Black	American White
American Black	81.0%	19.0%	American Black	84.6%	15.4%
American White	6.0%	94%	American White	4.0%	96.0%
% Correct	88.2%		*% Correct*	92.1%	
Cranial Dataset					
aNN			**QDA**		
Group	American Black	American White	**Group**	American Black	American White
American Black	79.2%	20.8%	American Black	75.0%	25.0%
American White	13.5%	86.5%	American White	13.5%	86.5%
% Correct	84.2%		*% Correct*	82.9%	
RFM			**SVM**		
Group	American Black	American White	**Group**	American Black	American White
American Black	65.5%	34.5%	American Black	76.0%	24.0%
American White	10.6%	89.4%	American White	9.8%	90.2%
% Correct	80.3%		*% Correct*	85.5%	
Postcranial Dataset					
aNN			**QDA**		
Group	American Black	American White	**Group**	American Black	American White
American Black	54.2%	45.8%	American Black	58.3%	41.7%
American White	11.5%	88.5%	American White	7.7%	92.3%
% Correct	77.6%		*% Correct*	81.6%	
RFM			**SVM**		
Group	American Black	American White	**Group**	American Black	American White
American Black	80.0%	20.0%	American Black	75.0%	25.0%
American White	19.7%	80.3%	American White	20.0%	80.0%
% Correct	80.3%		*% Correct*	78.9%	

The full QDA model using all variables (cranial and postcranial) performed well, misclassifying seven individuals: one American Black and six American Whites. Additionally, we observed this classification bias in the cross-validated QDA model, where nearly 12% of American White individuals misclassified, but only 4% of the American Black individuals misclassified. A stepwise QDA model incorporating two traits (SPB of the fifth cervical vertebra and nasal aperture width [NAW]) correctly classified 85.8% of the sample.

The aNN model correctly classified 100.0% of the training sample and nearly 91.0% of the

test sample. All of the misclassified individuals were American White, indicating bias with this model, as well. The RFM model correctly classified nearly 90.0% of the training sample and 88.0% of the testing sample. The OOB error for this RFM is 9.6%. Classification bias for the RFM was not significant: of the eight individuals misclassified, five were American Black and three were American White. Variable importance measures (VIM) suggest both cranial and postcranial variables are important for generating correct classifications (Fig. 1.4). The VIMs also suggest most of the cranial traits are more important in ancestry estimation than the postcranial traits. However, C3 spinous process bifurcation (C3 SPB) is consistently identified as the most important variable. In fact, four (Mean Decrease Accuracy) and three (Mean Decrease Gini) of the top five postcranial traits relate directly to bifidity. Finally, the SVM correctly classified 98.3% of the training sample and 92.1% of the test sample using the RBF kernel parameter with 96 support vectors. Applying the SVM to the training sample misclassified only six individuals: American Black (n = 4) and American White (n = 2).

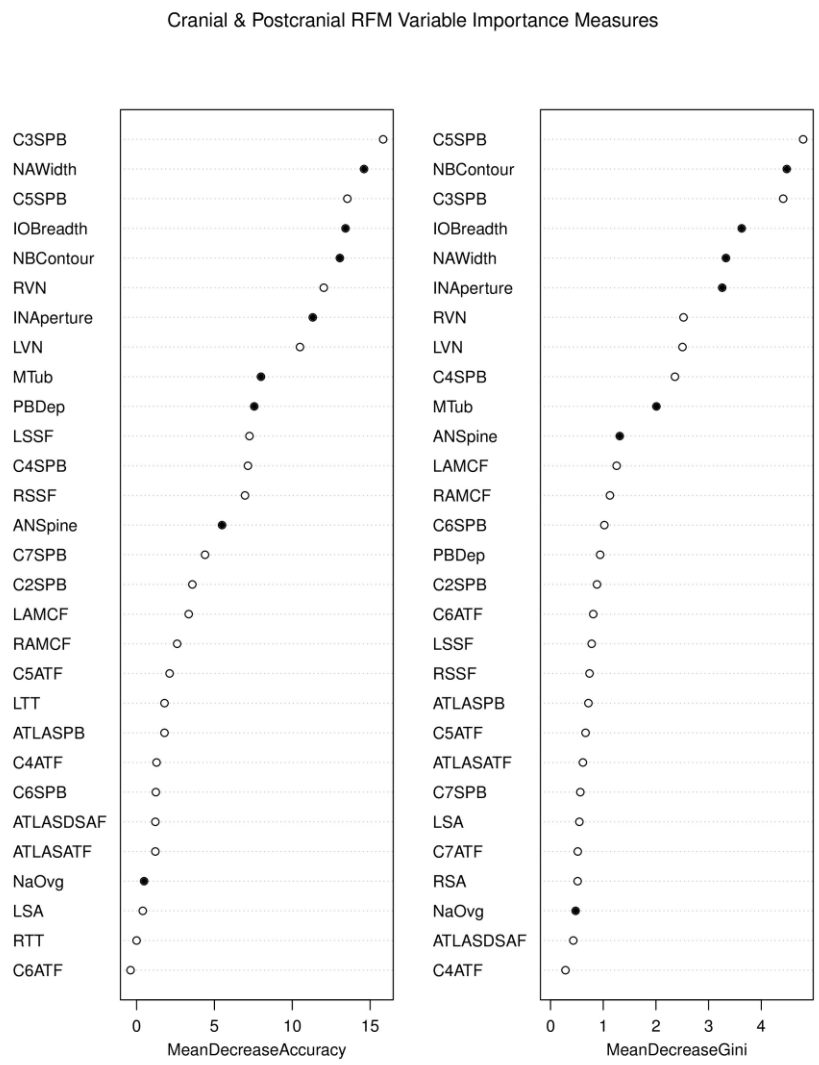

Figure 1.4 Variable Importance Measures (VIM) calculated from random forest modeling. Note: Black circles represent cranial traits; White circles represent postcranial data.

The results of the various multivariate analyses indicate bifidity are by far the most important postcranial morphology. To see just how important bifidity is, we dichotomized SPB (nonbifid= “0” and bifid = “1” or “2”) to generate a naïve estimator of ancestry. The probability of bifidity was determined for each cervical vertebra by ancestry (e.g., what is the probability of an individual being an American Black or American White if any one vertebra is bifid?). If the spinous process of C3 is not bifid, that individual is seven times more likely to be an American Black than an American White.

DISCUSSION

Refining methodological approaches to ancestry estimation are good science (Rao, 1997) and a direct response to modern judicial trends intended to fortify expert witness testimony and strengthen forensic science. The primary purpose of this study was to test a combined, paired dataset of cranial and postcranial MMS traits to decide if the inclusion of postcranial traits in models traditionally reliant on cranial MMS data improves ancestry estimations. This study also validated the importance of predictive, multivariate statistical frameworks, and machine learning models for improving accuracy in traditional forensic anthropological methods through probabilistic modeling.

The results of this study certainly indicate the inclusion of postcranial morphology more thoroughly informs ancestry estimation models and results in higher classification accuracies. The systematic definitions and illustrations of these traits facilitate incorporation into classification models. The general rugosity of postcranial MMS traits means they are more likely to withstand the taphonomic factors that so often damage their cranial counterparts. The incorporation of any new skeletal variable into forensic anthropological analyses necessitates fully understanding their distribution among groups and, when possible, the factors influencing trait manifestation.

We recommend cautious application of any model assuming trait independence (QDA, in particular) since there was a moderately strong but statistically significant correlation identified between cranial and postcranial traits. The higher frequency of asymmetrical trait manifestations in the American White sample requires additional study. While fluctuating asymmetry and developmental stress (Palmer, 1994; Meloro et al., 2019) may explain some of the disparities between American White and American Black postcranial morphologies, the most parsimonious explanation is patterned geographic variability. Measuring and interpreting differences between

ancestries using ordinal response variables may not elucidate the same causative forces as continuous data. An enduring problem with the application of postcranial MMS traits in ancestry estimation is their poorly understood etiology. However, collecting more data for more groups will mean a more thorough and comprehensive grasp of their distribution. These data, particularly if associated with geographic, climactic, and genomic datasets, will provide insight into the causative forces of patterned geographic variability. Consider, as an example, whether a cervical vertebra is bifid.

The power of bifidity as a single trait is of very little use to forensic anthropologists. However, the results of our simple heuristic naïve estimator warrant further investigation. As so little is known about the development and frequency of bifidity (on a global scale) further exploration into the ontogeny of this trait and other external influences on cervical bifidity are just the beginning.

The current analyses only include two groups, so a more thorough investigation of the frequency of these traits across additional populations—along with the underlying genetic and environmental factors contributing to their expression—is necessary. Among current and past two-group models, the combined cranial and postcranial models we presented outperform all others. The lowest accuracy from the combined dataset models (RFM: 88.2%) still exceeds the highest accuracy of cranial (SVM: 85.5%) or postcranial (QDA: 81.6%) models. The SVM model provided the highest CCR for the combined dataset (92.1%), and the aNN model has the lowest classification bias (test sample CCR: 90.8%). Analysts should focus on the aNN model. The relative stability (low classification bias) of the artificial neural network provides the most conservative classifications. Moreover, the appropriateness of the aNN over quadratic discriminant function leads us to recommend aNNs for future work. To facilitate implementation of that model,

we provide a web-based application.

In line with recent efforts to make statistical programs available for practitioners (Berg & Kenyhercz, 2017), a graphical user interface (GUI) was created utilizing the aNN model. This application, ComboMaMD Analytical v.0.1, was built using "shinyapp" (Chang et al., 2019) and R 3.6.0 (35), and is freely available at https:// www.macromorphoscopictraitanalysis.shinyapps.io/ combo_mamd or by contacting the authors for the source code. Scoring protocols follow Hefner (2009) and Spiros (2019) and are included in the guide. The model allows up to 35 cranial and postcranial MMS variables, and can handle the missing data seamlessly (Fig. 1.5). The output includes predicted ancestry and measures of model success including model accuracy, sensitivity, and specificity. The program collects no data and no aspect of an analysis is stored on the website.

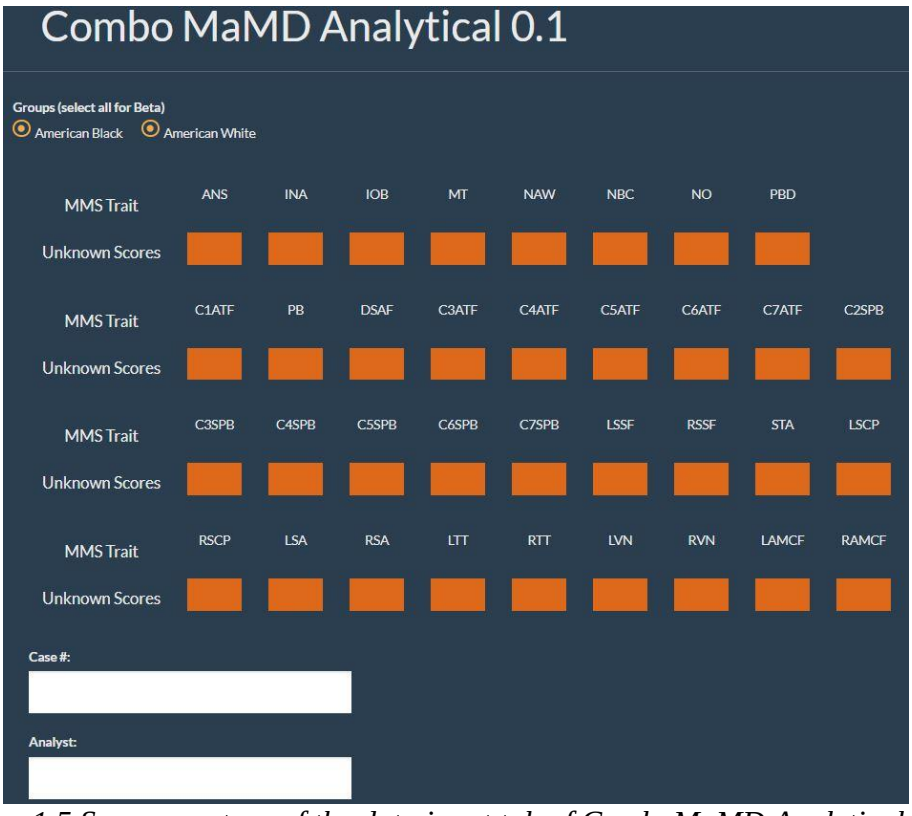

Figure 1.5 Screen capture of the data input tab of ComboMaMD Analytical v.0.1

CONCLUSIONS

Ancestry estimation methods have remained relatively unchanged in forensic anthropological research: the majority focus on metric analysis of the skull. However, at the turn of this century, focus has shifted to novel aspects of human skeletal remains, including the postcranial skeleton and trait variation. Our research utilizes cranial and postcranial MMS traits to estimate ancestry in a statistical framework. This approach is essential to validate and increase objectivity in ancestry estimation. The ComboMaMD Analytical v.0.1 permits forensic anthropologists to utilize the models we developed and includes measures of model success that are important for quantifying our evaluations.

The improved correct classification rates illustrate why both cranial and postcranial MMS traits should be used in ancestry estimation models and biodistance studies. Through continuous testing and revisions, forensic anthropological analyses can achieve the level of accuracy necessary for applying forensic science research to casework and expert witness testimony while concomitantly decreasing subjectivity and lowering rates of error.

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MANUSCRIPT 2. A HEURISTIC APPROACH TO THE DURAY METHOD: VALIDATION AND MODERN REFINEMENT

INTRODUCTION

Methodological standardization, validation, and improved accuracy have been at the forefront of forensic sciences in recent years, due in large part to reports critical of the forensic sciences (National Research Council, 2009). These are especially crucial when methods, such as the cervical spinous process bifurcation (SPB) (Duray et al., 1999), are included in standard operating procedures at national laboratories such as the Defense POW/MIA Accounting Agency's Central Identification Lab for population affinity estimation (DPAA Laboratory Manual 2020; Tallman & Winburn, 2015) and is listed as study material for the forensic anthropology board certification (ABFA, 2022). Validation studies of these methods are necessary following the call for higher admissibility criteria and evidentiary standards motivated by court cases (Grivas & Komar, 2008) and reports centered on the forensic sciences (National Research Council, 2009; PCAST, 2016). Validation of a method, alone, is not enough, however. Contemporary statistical analyses should also be applied to earlier methods to improve classification accuracy, calculate error rates, and refine applicability.

Human variation is an integral component of biological anthropology. In recent years, tests of how well morphological variations can be used to assess aspects of human variation have been conducted using new standards, assessing reliability (Christensen & Crowder, 2009; Francisco et al., 2017; Koot et al., 2005; Steyn et al. 2012) and applying modern statistical analyses (Hefner & Ousley, 2014; Hughes et al., 2011; Kamnikar et al., 2017; Kenyhercz et al., 2017; Tallman & Go, 2018; Scott et al., 2018; Spiros & Hefner, 2020). Cervical spinous process morphological variation has been researched since the late 1800s (Cunningham, 1886) and has continued into the modern

era (Finnegan, 1978; Duray et al., 1997; Barnes, 2012; Asvat, 2012; Mann et al., 2016; Spiros, 2019; Spiros & Hefner, 2020). Beyond biological anthropology, implications for skeletal variation in SPB have also been discussed in clinical (surgical) literature (Saluja et al. 2015).

In 1999, Duray and colleagues assessed the cervical vertebrae of 359 U.S. skeletons from the Hamman-Todd Collection at the Cleveland Museum of Natural History. The scoring methodology created by Duray and colleagues (1999) included three states of variation for the spinous process: 1) nonbifid; 2) partially bifid; and 3) completely bifid (Table 2.1; Figure 2.1). Duray and colleagues (1999) identified significant variation in the cervical vertebrae 3-6 (C3-C6) spinous processes between samples of Black and White individuals from the United States. Using a logistic regression analysis, they demonstrated C3 and C4 were most applicable, correctly classifying 76.1% (B= 72.1%; W= 80.3%) of the sample.

Table 2.1 Scoring Classification (Duray et al., 1999)

Character State	***Definition***
0: Nonbifid	The end of the spinous process is rounded or flattened. A median groove may be present but two distinct tubercles are not present
1: Partially Bifid	Two distinct tubercles at the end of the spinous process are present. The spinous process itself is not bifurcated and no cleft is present.
2: Bifid	The spinous process includes a clearly distinct cleft resulting in two elongated projections. The bifurcation must separate both the tubercles and part of the spinous process itself.

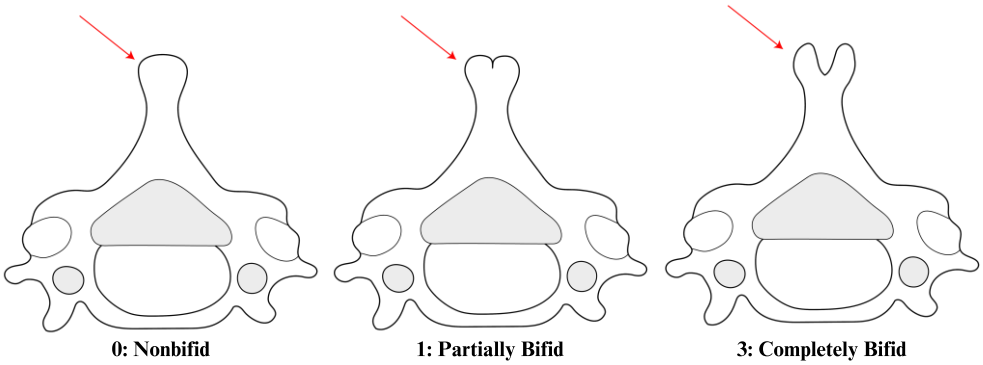

Figure 2.1 Spinous Process Bifurcation Character States (modified from Spiros, 2019)

Cervical vertebrae morphology can be used when the skull is absent, postcranial metrics are unavailable, or as an additional piece of evidence for a complete skeletal analysis. Incorporating multiple methods into analyses increases the accuracy of an estimation (Spiros & Hefner, 2020; Kamnikar, 2022). At the DPAA-CIL, the majority of missing service members are U.S. Black or White individuals (Belcher et al., 2021; Taylor et al., 2021; New et al., 2022) thus making this an applicable method.

The purpose of the current study is to test cervical SPB following Duray and colleagues (1999) on an independent collection of known individuals born during the same time period (19th century) as a validation sample and then to assess the impact of secular change on SPB morphology using a modern sample (20th century). First, the results from the original study (Duray et al., 1999) are compared to the Terry Collection model to assess differences between skeletal collections. Next, the method is tested to see how it performs on a sample of modern individuals (20th century birth years). The purpose of this approach is to determine if secular change impacts the expression of SPB. Then, a new model is built using the 20th century collection for modern utility. Finally, both 19th and 20th century data are modeled collectively to assess the classification power of this approach when the decedent is from an unknown temporal period.

MATERIALS & METHODS

Materials

A stratified random sample of 210 individuals was analyzed from the Robert J. Terry Collection for the preliminary validation study. Housed by the Smithsonian Institution, National Museum of Natural History (NMNH), this sample includes two broad cohorts representing U.S. Black and U.S. White individuals. These social classifications are based on records provided by NMNH curators (Table 2.2). Only individuals older than 18 years were included to control for developmental differences. Equal representation of both females and males stabilized sex differences. Individuals were included if the second through the seventh cervical vertebrae were present. If the cervical vertebrae showed traumatic, taphonomic, or pathological damage the individual was not included. The sample from the Terry Collection represents U.S. Black (n = 50) and U.S. White (n = 50) individuals with 19th century birth years, including females (n = 47) and males (n = 53) ranging in age from 19 to 91 years.

The second sample includes 214 individuals from the UTK Donated Skeletal Collection. This collection includes samples representing U.S. Black and White individuals. These social classifications are based on records provided by the University of Tennessee, Department of Anthropology (Table 2.2). The sample from the UTK Donated Skeletal Collection represents U.S. Black (n = 61) and U.S. White (n = 153) individuals with 19th and 20th century birth years, including females (n = 101) and males (n = 113) ranging in age from 23 to 97 years.

Table 2.2 Sample Demography (N= 314)

Terry Demography			
Population Affinity	***Females (n)***	***Males (n)***	***Total (N)***
U.S. Black	21	29	50
U.S. White	26	24	50
Total (N)	47	53	100
UTK Demography			
Population Affinity	***Females (n)***	***Males (n)***	***Total (N)***
U.S. Black	11	50	61
U.S. White	90	63	153
Total (N)	101	113	214

Methods

All data were collected following the definitions (Table 2.1) and character states (Figure 2.1). Missing data imputations were conducted using the "mice" package (van Buuren and Groothuis-Oudshoorn, 2010). Multivariate imputation by chained equations (MICE) generates multiple imputations using predictive mean matching against the full dataset.

Frequency distributions were calculated and tabulated in R. Pearson's chi-squared test was used to assess score differences between females and males. A chi-squared test was also used to check for statistical significance between U.S. Black and White individuals (Terry Collection), for comparability to Duray and colleagues (1999). A chi-square test was used to assess the UTK Donated Skeletal Collection for secular change in SPB presentation.

A heuristic method to dichotomize the three states of SPB, to maximize the differences between groups, was used. Previous researchers have utilized a similar method in forensic anthropology to analyze population affinity and sex with cranial traits (Hefner & Ousley, 2014; Kenyhercz et al., 2017; Tallman & Go, 2018). Using the tabulated trait frequencies for the associated skeletal assemblage, each trait state was dichotomized and assessed for statistical significance. Dichotomizing traits involves determining a cutoff point based on the cumulative frequencies of the trait values for each group, dividing the trait states into two categories

accordingly. Vertebrae with demonstrable significant differences between the two groups were utilized to build a model to assess SPB— cervical vertebrae 2-6 (C2-C6). Traits more prevalent within the U.S. Black sample were scored "0"; expressions more prevalent in the U.S. White sample were scored "1". After dichotomizing, all values were summed across vertebrae and summed distributions are reported.

Three models are generated: 1) one using Terry Collection data; 2) one using UTK Donated Collection data, and 3) one using those two samples in a combined analysis. Five iterations of this modeling are tested (Table 2.3). Model numbers are based on the training data and iteration is based on the test data.

Table 2.3 SPB Models

Model	*Iteration*	*Training Data*	*Test Data*	*Vertebrae*	*Purpose*
1	A	Terry	Terry	C3-C4	Duray Validation
1	B	Terry	Terry	C2-C6	19th Century
1	C	Terry	UTK	C2-C6	Secular Change
2	A	UTK	UTK	C2-C6	20th Century
3	A	Combined (Terry + UTK)	Combined (Terry + UTK)	C2-C6	Unknown Temporal

These iterations allow practitioners to utilize an appropriate method when temporal association is known/suspected. The summed values for each model range from 0-2 and 0-5, respectively. Error rates, sensitivity, specificity, positive predictive values (PPV), and negative predictive values (NPV) were calculated for each model (Table 2.4).

Table 2.4 Key Performance Indicators for Diagnostic Tests

Metric	***Formula***
Error Rate	100 - Correct Classification Rate
Sensitivity	Correctly Classified Black Individuals/ (Correctly Classified Black Individuals + White Individuals Classified as Black)
Specificity	Correctly Classified White Individuals/ (Correctly Classified White Individuals + White Individuals Classified as Black)
PPV *if Black*	Correctly Classified Black Individuals/ (Correctly Classified Black Individuals + Black Individuals Identified as White)
NPV *if White*	Correctly Classified White Individuals/ (Correctly Classified White Individuals + White Individuals Identified as Black)

RESULTS

No statistically significant differences ($p < 0.05$) were noted between the female and male data. As a result, these data were pooled to increase sample sizes for the Terry and UTK Donated collections. No bifurcated spinous processes were observed on a seventh cervical vertebrae (C7), so all C7 vertebrae were excluded from this study.

Duray Validation

Frequency distribution data for the Terry Collection are presented in Table 2.5, by population affinity. The chi-square tests demonstrate statistically significant differences (Table 2.6). Using the tabulated trait frequencies for the Terry Collection, each state was dichotomized based on the cumulative frequencies (Table 2.5) for a dichotomized score of "0" when the ordinal score was "0" or "1" and a "1" when the ordinal score was "2". This was repeated for every trait (Table 2.5).

Table 2.5 Terry Frequency Data & Dichotomized Scores

C2 SPB

	U.S. Black (n=50)			U.S. White (n=50)			
Trait State	***n***	***%***	***Cumulative %***	***n***	***%***	***Cumulative %***	***Dichotomized Score***
0	18	36	36	2	4	100	0
1	23	46	82	8	16	96	0
2	9	18	100	40	80	80	1

C3 SPB

	U.S. Black (n=50)			U.S. White (n=50)			
Trait State	***n***	***%***	***Cumulative %***	***n***	***%***	***Cumulative %***	***Dichotomized Score***
0	28	56	56	1	2	100	0
1	17	34	90	12	24	98	0
2	5	5	100	37	74	74	1

C4 SPB

	U.S. Black (n=50)			U.S. White (n=50)			
Trait State	***n***	***%***	***Cumulative %***	***n***	***%***	***Cumulative %***	***Dichotomized Score***
0	20	40	40	6	12	100	0
1	14	28	68	8	16	90	0
2	16	32	100	37	74	74	1

C5 SPB

	U.S. Black (n=50)			U.S. White (n=50)			
Trait State	***n***	***%***	***Cumulative %***	***n***	***%***	***Cumulative %***	***Dichotomized Score***
0	18	36	36	2	4	100	0
1	6	12	48	4	8	96	0
2	26	52	100	44	88	88	1

C6 SPB

	U.S. Black (n=50)			U.S. White (n=50)			
Trait State	***n***	***%***	***Cumulative %***	***n***	***%***	***Cumulative %***	***Dichotomized Score***
0	27	54	54	11	22	100	0
1	10	20	74	8	16	78	0
2	13	26	100	31	62	62	1

Table 2.6 Terry (19th Century) Chi-Square Results

Trait	*Results*
C2 Spinous Process Bifurcation	x^2=39.6703, df=2, p<0.0001*
C3 Spinous Process Bifurcation	x^2=50.3810, df=2, p<0.0001*
C4 Spinous Process Bifurcation	x^2=17.4874, df=2, p=0.0002*
C5 Spinous Process Bifurcation	x^2=17.8286, df=2, p=0.0001*
C6 Spinous Process Bifurcation	x^2=14.3227, df=2, p=0.0008*

**Statistically significant at $p \leq 0.05$*

When only using the third and fourth cervical vertebrae dichotomized scores, the sectioning point for individuals from the Terry Collection is 1.5 (<1 for U.S. Black individuals and ≥1 for U.S. White individuals (Table 2.5, Table 2.7). Summed scores were calculated for these data based on the dichotomized scores (Table 2.7). These summed scores were used to calculate estimated group membership. Creating a model to validate Duray and colleagues (1999), Model 1A isolated these two vertebrae for an overall CCR was 78% (B= 66%, W= 90%). The Model 1A classification statistics are listed in Table 2.8. For comparison, the C3-C4 SPB classification statistics for the original Hamann-Todd collection (Duray et al., 1999) are listed in Table 2.9.

Table 2.7 Terry Summed Score Distributions

	Summed Scores						***Totals***	
	0		***1***		***2***			
Group	*n*	*%*	*n*	*%*	*n*	*%*	*N*	*%*
U.S. Black	32	64.0	14	28.0	4	8.0	50	50.0
U.S. White	5	10.0	16	32.0	29	58.0	50	50.0
Total	37	37.0	30	30.0	33	33.0	100	100.0

Table 2.8 Duray Validation Classification Statistics (Model 1A)

Metric	***Percentage***
Correct Classification Rate	78.00%
Error Rate	22.00%
Sensitivity	86.84%
Specificity	72.58%
PPV *if Black*	66.00%
NPV *if White*	90.00%

Table 2.9 Duray (C3-C4) Classification Statistics (Duray et al. 1999)

Metric	***Percentage***
Correct Classification Rate	76.05%
Error Rate	23.95%
Sensitivity	79.49%
Specificity	73.03%
PPV *if Black*	72.09%
NPV *if White*	80.25%

19th Century Model

Assessing beyond the C3 and C4, chi-square analyses of C2-C6 indicated statistical significance between the two groups (Table 6), requiring further investigation. Using the same 19th century model to incorporate C2-C6, the distribution of the scores between U.S. Black and White individuals places the sectioning point at 2.5 (≤ 2 for U.S. Black individuals and > 2 for U.S. White individuals) (Table 2.5, Table 2.10). Summed scores were calculated (Table 2.10) and were used to calculate estimated group membership.

When using this model (Model 1B) to analyze SPB for C2-C6, the overall CCR was 83% (B= 76%, W= 90%). The classification statistics for Model 1B can be seen in Table 2.11.

Table 2.10 19th Century Summed Score Distributions (Model 1B)

	Summed Scores													
	0		***1***		***2***		***3***		***4***		***5***		***Totals***	
Group	*n*	*%*	*n*	*%*	*n*	*%*	*n*	*%*	*n*	*%*	*n*	*%*	*N*	*%*
U.S. Black	15	30.0	13	26.0	11	22.0	7	14.0	2	4.0	2	4.0	50	50.0
U.S. White	0	0.0	1	2.0	4	8.0	11	22.0	20	40.0	14	28.0	50	50.0
Total	15	15.0	14	14.0	15	15.0	18	18.0	22	22.0	16	16.0	100	100.0

Table 2.11 19th Century Classification Statistics (Model 1B)

Metric	***Percentage***
Correct Classification Rate	83.00%
Error Rate	17.00%
Sensitivity	88.37%
Specificity	78.95%
PPV *if Black*	76.00%
NPV *if White*	90.00%

Secular Change

The UTK Collection frequencies and dichotomized scores for cervical vertebrae two through six are presented, by population affinity, in Table 2.12. The distribution of the trait states for C2-C6 from each temporal sample is depicted in Figure 2.2. All traits, apart from C4, were significantly different between the 19th and 20th century cohorts (Table 2.13). Although, the results of the chi-square test for the 20th century cohort illustrate that the second through the sixth cervical vertebrae SPB still differ significantly between the two groups (Table 2.14). Three dichotomized scores shifted from the 19th to the 20th century cohorts (C3, C4, and C6 vertebrae) based on the cumulative frequency (Table 2.12).

Table 2.12 UTK Frequency Data & Dichotomized Scores

C2 SPB

	U.S. Black (n=61)			U.S. White (n=153)			
Trait State	***n***	***%***	***Cumulative %***	***n***	***%***	***Cumulative %***	***Dichotomized Score***
0	5	8	8	7	5	100	0
1	29	48	73	34	22	95	0
2	27	44	100	112	73	73	1

C3 SPB

	U.S. Black (n=61)			U.S. White (n=153)			
Trait State	***n***	***%***	***Cumulative %***	***n***	***%***	***Cumulative %***	***Dichotomized Score***
0	46	75	75	23	15	100	0
1	10	16	95	38	25	85	1*
2	5	8	100	92	60	60	1

C4 SPB

	U.S. Black (n=61)			U.S. White (n=153)			
Trait State	***n***	***%***	***Cumulative %***	***n***	***%***	***Cumulative %***	***Dichotomized Score***
0	38	62	62	21	14	100	0
1	11	18	89	32	21	86	1*
2	12	20	100	100	65	65	1

C5 SPB

	U.S. Black (n=61)			U.S. White (n=153)			
Trait State	***n***	***%***	***Cumulative %***	***n***	***%***	***Cumulative %***	***Dichotomized Score***
0	24	39	39	6	4	100	0
1	17	28	83	15	10	96	0
2	20	33	100	132	86	88	1

C6 SPB

	U.S. Black (n=61)			U.S. White (n=153)			
Trait State	***n***	***%***	***Cumulative %***	***n***	***%***	***Cumulative %***	***Dichotomized Score***
0	30	49	49	39	22	100	0
1	15	25	84	42	27	75	1*
2	16	26	100	72	47	47	1

** Score shift from the 19th century model*

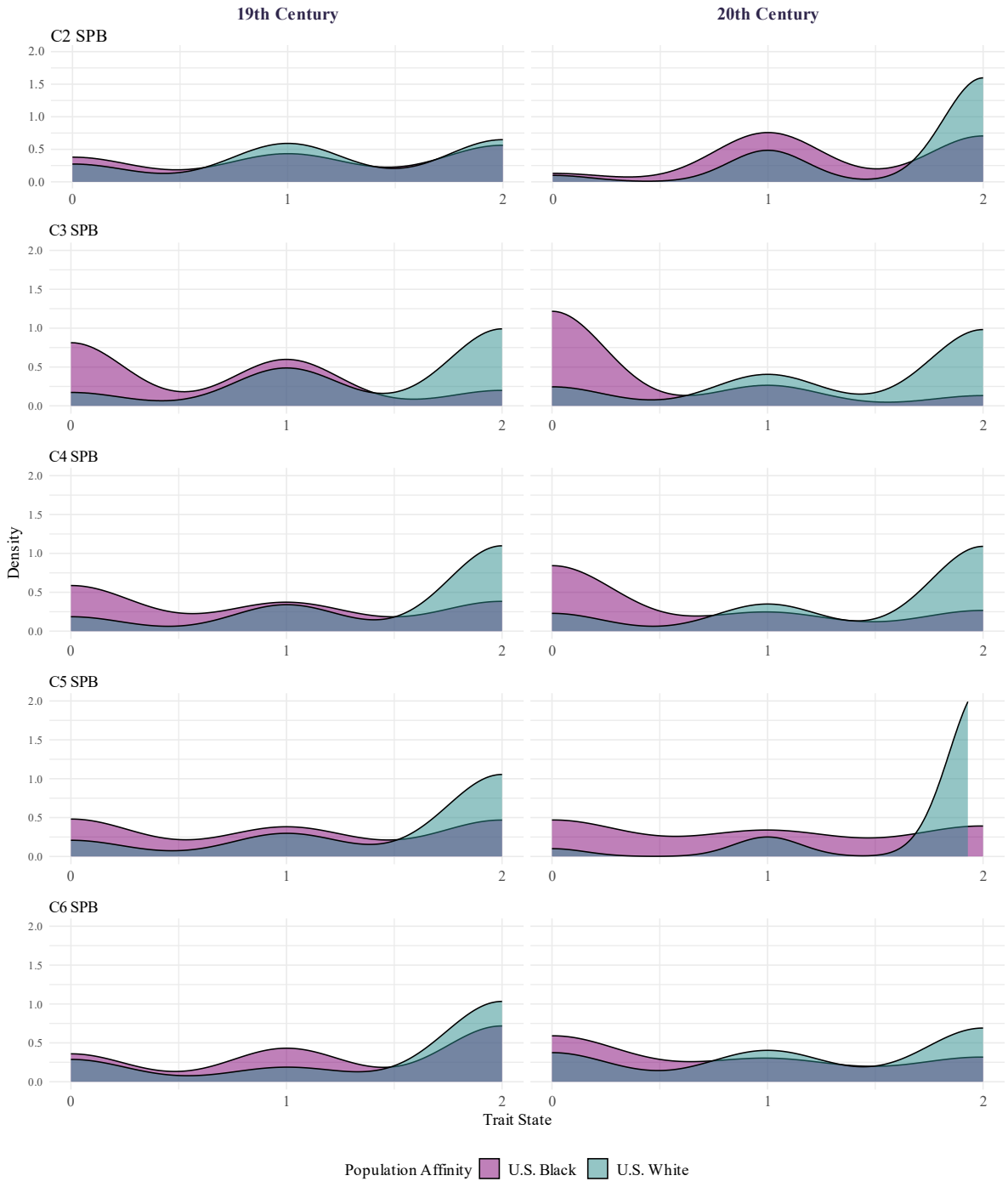

Figure 2.2 Density plot illustrating the distribution of SPB trait states between U.S Black and White individuals from the 19th and 20th centuries. Only C4 is not significant (Table 2.13).

Table 2.13 Chi-Square Results between 19th & 20th Centuries

Trait	*Results*
C2 Spinous Process Bifurcation	x^2=33.907, df=2, p<0.0001*
C3 Spinous Process Bifurcation	x^2=6.8017, df=2, p=0.0336*
C4 Spinous Process Bifurcation	x^2=1.2198, df=2, p=0.5434
C5 Spinous Process Bifurcation	x^2=17.2640, df=2, p=0.0002*
C6 Spinous Process Bifurcation	x^2=12.4810, df=2, p=0.0019*

**Statistically significant at $p \leq 0.05$*

Table 2.14 UTK (20th Century) Chi-Square Results

Trait	*Results*
C2 Spinous Process Bifurcation	x^2= 16.1402, df=2, p= 0.0003*
C3 Spinous Process Bifurcation	x^2= 76.6450, df=2, p <0.0001*
C4 Spinous Process Bifurcation	x^2= 54.8904, df=2, p <0.0001*
C5 Spinous Process Bifurcation	x^2= 66.1202, df=2, p <0.0001*
C6 Spinous Process Bifurcation	x^2= 12.3265, df=2, p =0.0021*

**Statistically significant at $p \leq 0.05$*

To compare datasets to assess secular change, the 20th century (UTK) data were analyzed with the model built using the 19th century data (Model 1C) and subsequently through a new model using the 20th century data (Model 2A; see next section). For Model 1C, applying the dichotomized scores from the Terry model, the distribution of the UTK scores between U.S. Black and White individuals still suggests a sectioning point of 2.5 (≤ 2 for U.S. Black individuals and > 2 for U.S. White individuals) (Table 2.12, Table 2.15). Summed scores were calculated (Table 2.15) and used to calculate estimated group membership. When utilizing Model 1C, the overall CCR was 79.9% (B= 80.3%, W= 79.7%). The UTK classification statistics using the 19th century model are listed in Table 2.16.

Table 2.15 Secular Change Summed Score Distributions (Model 1C)

	Summed Scores												***Totals***	
	0		***1***		***2***		***3***		***4***		***5***			
Group	*n*	*%*	*n*	*%*	*n*	*%*	*n*	*%*	*n*	*%*	*n*	*%*	*N*	*%*
U.S. Black	12	19.7	17	27.9	20	32.8	8	13.1	4	6.6	0	0	61	28.5
U.S. White	2	1.3	11	7.2	18	11.8	39	25.5	56	36.6	27	17.6	153	71.5
Total	14	6.5	28	13.1	38	17.8	47	22.0	60	28.0	27	12.6	214	100.0

Table 2.16 Secular Change Classification Statistics (Model 1C)

Metric	***Percentage***
Correct Classification Rate	79.91%
Error Rate	20.09%
Sensitivity	61.25%
Specificity	91.04%
PPV *if Black*	80.33%
NPV *if White*	79.74%

20th Century Model

Building a new model using the 20th century (UTK) data (Model 2A), the distribution suggests a sectioning point of 2.5 (≤ 2 for U.S. Black individuals and > 2 for U.S. White individuals) (Table 2.12, Table 2.17). Summed scores were calculated (Table 2.17) and were used to calculate estimated group membership. This model correctly classifies 85.5% of the sample (B= 68.9%, W= 92.2%), but is disproportionately classifying U.S. White individuals. The UTK classification statistics using Model 2A are listed in Table 2.18.

Table 2.17 20th Century Summed Score Distributions (Model 2A)

	Summed Scores												***Totals***	
	0		***1***		***2***		***3***		***4***		***5***			
Group	*n*	*%*	*n*	*%*	*n*	*%*	*n*	*%*	*n*	*%*	*n*	*%*	*N*	*%*
U.S. Black	10	16.4	17	27.9	15	24.6	10	16.4	6	9.8	3	4.9	61	28.5
U.S. White	0	0.0	6	3.9	6	3.9	26	17.0	51	33.3	64	41.8	153	71.5
Total	10	4.7	23	10.7	21	9.8	36	16.8	57	26.6	67	31.3	214	100.0

Table 2.18 20th Century Classification Statistics (Model 2A)

Metric	***Percentage***
Correct Classification Rate	85.51%
Error Rate	14.49%
Sensitivity	77.78%
Specificity	88.13%
PPV *if Black*	68.85%
NPV *if White*	92.16%

Combined Temporal Model

A combined model based on both the Terry and UTK data was created (Model 3A). The distribution of the Terry and UTK scores between U.S. Black and White individuals remains to suggest a 2.5 sectioning point (≤ 2 for U.S. Black individuals and > 2 for U.S. White individuals) (Table 2.19). Summed scores were calculated (Table 2.19) and, when utilizing the combined model, the overall CCR is 75.2% (B= 78.3%, W= 73.3%). The classification statistics using Model 3A are listed in Table 2.20.

Table 2.19 Combined Summed Score Distributions (Model 3A)

	Summed Scores												***Totals***	
	0		***1***		***2***		***3***		***4***		***5***			
Group	*n*	*%*	*n*	*%*	*n*	*%*	*n*	*%*	*n*	*%*	*n*	*%*	*N*	*%*
U.S. Black	36	21.7	57	34.3	37	22.3	23	13.9	12	7.2	1	0.6	166	39.2
U.S. White	6	2.3	19	7.4	44	17.1	70	27.1	82	31.8	37	14.3	258	60.8
Total	42	9.9	76	17.9	81	19.1	93	21.9	94	22.2	38	9.0	424	100.0

Table 2.20 Combined Classification Statistics (Model 3A)

Metric	***Percentage***
Correct Classification Rate	75.42%
Error Rate	24.76%
Sensitivity	65.33%
Specificity	84.00%
PPV *if Black*	78.31%
NPV *if White*	73.26%

DISCUSSION

This study reviewed the evaluation of cervical SPB for population affinity estimation. In 1999, Duray and colleagues found consistent, significant variations in the SPB frequencies between U.S. Black and White individuals at C3-C6, where both C3 and C4 led to the highest correct classification. The results of the current study, which used a temporally similar collection, corroborates their results (Duray et al., 1999) identifying significant differences in the expression of cervical vertebrae spinous processes. Contrary to the 1999 findings, the current analysis of the Terry collection found that SPB variations of the second cervical vertebra were statistically significant between the two groups for both the Terry and UTK collections.

Duray and colleagues (1999) achieved an overall CCR of 76.05% using a logistic regression analysis on the C3 and C4 vertebrae (U.S. White = 80.25%; U.S. Black = 72.09%). When the Duray validation model (Model 1A) was applied to analyze the C3/C4 vertebrae, the overall CCR for population affinity was greater than achieved by the Duray study. While the correct classification of U.S. White individuals increased by ~10%, the classification of U.S. Black individuals decreased by ~6%. These classification rates outperformed the logistic regression by seven percent. Comparing the results between Duray et al. (1999) and the validation model (Model 1A) herein, there was fa modest increase in correct classifications (~2%); however, there was a 28% increase in CCR over random allocation. There was a classification bias toward the U.S. White sample. In contrast, the 19th century model (Model 1B) built on the Terry data using C2-C6 led to an overall CCR of 83%, correctly classifying 76% of the U.S. Black sample 90% of the U.S. White sample. Moving beyond the C3/C4 model, the 19th century model (Model 1B) had approximately a 7% increase from the Duray et al. (1999) C3-C4 results.

Even though there were shifts in significant difference from the 19th to 20th century (apart

from C4), spinous process bifurcation still illustrates significant differences for C2-C6 within the 20th century cohort. Testing if this secular change is meaningful (Model 1C), the secular change model correctly classified nearly 80% of the sample, equally classifying both groups. Applying the 19th century model to the 20th century collection (Model 1C) improved correct classification over the Duray and colleagues (1999) C3-C4 model by 3.86% with the added benefit of similar classification rates between the groups. An increase in ~30% from random, even with the shift in dichotomized scores for the third, fourth, and sixth cervical vertebrae.

Further comparing Model 1B (19th Century Model) and Model 1C (Secular Change model) though, Model 1C decreases accuracy overall. When looking at the predictive values for each group, the proportion of individuals correctly classified among individuals identified as that group by the model decreases for white individuals but increases for black individuals. Although, looking at the sensitivity and specificity, the proportions that represent individuals correctly classified as the group they are from among all individuals who are actual from that group, the increase for white individuals but decreases for black individuals. This fits the models we see in other osteological studies of U.S. secular change where there is a trend towards homogeneity in American Black individuals across time (Meadows Jantz & Jantz, 1999; Algee-Hewitt, 2016).

The 20th century model (Model 2A) correctly classified 85.51% of the sample with U.S. White individuals correctly classified 92.16% of the time and U.S. Black individuals correctly classified 68.85% of the time, highlighting a strong classification bias. The combined temporal model (Model 3A) had an overall CCR of 75.42% with U.S. White individuals correctly classified 73.26% of the time while U.S. Black individuals correctly classified 78.31% of the time. Utilizing the 20th century model on the UTK collection, the overall classification rate improved over the Duray and colleagues (1999) model by 9.46%. An increase in 35.51% from random classification,

although with a classification bias towards U.S. White individuals. Finally, the combined model of 19th and 20th century (Model 3A) classification decreases from Duray et al. (1999) by less than 1%. The classification bias on this model highlight similarities between groups and the model still increases the classification of an individual by 25.42% from random.

Although the overall best CCR was the 20th century model (Model 2A), there is a large bias between groups. The highest CCR with stabilization between groups was seen in the secular change model (Model 1C) with the combined model (Model 3A) being the second highest CCR with the stabilized bias between the two groups. This highlights that the combined model would be useful for all individuals with the least amount of bias.

CONCLUSION

Overall, this study validates significant differences between groups when analyzing cervical SPB character states outlined by Duray and colleagues (1999). Subsequently, this study illustrated the impact of time on the plasticity of the human skeleton validated the utilization of spinous process bifurcation of the cervical vertebrae in 19th century, 20th century, and combined temporal cohorts. The SPB character states can be used to estimate population affinity using statistical analyses such as the adapted dichotomized model used herein (or the logistic regression models incorporated in the original study), although analysis of the second through sixth vertebrae produced the best classification rate. Spiros (2019) addressed the C3/C4 vertebrae for postcranial macromorphoscopic research, previously; and, like that study we suggest future applications of SPB should include the second through the sixth vertebrae, as demonstrated by Spiros & Hefner (2020) and reinforced in this study.

Although there is evidence for secular change based on variation in the classification rates between the 19th to 20th century birth cohorts and a shift in C3, C4, and C6 dichotomized scores,

the correct classification rates are still well over random and consistent across temporal cohorts. Though the threshold shifted, the correct classification rates highlight that this change does not seem to be significant enough to render the utility of this method impractical from the 19th to the 20th century. The significant differences between the time periods illustrate this noteworthy secular change, possibly due to a shift towards homogeneity, though testing the utility of the traits within the 20th century cohort still illustrates the applicability of spinous process bifurcation in a modern skeletal analysis. Future studies should explore models that decrease between-group biases, employing more rigorous methods of classification to stabilize group classifications. Studies utilizing more geographically, socially diverse samples are imperative for future applicability of this method.

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MANUSCRIPT 3. ONTOGENETIC AND PUBERTY INFLUENCES ON POSTCRANIAL MORPHOLOGICAL VARIATION

INTRODUCTION

Postcranial nonmetric traits have been only rarely studied, generally as isolated variables to identify functional or for surgical morphological significance (Bolanowski et al., 2005; Bradshaw et al., 2020; Lozanoff et al., 1985; Paraskevas et al., 2012). Some of these traits are documented in the paleoanthropological literature, for example, the septal aperture (Trinkaus et al., 2007; Walker et al., 2011); however, very little effort has been made to understand the incidence of postcranial nonmetric traits among anatomically modern humans. The influences of sociocultural behavior, environmental stressors, and diet on ossification patterns, laterality, size/robusticity, and cross-sectional morphology have been explored using metric analyses of the postcranial skeleton (Cameron et al., 2017; Cowgill, 2010, 2014; Donisch & Trapp, 1971; Garn et al., 1973; Özener, 2010; Prang, 2015a,b; Prang, 2016; Ruff, 1994; Ruff et al., 1994; Ruff et al., 2013; Schaefer et al., 2015; Spradley & Jantz, 2011). Nonetheless, currently there is little known about the formation of these traits, their timing in growth and development, or their expression within and between groups of humans. Human adaptability scholarship centers on understanding variation and informs evolutionary histories to explain diversity in humans', past and present. This study tests the influence of multiple interactive biocultural variables on 11 postcranial traits (Spiros, 2019) to identify the ontogenetic origins of these trait manifestations.

Ontogeny (i.e., growth and development) is influenced by genetics and the environment in non-linear, but quantifiable ways. These interactions may include maternal stress, nutrition, socioeconomic status, seasonality, climate, or population history. No matter the influence, growth is a change in the size of an organism; development is a change in morphology.

Ruff and colleagues (2013) explore the impact on skeletal morphology of human skeletal growth and environment, diet, and mechanical influences using samples derived from past and modern human populations. They identified varying rates of growth in skeletal regions, potentially indicating biomechanical and functional influences from different environmental factors (Ruff et al., 2013). What is not known is whether hormonal changes influence postcranial morphology in regions not traditionally related to indicators of sex in the human skeleton. Regional studies of postnatal growth and development using a multifactorial approach are warranted to understand whether genetics, environment, and/or skeletal functional morphology impact how these traits manifest.

Plasticity is important in evolutionary theory, identifying the interaction between flexible behavioral patterns and flexible morphological development. This flexibility is reflected in the interactions between biology and culture; plasticity results from established behavioral changes and the morphological adaptations that follow (West-Eberhard, 1989; West-Eberhard, 2003). Phenotypic plasticity is the observable variation produced when environmental factors influence expression (genetic and morphological) (Agarwal, 2016; Agarwal & Beauchesne, 2011; Duncan et al., 2014; Meloni, 2015; West-Eberhard, 1989). Developmental plasticity identifies a phenotype threshold via the genome dependent on extrinsic factors impacting morphology during development. As such, an individual's phenotype may not realize the genome's full potential (West-Eberhard, 1989). Thus, development and plasticity are closely intertwined.

Eleven postcranial MMS traits are assessed following Spiros (2019) (Table 1). The postcranial MMS protocol expanded certain traits beyond binary representations and standardized scoring methods for usability and applicability in modern skeletal analysis. The purpose of this manuscript

is to assess these less frequently researched postcranial MMS traits (Spiros, 2019; Spiros & Hefner 2020) from birth through adulthood using a comparative ontogenetic and biocultural framework.

Studies have demonstrated the potential of postcranial MMS traits as a tool to study human variation (Spiros, 2019; Spiros & Hefner, 2020). Unfortunately, these early studies lacked a diverse sample and only incorporated adult individuals into their analysis. Very little research has been done to understand the impact of age on the development of nonmetric skeletal morphology (Wood, 2015). One study (Wood, 2015) examined at the expression of cranial morphological traits at different age intervals (from 0-20 years) and identified varying levels of character state expression and developmental timing across populations (Wood, 2015). While there have been studies exploring how environmental and biocultural factors impact the growth and development of postcranial morphological variation, these have predominately focused on metric approaches, leaving a relatively broad knowledge gap concerning nonmetric, morphological studies capturing trait expression and timing. Understanding trait timing is important for two reasons. First, knowing when and how these traits appear across age groups can increase data availability by including individuals beyond the adult cohorts; and second, understanding when these traits appear may highlight factors influencing their manifestations.

The appearance of certain bony morphologies following the onset of puberty and the concomitant hormonal differences between males and females is well documented (Cunningham et al., 2016). To date, there is no research exploring the effect of age and/or puberty on postcranial nonmetric trait expression. Growth and development studies detail the broad skeletal regions where these traits occur. Beyond that, very little is known regarding their growth and development. The traits are believed to result from incomplete ossification in a specific region, the occurrence of bone exostosis during ossification, or anomalies linked to fusion variability. The appearance of

primary and secondary centers of ossification and fusion/complete ossification times for the adjacent skeletal regions are provided in Table 3.1. The third trochanter has been seen to have a similar growth and development rate as the lesser trochanter (Cunningham et al., 2016) and, as such, the ontogeny of the lesser trochanter is used as a proxy estimate for the third trochanter.

Table 3.1. Postcranial MMS Traits & Estimated Associated Ontogenetic Information (Age)

Trait *(Spiros, 2019)*	**Abbreviation**	**Score**	**Associated Ossification Center Appearance** *(Cunningham et al., 2016)*	**Fusion/Complete Ossification** *(Cunningham et al., 2016)*
Posterior Bridging	PB	0-2	Atlas Lateral Mass Primary Center (7 weeks *in utero)*	Atlas Complete Fusion (5-6 years)
Atlas Accessory Transverse Foramen	Atlas ATF	0-2	Atlas Lateral Mass Primary Center (7 weeks *in utero)*	Anterior & Posterior Bar Fusion (3-4 years)
C2-C7 Accessory Transverse Foramen	C2-C7 ATF	0-2	Neural Arch Primary Center (2-3 months *in utero)*	Anterior & Posterior Bar Fusion (3-4 years)
C2 Spinous Process Bifurcation	C2 SPB	0-2	Spinous Process Secondary Center (Puberty)	Posterior Synchondrosis Fusion (3-4 years)
C3-C7 Spinous Process Bifurcation	C3-C7 SPB	0-2	Spinous Process Secondary Center (Puberty)	Posterior Synchondrosis Fusion (2 years)
Sternal Aperture	STA	0-1	Sternebrae Primary Centers (5 months *in utero*- 1 year)	Sternebrae Fusion (4-Puberty)
Suprascapular Foramen	SSF	0-1	Scapula Primary Center (2 months *in utero*)	Coracoid & Scapular Body Fusion (11-22 years)
Supracondyloid Process	SCP	0-1	Humeral Shaft Primary Center (8-9 weeks *in utero*)	Distal Humerus Ossification (6 months *in utero*)
Septal Aperture	SA	0-3*	Humeral Shaft Primary Center (8-9 weeks *in utero*)	Olecranon Fossa Ossification (6 months *in utero*)
Third Trochanter	TT	0-1	Lesser Trochanter Secondary Center (7-11 years)	Lesser Trochanter Fusion (16-17 years)
Vastus Notch	VN	0-1	Patella Primary Center (18 months- 6 years)	Complete Patella Ossification (14- 16 years)

**Translucency (state of '1') not scored for this study*

The range of puberty onset in the United States is 8-14 years of age (Wolf & Long, 2016). In the clinical literature puberty is defined as the period of biological maturation across several body systems (Aris et al., 2022) and is measured in various ways including the timing of menarche among females, physical (bodily) changes, the development of secondary sexual characteristics, and skeletal maturation.

An increase in hormones and sex steroids during puberty impacts bone growth and development, leading to higher bone turnover through modeling and remodeling (Saggese et al., 2002). Life course perspectives on puberty and timing of maturation link social influences to adolescent growth and development (Hoyt et al., 2020). Studies show that the interaction of social, environmental, cultural, and biological factors can impact growth and development (O'Donnell et al., 2022; Williams et al., 2010; Willey et al., 2022).

Race is not biological, although social race is reflected in the physical body because of the interactions between racism (e.g., structural, environmental, political, legal), evolutionary processes associated with climatic and geographic influences, and geographic ancestry. In medical, sociological, and anthropological research, social race has been used to model inequalities in health and to study aspects of human variation, although to the latter has led to the oversimplification of the concept and signaling biological determinism. Biological, or genetic, determinism is the key facet of scientific racism, and remains an issue today (Blakey, 2020). Blakey (2020) equates grouped variations to genetic histories of societal inequalities, arguing that "the study of physiological effects of racism (social analysis) is different from biodeterministic studies of race (racial biological analysis)" (Blakey, 2020, p. 12). To understand the social implications social race imparts on the human body, a multivariate approach is essential to study how race becomes embodied (Gravlee, 2009). Understanding a human beyond their genetic make-up requires

understanding their life course in addition to environmental factors, the impact of phenotypic plasticity, and the overall multilevel causal influences modeled by embodiment. Of course, this approach has shortcomings. The individuals used in this study have a reported race. In this study, the utilization of social race underscores the implications biological processes (e.g., acclimatization) and societal factors (e.g., racism, assortative mating) on human variation, despite their lack of direct influence on the genome.

Three research questions are used to investigate the variation and ontogeny of postcranial MMS traits. First, is age a significant contributing factor in the ontogeny of postcranial traits? Second, is there a relationship between puberty and the frequency distribution of postcranial MM traits? Finally, is there significant variation in the appearance of these postcranial MMS traits between sexes and/or across social race cohorts?

MATERIALS AND METHODS

Materials

To address these questions, postcranial MMS trait data were collected from modern adult and juvenile skeletons. The New Mexico Decedent Image Database (NMDID) was utilized. The NMDID is a novel database of computed tomography (CT) scans of decedents with associated metadata (age, sex, social race) (Berry & Edgar, 2019; Berry et al., 2021). The database includes thin bone Digital Imaging and Communications in Medicine (DICOM) files either encompassing the whole body (for small or young individuals) or separated by bodily region (e.g., upper extremity, torso, lower extremity).

Our overall sample includes 646 individuals (Table 3.2). To calculate trait frequencies, the sample was divided into juveniles (<18) and adults (≥18). These data are explored using cohorts related to puberty: pre-pubescent, pubescent, and post-pubescent. The distribution of age cohorts

is provided in Figure 3.1. These age cohorts are broadly based on Buikstra & Ubelaker's (1994) standards for data collection from human skeletal remains and are used to assess age-at-stabilization for each trait.

Table 3.2 Sample demography (N= 646)

Juvenile Demography (<18 years)			
Social Race	***Females (n)***	***Males (n)***	***Total (N)***
U.S. Black	21	29	35
U.S. Hispanic	49	53	102
U.S. Native American	47	56	103
U.S. White	48	55	103
Total (N)	161	182	343
Adult Demography (≥ 18 years)			
Social Race	***Females (n)***	***Males (n)***	***Total (N)***
U.S. Black	13	40	53
U.S. Hispanic	38	45	83
U.S. Native American	30	37	67
U.S. White	49	51	100
Total (N)	130	173	303

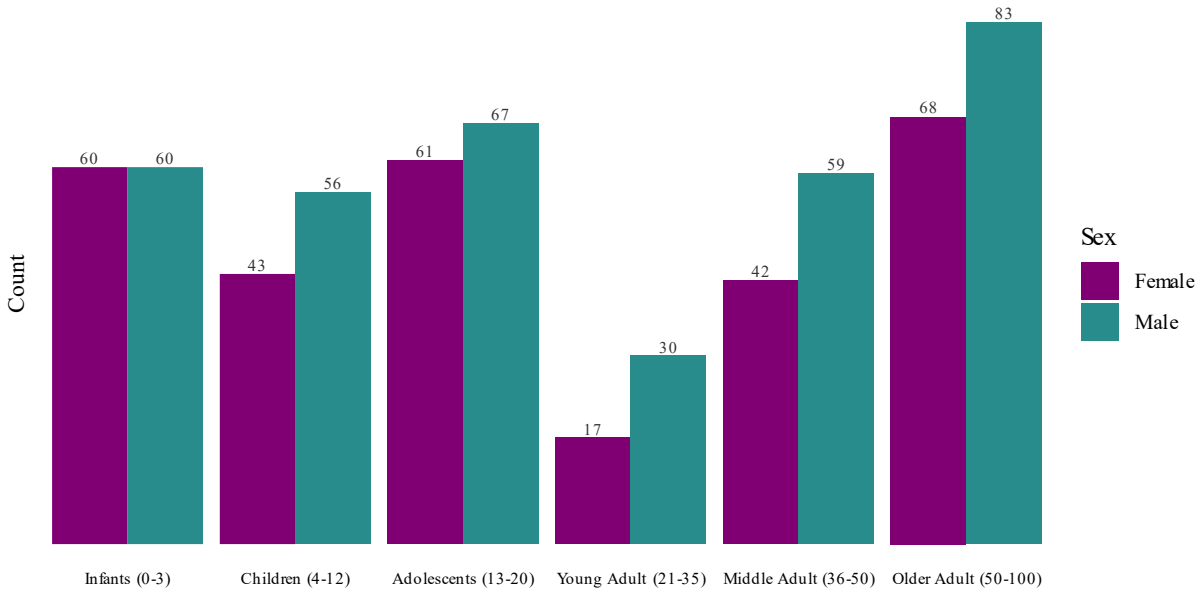


Figure 3.1. Age Distribution by Sex

Data Collection

Three-dimensional skeletal models were generated from the NMDID CT scans to facilitate

data collection. Utilizing the methodology outlined by Stull and colleagues (2021), thin-slice DICOM stacks from the NMDID CT scans were imported into the Amira™ 3D 2022.2 software (Thermo Fisher Scientific, 2023). A volume render was generated for each individual and a surface model (three-dimensional) was reconstructed from the 2D slices to generate a 3D representation of the element. Following Spiros (2019), the cervical vertebrae, scapulae, sternum, humeri, femora, patellae, and calcanei must be present. Due to the articulation points of the calcaneus and talus, the double superior articular facet (DSAF) and the anterior and middle calcaneal facets (AMCF) were not scored. Translucency ("1") was not scored in this study. The assessment of these skeletal elements follows the standard scoring procedures for postcranial MMS variation (Spiros, 2019). Each trait is assigned a nominal score based on the associated definition and line drawings for each character state (Spiros 2019). A score of "7" was recorded when a trait could not be scored because the region or bone was unfused (i.e., the region was not fully developed). For the patella, "7" was used when the border of the bone was scalloped.

To evaluate puberty, assessment of the Risser sign is employed. The Risser sign is a metric initially described by Risser (1958) to measure the ossification and fusion stages of the iliac crest. The Risser sign has a direct correlation to hormonal fluctuations in both males and females. Notably, in females, the Risser sign typically manifests within six months following menarche. Furthermore, the Risser sign is directly correlated with various other markers indicative of the onset of puberty in both sexes. The Risser sign is assessed on a scale from "0" to "5". A "0" signifies the absence of iliac crest ossification, indicative of a pre-pubertal stage. Sequential scores from "1" to "4" represent progressive stages of iliac crest fusion, each stage correlating with advancing development. The final stage, indicated by a score of "5", denotes complete formation and fusion of the iliac crest, which typically coincides with the conclusion of puberty (Shapland

& Lewis, 2013; Scoles et al., 1988).

Statistical Analyses

Missing data imputation is accomplished using the R package, *"mice"* (van Buuren & Groothuis-Oudshoorn, 2015). Imputations are performed separately on the juvenile and adult age cohorts to control for the influence of age. Laterality is assessed using the Pearson's chi-square. To explore trait development, summary statistics are calculated. The R package *"corrplot"* (Wei et al., 2017) is used to calculate the Spearman correlation coefficients for each trait. The Kruskal-Wallis rank sum, a non-parametric test, is applied to each trait in the overall dataset to assess age stabilization, by age cohort. Subsequently, a one-sided Dunn's test for *post hoc* pairwise comparison is used to examine significant differences between each age cohort. Stabilization is determined as the youngest cohort that does not have significant differences from the subsequent cohort. A Kruskal-Wallis test is then used to determine whether there is a significant difference between each postcranial trait and puberty. Again, a one-sided Dunn's test for *post hoc* pairwise comparisons is used to test the significant differences between each postcranial trait and each puberty stage.

After evaluating age and puberty, trait counts and frequencies are calculated. The Kruskal-Wallis rank sum test is used to assess each trait compared to social race. The dataset is separated by juvenile and adult cohorts to control for age/puberty. A one-sided Dunn's test for *post hoc* pairwise comparison measures the significant differences between individual groups. To assess the significance of sex, the Mann-Whitney U test (a non-parametric test alternative to the Kruskal-Wallis test to compare two independent groups) is used. A MANOVA model assessed interactions among the overall dataset (juveniles and adults), with *post hoc* univariate ANOVA tests to assess interactions by trait.

RESULTS

Missing Data

A little over three percent of these data are missing, predominately due to the clarity of the CT scans, trauma, or incomplete full body scans. The distribution of missing data, by trait, is shown in Figure 3.2.

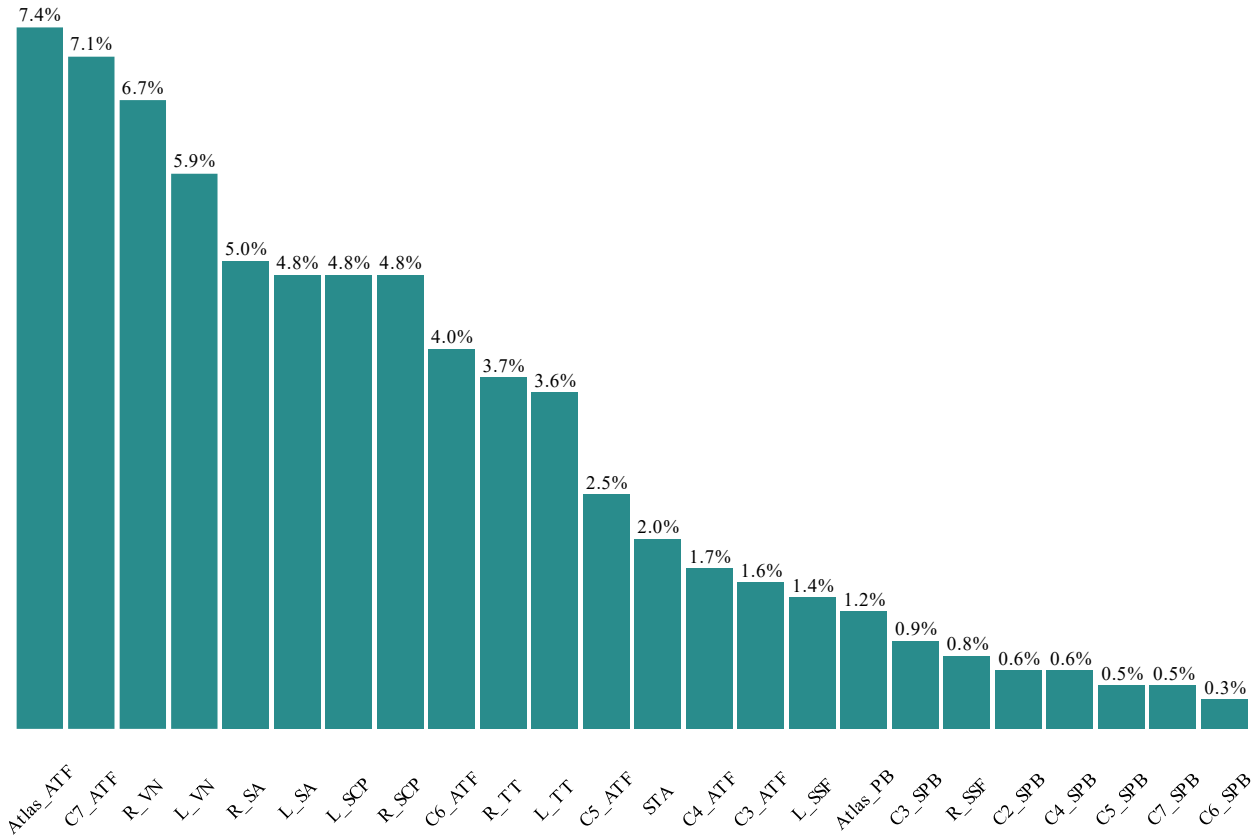


Figure 3.2. Percentage of Missing Data by Variable

Laterality

Laterality was assessed for suprascapular foramen, supracondyloid process, septal aperture, third trochanter, and vastus notch. Among both the juvenile and adult datasets, significant differences between the left and right were identified for each of these traits (Table 3.3).

Table 3.3. Laterality

Trait	***Juvenile***	***Adult***
Suprascapular Foramen	χ^2 = 339.01, df = 1, p-value < 0.0001*	χ^2 = 27.73, df = 1, p-value < 0.0001*
Supracondyloid Process	χ^2 = 27.917, df = 1, p-value < 0.0001*	χ^2 = 49.335, df = 2, p-value < 0.0001*
Septal Aperture	χ^2 = 144.18, df = 4, p-value < 0.0001*	χ^2 = 101.04, df = 6, p-value < 0.0001*
Third Trochanter	χ^2 = 77.106, df = 1, p-value < 0.0001*	χ^2 = 26.657, df = 1, p-value < 0.0001*
Vastus Notch	χ^2 = 522.76, df = 4, p-value < 0.0001*	χ^2 = 135.58, df = 1, p-value < 0.0001*

**Statistically significant*

Age & Puberty

Density plots illustrate the lack of fusion (score "7") for each trait (Figure 3). Summary statistics, by sex, are provided in Figure 3.3.

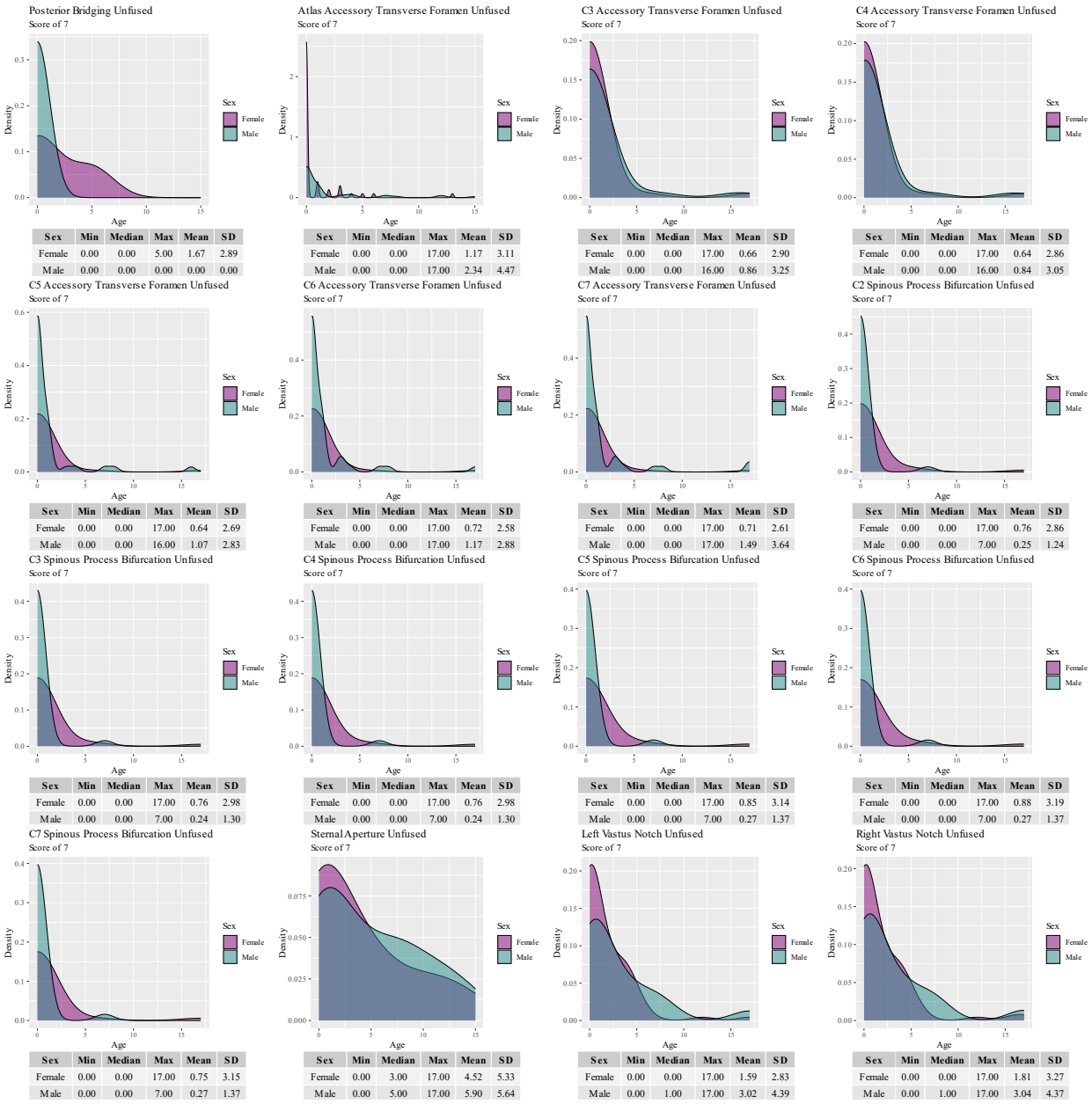


Figure 3.3. Density plots and age summary statistics of unfused region by trait

Trait correlations are illustrated in Figure 3.4. The undeveloped score ("7") may skew these data, so for this particular analysis, scores of "7" were removed. Traits that have one or less occurrence in the juvenile dataset (right supracondyloid process, left/right suprascapular foramen)

were also excluded. All traits were included in the analysis of the adult correlations.

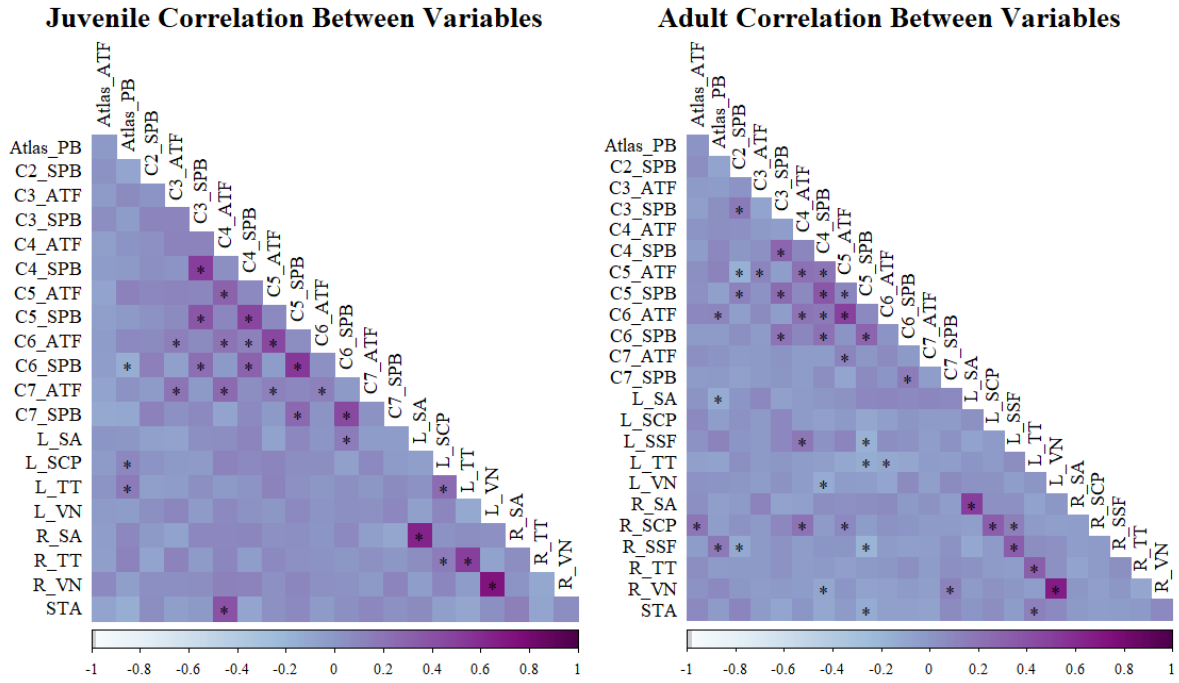


Figure 3.4. Trait correlation by age

Summary age for all of the trait's character states are outlined by mean, median, minimum, and maximum age of appearance in Table 3.4.

Table 3.4. Summary age data (in years), by trait and character state.

Trait & States	***Mean***	***Median***	***Min***	***Max***	***Trait & States***	***Mean***	***Median***	***Min***	***Max***
Posterior Bridging					*Atlas ATF*				
0	29	17	0	96	*0*	35	32	0	99
1	40	41	3	99	*1*	44	*31*	0	94
2	*33*	31	0	74	*2*	43	43	1	87
7	*1*	0	0	5	*7*	2	0	0	17
C3 Accessory Transverse Foramen					*C4 Accessory Transverse Foramen*				
0	33	25	0	99	*0*	33	27	0	99
1	20	16	4	43	*1*	25	16	1	78
2	0	0	0	0	*2*	30	25	4	79
7	1	0	0	17	*7*	1	0	0	17
C5 Accessory Transverse Foramen					*C6 Accessory Transverse Foramen*				
0	33	25	0	96	*0*	38	36	0	99
1	37	36	0	99	*1*	26	17	0	94
2	36	36	1	85	*2*	35	32	0	90
7	1	0	0	17	*7*	1	0	0	17

Table 3.4 (cont'd)

C7 Accessory Transverse Foramen					*C2 Spinous Process Bifurcation*				
0	36	34	0	99	*0*	36	37	1	86
1	26	15	2	94	*1*	56	55	16	99
2	17	6	0	84	*2*	33	24	0	96
7	1	0	0	17	*7*	1	0	0	17
C3 Spinous Process Bifurcation					*C4 Spinous Process Bifurcation*				
0	33	27	0	90	*0*	30	16	1	90
1	32	17	0	96	*1*	31	17	0	95
2	33	28	0	99	*2*	34	28	0	99
7	1	0	0	17	*7*	1	0	0	17
C5 Spinous Process Bifurcation					*C6 Spinous Process Bifurcation*				
0	27	16	0	87	*0*	34	28	0	96
1	28	17	0	90	*1*	31	20	0	99
2	34	28	0	99	*2*	32	24	0	94
7	1	0	0	17	*7*	1	0	0	17
C7 Spinous Process Bifurcation					*Sternal Aperture*				
0	38	38	0	99	*0*	44	43	0	99
1	13	9	0	96	*1*	45	47	4	90
2	11	*7*	0	51	*7*	5	4	0	17
7	1	0	0	17					
Left Suprascapular Foramen					*Rights Suprascapular Foramen*				
0	29	17	0	99	*0*	29	17	0	99
1	59	56	34	91	*1*	57	51	0	91
Left Supracondyloid Process					*Right Supracondyloid Process*				
0	29	17	0	99	*0*	29	17	0	99
1	28	26	0	58	*1*	37	41	11	58
Left Septal Aperture					*Right Septal Aperture*				
0	29	17	0	99	*0*	30	17	0	96
2	39	42	0	95	*2*	34	17	0	99
3	28	17	0	90	*3*	28	17	0	90
Left Third Trochanter					*Right Third Trochanter*				
0	30	17	0	99	*0*	29	17	0	96
1	21	13	0	82	*1*	30	17	0	84
Left Vastus Notch					*Right Vastus Notch*				
0	39	38	0	96	*0*	40	39	0	95
1	34	30	0	90	*1*	33	27	0	96
7	2	1	0	17	*7*	2	1	0	17

Age stabilization data are provided in Table 3.5. Age cohorts are broadly based on Buikstra & Ubelaker's (1994) standards for data collection from human skeletal (Figure 3.1). The supracondyloid process, observed bilaterally, is the only trait to stabilize during the 'infant' phase

(0-3 years). Nine traits stabilize during the 'children' phase (4-12 years), three within the 'adolescent' phase (13-20 years), and nine during the 'young adult' phase (21-35 years).

Table 3.5. Kruskal-Wallis and Dunn's test results showing the effects of age on postcranial trait expression.

Trait	***Overall Significance (Kruskal-Wallis p-value)***	***Unstable (Dunn's Test ≤ 0.05)***	***Stabilized (Dunn's Test >0.05)***
Posterior Bridging	*0.0945*	Infant (0-3)	Children (4-12)
Atlas Accessory Transverse Foramen	*<0.0001**	Infant (0-3)	Children (4-12)
C3 Accessory Transverse Foramen	*<0.0001**	Infant (0-3)	Children (4-12)
C4 Accessory Transverse Foramen	*<0.0001**	Infant (0-3)	Children (4-12)
C5 Accessory Transverse Foramen	*<0.0001**	Infant (0-3)	Children (4-12)
C6 Accessory Transverse Foramen	*<0.0001**	Infant (0-3)	Children (4-12)
C7 Accessory Transverse Foramen	*<0.0001**	Infant (0-3) Children (4-12)	Adolescent (13-20)
C2 Spinous Process Bifurcation	*<0.0001**	Infant (0-3) Children (4-12)	Adolescent (13-20)
C3 Spinous Process Bifurcation	*<0.0001**	Infant (0-3) Children (4-12)	Adolescent (13-20)
C4 Spinous Process Bifurcation	*<0.0001**	Infant (0-3)	Children (4-12)
C5 Spinous Process Bifurcation	*<0.0001**	Infant (0-3)	Children (4-12)
C6 Spinous Process Bifurcation	*<0.0001**	Infant (0-3)	Children (4-12)
C7 Spinous Process Bifurcation	*<0.0001**	Infant (0-3) Children (4-12) Adolescent (13-20)	Young Adult (21-35)
Sternal Aperture	*<0.0001**	Infant (0-3) Children (4-12) Adolescent (13-20)	Young Adult (21-35)

Table 3.5 (cont'd)

Left Suprascapular Foramen	*0.0041**	Infant (0-3) Children (4-12) Adolescent (13-20)	Young Adult (21-35)
Right Suprascapular Foramen	*0.0041**	Infant (0-3) Children (4-12) Adolescent (13-20)	Young Adult (21-35)
Left Supracondyloid Process	*0.9461*	*N/A*	Infant (0-3)
Right Supracondyloid Process	*0.5827*	*N/A*	Infant (0-3)
Left Septal Aperture	*<0.0001**	Infant (0-3) Children (4-12) Adolescent (13-20)	Young Adult (21-35)
Right Septal Aperture	*<0.0001**	Infant (0-3) Children (4-12) Adolescent (13-20)	Young Adult (21-35)
Left Third Trochanter	*0.2745*	Infant (0-3) Children (4-12) Adolescent (13-20)	Young Adult (21-35)
Right Third Trochanter	*0.0730*	Infant (0-3) Children (4-12) Adolescent (13-20)	Young Adult (21-35)
Left Vastus Notch	*<0.0001**	Infant (0-3) Children (4-12)	Adolescent (13-20)
Right Vastus Notch	*<0.0001**	Infant (0-3) Children (4-12) Adolescent (13-20)	Young Adult (21-35)

**Statistically significant at $p \leq 0.05$*

Table 3.6 outlines the Risser score and the frequencies of puberty stages utilizing the iliac crest as the indicator of an individual's pubertal development. Subsequently, condensed puberty stages derived from the Risser scores, by sex, are demonstrated in Figure 3.5.

Table 3.6. Risser scores and puberty frequencies, by stage (N=646)

Risser Score	***n (%)***
0	227 (35.1%)
1	11 (1.7%)
2	8 (1.2%)
3	6 (0.9%)
4	49 (7.6%)
5	345 (53.4%)

Table 3.6 (cont'd)

Puberty Stage	***n (%)***
Pre-Pubescent	227 (35.1%)
Pubescent	74 (11.5%)
Post-Pubescent	345 (53.4%)

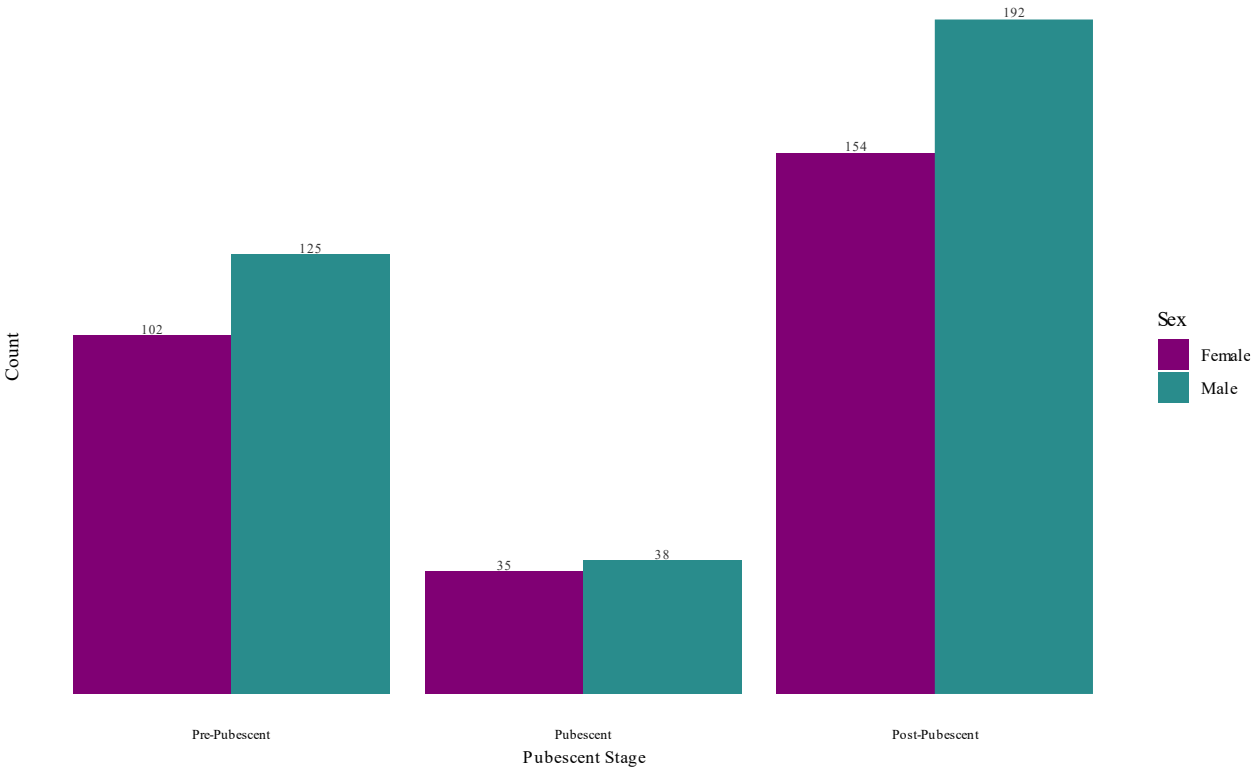
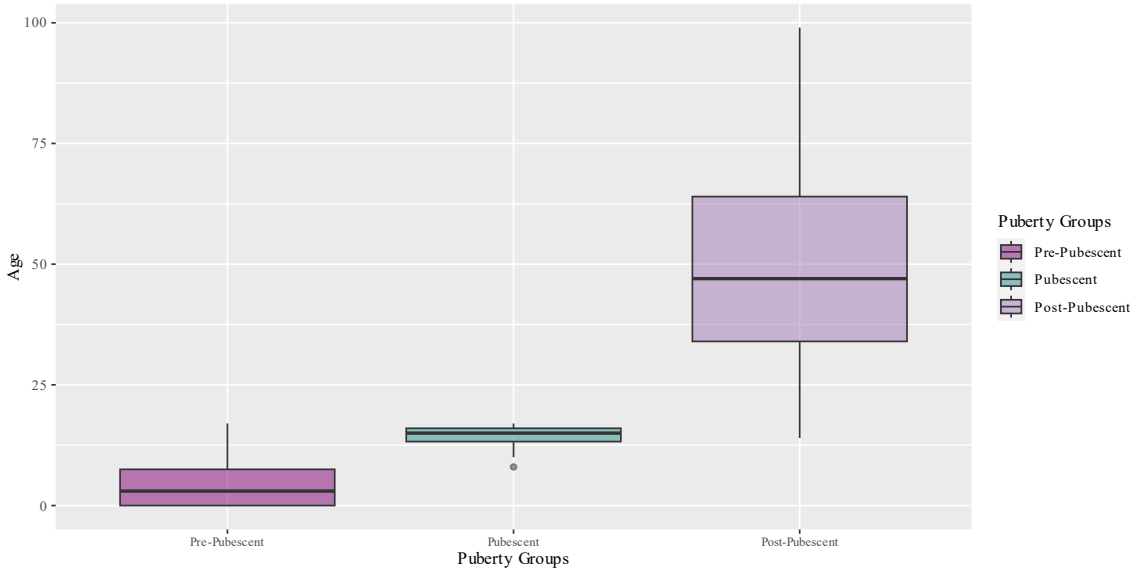


Figure 3.5. Puberty distribution by sex

Summary statistics of each pubescent stage are provided in Figure 3.6. The median age for puberty is comparable between the male and female cohorts, although the pre-pubescent stage shows a slight, two-year difference between sexes.



Puberty	Sex	Median Age	Lower Quartile	Upper Quartile	Minimum Age	Maximum Age
Pre-Pubescent	Female	2	0.00	5.00	0	17
Pre-Pubescent	Male	4	0.00	9.00	0	17
Pubescent	Female	14	13.00	16.00	10	17
Pubescent	Male	15	14.00	16.00	8	17
Post-Pubescent	Female	47	34.00	66.00	14	99
Post-Pubescent	Male	48	34.75	63.25	15	96

Figure 3.6. Sample distribution of puberty and age

Figure 3.7 provides the distribution frequency data of each trait's character states, by developmental puberty stage. Left suprascapular foramen was not present in the juvenile dataset. The Kruskal-Wallis test identified significant differences (p-values were considered statistically significant at the $\alpha = 0.05$ level) in trait expression between the various stages capturing the onset of puberty, with the exception of the left/right suprascapular process, right suprascapular foramen, and the left third trochanter (Table 3.7). *Post hoc* pairwise comparisons revealed significant differences in all trait expressions between pre-pubescent and pubescent stages, with the exception of posterior bridging, left suprascapular foramen, right suprascapular foramen, and left suprascapular process (Table 3.7). However, the expression of posterior bridging is significantly different between pre- and post-pubescent stages. Only four traits were significantly different in

their expressions between the pubescent and post-pubescent stages: C7 spinous process bifurcation, left septal aperture, and both left/right vastus notches.

Figure 3.7. Trait states by puberty status

Table 3.7. Kruskal-Wallis and Dunn's test results showing the effects of puberty on postcranial trait expression (p-value)

Trait	*Overall Significance (Kruskal-Wallis)*	*Pre-Pubescent *Pubescent (Dunn's Test)*	*Pre-Pubescent *Post-Pubescent (Dunn's Test)*	*Pubescent *Post-Pubescent (Dunn's Test)*
Posterior Bridging	0.0509	0.1083	0.0105*	0.1273
Atlas Accessory Transverse Foramen	<0.0001*	<0.0001*	<0.0001*	0.1112
C3 Accessory Transverse Foramen	<0.0001*	0.0001*	<0.0001*	0.3428
C4 Accessory Transverse Foramen	<0.0001*	<0.0001*	<0.0001*	0.4837
C5 Accessory Transverse Foramen	<0.0001*	<0.0001*	<0.0001*	0.2110
C6 Accessory Transverse Foramen	<0.0001*	<0.0001*	<0.0001*	0.0598
C7 Accessory Transverse Foramen	<0.0001*	<0.0001*	<0.0001*	0.4149
C2 Spinous Process Bifurcation	<0.0001*	<0.0001*	<0.0001*	0.2956
C3 Spinous Process Bifurcation	0.0009*	0.0015*	0.0027*	0.3687
C4 Spinous Process Bifurcation	0.0006*	0.0004*	0.0055*	0.4453
C5 Spinous Process Bifurcation	<0.0001*	<0.0001*	0.0029*	0.2187
C6 Spinous Process Bifurcation	0.0006*	0.0004*	0.0065*	0.4260
C7 Spinous Process Bifurcation	<0.0001*	<0.0001*	<0.0001*	0.0286*
Sternal Aperture	<0.0001*	<0.0001*	<0.0001*	0.0040
Left Suprascapular Foramen	*N/A*	*N/A*	*N/A*	*N/A*
Right Suprascapular Foramen	0.7719	0.2703	0.3112	0.5000
Left Supracondyloid Process	0.7513	0.3544	0.2842	0.2249
Right Supracondyloid Process	0.1624	0.0308*	0.5000	0.0959
Left Septal Aperture	<0.0001*	<0.0001*	0.0283*	0.0073*
Right Septal Aperture	<0.0001*	<0.0001*	<0.0001*	0.4767
Left Third Trochanter	0.0810	0.0130*	0.4303	0.0804
Right Third Trochanter	0.0039*	0.0005*	0.1388	0.0865
Left Vastus Notch	<0.0001*	<0.0001*	0.4774	<0.0001*
Right Vastus Notch	<0.0001*	<0.0001*	0.3648	<0.0001*

**Statistically significant at $p \leq 0.05$*

Trait Frequencies

Frequency distributions for the individual character states, by social race and juvenile and

adult stages are detailed in Table 3.8. For the juvenile sample, only the left suprascapular foramen is not present. Every trait is observed at least once in the adult sample; however, traits among less than 5% of the adult sample include: C3 accessory transverse foramen, C4 accessory transverse foramen, C7 accessory transverse foramen, C7 spinous process bifurcation, left suprascapular foramen, right suprascapular foramen, left supracondyloid process, right supracondyloid process, left third trochanter, and right third trochanter.

Table 3.8. Counts and frequencies of postcranial trait character states (N=646).

Trait	***Juvenile***				***Adult***			
PB	***Black[1]***	***Hispanic[1]***	***Native American[1]***	***White[1]***	***Black[1]***	***Hispanic[1]***	***Native American[1]***	***White[1]***
0	*31 (89%)*	*91 (89%)*	*95 (92%)*	*93 (90%)*	*42 (79%)*	*72 (87%)*	*55 (82%)*	*86 (86%)*
1	*1 (2.9%)*	*6 (5.9%)*	*4 (3.9%)*	*6 (5.8%)*	*7 (13%)*	*9 (11%)*	*8 (12%)*	*8 (8.0%)*
2	*2 (5.7%)*	*4 (3.9%)*	*2 (1.9%)*	*3 (2.9%)*	*4 (7.5%)*	*2 (2.4%)*	*4 (6.0%)*	*6 (6.0%)*
7	*1 (2.9%)*	*1 (1.0%)*	*2 (1.9%)*	*1 (1.0%)*				
Atlas ATF	***Black[1]***	***Hispanic[1]***	***Native American[1]***	***White[1]***	***Black[1]***	***Hispanic[1]***	***Native American[1]***	***White[1]***
0	*16 (46%)*	*76 (75%)*	*57 (55%)*	*71 (69%)*	*45 (85%)*	*76 (92%)*	*65 (97%)*	*91 (91%)*
1	*1 (2.9%)*	*4 (3.9%)*	*0 (0%)*	*1 (1.0%)*	*4 (7.5%)*	*3 (3.6%)*	*0 (0%)*	*2 (2.0%)*
2	*0 (0%)*	*0 (0%)*	*3 (2.9%)*	*0 (0%)*	*4 (7.5%)*	*4 (4.8%)*	*2 (3.0%)*	*7 (7.0%)*
7	*18 (51%)*	*22 (22%)*	*43 (42%)*	*31 (30%)*				
C3 ATF	***Black[1]***	***Hispanic[1]***	***Native American[1]***	***White[1]***	***Black[1]***	***Hispanic[1]***	***Native American[1]***	***White[1]***
0	*20 (57%)*	*92 (90%)*	*75 (73%)*	*86 (83%)*	*53 (100%)*	*82 (99%)*	*67 (100%)*	*100 (100%)*
1	*0 (0%)*	*1 (1.0%)*	*0 (0%)*	*2 (1.9%)*	*0 (0%)*	*1 (1.2%)*	*0 (0%)*	*0 (0%)*
2	*0 (0%)*	*0 (0%)*	*1 (1.0%)*	*0 (0%)*	*0 (0%)*	*0 (0%)*	*0 (0%)*	*0 (0%)*
7	*15 (43%)*	*9 (8.8%)*	*27 (26%)*	*15 (15%)*				
C4 ATF	***Black[1]***	***Hispanic[1]***	***Native American[1]***	***White[1]***	***Black[1]***	***Hispanic[1]***	***Native American[1]***	***White[1]***
0	*20 (57%)*	*83 (81%)*	*70 (68%)*	*20 (57%)*	*53 (100%)*	*78 (96%)*	*65 (98%)*	*97 (97%)*
1	*0 (0%)*	*6 (5.9%)*	*2 (1.9%)*	*0 (0%)*	*0 (0%)*	*2 (2.5%)*	*1 (1.5%)*	*1 (1.0%)*
2	*0 (0%)*	*2 (2.0%)*	*1 (1.0%)*	*0 (0%)*	*0 (0%)*	*1 (1.2%)*	*0 (0%)*	*2 (2.0%)*
7	*15 (43%)*	*11 (11%)*	*30 (29%)*	*15 (43%)*				
C5 ATF	***Black[1]***	***Hispanic[1]***	***Native American[1]***	***White[1]***	***Black[1]***	***Hispanic[1]***	***Native American[1]***	***White[1]***
0	*17 (49%)*	*56 (55%)*	*52 (50%)*	*64 (62%)*	*39 (74%)*	*56 (67%)*	*50 (75%)*	*56 (56%)*
1	*1 (2.9%)*	*20 (20%)*	*11 (11%)*	*13 (13%)*	*9 (17%)*	*16 (19%)*	*13 (19%)*	*32 (32%)*
2	*0 (0%)*	*10 (9.8%)*	*2 (1.9%)*	*7 (6.8%)*	*5 (9.4%)*	*11 (13%)*	*4 (6.0%)*	*12 (12%)*
7	*17 (49%)*	*16 (16%)*	*38 (37%)*	*19 (18%)*				
C6 ATF	***Black[1]***	***Hispanic[1]***	***Native American[1]***	***White[1]***	***Black[1]***	***Hispanic[1]***	***Native American[1]***	***White[1]***
0	*10 (29%)*	*31 (30%)*	*31 (30%)*	*31 (30%)*	*30 (57%)*	*38 (46%)*	*38 (57%)*	*49 (49%)*
1	*4 (11%)*	*23 (23%)*	*15 (15%)*	*22 (21%)*	*9 (17%)*	*12 (14%)*	*14 (21%)*	*11 (11%)*
2	*4 (11%)*	*30 (29%)*	*17 (17%)*	*27 (26%)*	*14 (26%)*	*33 (40%)*	*15 (22%)*	*40 (40%)*
7	*17 (49%)*	*18 (18%)*	*40 (39%)*	*23 (22%)*				

Table 3.8 (cont'd)

C7 ATF	Black[1]	Hispanic[1]	Native American[1]	White[1]	Black[1]	Hispanic[1]	Native American[1]	White[1]
0	17 (49%)	71 (70%)	56 (54%)	68 (66%)	51 (96%)	81 (98%)	63 (94%)	97 (97%)
1	0 (0%)	10 (9.8%)	6 (5.8%)	7 (6.8%)	1 (1.9%)	2 (2.4%)	4 (6.0%)	2 (2.0%)
2	1 (2.9%)	3 (2.9%)	1 (1.0%)	5 (4.9%)	1 (1.9%)	0 (0%)	0 (0%)	1 (1.0%)
7	17 (49%)	18 (18%)	40 (39%)	23 (22%)				
C2 SPB	**Black[1]**	**Hispanic[1]**	**Native American[1]**	**White[1]**	**Black[1]**	**Hispanic[1]**	**Native American[1]**	**White[1]**
0	0 (0%)	1 (1.0%)	2 (1.9%)	1 (1.0%)	2 (3.8%)	2 (2.4%)	3 (4.5%)	3 (3.0%)
1	0 (0%)	1 (1.0%)	1 (1.0%)	1 (1.0%)	3 (5.7%)	5 (6.0%)	1 (1.5%)	4 (4.0%)
2	20 (57%)	89 (87%)	69 (67%)	84 (82%)	48 (91%)	76 (92%)	63 (94%)	93 (93%)
7	15 (43%)	11 (11%)	31 (30%)	17 (17%)				
C3 SPB	**Black[1]**	**Hispanic[1]**	**Native American[1]**	**White[1]**	**Black[1]**	**Hispanic[1]**	**Native American[1]**	**White[1]**
0	7 (20%)	31 (30%)	25 (24%)	17 (17%)	26 (49%)	21 (25%)	12 (18%)	25 (25%)
1	6 (17%)	21 (21%)	15 (15%)	26 (25%)	13 (25%)	17 (20%)	10 (15%)	22 (22%)
2	6 (17%)	40 (39%)	37 (36%)	45 (44%)	14 (26%)	45 (54%)	45 (67%)	53 (53%)
7	16 (46%)	10 (9.8%)	26 (25%)	15 (15%)				
C4 SPB	**Black[1]**	**Hispanic[1]**	**Native American[1]**	**White[1]**	**Black[1]**	**Hispanic[1]**	**Native American[1]**	**White[1]**
0	6 (17%)	18 (18%)	17 (17%)	9 (8.7%)	16 (30%)	9 (11%)	9 (13%)	8 (8.0%)
1	6 (17%)	16 (16%)	14 (14%)	17 (17%)	10 (19%)	8 (9.6%)	13 (19%)	14 (14%)
2	7 (20%)	59 (58%)	48 (47%)	62 (60%)	27 (51%)	66 (80%)	45 (67%)	78 (78%)
7	16 (46%)	9 (8.8%)	24 (23%)	15 (15%)				
C5 SPB	**Black[1]**	**Hispanic[1]**	**Native American[1]**	**White[1]**	**Black[1]**	**Hispanic[1]**	**Native American[1]**	**White[1]**
0	2 (5.7%)	16 (16%)	15 (15%)	8 (7.8%)	9 (17%)	5 (6.0%)	6 (9.0%)	7 (7.0%)
1	6 (17%)	14 (14%)	9 (8.7%)	10 (9.7%)	6 (11%)	9 (11%)	13 (19%)	5 (5.0%)
2	12 (34%)	65 (64%)	56 (54%)	70 (68%)	38 (72%)	69 (83%)	48 (72%)	88 (88%)
7	15 (43%)	7 (6.9%)	23 (22%)	15 (15%)				
C6 SPB	**Black[1]**	**Hispanic[1]**	**Native American[1]**	**White[1]**	**Black[1]**	**Hispanic[1]**	**Native American[1]**	**White[1]**
0	6 (17%)	33 (32%)	25 (24%)	20 (19%)	18 (34%)	24 (29%)	20 (30%)	28 (28%)
1	9 (26%)	19 (19%)	21 (20%)	18 (17%)	13 (25%)	16 (19%)	22 (33%)	19 (19%)
2	5 (14%)	43 (42%)	34 (33%)	51 (50%)	22 (42%)	43 (52%)	25 (37%)	53 (53%)
7	15 (43%)	7 (6.9%)	23 (22%)	14 (14%)				
C7 SPB	**Black[1]**	**Hispanic[1]**	**Native American[1]**	**White[1]**	**Black[1]**	**Hispanic[1]**	**Native American[1]**	**White[1]**
0	12 (34%)	58 (57%)	47 (46%)	47 (46%)	50 (94%)	78 (94%)	65 (97%)	96 (96%)
1	6 (17%)	30 (29%)	29 (28%)	33 (32%)	3 (5.7%)	2 (2.4%)	2 (3.0%)	4 (4.0%)
2	2 (5.7%)	8 (7.8%)	4 (3.9%)	9 (8.7%)	0 (0%)	3 (3.6%)	0 (0%)	0 (0%)
7	15 (43%)	6 (5.9%)	23 (22%)	14 (14%)				
STA	**Black[1]**	**Hispanic[1]**	**Native American[1]**	**White[1]**	**Black[1]**	**Hispanic[1]**	**Native American[1]**	**White[1]**
0	6 (17%)	39 (38%)	20 (19%)	31 (30%)	46 (87%)	70 (84%)	59 (88%)	91 (91%)
1	1 (2.9%)	5 (4.9%)	2 (1.9%)	2 (1.9%)	7 (13%)	13 (16%)	8 (12%)	9 (9.0%)
7	28 (80%)	58 (57%)	81 (79%)	70 (68%)				
L SSF	**Black[1]**	**Hispanic[1]**	**Native American[1]**	**White[1]**	**Black[1]**	**Hispanic[1]**	**Native American[1]**	**White[1]**
0	35 (100%)	102 (100%)	103 (100%)	103 (100%)	50 (94%)	78 (94%)	65 (97%)	97 (97%)
1	0 (0%)	0 (0%)	0 (0%)	0 (0%)	3 (5.7%)	5 (6.0%)	2 (3.0%)	3 (3.0%)
7	0 (0%)	0 (0%)	0 (0%)	0 (0%)				

Table 3.8 (cont'd)

R SSF	***Black***[1]	***Hispanic***[1]	***Native American***[1]	***White***[1]	***Black***[1]	***Hispanic***[1]	***Native American***[1]	***White***[1]
0	*35 (100%)*	*102 (100%)*	*102 (99%)*	*103 (100%)*	*49 (92%)*	*80 (96%)*	*63 (94%)*	*96 (96%)*
1	*0 (0%)*	*0 (0%)*	*1 (1.0%)*	*0 (0%)*	*4 (7.5%)*	*3 (3.6%)*	*4 (6.0%)*	*4 (4.0%)*
7	*0 (0%)*	*0 (0%)*	*0 (0%)*	*0 (0%)*				
L SCP	***Black***[1]	***Hispanic***[1]	***Native American***[1]	***White***[1]	***Black***[1]	***Hispanic***[1]	***Native American***[1]	***White***[1]
0	*34 (97%)*	*101 (99%)*	*103 (100%)*	*102 (99%)*	*53 (100%)*	*82 (99%)*	*67 (100%)*	*96 (96%)*
1	*1 (2.9%)*	*1 (1.0%)*	*0 (0%)*	*1 (1.0%)*	*0 (0%)*	*1 (1.2%)*	*0 (0%)*	*4 (4.0%)*
7	*0 (0%)*	*0 (0%)*	*0 (0%)*	*0 (0%)*				
R SCP	***Black***[1]	***Hispanic***[1]	***Native American***[1]	***White***[1]	***Black***[1]	***Hispanic***[1]	***Native American***[1]	***White***[1]
0	*35 (100%)*	*101 (99%)*	*103 (100%)*	*103 (100%)*	*53 (100%)*	*83 (100%)*	*66 (99%)*	*98 (98%)*
1	*0 (0%)*	*1 (1.0%)*	*0 (0%)*	*0 (0%)*	*0 (0%)*	*0 (0%)*	*1 (1.5%)*	*1 (1.0%)*
7	*0 (0%)*	*0 (0.0%)*	*0 (0%)*	*0 (0%)*				
L SA	**Black**[1]	**Hispanic**[1]	**Native American**[1]	**White**[1]	**Black**[1]	**Hispanic**[1]	**Native American**[1]	**White**[1]
0	30 (86%)	81 (79%)	82 (80%)	76 (74%)	44 (83%)	63 (76%)	57 (85%)	75 (75%)
2	1 (2.9%)	2 (2.0%)	0 (0%)	3 (2.9%)	2 (3.8%)	5 (6.0%)	0 (0%)	7 (7.0%)
3	4 (11%)	19 (19%)	21 (20%)	24 (23%)	7 (13%)	15 (18%)	10 (15%)	18 (18%)
7	0 (0%)	0 (0%)	0 (0%)	0 (0%)				
R SA	**Black**[1]	**Hispanic**[1]	**Native American**[1]	**White**[1]	**Black**[1]	**Hispanic**[1]	**Native American**[1]	**White**[1]
0	30 (86%)	78 (76%)	84 (82%)	74 (72%)	45 (85%)	66 (80%)	60 (90%)	87 (87%)
2	0 (0%)	4 (3.9%)	1 (1.0%)	4 (3.9%)	2 (3.8%)	4 (4.8%)	0 (0%)	0 (0%)
3	5 (14%)	20 (20%)	18 (17%)	25 (24%)	6 (11%)	13 (16%)	7 (10%)	13 (13%)
7	0 (0%)	0 (0%)	0 (0%)	0 (0%)				
L TT	**Black**[1]	**Hispanic**[1]	**Native American**[1]	**White**[1]	**Black**[1]	**Hispanic**[1]	**Native American**[1]	**White**[1]
0	34 (97%)	94 (92%)	100 (97%)	96 (93%)	53 (100%)	80 (96%)	64 (96%)	97 (97%)
1	1 (2.9%)	8 (7.8%)	3 (2.9%)	7 (6.8%)	0 (0%)	3 (3.6%)	3 (4.5%)	3 (3.0%)
7	0 (0%)	0 (0%)	0 (0%)	0 (0%)				
R TT	**Black**[1]	**Hispanic**[1]	**Native American**[1]	**White**[1]	**Black**[1]	**Hispanic**[1]	**Native American**[1]	**White**[1]
0	34 (97%)	98 (96%)	99 (96%)	100 (97%)	53 (100%)	81 (98%)	62 (93%)	98 (98%)
1	1 (2.9%)	4 (3.9%)	4 (3.9%)	3 (2.9%)	0 (0%)	2 (2.4%)	5 (7.5%)	2 (2.0%)
7	0 (0%)	0 (0%)	0 (0%)	0 (0%)				
L VN	**Black**[1]	**Hispanic**[1]	**Native American**[1]	**White**[1]	**Black**[1]	**Hispanic**[1]	**Native American**[1]	**White**[1]
0	8 (23%)	52 (51%)	28 (27%)	43 (42%)	34 (64%)	62 (75%)	57 (85%)	83 (83%)
1	5 (14%)	16 (16%)	17 (17%)	16 (16%)	19 (36%)	21 (25%)	10 (15%)	17 (17%)
7	22 (63%)	34 (33%)	58 (56%)	44 (43%)				
R VN	**Black**[1]	**Hispanic**[1]	**Native American**[1]	**White**[1]	**Black**[1]	**Hispanic**[1]	**Native American**[1]	**White**[1]
0	8 (23%)	48 (47%)	28 (27%)	44 (43%)	35 (66%)	65 (78%)	53 (79%)	84 (84%)
1	5 (14%)	22 (22%)	17 (17%)	15 (15%)	18 (34%)	18 (22%)	14 (21%)	16 (16%)
7	22 (63%)	32 (31%)	58 (56%)	44 (43%)				

[1]n (%)

Social Race

The results from the Kruskal-Wallis test (Table 3.9) reveal significant differences in the vertebrae and the left patella (C5 ATF, C3-C5 SPB, and L VN) among all adults. The subsequent *post hoc* Dunn's test (Table 3.10) identified significant differences in trait manifestations for vertebrae (Atlas ATF, C5 ATF, C6 ATF, C3-C5 SPB), the left scapula (L SCP), the right femur (R TT), and both patellae (L/R VN). Among all social race groups, only C5 accessory transverse foramen is significant for the juvenile sample. The only trait consistent between the adult and juvenile samples is C4 spinous process bifurcation between the following pairs: Black-Hispanic, Black-Native American, and Black-White.

Table 3.9. Kruskal-Wallis test results showing the effect of social race on postcranial trait expression (p-value)

Trait	***Adult***	***Juvenile***
Posterior Bridging	0.5891	0.7261
Atlas Accessory Transverse Foramen	0.1868	0.5978
C3 Accessory Transverse Foramen	0.4487	0.8528
C4 Accessory Transverse Foramen	0.5144	0.3172
C5 Accessory Transverse Foramen	0.0391*	0.0234*
C6 Accessory Transverse Foramen	0.1663	0.4783
C7 Accessory Transverse Foramen	0.8120	0.8755
C2 Spinous Process Bifurcation	0.9028	0.7894
C3 Spinous Process Bifurcation	<0.0001*	0.3021
C4 Spinous Process Bifurcation	0.0004*	0.0683
C5 Spinous Process Bifurcation	0.0243*	0.2354
C6 Spinous Process Bifurcation	0.1825	0.0962
C7 Spinous Process Bifurcation	0.7861	0.6658
Sternal Aperture	0.5867	0.7767
Left Suprascapular Foramen	0.6758	N/A
Right Suprascapular Foramen	0.5546	0.7033
Left Supracondyloid Process	0.2877	0.1387
Right Supracondyloid Process	0.4632	0.5006
Left Septal Aperture	0.6126	0.4457
Right Septal Aperture	0.3872	0.2435
Left Third Trochanter	0.6599	0.3957
Right Third Trochanter	0.1125	0.9699

Table 3.9 (cont'd)

Left Vastus Notch	0.0597*	0.4719
Right Vastus Notch	0.1714	0.7157

**Statistically significant at $p \leq 0.05$*

Table 3.10. One-sided Dunn's test results showing the effect of social race on postcranial trait expression (p-value)

Trait	*Black - Hispanic*	*Black - Native American*	*Hispanic - Native American*	*Black - White*	*Hispanic - White*	*Native American - White*
PB (Adult)	0.1098	0.3313	0.2045	0.1433	0.4074	0.2616
PB (Juv)	0.4329	0.2798	0.1446	0.3440	0.2104	0.3983
Atlas ATF (Adult)	0.0522	0.0120*	0.2157	0.0628	0.4324	0.1639
Atlas ATF (Juv)	0.4276	0.4240	0.4913	0.1914	0.1231	0.1422
C3 ATF (Adult)	0.1165	0.5000	0.1008	0.5000	0.0789	0.5000
C3 ATF (Juv)	0.3578	0.3287	0.4443	0.2241	0.2546	0.3128
C4 ATF (Adult)	0.0864	0.2966	0.1945	0.1190	0.3959	0.2586
C4 ATF (Juv)	0.0590	0.2363	0.0963	0.2158	0.0996	0.4663
C5 ATF (Adult)	0.2127	0.4064	0.1317	0.0214*	0.0846	0.0070*
C5 ATF (Juv)	0.0041*	0.1135	0.0137*	0.0481	0.0502	0.2519
C6 ATF (Adult)	0.0690	0.4162	0.0340*	0.0953	0.3980	0.0490*
C6 ATF (Juv)	0.1758	0.3688	0.1802	0.1225	0.3475	0.1023
C7 ATF (Adult)	0.3329	0.2697	0.1252	0.4007	0.4114	0.1623
C7 ATF (Juv)	0.2061	0.2816	0.3629	0.2562	0.3940	0.4612
C2 SPB (Adult)	0.4093	0.2497	0.3049	0.2964	0.3668	0.4165
C2 SPB (Juv)	0.2405	0.1921	0.3855	0.1631	0.3217	0.4414
C3 SPB (Adult)	0.0003*	<0.0001*	0.0678*	0.0003*	0.4626	0.0505
C3 SPB (Juv)	0.2605	0.1561	0.2646	0.0615	0.0626	0.2004
C4 SPB (Adult)	0.0001*	0.0131*	0.0658	0.0001*	0.4713	0.0667
C4 SPB (Juv)	0.0201*	0.0345*	0.3675	0.0045*	0.1663	0.1030
C5 SPB (Adult)	0.0373*	0.4175	0.0470*	0.0068*	0.2385	0.0079*
C5 SPB (Juv)	0.4060	0.3057	0.3259	0.0885	0.0311*	0.0897
C6 SPB (Adult)	0.1463	0.4685	0.1121	0.1085	0.4339	0.0777
C6 SPB (Juv)	0.2176	0.1948	0.4396	0.0252*	0.0239*	0.0405*
C7 SPB (Adult)	0.4433	0.2466	0.1789	0.3227	0.2435	0.3811
C7 SPB (Juv)	0.3910	0.4710	0.3711	0.3255	0.1107	0.1991
STA (Adult)	0.3351	0.4168	0.2448	0.2251	0.0856	0.2851
STA (Juv)	0.4018	0.3392	0.3816	0.2278	0.1775	0.3177
L SSF (Adult)	0.4594	0.2367	0.1810	0.2202	0.1578	0.4981
L SSF (Juv)	N/A	N/A	N/A	N/A	N/A	N/A
R SSF (Adult)	0.1516	0.3465	0.2546	0.1683	0.4524	0.2829
R SSF (Juv)	0.5000	0.1790	0.0990	0.5000	0.5000	0.0985
L SCP (Adult)	0.2956	0.5000	0.2827	0.0325*	0.0701	0.0235*
L SCP (Juv)	0.1521	0.0587	0.2258	0.1506	0.4971	0.2275
R SCP (Adult)	0.5000	0.2073	0.1805	0.1172	0.0869	0.3709

Table 3.10 (cont'd)

R SCP (Juv)	0.1770	0.5000	0.0968	0.5000	0.0968	0.5000
L SA (Adult)	0.1673	0.4289	0.1087	0.1347	0.4518	0.0812
L SA (Juv)	0.2798	0.2706	0.4851	0.0785	0.1223	0.1294
R SA (Adult)	0.1973	0.2620	0.0521	0.3975	0.0959	0.3220
R SA (Juv)	0.3047	0.4536	0.1895	0.1020	0.1441	0.0258*
L TT (Adult)	0.1134	0.0760	0.3786	0.1496	0.4039	0.2910
L TT (Juv)	0.1272	0.4949	0.0570	0.2485	0.2589	0.1746
R TT (Adult)	0.2101	0.0085*	0.0352*	0.2444	0.4356	0.0209*
R TT (Juv)	0.3839	0.3878	0.4941	0.4939	0.3473	0.3525
L VN (Adult)	0.0745	0.0031*	0.0643	0.0038*	0.0893	0.3760
L VN (Juv)	0.1190	0.3570	0.0983	0.1854	0.3181	0.2053
R VN (Adult)	0.0456*	0.0428*	0.4536	0.0053*	0.1771	0.2266
R VN (Juv)	0.1944	0.3042	0.2967	0.1565	0.3912	0.2216

**Statistically significant at $p \leq 0.05$*

Sex

The results of the Kruskal-Wallis test (Table 3.11) indicate significant differences among the adult sample for left suprascapular foramen, left/right septal apertures, and left/right vastus notches. However, among juveniles, only C5 accessory transverse foramen and sternal aperture significantly differs between females and males.

Table 3.11. Mann-Whitney U test results showing the effect of sex on postcranial trait expression (p-value)

Trait	***Adult***	***Juvenile***
Posterior Bridging	0.0689	0.6514
Atlas Accessory Transverse Foramen	0.7684	0.8040
C3 Accessory Transverse Foramen	0.2514	0.0729
C4 Accessory Transverse Foramen	0.4619	0.9349
C5 Accessory Transverse Foramen	0.7389	0.0178*
C6 Accessory Transverse Foramen	0.7125	0.0580
C7 Accessory Transverse Foramen	0.2740	0.1352
C2 Spinous Process Bifurcation	0.9379	0.9475
C3 Spinous Process Bifurcation	0.4677	0.2095
C4 Spinous Process Bifurcation	0.4256	0.1531
C5 Spinous Process Bifurcation	0.4104	0.0456*
C6 Spinous Process Bifurcation	0.8033	0.4332
C7 Spinous Process Bifurcation	0.0993	0.6136
Sternal Aperture	0.3095	0.0444*
Left Suprascapular Foramen	0.5797	N/A
Right Suprascapular Foramen	0.2720	0.3499
Left Supracondyloid Process	0.0454*	0.6382

Table 3.11 (cont'd)

Right Supracondyloid Process	0.7368	0.2903
Left Septal Aperture	<0.0001*	0.0636
Right Septal Aperture	0.0011*	0.9470
Left Third Trochanter	0.2582	0.1459
Right Third Trochanter	0.2684	0.4224
Left Vastus Notch	0.0260*	0.1903
Right Vastus Notch	0.0121*	0.3330

**Statistically significant at ≤ 0.05*

Interactions

A MANOVA conducted among postcranial traits in the dataset (including both juveniles and adults) reveals significant differences by social race, sex, and puberty. The MANOVA analysis revealed significant interactions between sex and puberty, as well as between social race and puberty. The *post hoc* univariate ANOVA results for each trait and interactions are provided in Table 3.12. No single trait had interactive effects between social race and sex (Table 3.13). The only significant interactions involve puberty and either social race (C4-C5 accessory transverse foramen, C2-C7 spinous process bifurcation, sternal aperture), sex (C3 accessory transverse foramen, C7 accessory transverse foramen, C2 spinous process bifurcation, C7 spinous process bifurcation, right septal aperture, left third trochanter), or both (left septal aperture). When examining the interactions within the adult dataset, both social race and sex significantly influenced trait manifestation (Table 3.14). *Post hoc* univariate ANOVA results suggest no statistically significant interactions between social race and sex in the adult data when evaluating each trait individually.

Table 3.12. MANOVA results showing the effect of puberty, sex, and social race on adult and juvenile postcranial trait expression.

Response Variables	*Df*	*Wilks' Lambda*	*Approximate F-Statistic*	*Num Df*	*Den Df*	*Pr(>F)*
Social Race	3	0.8006	1.925	72.0	1794.0	<0.0001*
Sex	1	0.93012	1.878	24.0	600.0	0.0007*
Puberty	2	0.16282	36.956	48.0	1200.0	<0.0001*
*Social Race*Sex*	3	0.89599	0.933	72.0	1794.0	0.6380
*Social Race*Puberty*	6	0.71638	1.433	144.0	3514.4	0.0007*
*Sex*Puberty*	2	0.8994	1.361	48.0	1200.0	0.0531*
*Social Race*Sex*Puberty*	5	0.79955	1.146	120.0	2953.7	0.1359

**Statistically significant at < 0.05*

Table 3.13. Univariate ANOVA results showing the effect of puberty, age, sex, and social race on individual postcranial traits (p-value)

Trait	*Social Race*Sex*	*Social Race*Puberty*	*Sex*Puberty*	*Social Race*Sex*Puberty*
Posterior Bridging	0.1408	0.9575	0.6339	0.3689
Atlas Accessory Transverse Foramen	0.8882	0.5401	0.0584	0.8661
C3 Accessory Transverse Foramen	0.6301	0.0513	0.0020*	0.3789
C4 Accessory Transverse Foramen	0.4682	0.0335*	0.0065*	0.2917
C5 Accessory Transverse Foramen	0.9758	0.0137*	0.1098	0.6217
C6 Accessory Transverse Foramen	0.7156	0.0865	0.1143	0.4328
C7 Accessory Transverse Foramen	0.8297	0.2036	0.0473*	0.5984
C2 Spinous Process Bifurcation	0.8512	0.0277*	0.0046*	0.4939
C3 Spinous Process Bifurcation	0.4564	0.0043*	0.1935	0.8087
C4 Spinous Process Bifurcation	0.5463	0.0038*	0.3851	0.3663
C5 Spinous Process Bifurcation	0.2134	0.0060*	0.1221	0.2359
C6 Spinous Process Bifurcation	0.3405	0.0211*	0.1399	0.7969
C7 Spinous Process Bifurcation	0.3600	0.0024*	0.0312*	0.6693
Sternal Aperture	0.6787	0.0472*	0.0913	0.9316
Left Suprascapular Foramen	0.7626	0.9950	0.9040	0.9552
Right Suprascapular Foramen	0.5154	0.9558	0.6078	0.9311
Left Supracondyloid Process	0.5599	0.6822	0.0787	0.7677

Table 3.13 (cont'd)

Right Supracondyloid Process	0.5669	0.9745	0.6938	0.9222
Left Septal Aperture	0.1239	0.1407	0.6683	0.0004*
Right Septal Aperture	0.9270	0.6235	0.0001*	0.1935
Left Third Trochanter	0.1253	0.2593	0.0051*	0.1319
Right Third Trochanter	0.6817	0.2160	0.1467	0.2658
Left Vastus Notch	0.7403	0.0695	0.7066	0.6436
Right Vastus Notch	0.8359	0.1264	0.6375	0.6456

**Statistically significant at < 0.05*

Table 3.14. MANOVA results showing the effect of age, sex, and social race on adult postcranial trait expression.

Response Variables	*Df*	*Wilks' Lambda*	*Approximate F-Statistic*	*Num Df*	*Den Df*	*Pr(>F)*
Social Race	3	0.7037	1.3687	72.0000	789.8200	0.0268*
Sex	1	0.8609	1.7768	24.0000	264.0000	0.0161*
Age	1	0.9084	1.1096	24.0000	264.0000	0.3327
*Social Race*Sex*	3	0.7912	0.8942	72.0000	789.8200	0.7202
*Social Race*Age*	3	0.7898	0.9013	72.0000	789.8200	0.7051
*Sex*Age*	1	0.9147	1.0253	24.0000	264.0000	0.4338
*Social Race*Sex*Age*	3	0.8197	0.7545	72.0000	789.8200	0.9340

**Statistically significant at < 0.05*

DISCUSSION

Exploring these postcranial traits across age, puberty, sex, and social race cohorts provided insight regarding their developmental patterns. A notable shift is observed in those traits showing significant differences in character state expressions compared to Spiros' (2019) study. The 2019 research identified only one trait was significant when assessing laterality (i.e., septal aperture), whereas the current findings reveal significant differences in the septal aperture, suprascapular foramen, supracondyloid process, third trochanter, and vastus notch. Interestingly, the suprascapular foramen, supracondyloid process, and third trochanter each exhibit relatively low presence frequency (< 10%) even when the left and right sides are combined. This shift in laterality

may be attributable to the more diverse and representative sample in the current study or to changes in biomechanical influences not captured in the original work. Or, the most likely explanation, secular change between the original 19th-century sample and the more modern sample represented herein. This progression underscores the dynamic nature of laterality and its potential influence on postcranial trait expressions.

In both the juvenile and adult groups, a notable positive correlation exists among MMS features found on the cervical vertebrae (spinous process bifurcation and accessory transverse foramina). However, there are also observable shifts in the significance of specific vertebrae when transitioning from juvenile to adult. This is not true of all traits, however. Take, for example, spinous process bifurcation and accessory transverse foramina, which are consistently correlated throughout life history. The expression of traits on the left and right traits is also consistent throughout growth and development, remaining positively and significantly correlated between the juvenile and adult samples.

Undeveloped traits show the highest density peaks around birth (age = 0) and continue to decrease throughout an individual's life. This suggests any attempts to score these traits prior to fusion would be ill advised, since unfused bones may not provide an accurate representation of the adult threshold. The sternal aperture and the left/right vastus notches are the only traits that fuse past birth. All postcranial MMS traits are fully fused (i.e., can be assessed) by two years, except for the atlas accessory transverse foramen and still the sternal aperture and the left/right vastus notches remain unfused. All traits can be assessed by the age of one, except for sternal aperture (4 years), left suprascapular foramen (34 years), and right supracondyloid process (11 years).

Trait stabilization appears to be more dependable than just determining whether fusion has occurred. For example, in the fusion model, sternal aperture cannot be scored until the sternum is

completely fused which may occur as late as 16-25 years (Bayaroğulları et al. 2014). While these data show the minimum age of appearance of the sternal aperture is ca. 4 years old, a finding consistent with sternebrae fusion (Table 3.1), stabilization of this trait does not occur until individuals reach the 'young adult' stage (Table 3.5), and not until post-puberty (Table 3.7).

Not all traits explored were significantly impacted by age (i.e., PB, L SCP, R SCP, L RR, and R TT) or puberty (i.e., L SSF, R SSF, and L SCP). The influence of chronological age on trait manifestation is highlighted by the results using age cohorts and puberty. It is shown that age cohorts may be too broad to encompass age changes among the juvenile sub-groups. Posterior bridging, for example, is unstable amongst infants (0-3 years) but stabilizes by the fourth year (4-12 years). The influence of puberty on posterior bridging seems clear: there is no difference in trait manifestation between the pre-pubescent and pubescent samples nor between the pubescent and post-pubescent age groups. However, there is a significant difference in posterior bridging between the pre-pubescent and post-pubescent samples. In other words, posterior bridging can be reliably scored by puberty, although the exact age within the 4-to-12-year range is unknown. Complete fusion of the atlas between 5-6 years of age could provide a better indication of when to score posterior bridging.

Most traits, mainly related to the cervical vertebrae (i.e., Atlas ATF, C3 ATF, C4 ATF, C5 ATF, C6 ATF, C7 ATF, C2 SPB, C3 SPB, C4 SPB, C5 SPB, C6 SPB), the sternal aperture, and right septal aperture can be safely scored once an individual has reached puberty. Although the age cohort data shows these traits stabilize broadly within either the 'children' (4-12 years), 'adolescent' (13-20 years), or 'young adult' (21-35 years) stage, puberty may serve as a more precise indicator of stability. Four traits— C7 spinous process bifurcation, left septal aperture, left vastus notch, and right vastus notch— do not develop until after puberty. Left vastus notch

stabilizes within the ‘adolescent’ stage (13-20 years) while the other three (C7 spinous process bifurcation, left septal aperture, right vastus notch) do not stabilize until the ‘young adult’ stage (21-35 years).

Exploring interactions to comprehend how sex, puberty, and social race relate concerning individual traits, puberty is the crucial interaction. Social race and sex do not demonstrate significant interactions unless puberty is a factor (i.e., left septal aperture). When examining the influence of sex on the traits, only left/right septal aperture and right vastus notch exhibit a statistically significant difference between adult males and females. Investigating the association between postcranial traits and social race, those that exhibit notable differences across at least two groups include: the atlas accessory transverse foramen, C5- C6 accessory transverse foramina, C3-C5 spinous process bifurcation, left supracondylar process, right third trochanter, and both vastus notches. Although, the left supracondylar process was only present overall in five of the 303 individuals, 1.7% of the adult sample questioning the practicality of the trait’s use.

The in-depth examination of these traits in this study showcases a more comprehensive analysis of postcranial features. Spiros (2019) pooled all the cervical vertebrae accessory transverse foramina and only included C3-C4 spinous process bifurcation (following Duray et al. 1999). In contrast to Spiros (2019), the significance of septal aperture between social race groups has transitioned from a noteworthy observation to a non-significant finding in this study. Given the data collection method employed (CT scans) for this research, transparency as a state was not assessed and should be included in future investigations to gain a comprehensive understanding of the variation.

CONCLUSION

This study is the first to investigate the ontogenetic variation of postcranial MMS traits.

Age is a significant contributing factor in the ontogeny of postcranial traits, particularly when focusing on puberty and age-of-attainment for adult morphology. Only the left supracondyloid process, left/right septal apertures, and left/right vastus notches demonstrate variation between sexes. Among adults, social race impacts the expression of traits ranging from the vertebrae (i.e., Atlas ATF, C5 ATF, C6 ATF, C3 SPB, C4 SPB, C5 SPB), the humeri (i.e., L SCP), the femora (i.e., R TT), and patella (i.e., L/R VN). In this sample of juveniles and adults sex and social race, in tandem, do not seem to contribute to differences in trait manifestation. These results (*writ large)* suggest postcranial MMS traits should not be collected from individuals who have not reached puberty for assessment of social race or sex. The stabilization of traits occurs at distinct points in time; puberty is the best indicator of stability for most of these traits. The absence of age, sex, and social race influences on specific traits underscores the importance of future investigations into biomechanical factors.

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MANUSCRIPT 4. EMBODIMENT OF SOCIOCULTURAL INFLUENCES ON POSTCRANIAL SKELETAL MORPHOLOGY

INTRODUCTION

There is no gene for social race, but due to the dynamic nature of the human body, there is biological patterning to embodied racism. Social race itself is interpreted in a multitude of ways, dependent on context. As such, social race is defined for this research as a sociocultural concept, reinforced through population history, self-identity, cultural practices, political categories, and legal policies. In other words, the 'social' aspect of social race emphasizes that it is a concept completely dependent on society. Specifically, for this study, the social race groups explored parallel the social race assessed at time-of-death in the New Mexico Office of the Medical Investigation (i.e., U.S. Black, Hispanic, Native American, and U.S. White individuals).

The complexity of human variation has been a pivotal and key discussion of biological anthropologists for years and the belief that institutional racism impacts the skeleton is not a new one in forensic anthropology (*c.f.* Dunn et al., 2020; Gross & Edgar, 2021; Ousley et al., 2009; Ousley et al., 2017;). In the literature devoted to macromorphoscopic (MMS) trait research, the embodiment of racism is discussed as a component influencing the nonzero correlation between geographic ancestry and skeletal variation (DiGangi & Hefner, 2013; Pilloud & Hefner, 2016; Hefner & Redfern, 2021).

Macromorphoscopic traits (binary or continuous skeletal variants) are one type of data used to capture human variation and assess population affinity of an unknown individual in forensic anthropological casework (Hefner & Linde, 2018; Pilloud et al., 2018). Defining population affinity estimation as the "prediction of the peer-perceived ancestry of an individual" (Hefner, 2009, p. 985), MMS trait analyses highlighting the frequencies of traits between groups,

demonstrating the reliability of these variations within a statistical framework, illustrating that single trait expressions are not reliable or valid for the estimation of population affinity, as such moving past the outdated, one-to-one correlation of single trait–to-population fallacy (Hefner, 2009). Since the inception of the cranial macromorphoscopic approach, researchers have distanced the approach from antiquated typology wherein one trait expression equals one social race; for example, Hefner showed that, "a combination of supposedly ancestrally diagnostic traits in many individuals shows the fallacy of the typological approach to ancestry prediction and reveals variation in morphoscopic [sic] traits within ancestral groups" (Hefner, 2009, p. 994). This is very much in line with Lewontin's (1972) assertion that there is more genetic variation within groups than between groups of geographic populations. Building on the shift away from antiquated typological approaches in anthropological research, it becomes imperative to examine how societal structures that perpetuate harm and inequity become embodied. Structural violence, a concept rooted in the understanding of societal systems, extends our comprehension beyond individual skeletal traits to encompass broader systemic issues.

Structural violence can be defined as productions of society (e.g., policies, laws, cultural practices, and economic structures) that endanger, harm, or injure communities. These structures reinforce the broader concept of systemic violence, in which entire systems (e.g., political, legal educational, economic, housing, criminal justice, and healthcare systems) put communities at risk, tolerate inequity, and perpetuate discrimination (O'Donnell & Edgar, 2021; Sharif et al., 2022; Farmer, 2004). Studies exploring structural violence and the interrelatedness on population-specific skeletal variation have used metric analyses of the cranium (Weisensee & Spradley, 2018), metric analyses of the postcranium (Znachko et al., 2019; Corron et al., 2021), and dentition (O'Donnell and Edgar, 2021), but there have been no attempts to use postcranial

macromorphoscopic traits to explore the effects of structural violence. Structural racism, a form of structural violence, is the concept in which the oppression of marginalized peoples is created, embedded, and normalized within the systems, institutions, and structures of society both implicitly and explicitly based on race (Braveman et al., 2022; Sharif et al., 2022). These systems of inequity and harm can become embodied (Gravlee, 2009).

Biological distance (biodistance) analyses rely on measures of similarity/dissimilarity for populations or individuals. In osteological research, various scales for assessing biodistance based on social structures are utilized. From small scale analyses analyzing kinship, to large continental-level scales that include population history, biodistance studies rely on statistical analyses (Hefner et al. 2016; Hefner 2016). It is known that there is morphological variation across populations, and that this variation is reflected in population-specific ways. For example, global environmental factors (such as climate and temperature) influence body form, such as Allen's Rule (Allen, 1877) and size, such as Bergmann's Rule (Bergman, 1847) and thus can be correlated with geographic ancestry.

Many of the methods forensic anthropologists use to construct the biological profile rely on population-specific standards to account for ecogeographical pattering, human adaptability, and epigenetic influences (Adams et al., 2019; Liebenberg et al., 2019; Spradley, 2016; Plemons, 2022). The variation these methods account for is reflected in population studies including the skull (Atkinson & Tallman, 2020; Berg & Kenyhercz, 2017; Hefner, 2009, 2018; Kamnikar, 2022; Maier, 2019; Plemons & Hefner, 2016; Plemons, 2022; Spradley & Jantz, 2016;), dentition (Adams et al., 2019; Edgar, 2013; Edgar & Ousley, 2013; Pilloud et al., 2019; Scott et al. 2018), and the postcranium (Duray et al., 1999; Spiros, 2019; Spiros & Hefner, 2020; Spradley, 2017;

Kindschuh et al., 2012; Bidmos et al., 2018; Liebenberg et al., 2015) exploring various data types and statistical approaches to understanding how skeletal variation is modeled.

And yet, our understanding of biocultural influences and the etiology of morphological variation is limited (Bethard & DiGangi, 2020; Dunn et al., 2020; Ross & Pilloud, 2021; Stull et al., 2021). Because of this, a more detailed understanding of how neutral evolutionary forces, mechanisms that occur regardless of fitness or survival (e.g., genetic drift, mutation), influence and impact human variation and population affinity is necessary (Ross & Pilloud, 2021; Plemons, 2022). Systemic and structural racism has been linked to aspects of modern human variation (e.g., anti-miscegenation/Jim Crow laws were legal until the late 1960s), but it is important to understanding if structural racism has an impact on the human skeleton. By exploring the prevalence of postcranial macromorphoscopic traits in a sample of modern Americans, this research aims to explore the sociocultural impacts (i.e., socioeconomic status, education, and social race) on skeletal morphology and how understanding these interactions can refine our understanding of human variation.

The dynamic nature of bone provides an interesting conduit for studying growth and development in the context of evolutionary and embodiment theories. The flexibility of biology, known as plasticity, reflects the embodiment of social, behavioral, and cultural patterns (West-Eberhard, 1989). With a focus on phenotypic plasticity—the observable variation produced by environmental factors—a postgenomic approach is necessary to understand human variation (Agarwal, 2016; Agarwal & Beauchesne, 2011; Duncan et al., 2014; Meloni, 2015; West-Eberhard, 1989). Developmental systems theory (DST) links sociocultural impacts to biology, and thus to inequity and privilege embodiment (Duncan et al., 2014; Hicks & Leonard, 2014; Mansfield & Guthman, 2015; Meloni, 2015). Through this perspective, DST emphasizes

biocultural influences on development while specifically focusing on the inheritance of sociocultural factors (e.g., income, education, employment) in a postgenomic framework (Agarwal & Beauchesne, 2011; Meloni, 2015; Oyama et al., 2001). This theoretical approach suggests heredity does not just impact genes; instead, developmental variations, such as methylation and/or histone modifications, can be inherited alongside the genome (Agarwal, 2016; Agarwal & Beauchesne, 2011; Hicks & Leonard, 2014; Jablonka & Lamb, 2002; Robert et al., 2001). Epigenetic research has shown how these modifications represent (biologically) lived experiences at the genetic level by changing how genes are expressed without altering the underlying DNA sequence (Lock, 2013). Using DST as a framework for the theoretical keystones of developmental changes, this study explores the implications of geographical ancestry, economic status, racism, and privilege on the postcranial skeleton.

A biocultural interpretation of data allows anthropologists to explore the effects of sociocultural influences (e.g., wealth, health behaviors, psychosocial stress, social structure/cultural context) and biology in tandem to model inequalities in health and human variation (Gravlee, 2009). This concept dispels the erroneous idea that race is biological and, instead, identifies cultural factors, such as structural racism, as some of the prime influencers on our biology. For example, while the risk of morbidity and mortality is higher among Black individuals in the United States, it is not a genetic difference causing these inequities, but structural violence and systemic racism (Yearby, 2018; Williams et al., 2016). Understanding how sociopolitical constructs (e.g., social race and racism) become entwined with biology is necessary to understand modern human variation.

The connection between socioeconomic status (SES) and the health-wealth gradient, for example, highlights this interconnection. Generally, SES relies on sorting individuals into groups

based on income, at times using an ordinal expression like ‘low’, ‘middle’, or ‘high’. However, researchers use additional measures—education, poverty, net worth, occupation—to capture different aspects of the social experience. Though some measurements are stronger than others, regardless of the metric, SES is a robust determinant of variation in health outcome expectations (LaVeist, 2005).

Using wealth as a proxy for security (e.g., food security, healthcare, housing), it has been shown that wealth influences health (e.g. mental, behavioral, emotional, and physical health) (DeWitte et al 2016). This process includes environmental stressors, biological responses, consequences of the responses, and moderators illustrating variations between individuals (McDade, 2008). Understanding the living conditions of a population is traditionally captured through broad concepts of environment and adaptability; this study works under the perspective that adaptability is a response to environmental adversity over the lifetime of an individual and cross-generationally, integrating biology and culture to understand postcranial variation manifestation and development (Chapter 4).

The social realities of racism and institutional racism have repercussions that lead to the embodiment of social inequalities. Gravlee (2009) proposes three foci essential to center discussions of social race and biology. These include: 1) Race does not equal human genetic variation; 2) biology does not equal genetics; and 3) race is not a myth. No human is defined solely by their genetic make-up, so this paper explores beyond the antiquated one-to-one typological ideology that one variant equates to a specific race. An individual’s life course must be contextualized including the environmental factors influencing the expression of their genome, the phenotypic plasticity expressed as some threshold of said genome, and the multilevel causal influences. Krieger’s ecosocial theory of epidemiology can model each of these as constructs of

embodiment through the correlation between biology and society (Krieger, 2001; Krieger, 2021). Krieger's idea of embodiment in social theory illustrates how bridging biology and society using epigenetics contributes to the breakdown between the natural/social divide. Under "body economics", the author illustrates this idea and shows how policies and inequalities, specifically SES, equate directly to risk factors related to the health-wealth gradient. There is already a body of literature illustrating the correlation between low SES and high mortality, negative immune responses, and an overall increase in disease risk factors (Krieger, 2001; Meloni, 2015). This suggests or outright implies that epigenetics and embodiment are interdependent. Meloni (2015) suggests "embodied constructivism" should be used in the context of DST; that is that a non-hierarchical, cyclical relationship of social structures influencing biological factors influencing social structures.

The oversimplified (but perhaps not stated enough) fact is that it is known that race is not biological, but *racism* can be biologically expressed as an embodiment of the entire process (McDade, 2008). Disembodiment, the reluctance to recognize human variation and phenotypic differences, was an issue in anthropological scholarship resulting from hard opposition to genetic reductionists (Lock, 2013). However, as the relationship between biology and culture was better understood, the need to incorporate a biocultural approach became apparent. Sociological and cultural structures need to be documented as much as biology since these external factors can generate changes in genetic expression (Dressler, 2009). While the patterns between SES, education, and social race have been used to illustrate and discuss the connection between biology and structural racism (Gravlee, 2009; LaVeist, 2005; McDade, 2008; Meloni, 2015; Sharif et al., 2022; Williams et al., 2016; Yearby, 2018), it is important to note that the significant differences and patterns could also be due to cultural difference (i.e., different emphasis on educational

obtainment or career choices) or migration patterns (i.e., economic opportunities). This manuscript investigates wealth/income, education, and social race, each separately and simultaneously, to explore the human variation through the embodiment of race and racism. As such, this paper conducts a data-driven exploration of the impact of biocultural influences on the skeleton.

Three research aims guide this study— the first objective of this manuscript is to understand and quantify the underlying structure and relationships of postcranial MMS traits. Second, this manuscript aims to identify patterns or relationships in the expression of these postcranial traits and a number of sociodemographic variables both on a broad scale and then more refined levels of analysis. The final objective is to assess the association and interaction between these sociodemographic variables and postcranial morphology. In particular, this research is guided by the hypothesis that due to the embodiment of social inequity and evolutionary processes related to geographic ancestry, sociodemographic variables— sex, social race, socioeconomic status, and education— will influence morphological variation of the postcranial skeleton.

MATERIALS AND METHODS

Sample

Data were collected for postcranial MMS traits from adult individuals whose deathplace was New Mexico. We used data from the New Mexico Decedent Image Database (NMDID), a novel database of CT scans with associated HIPPA-compliant metadata (i.e., sex, social race, socioeconomic status as a child, socioeconomic status as an adult, education level, etc.) connected directly to individuals in the collection (Berry & Edgar, 2020; Berry et al., 2021). The complete sample includes 303 individuals (Table 4.1). All individuals included are over 18 years of age to control for pubertal variability (Chapter 4). The social race of the individuals was reported in the

NMDID based on VAST, the New Mexico Office of the Medical Investigator's database and as recorded through next of kin interviews (Berry & Edgar, 2020).

In the NMDID, socioeconomic status[1] during an individual's childhood and adulthood and their education level are established through next-of-kin interviews (Berry & Edgar, 2020). During the next-of-kin interviews socioeconomic status responses accepted included: lower class, lower middle class, middle class, upper middle class, and upper class. For this study, lower class/lower middle, and upper middle class/upper class were pooled to improve sample sizes. Demography data by SES and education are presented, by social race, in Figure 4.1. At least one individual from every county in New Mexico, with the exceptions of Hidalgo, De Baca, Mora, Colfax, Harding, and Union counties, are included in this study (Figure 4.2). For comparative purposes, the percentage of the populace (by county) living in poverty is also illustrated in Figure 4.2 (U.S. Census, 2022).

[1] A state analysis of income trends demonstrated that, on average, New Mexico has the greatest income inequality between the top 20% and bottom 20% (McNichol et al., 2012). The New Mexico average income between 2008-2010 (adjusted for inflation to be represented by 2009 US dollars) for the bottom fifth ($16,319), middle fifth ($51,136), and top fifth ($161,162) income are lower compared to the United States averages for the bottom fifth ($20,510) and top fifth ($164,490) income (McNichol et al., 2012).

Table 4.1 Summary of sociodemographic sample characteristics (N= 303).

Social Race	***Females (n)***	***Males (n)***	***Total (N)***
U.S. Black	13	40	53
U.S. Hispanic	38	45	83
U.S. Native American	30	37	67
U.S. White	49	51	100
Total (N)	130	173	303
Childhood SES	***Females (n)***	***Males (n)***	***Total (N)***
Low SES	48	63	11
Middle SES	61	70	131
High SES	21	40	61
Total (N)	130	173	303
Adult SES	***Females (n)***	***Males (n)***	***Total (N)***
Low SES	51	63	114
Middle SES	50	63	113
High SES	29	47	76
Total (N)	130	173	303
Education	***Females (n)***	***Males (n)***	***Total (N)***
Unknown	4	3	7
No HS Degree	23	41	64
HS Degree	40	59	99
Some College Credit	19	28	47
College Degree	44	42	86
Total (N)	130	173	303

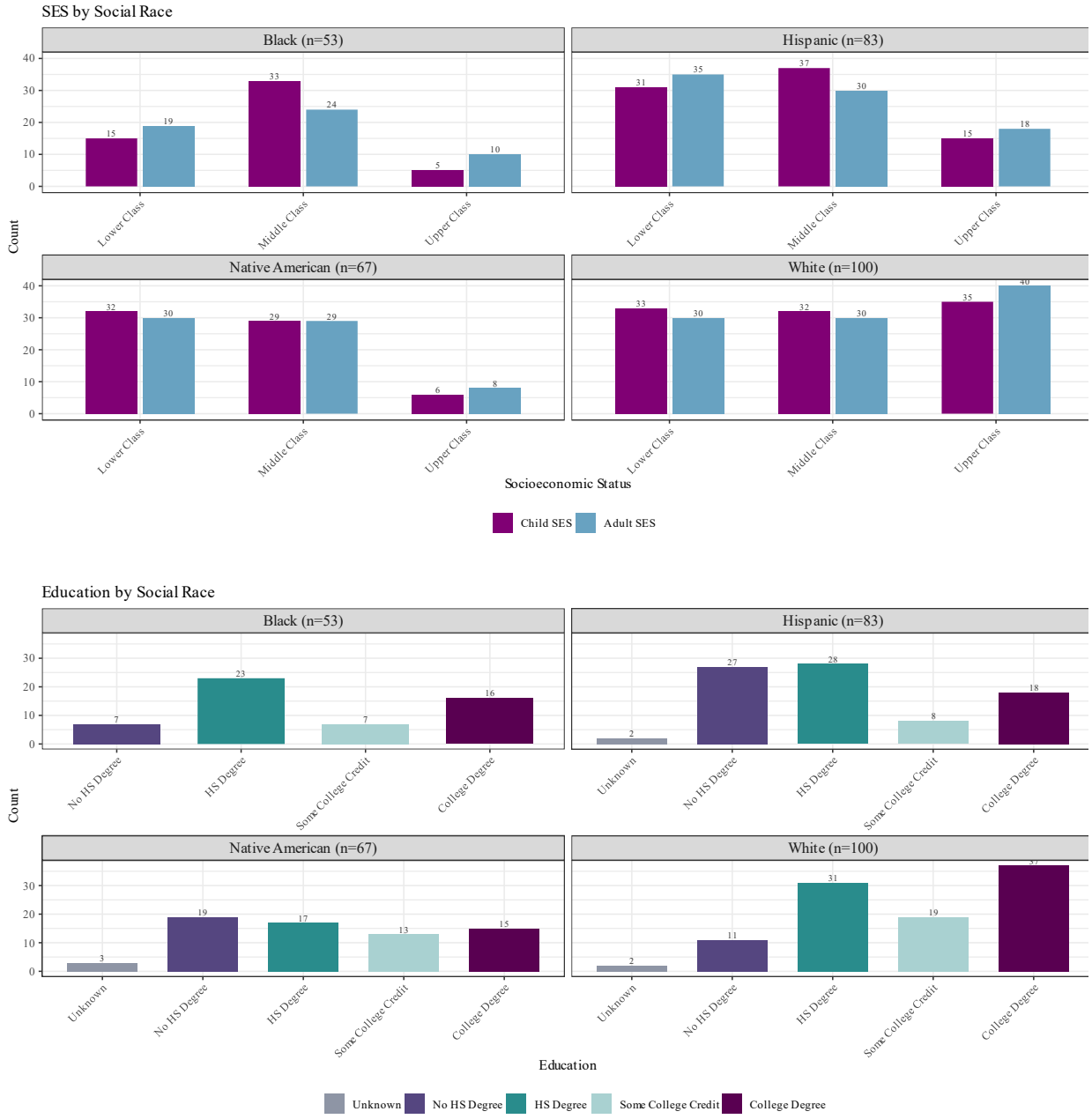

Figure 4.1 Sample Demography by Social Race

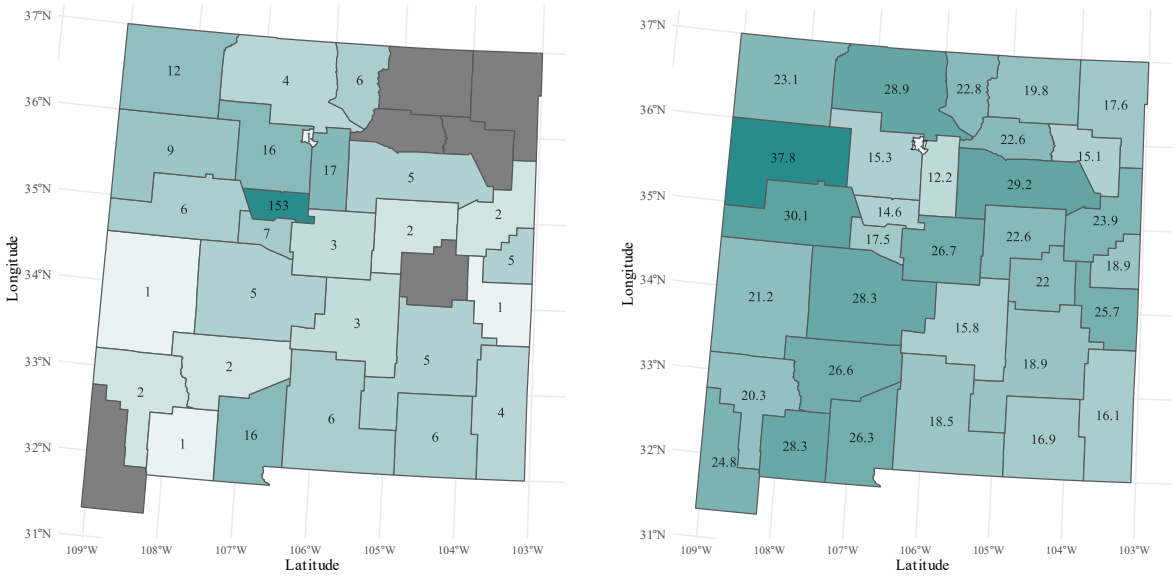

Figure 4.2. Sample count distribution by county (left); Percentage of poverty by county population (right). The darker the green the higher the frequency. Grey counties indicate that no data was collected.

Data Collection

Skeletal elements were modeled in three-dimensional space using CT scans from the NMDID to collect each postcranial MMS trait score. Thin-slice DICOM stacks from the NMDID CT scans were imported into the Amira™ 3D 2022.2 software (Thermo Fisher Scientific, 2023). A volume render was generated for each individual and a 3D surface model was reconstructed from the 2D slices, following the procedures recommended by Stull and colleagues (2021). The assessment of postcranial variation follows the standard scoring procedures for postcranial MMS traits (Spiros 2019). Spiros (2019) introduced a protocol to collect data on the cervical vertebrae, scapulae, sternum, humeri, femora, patellae, and calcanei. Due to the articulation points of the calcaneus and talus, the double superior articular facet (DSAF) and the anterior and middle calcaneal facets (AMCF) were not scored. Translucency (“1”) was not scored in this study. Each trait is assigned a nominal score based on the associated definition and line drawings for each character state (Spiros 2019). Any trait that did not exhibit significant variability in expression

(presence of < 5% and no significance between social race groups) was removed. The eight retained traits are outlined in Table 4.2.

Table 4.2 Retained postcranial MMS traits.

Trait (Spiros 2019)	Abbreviation	Score
Posterior Bridging	PB	0-2
Atlas Accessory Transverse Foramen	Atlas ATF	0-2
C5-C6 Accessory Transverse Foramen	C5-C6 ATF	0-2
C2-C6 Spinous Process Bifurcation	C3-C6 SPB	0-2
Sternal Aperture	STA	0-1
Left & Right Septal Aperture	L/R SA	0-3*
Left Third Trochanter	L TT	0-1
Left & Right Vastus Notch	L/R VN	0-1

**Translucency (state of '1') not scored for this study*

Statistical Analyses

All analyses were conducted in the R environment. Missing data were imputed using the "mice" package (van Buuren & Groothuis-Oudshoorn, 2010). In multivariate imputation by chained equations (MICE), predictive mean matching was used selecting, for each missing value, a matching observed value from the dataset based on its predicted mean and imputing the missing value with a matched value. Chi-square tests were employed to measure the association between the sociodemographic variables (sex, social race, childhood socioeconomic status, adult socioeconomic status). Cramér's V was utilized to quantify the strength of the relationships between the sociodemographic variables. Using a test of equality of proportions, socioeconomic statuses were compared between the childhood and adult categories. Hierarchical clustering analysis, and an associated dendrogram, was used to explore postcranial MMS trait manifestations. These data are explored prior to incorporating the sociodemographic data to understand the underlying structure of the similarities between the traits allowing for understanding the associations between the traits. The degree of correlation between these traits is quantified using

Pearson's correlation as the distance metric in the analysis.

Multiple Correspondence Analysis (MCA) is a statistical technique suitable for visualizing the relationship between two or more variables (Husson et al., 2011). First, an MCA was used to assess the relationship of the sociodemographic variables (social race, sex, education, and SES) to the known New Mexico population, in an effort to understand if our sample is representative of the New Mexican demography. These analyses used the 'FactoMineR" package (Lê et al., 2008). Next, the postcranial character states are incorporated to assess the relationship of all independent and dependent variables. The contribution and squared cosine (cos^2) measurements quantify the relationships between these data. Contribution measures how much a category provides for the variability by each dimension while cos^2 represents the quality of representation of each category on the dimensions.

Group differences were assessed using a Kruskal–Wallis test ($\alpha = 0.05$) and the 'stats' package (R Core Team, 2019). Subsequently, the *kwAllPairsDunnTest* function from the 'PMCMRplus' package (Pohlert, 2020) was applied for the Kruskal–Wallis *post hoc* two-sided Dunn's test to assess significant differences between sociodemographic variables (social race, childhood SES, adult SES, education, and sex) and the postcranial MMS traits. A multivariate analysis of variance (MANOVA) model using the 'jmv' package (Selker et al., 2022) assessed interactions between all variables, with *post hoc* univariate analysis of variance (ANOVA) tests to assess interactions by trait.

RESULTS

A little under three percent of data is missing, due in large part to the clarity of the CT scans, followed by trauma, then incomplete full body scans. The distribution of missing data, by trait, is shown in Table 4.3.

Table 4.3 Missing data by trait.

Variable	*Missing (Count)*	*Missing (%)*
Right Vastus Notch	23	7.59
Atlas Accessory Transverse Foramen	19	6.27
Left Vastus Notch	17	5.61
C6 Accessory Transverse Foramen	15	4.95
Left Septal Aperture	15	4.95
Right Septal Aperture	13	4.29
Right Third Trochanter	12	3.96
C5 Accessory Transverse Foramen	7	2.31
Sternal Aperture	3	0.99
Posterior Bridging	2	0.66
C3 Spinous Process Bifurcation	2	0.66
C2 Spinous Process Bifurcation	1	0.33
C4 Spinous Process Bifurcation	1	0.33
C5 Spinous Process Bifurcation	0	0.00
C6 Spinous Process Bifurcation	0	0.00

All the sociodemographic variables are significantly associated with each other, except for sex, which is only statistically significant when associated with social race (Table 4.4). The strongest effect between groups is adult SES and childhood SES, followed by education and adult SES, and then social race and childhood SES.

Table 4.4 Summary data for the Chi-square tests.

Categories	χ^2	*df*	*p-value*	*Cramér's V*
Social Race + Sex	9.1994	3	0.0268*	0.17
Social Race + Adult SES	20.6470	6	0.0021*	0.18
Social Race + Childhood SES	29.3600	6	<0.0001*	0.22
Social Race + Education	27.2040	12	0.0072*	0.17
Education + Sex	4.6123	4	0.3294	0.12
Education + Adult SES	31.905	8	<0.0001*	0.23
Education + Childhood SES	26.443	8	0.0009*	0.21
Adult SES + Sex	0.9385	2	0.6255	0.06
Adult SES + Childhood SES	99.886	4	<0.0001*	0.41
Childhood SES + Sex	2.5117	2	0.2848	0.09

**Statistically significant at $p < 0.05$*

Comparing childhood and adult proportions for the lower-, middle-, and upper-class

samples identified no statistically significant differences (α = 0.05; Table 4.5).

Table 4.5 Test of equality of proportions by childhood and adult SES.

Variable	*Childhood Prop.*	*Adult Prop.*	χ^2	*df*	*p-value*
Lower Class	0.3663	0.3762	0.0283	1	0.8665
Middle Class	0.4323	0.3729	1.9828	1	0.1591
Upper Class	0.2013	0.2508	1.8486	1	0.1740

**Statistically significant at p < 0.05*

Figure 4.3 illustrates correlations among sociodemographic variables. Notably, despite the absence of significant differences, the highest correlation coefficient is observed between childhood SES and adult SES.

Figure 4.3 A visual representation of correlations between variables, where color intensity signifies correlation coefficient strength. The labels denote the correlation coefficients. No correlations are significant (α = 0.05).

The hierarchical clustering analysis revealed two primary clusters, subdivided into 11

subclusters (Figure 4.4). The first cluster comprises the traits associated with the patellas, humeri, sternum, one first vertebra trait (e.g., atlas accessory transverse foramen), and the second cervical vertebra. The second cluster includes one first cervical vertebra (e.g., posterior bridging), cervical vertebrae 3-6, and the femur. These clusters introduce the relationship between the traits allowing for more nuanced interpretation of their etiology.

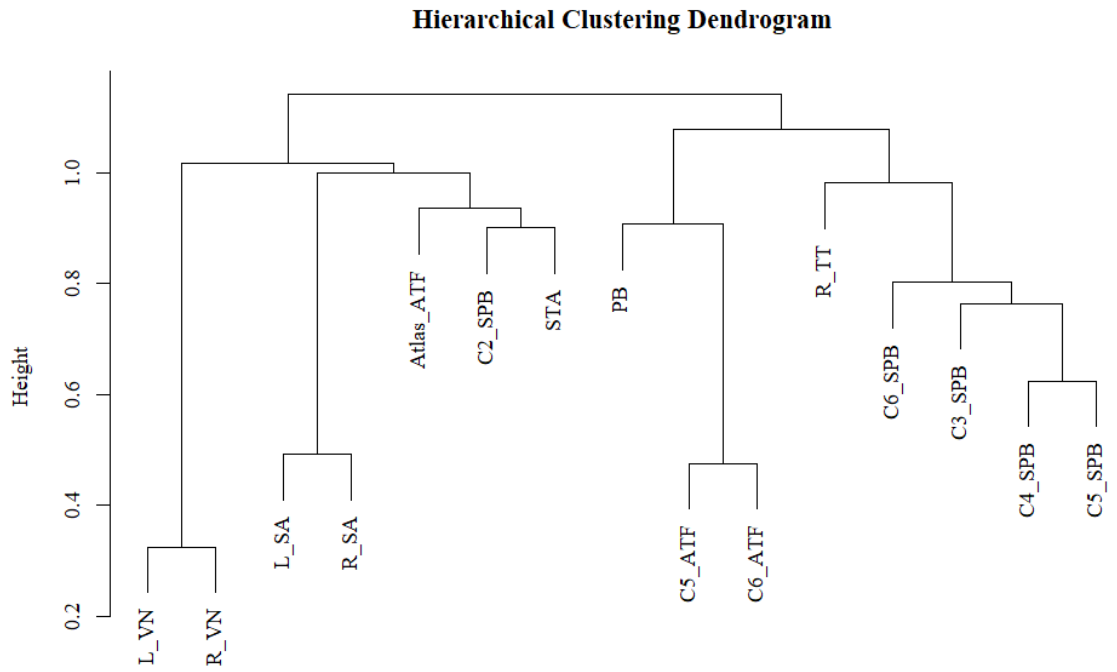

Figure 4.4 Visual representation of hierarchical clustering dendrogram, revealing the underlying structure and relationships among data points. Method: Complete Linkage, Distance Metric: 1- Pearson Correlation.

The MCA exploring the sociodemographic data (Figure 4.5), first without the postcranial MMS traits, revealed clustering along the two principal dimensions. The cos^2 values are observed represented via a color gradient (Figure 4.5). Overall, white, upper-class male individuals with some level of college education are separated by the first dimension from everyone else. The second dimension then separates Black, middle-class males with a high school degree or higher from the rest of the individuals.

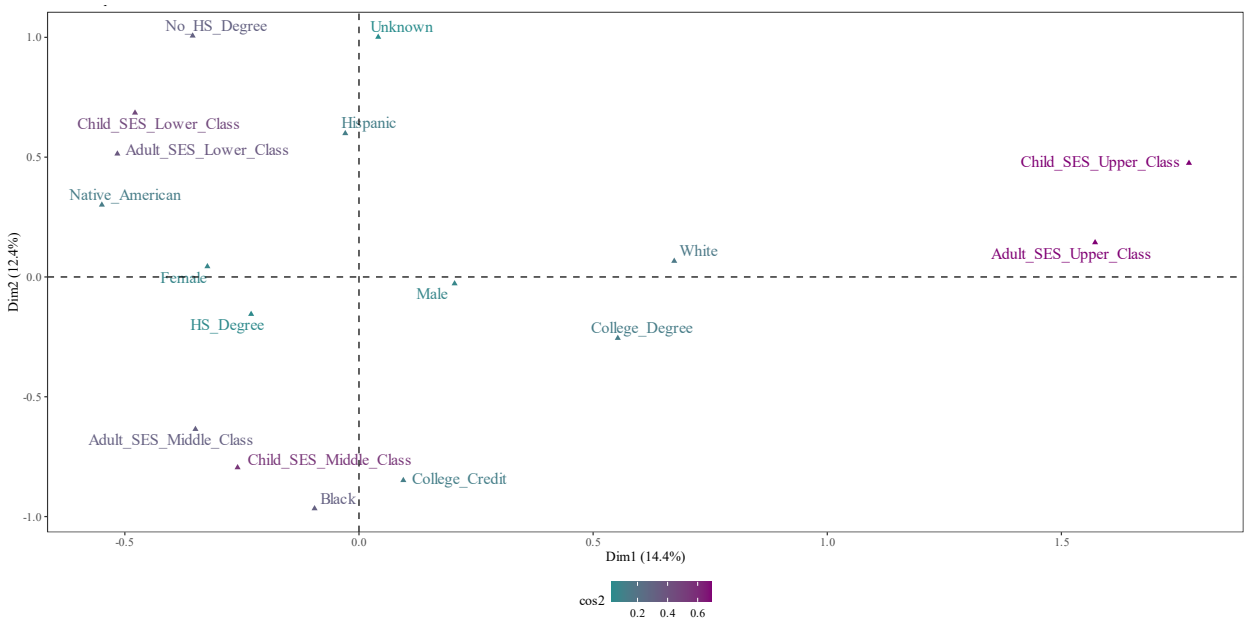

Figure 4.5 MCA plot illustrating the interrelationships among sociodemographic variables social race, SES, sex, and education (Downsampled to the smallest social race group).

The MCA plot for sociodemographic variables and postcranial MMS character states combined (Figure 4.6) revealed clustering of categories along the two principal dimensions, indicating patterns within the dataset with each variable highlighted by $\cos^2$ values. The $\cos^2$ values are observed represented via a color gradient (Figure 4.6). A biplot with confidence ellipses around the means of social race is provided in Figure 4.7 to illustrate the distributions of the groups. Overall, the MCA plot, provided valuable insights into the underlying structure of the data, facilitating the identification of meaningful associations between categories.

The MCA biplot revealed distinctive patterns along its dimensions. Specifically, variables positioned to the left (negative) of zero on the first-dimension axis represent characteristics associated with one another, while variables positioned to the right (positive) of zero represent characteristics associated with a second group. Dimension 1 highlights that the postcranial MMS and sociodemographic variables contributing to this dimension are distinctly separate categories. For instance, this first dimension effectively separates females (left of first axis) from males (right

of first axis); Hispanic and U.S. White individuals (left of first axis) from U.S. Black and Native American individuals (right of first axis); upper class (left of first axis) from middle to lower class SES (right of first axis); and individuals with college-level coursework or higher (left of first axis) from individuals with a high school degree or lower (right of first axis).

The second dimension essentially separates females (above the second axis) from males (below the second axis); Hispanic, U.S. Black, and Native American individuals (above the second axis) and U.S. White individuals (below the second axis); lower and middle class (above the second axis) from upper class SES (below the second axis); and individuals with no college degree (above the second axis) from individuals with a college degree (below the second axis).

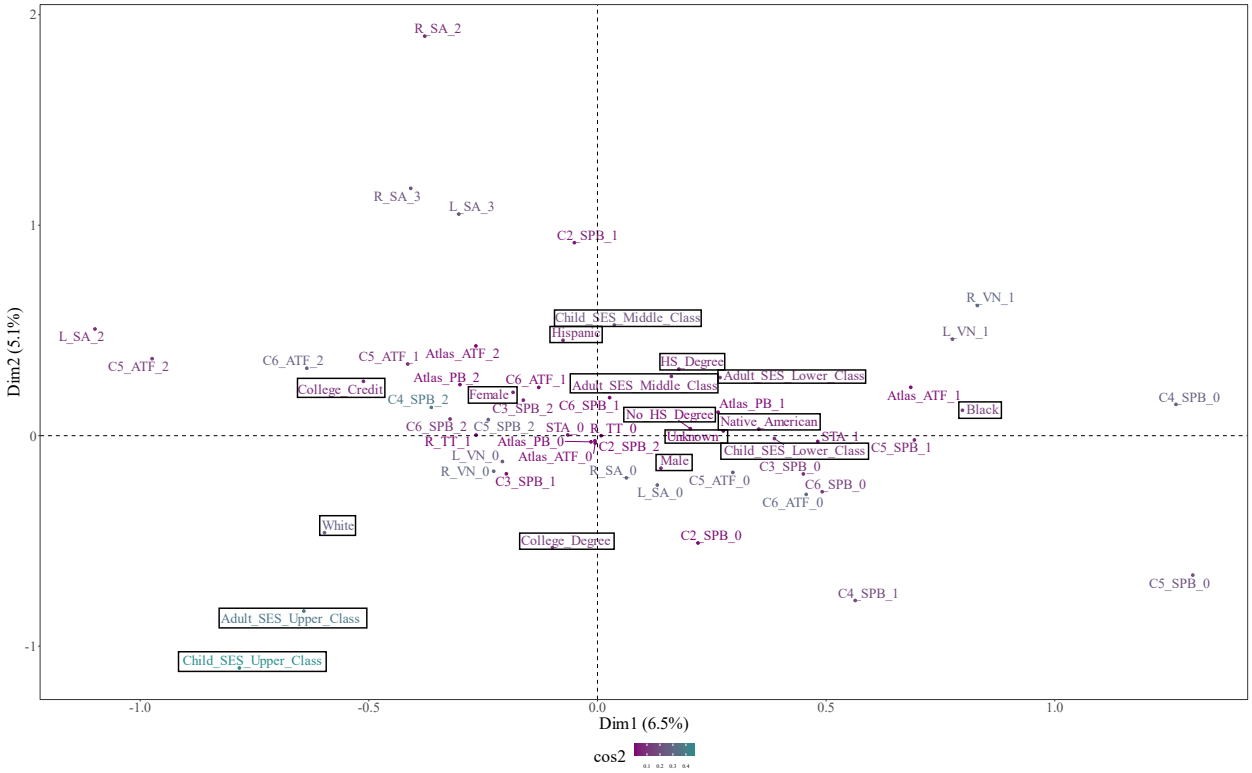

Figure 4.6 Visualization of MCA results for variable contributions, highlighting the strength and directionality of associations. Variable labels are colored proportionally to their contributions (cos2), with a gradient representing the magnitude of variance. Sociodemographic variables are illustrated with black rectangles.

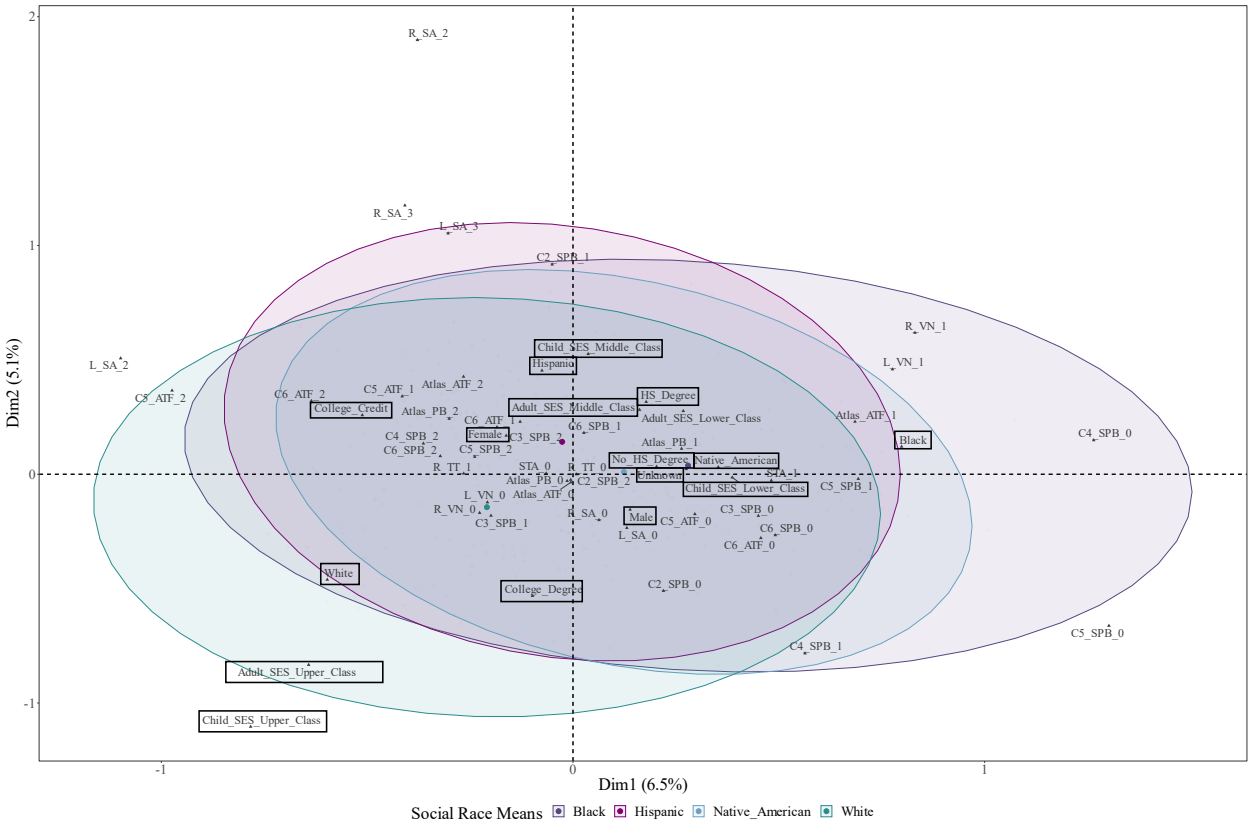

Figure 4.7 Biplot representation of MCA showcasing the relationships between categories and observations (Figure 4.6) with added confidence ellipses around the mean point of social race categories. Sociodemographic variables are illustrated with black rectangles.

The results from the Kruskal-Wallis test for social race (Figure 4.8) reveal significant differences in C3-C5 SPB overall. The subsequent *post hoc* Dunn's test (Figure 4.8) identified significant differences in character state manifestations for: C5-C6 accessory transverse foramen, C3-C5 spinous process bifurcation, right septal aperture, right third trochanter, and both vastus notches.

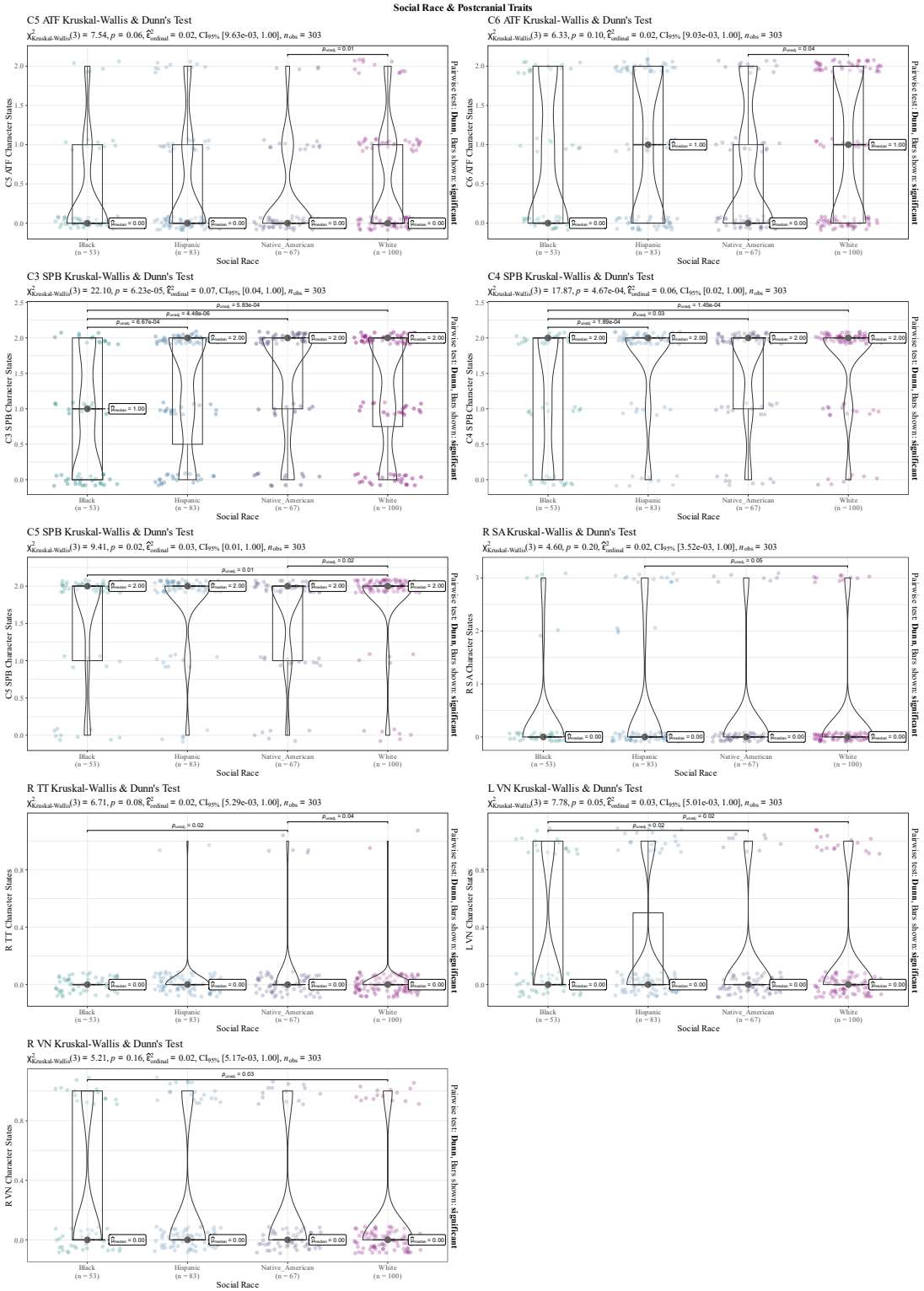

Figure 4.8 Boxplot & violin plot showing the distribution of significant postcranial MMS traits among social race groups, with statistical analysis using Kruskal-Wallis test. The horizontal p-bars shown at the top of the plot illustrate which groups are significant via Dunn's post hoc test for multiple comparisons.

The results from the Kruskal-Wallis test for childhood SES (Figure 4.9) reveal significant differences for C3-C4 accessory transverse foramina. The subsequent *post hoc* Dunn's test (Figure 4.9) identified significant differences in character state manifestations for: C5-C6 accessory transverse foramina, C4 spinous process bifurcation, and the right vastus notch. The results from the Kruskal-Wallis test for adult SES reveal no significant differences for the overall traits. The subsequent *post hoc* Dunn's test identified no significant differences in character state manifestations.

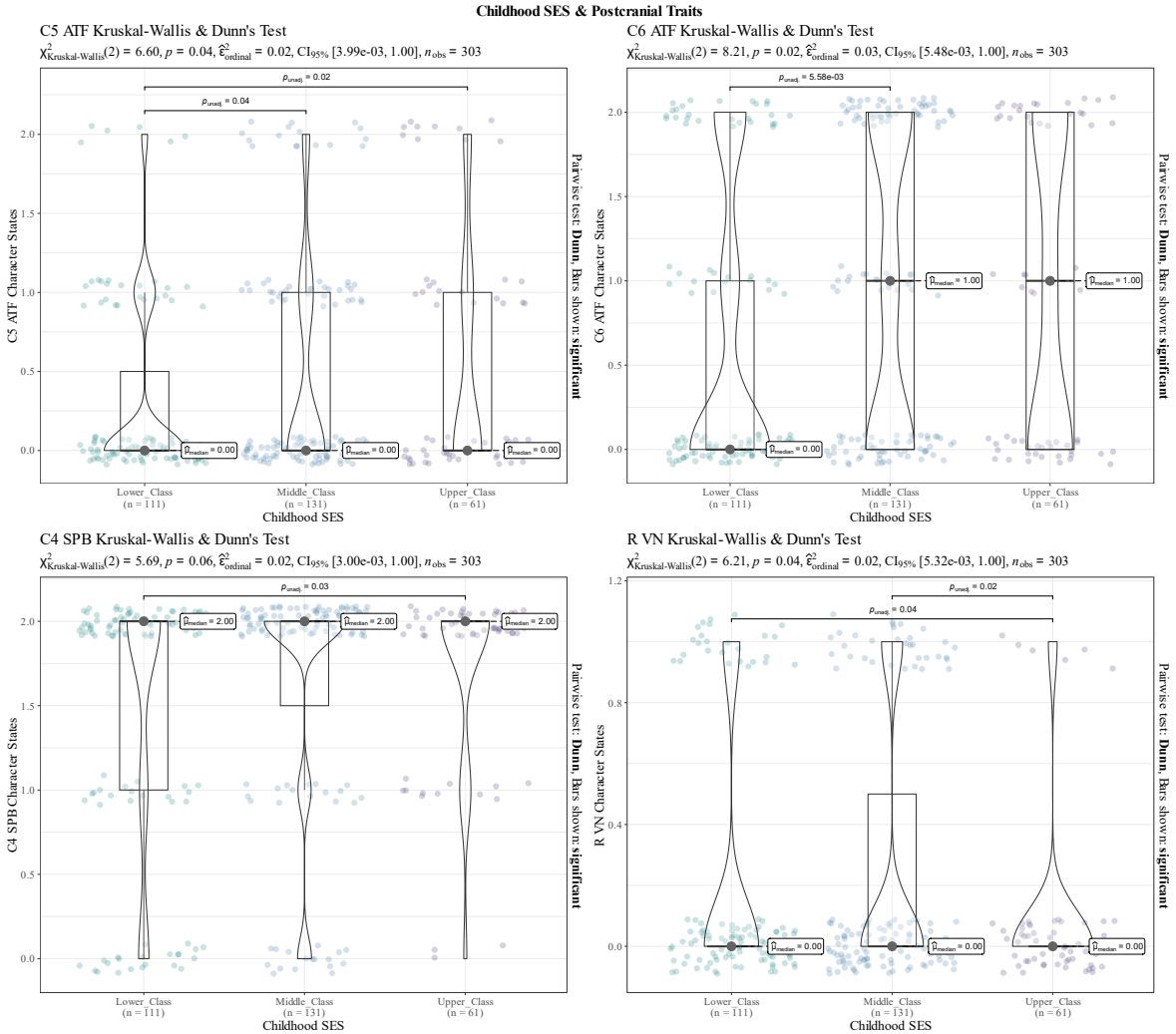

Figure 4.9 Boxplot & violin plot showing the distribution of significant postcranial MMS traits among childhood SES groups, with statistical analysis using Kruskal-Wallis test. The horizontal p-bars shown at the top of the plot illustrate which groups are significant via Dunn's post hoc test for multiple comparisons.

The results from the Kruskal-Wallis test for education (Figure 4.10) reveal significant no significant differences for the overall traits. The subsequent *post hoc* Dunn's test (Figure 4.10) identified significant differences in character state manifestations for: C3-C6 spinous process bifurcation and the left vastus notch.

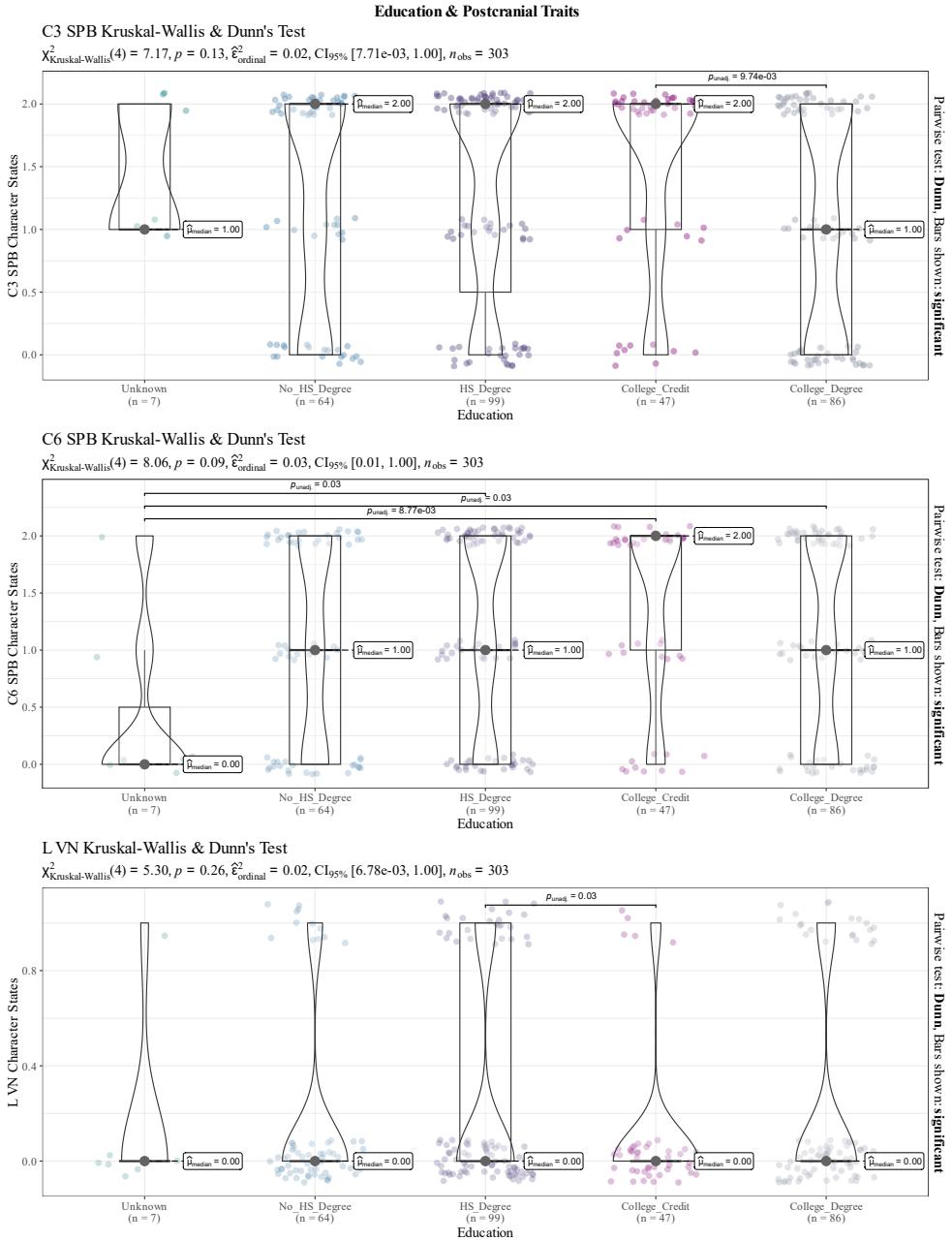

Figure 4.10 Boxplot & violin plot showing the distribution of significant postcranial MMS traits among education groups, with statistical analysis using Kruskal-Wallis test. The horizontal p-bars shown at the top of the plot illustrate which groups are significant via Dunn's post hoc test for multiple comparisons.

The results from the Mann-Whitney U test for sex (Figure 4.11) reveal significant differences between males and females for the left and right septal aperture and vastus notches.

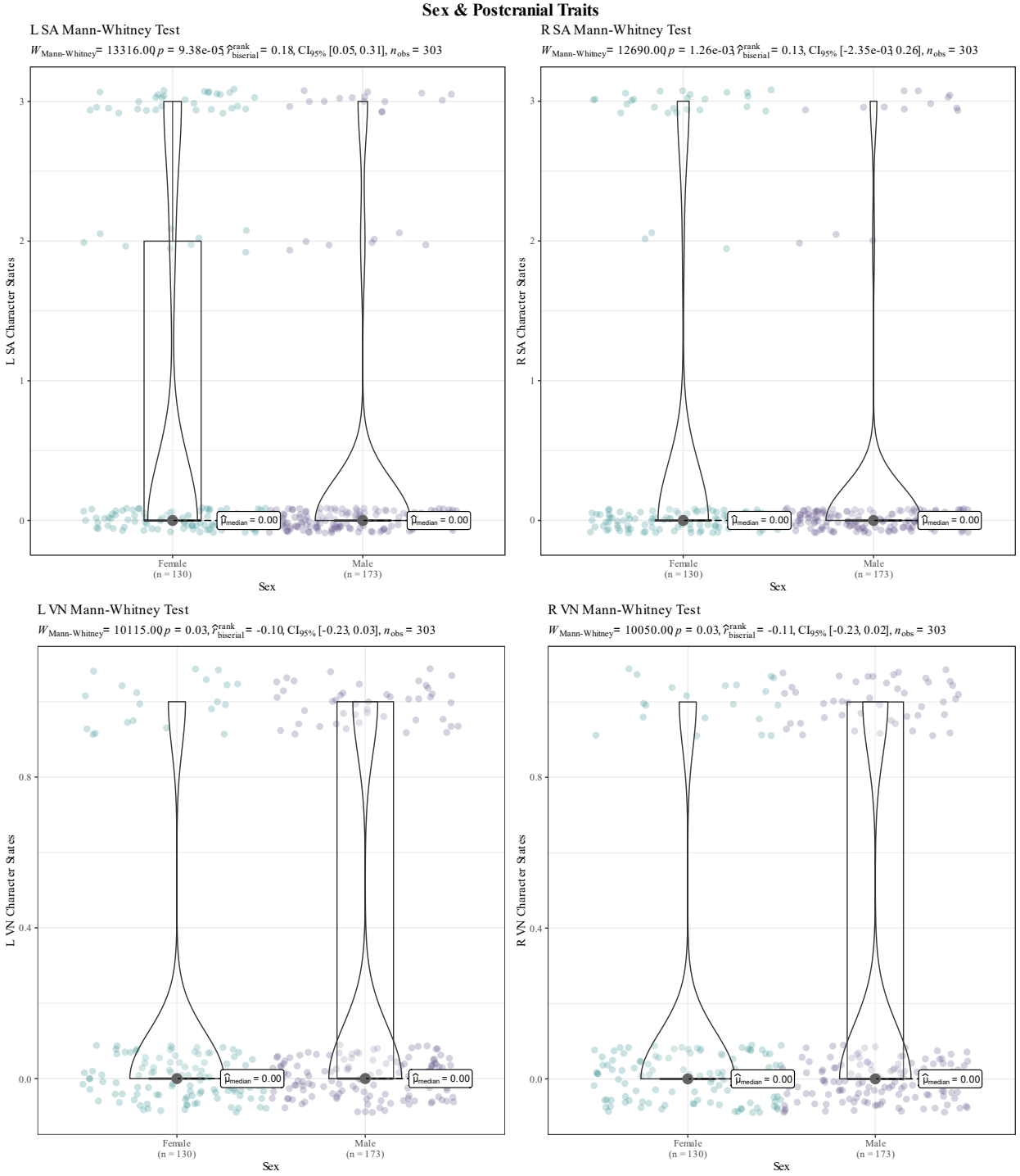

Figure 4.11 Boxplot & violin plot showing the distribution of the significant (α = 0.05) postcranial MMS traits between the sexes with statistical analysis using the Mann-Whitney test.

Adult SES was not included in the MANOVA due to prioritize significant interactions. Overall, the MANOVA found no significant interactions (Traits ~ Social Race*Child SES*Education Level). *Post hoc* univariate ANOVA analyses were run for every individual trait with 2 and 3-way interactions. All univariate tests showed no significant interactions.

DISCUSSION

By first investigating social race, SES, education, and sex without regard to the postcranial variation, we explore connections within the sample and assess how these variables are associated. The chi-square results found significant associations, except for sex which was only significantly distributed by social race. The only significant differences in postcranial morphology and sex are the left septal aperture ($p < 0.0001$), the right septal aperture ($p < 0.0001$), the left vastus notch ($p = 0.03$), and the right vastus notch ($p = 0.03$).

The strongest effect between groups is adult and childhood SES. While there is a significant shift between the groups, the test of equality of proportions identified no significant differences in SES among levels of SES from childhood to adulthood. The strong difference between education and adult SES demonstrates individuals with different levels of education attain significantly different levels of socioeconomic status in adulthood. The next greatest interaction, social race and childhood SES, highlights the inequity at an economic level beginning in childhood. A parent's educational attainment is likely a better marker for the effects of SES than even income alone, highlighting generational wealth and systemic racism. Although this is the strongest effect between social race and the other categories, all aspects of SES levels (childhood SES, adult SES, and education) are statistically significant in this sample. The correlation association suggests a potential continuity in socioeconomic status from childhood into adulthood, understandably, though the correlation is not significant and thus both variables are explored.

Although other correlations lack significance, this finding underscores the importance of understanding the relationship of socioeconomic status across an individuals' lifespan.

In New Mexico, the population sociodemographic composition by social race is: Hispanic (50.2%), White (not Hispanic/Latino) (46.4.7%), American Indian/Alaska Native (9.2%), and Black/African American individuals (2.1%) (U.S. Census, 2022). American Indian/Alaska Native individuals had the lowest median income at ca. $43,317, Hispanic/Latino individuals ($52,568), followed by Black/African American individuals ($55,344), and then the White (not Hispanic/Latino) individuals ($66,903) (U.S. Census, 2022). The highest percentage of "No high school diploma" were Hispanic/Latino (19.1%) and Native American (15.6%), those with a "high school degree" were Hispanic/Latino (31.8%) and Native American (31.4%) individuals, for "some college credit or associate degree" included Black/African American individuals (40.5%), and for "bachelor's degree or higher" were White individuals (39.8%) (U.S. Census, 2022). These patterns are also identified in the MCA analyses of the sociodemographic variables without the postcranial morphology. So, once the postcranial MMS data are incorporated, we can explore potential connections between trait expression (i.e., frequency distributions) and these sociodemographic variables. Those connections can then be compared to the *a priori* hierarchical clustering, Kruskal-Wallis, and Dunn's tests.

The hierarchical clustering highlighted the laterality between traits. All of the cervical vertebrae traits were closely connected, with the exception of the atlas accessory transverse foramen and the C2 spinous process bifurcation. The majority of spinous processes of the second cervical vertebra are completely bifid which may be why this is the only cervical vertebra not clustering with the others. On the whole, this highlights that the etiology of the clustered traits may be associated and should be further explored.

When incorporating postcranial MMS traits in the multiple correspondence analysis (MCA), the first dimension broadly separates Hispanic/White, college-educated, upper-class females from Native American/Black, lower class, less educated males. The second dimension separates White, college-educated, upper-class males from everyone else. Overall, the biplot illustrates the intricate relationships between the MMS traits and sociodemographic variables, illuminating their positioning and associations within the analyzed dataset.

All the postcranial MMS significant influenced by either education or SES were also significant for social race. Interestingly, the traits that were significant for social race and childhood SES (C5-C6 accessory transverse foramen, C4 spinous process bifurcation, and the right vastus notch) do not correspond to the traits that were significant for social race and education (C3/C6 spinous process bifurcation and the left vastus notch). However, the only significant difference identified for C6 spinous process bifurcation was the "unknown" education group, which had a relatively small sample size (n = 7). Significant differences in postcranial MMS trait expressions were identified among the social race groups for the C5 spinous process bifurcation, right septal aperture, and right third trochanter, suggesting a genetic or evolutionary processes related to climate, acclimatization, etc. could play a role in their expression (Plemons, 2022). Though there are no significant interactions between sex and race/SES/education, between the chi-square association of race and sex and the significance of the septal apertures and vastus notches between the sexes, future exploration of these traits without pooling sex is necessary.

Posterior bridging, the atlas accessory transverse foramen, C2 spinous process bifurcation, and sternal aperture were the only traits not significantly different between social race, SES, education, or sex. These should be explored more fully to identify other potential reasons for the variability documented in future studies.

CONCLUSION

Studying social categories in relationship to biology and forensic anthropological approaches to population affinity is important, especially when studies confound race and SES-related health disparities. Patterns of embodiment in structural racism can be correlated in various postcranial MMS traits as variation within and between social races and SES and/or education. These include C5-C6 accessory transverse foramina, C3/C4/C6 spinous process bifurcation, and both vastus notches. C5 spinous process bifurcation, right septal aperture and the right third trochanter show significant differences between social race alone. This does not mean that social race is biological in relation to these three traits, rather there should be further exploration of all postcranial traits in an evolutionary model related to geographic ancestry, climate, genetic flow, and genetic drift.

SES and education are the only two variables related to the health-wealth gradient being explored; as such, other measures of wealth, health, and inequality should be explored. Further studies of environmental impacts socially and evolutionarily are necessary to tease out some of the other possible confounding factors. With access to novel databases such as the NMDID, forensic anthropologists can more accurately, and to a more specific degree, understand societal impacts on bone. Overall, the goal is to better understand what influences the variability of skeletal morphology. Whether that is evolutionary processes of climate impacts and migration correlated with geographic ancestry or structural violence influencing the health of groups of individuals and, thus, the production (or lack thereof) of bone in certain patterns, this paper shows that there is a call for a more comprehensive approach of mixed-methods to incorporate more multivariate, refined, multiregional approaches to understand the full picture of human variation across the human skeleton.

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CONCLUSION

The purpose of this dissertation was to determine how biological and cultural factors influence and interact with the expression of postcranial morphology using a series of 11 traits I previously outlined for use in forensic anthropological research. These traits have been used for decades, but without a deeper understanding of why they are expressed in some individuals but not in others. To understand how (and when) they develop, this dissertation approached their analysis in terms of 1) human variation and population history, through a combined cranial and postcranial MMS trait approach to assess population affinity; 2) secular change through an exploration of two US samples from different temporal periods; 3) growth and development using a sample of children and adults from the NMDID, and a, 4) biocultural model utilizing sociodemographic parameters as proxies for embodied inequity of wealth and health. These frameworks coincide to the four manuscripts generated for this dissertation.

Manuscript 1 ("Ancestry Estimation Using Cranial and Postcranial Macromorphoscopic Traits") explored the use of a mixed model approach to skeletal variation exploring both cranial and postcranial MMS traits concomitantly. To test the applicability of the traits in a forensic context, I explored various classification models to assess which multivariate statistical framework would allow the highest classification between two U.S. populations while remaining stable. This manuscript highlighted that the artificial neural network was the more robust model due to high accuracy and low bias. This model was incorporated into a web-based application to facilitate analysis when the reference groups are appropriate for the case context. At the time of submission of this dissertation, Manuscript 1 ("Ancestry Estimation Using Cranial and Postcranial Macromorphoscopic Traits") has been published in the Journal of Forensic Sciences (Spiros & Hefner, 2020).

Manuscript 2 ("A Heuristic Approach to The Duray Method: Validation and Modern Refinement") explored the impact of time on the plasticity of the human skeleton. With the importance of methodological validation, reliability, and application of statistical frameworks in the forensic context, this manuscript validated the utilization of spinous process bifurcation of the cervical vertebrae in 19th century, 20th century, and unknown cohorts building on the Duray and colleagues (1999) model. Studying the temporal shift of the frequency data from one century to the next, there is evidence for secular change though not significant enough to not utilize this method for estimating population affinity in a case.

For Manuscript 3 ("Ontogenetic and Puberty Influences on Postcranial Morphological Variation"), the goal was to assess the growth and development of the postcranial MMS traits and how puberty might impact their emergence. Scoring the traits for 646 individuals ranging in age from 0 to 100 while simultaneously evaluating their pubertal stage at time-of-death, analyses show that trait stabilization is more appropriate for deeming when to score these traits rather than bone fusion alone. Though not all the traits were influenced by age and puberty, most traits can be scored once the individual has reached puberty with only four not developing until after puberty. Exploring these postcranial traits across age, puberty, sex, and social race cohorts provided insight into patterns that may inform the age-of-attainment for adult morphology for applicability within forensic methods as well as further understanding the impact of puberty on the skeletal system.

And finally, Manuscript 4 ("Embodiment of Biocultural Influences on Postcranial Skeletal Morphology") explores the influence of geographic ancestry and social race on the human body. Using the postcranial MMS traits, this manuscript addresses the question of how racism can be embodied in a data-drive, quantifiable manner. By looking at sociodemographic variables (social race, SES, and education) as proxies for geographic ancestry and/or systemic racism, this

manuscript identifies which traits are significantly different between various sociodemographic variables. All traits that are significantly different between either education or SES were also significant between social races highlighting the fact that embodied racism could be the initiating factor for the development of these traits whether that is due to lack of resources (e.g., nutritional deficiencies) or sociocultural stressors affecting the body through the lifetime causing or inhibiting bone to form in a specific way rather than a neutral selection or climatic/environmental impetus for change.

Morphological research is important to understanding the intrinsic and extrinsic factors that influence the human body. These manuscripts are relevant not only for forensic anthropologists to explore beyond the four-pillar biological profile paradigm, but also lends to further explorations through interdisciplinary lens of evolutionary biology, sociocultural studies, and public health initiatives. These manuscripts demonstrate how the application of mixed models and machine learning algorithms (manuscript one) more effectively capture and model morphological variation; how secular change (manuscript two) and ontogeny & puberty (manuscript three) impact the distribution and expression of that variation, and how biological anthropologists can utilize biocultural factors (manuscript four) to generate a more robust theoretical explanation of modern human variation.