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The Evaluation and Refinement of Nonmetric Sex and Ancestry Assessment Methods in Modern Japanese and Thai Individuals

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To the Graduate Council:

I am submitting herewith a dissertation written by Sean D. Tallman entitled "The Evaluation and Refinement of Nonmetric Sex and Ancestry Assessment Methods in Modern Japanese and Thai Individuals." I have examined the final electronic copy of this dissertation for form and content and recommend that it be accepted in partial fulfillment of the requirements for the degree of Doctor of Philosophy, with a major in Anthropology.

Dawnie W. Steadman, Major Professor

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The Evaluation and Refinement of Nonmetric Sex and Ancestry Assessment Methods in Modern Japanese and Thai Individuals

A Dissertation Presented for the
Doctor of Philosophy
Degree
The University of Tennessee, Knoxville

Sean D. Tallman
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ABSTRACT

Effective biological profiles in forensic anthropology and bioarchaeology depend on the development, validation, and refinement of population-specific methods. However, most methods were developed in North America on individuals of African and European descent, and it is unlikely that such methods can generate accurate biological profiles for Asian individuals. Moreover, Native Americans have served as biological proxies for Asians due to their distantly shared genetic history, resulting in largely untested assumptions that Native Americans and Asians are homogenous and share nonmetric sexually dimorphic skeletal features and a unique suite of cranial traits that can be used in ancestry assessment.

This study explores nonmetric sexual dimorphism and cranial nonmetric variability in 1,397 modern Japanese and Thai individuals 17 to 96 years of age. The first objective tests and refines the methods based on 15 traits used to predict sex from the cranium, pelvis, clavicle, and humerus that were developed on non-Asian populations. The second objective establishes 37 cranial and mandibular trait frequencies to determine if the Japanese and Thai differ from each other and from Native Americans in trait expressions. Further, the affects of sex, age, population, inter-trait correlations, intraobserver error, and secular change on the traits are assessed.

The results indicate that population-specific sex assessment methods perform better in classifying the Japanese and Thai compared to those developed on non-Asian populations, producing correct classification rates of 66-98%. Additionally, the majority of cranial and mandibular traits used in ancestry assessment significantly differ in frequency between the Japanese and Thai, resulting in correct classification rates of 60-90%. Further, the Japanese and Thai are different from Native Americans in the expression of nonmetric traits. However, sex, age, population, intraobserver error, and secular change affect many nonmetric traits, thereby complicating their use in sex and ancestry assessment.

This study demonstrates that the Japanese, Thai, and Native Americans are not skeletally homogenous, as they exhibit differences in sexual dimorphism and in the expression of cranial trait frequencies due to unique population histories. Moreover, the findings of this research underscore the importance of developing population-specific biological profile methods for diverse Asian populations, such as those provided here.

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CHAPTER I: Introduction

Subsequent to deaths resulting from natural disasters, armed conflicts, and homicides, the identification of decedents is paramount and depends upon the accuracy of the scientific methods employed in the biological profile (Hunt and Albanese 2004; Komar and Buikstra 2008; Komar and Grivas 2008). Accurate biological profile methods require that they be developed, validated, and refined on contemporaneous skeletal assemblages that share a genetic history with the decedents. Most biological profile methods were developed in North America on individuals of African and European descent, and therefore it is unlikely that such methods accurately determine biological profiles for modern-day Asian individuals. Further, data from Native American skeletons have been utilized to represent Asian populations, resulting in the largely untested assumption that Native Americans and all Asian groups are skeletally similar in their sexual dimorphism and cranial trait expressions that are used to ascertain sex and ancestry. As such, Native American and Asian populations have been viewed as skeletally homogenous, despite significant differences in population histories. The continued reliance on methods developed from non-Asian populations is especially problematic in forensic contexts where Asian remains are likely to be recovered, including large western U.S. cities where significant populations of East and Southeast Asians reside, and in mass disasters (i.e., tsunamis, earthquakes, typhoons, armed conflicts, aircraft crashes).

The development and refinement of accurate biological profile methods requires documented skeletal collections consisting of contemporary individuals of known sex, age, ancestry, and stature. In order for the biological profile methods to be applicable to forensic contexts within a particular population, the methods should be developed from skeletal assemblages that are contemporaneous and share a genetic history with the population from which the unknown individuals originate. However, most biological profile methods currently used in skeletal biology were developed and refined in North America using documented skeletal collections established in the late 19th and early 20th centuries (Komar and Buikstra 2008). The Terry and Hamman-Todd collections are two of the most heavily studied of the 12 documented skeletal collections currently available for research in the U.S. and Canada, and consist of individuals who were largely born during the 1800s. While numerous important biological profile methods were developed on these collections (e.g., DiBennardo and Taylor 1983; Giles and Elliot 1962, 1963; Klales 2016; Klales *et al.* 2012; Osborne *et al*. 2004; Phenice 1969; Todd 1920), it has been demonstrated that phenotypic differences exist between individuals originating from the 1800s and modern populations. In particular, cranial morphology, limb proportions, and stature differ significantly between these two time periods (Jantz 2001; Jantz and Meadows Jantz 2000; Klales 2016; Meadows and Jantz 1995; Meadows Jantz and Jantz 1999; Ousley and Jantz 2005). These population differences affect the accuracy of biological profile methods and underscore the importance of developing contemporary population-specific methods.

The ancestral composition of the collections historically available for skeletal biology research largely reflects the demographics of North America prior to the 1950s (Komar and Buikstra 2008). The collections are comprised mainly of individuals of African and European descent, and thus, most biological profile methods were developed on these two ancestral groups. Until fairly recently, large samples of documented Asian skeletons were not available to Western researchers, so it was impossible to test whether the methods developed on individuals of

African and European descent can generate accurate biological profiles for Asian individuals. As such, this research applies nonmetric visual sex assessment methods to adults in documented anatomical collections in East (Japan) and Southeast (Thailand) Asia, and establishes nonmetric cranial trait frequencies in order to determine their utility in sex and ancestry assessment for these two Asian groups.

Sex estimation is one of the most important components of the biological profile as it dictates the methods used later in the assessment of age, ancestry, and stature. Sex can be accurately determined through the visual assessment of robust or gracile features present on the pelvis and cranium. Sexually dimorphic features are normally assigned an ordinal score that indicates gracile ("female-like") or robust ("male-like") morphology (Buikstra and Ubelaker 1994; Klales *et al*. 2012; Walker 2008). In the absence of the pelvis and cranium, skeletal biologists can nonmetrically asses other postcranial elements to determine sex, including features on the clavicle and distal humerus (Rogers 1999; Rogers *et al.* 2000; Vance *et al.* 2011). These regions are important because they are often preserved in highly fragmentary and incomplete cases. These cranial and postcranial nonmetric sex assessment methods are applied to numerous populations throughout the world; however, they were developed largely on individuals of African and European descent, and little work has tested their efficacy on Asian populations. Consequently, the application of current visual sex assessment methods to Asian remains may misclassify individuals, thereby hindering or preventing identifications in forensic contexts and skewing demographic data in bioarchaeological contexts.

Nonmetric ancestry assessment is often considered the most difficult, least accurate, and most subjective of the biological profile methods; however, forensic anthropologists are frequently expected to provide information on a decedent's most likely ancestral origins. "Race" (i.e., Black or White) may indicate an individual's sociocultural group membership, and is often reported through family members in missing-person's reports. Conversely, the anthropological assessment of ancestry for skeletonized remains is a biogeographical estimate that reflects the genetic origin of population variation (Konigsberg *et al.* 2009; Relethford 2009). Group similarities and differences in cranial and postcranial morphometrics can be attributable to micro-evolutionary processes (i.e., genetic drift, gene flow, mutation, and selection) in human populations (AAPA 1996; Konigsberg *et al.* 2009; Relethford 1994, 2009). While studies have demonstrated that the entirety of human cranial morphological diversity cannot be explained by genetic inheritance alone, the vast majority of the cranial morphometric studies indicate that there is a significant correlation between genetics and cranial morphology (Berry and Berry 1967; Cheverud 1988; Hartl and Clark 2007; Relethford 1994). Individual traits may have adaptive significance; however, on a multivariate level, craniofacial morphology reflects genetics (Relethford 2009). Cranial morphometric variables are inherited from generation to generation and reflect genetic relationships that are geographically clustered (Brace *et al.* 2001). Other, adaptive features associated with air conditioning (nasal region) and mastication (mandible) may also pattern geographically (Berg 2008; Guglielmino-Matessi *et al.* 1979; Parr 2005, 2006; Yokley 2009). Thus, ancestry can be ascertained through the visual assessment of nonmetric cranial traits within a statistical framework, and/or by statistical analyses of cranial and postcranial measurements.

The first objective of this study is to address the following questions: How do the nonmetric sex assessment methods using the cranium, clavicle, humerus, and pelvis that were developed on individuals of African and European descent perform in classifying Japanese and Thai individuals of known sex? Further, will the statistical refinement of the cranial and postcranial sex assessment methods provide more accurate classification rates for individuals of East and Southeast Asian origin? Sexually dimorphic regions on the cranium, clavicle, humerus, and pelvis were assessed visually and assigned an ordinal score based on their robust or gracile expression. The scores and documented sexes were analyzed statistically to identify the traits that best indicate female or male, while also testing the hypotheses that these two Asian populations exhibit sexually dimorphic differences when compared to each other, and reduced sexual dimorphism when compared to non-Asian groups.

The second objective of this project is to address the following questions: How do the cranial trait expressions and frequencies identified in pre-contact Native American skeletal remains perform in classifying contemporary Japanese and Thai individuals as is commonly practiced today? In the absence of Asian populations available for study in North America, skeletal biologists used data gathered from pre-contact Native American assemblages to define a suite of cranial traits expected to be present in Asians (Bass 1995; Gill 1998; Rhine 1990). Cranial trait shapes are typically scored by the degree of expression or presence/absence, and are used to differentiate three very broad biogeographic ancestries: African, Asian, and European (Bass 1995; Gill 1998; Rhine 1990). Therefore, this project investigates the frequencies of the cranial and mandibular traits used in identifying Native Americans in modern Japanese and Thai individuals, and to determine if differences exist in the trait frequencies and expressions between Japanese and Thai individuals. The nonmetric cranial traits commonly used to identify Native Americans were ordinally or dichotomously scored following Hefner (2009, 2012), Rhine

(1990), and Parr (2006) to test the hypothesis that Japanese and Thai individuals differ from Native Americans and each other in their trait expressions and frequencies.

The continued refinement of nonmetric sex and ancestry assessment methods is of utmost importance in the current judicial climate, which is dictated by the *Daubert* ruling of 1993 and requires rigorous testing of scientific methods (U.S. Supreme Court 1993). Thus, as highlighted in the National Research Council's (2009) report on the state of forensic science, it is necessary to develop more quantifiable, reliable, and objective visual assessment methods that can be used to satisfy this ruling. Therefore, this research will provide revised, population-specific methods to improve the accuracy in identifying individuals belonging to East and Southeast Asian groups.

Hypotheses

The purpose of this study is to: a) Statistically test and refine the cranial and postcranial nonmetric sex assessment methods developed from individuals of African, European, and Native American descent on documented modern Japanese and Thai individuals; and b) Through the establishment of cranial trait frequencies, determine if the nonmetric cranial trait expressions and frequencies believed to be useful in identifying Native Americans are present in and/or different between Japanese and Thai individuals. To achieve these goals four hypotheses will be tested:

1. Differences in the nonmetric expression of sexual dimorphism exist between Japanese/Thai individuals and non-Asian groups such that the sex assessment methods developed on individuals of African, European and Native American descent will not accurately classify Japanese or Thai individuals. If this hypothesis is supported, the methods developed on non-Asian populations will

not be advocated for Japanese and Thai individuals specifically, and Asian populations more generally.

2. Differences in the nonmetric expression of sexual dimorphism exist between Japanese and Thai individuals. If this hypothesis is supported, then these two Asian groups should not be considered homogenous, and separate nonmetric sex assessment methods will be established for Japanese and Thai individuals. If this hypothesis is not supported, pooled Japanese and Thai methods will be established.
3. Differences in nonmetric cranial and mandibular trait expressions and frequencies used in ancestry assessment exist between Japanese and Thai individuals. If this hypothesis is supported, then inter-group variation exists among these two Asian populations, and cranial trait frequencies and associated statistical models will be established separately for the Japanese and Thai individuals.
4. Differences in the nonmetric cranial and mandibular trait expressions and frequencies exists between Japanese/Thai and Native American individuals, such that the traits used to identify pre-contact Native Americans will not accurately classify contemporary Japanese or Thai individuals in forensic contexts. If this hypothesis is supported, pre-contact Native Americans should not be used as biological proxies for modern Japanese or Thai individuals.

Organization of Chapters

Chapter II of this study discusses the theoretical and methodological approaches to studying and understanding sex and ancestry within biological anthropology. In particular, the morphological approaches to sex estimation are discussed for the cranium, pelvis, clavicle, and humerus, as are the biological underpinnings that contribute to sexual dimorphism for these traits. Additionally, this chapter covers the history of the typological race concept within physical anthropology and the emergence of modern biogeographic perspectives on ancestry. Further, the factors that contribute to cranial nonmetric morphological variability and how nonmetric traits are employed in forensic biogeographic ancestry assessment are highlighted. Chapter III briefly discusses the population histories of Japan and Thailand, emphasizing the markedly different migrations and environmental factors that contribute to the genetic make-up of modern Japanese and Thai individuals. Subsequently, the methodology of this study is discussed in Chapter IV, including: the Japanese and Thai skeletal collections, the nonmetric ordinal scoring procedures, and the statistical procedures used in the analysis of the nonmetric traits. Chapter V presents the results of the statistical analyses for the sexually dimorphic cranial, pelvic, clavicular, and distal humerus traits, as well as the results for the cranial and mandibular ancestral traits. Chapter VI discusses the results of the statistical analyses, particularly addressing whether the results support or reject the five hypotheses presented in this chapter. Additionally this chapter discusses the affects of age, sex, population, inter-trait correlations, intraobserver error, and secular change on the expression of sexually dimorphic and biogeographical ancestry traits. Lastly Chapter VII discusses the broader implications of this study, including how the results satisfy the *Daubert* criteria. This final chapter concludes with a brief discussion regarding the potential future directions of research aimed at understanding sexual dimorphism and ancestry differences within and between diverse Asian populations.

A Note on Terminology

The terms Caucasoid, Mongoloid, and Negroid were first used to denote biological and behavioral/cultural differences between worldwide populations, and were used by early 19th and 20th century physical anthropologists and anatomists to rather simplistically and oftentimes wrongly classify and explain human population variation (e.g., Coon 1939; Coon *et al.* 1950). The suffix "-oid" was used to represent specific and expected craniofacial forms and body types, largely irrespective of geography: Caucasoid categorized Europeans and light-skinned North Americans; Mongoloid categorized Asians, Native Americans, and Pacific Islanders; and Negroid categorized Africans and dark-skinned North Americans. Due to the racist, typological, and hierarchical connotations that are inherent in these antiquated and harmful terms, they were replaced over time by a mix of skin color and geographic terms (i.e., White, Asian, and Black), and are seldom, if ever, used in modern anthropological perspectives (e.g., Gill 1998; Klales 2016; Klales *et al.* 2012). However, the use of Black and White reduces population variation mainly to skin color, which fails to explain variation that arises from unique population histories and reinforces the oft-perceived myth that forensic anthropologists can determine skin color, hair texture, and eye form through skeletal analyses (Brace 1995). Further, the definitions of Black and White have changed over the years due to evolving folk taxonomies that conflate biology and culture (Edgar 2009; Watkins 2012). Such changes are due in part to the observation that racial terms, such as Black and White, elicit differing emotional responses from people, and each person imposes their own definition of what the terms mean (Montagu 1962). In response, anthropologists somewhat more recently began employing biogeographic and biocultural ancestral terms such as African, African American, European American, Hispanic, and Native American, in addition to myriad other geographically centered group labels (e.g., Hefner 2009; Hefner *et al.* 2014; Ross *et al.* 2004; Spradley *et al.* 2008).

While not perfect, the current use of biogeographic nomenclature is more useful and scientifically valid than those based on skin color because they explicitly or implicitly incorporate underlying micro-evolutionary, genetic, adaptive, and biomechanical processes that contribute to differences between populations and are potentially reflected in skeletal morphology. Terminology aimed at grouping human populations has been and will continue to be important in anthropological studies. Consistencies in terminology extend beyond simple semantics, as the way in which anthropologists group and supposedly define human populations have ramifications for the way in which the society and culture where we live and conduct research conceptualizes similarities and differences within and between groups. Accordingly, anthropologists should take the lead and serve as role models for the more accurate and meaningful use of ancestral terms. While this study adopts a biogeographic perspective on ancestry and uses geographically oriented terminology in explaining human groups, the terminology used by previous researchers in studies of sex and ancestry is maintained to avoid potentially wrongful assumptions regarding past researchers' perspectives on ancestry, and to accurately convey the original research parameters

CHAPTER II: Sex And Ancestry Assessment In Biological Anthropology

This chapter discusses the role of sex and ancestry estimation in the biological profile largely from a historical perspective, highlighting the significant events, theories, studies, and methods that have contributed to modern perspectives. The first section addresses the morphological and metric methods used in the estimation of sex from skeletal remains, focusing on the methods developed on the cranium, mandible, pelvis, humerus, and clavicle. The second section briefly addresses the history of ancestry or race in physical and forensic anthropology, the biological basis for skeletal variation, and modern perspectives on ancestry and population variation. The last section of this chapter discusses the need for Asian-specific biological profile methods, as Asian populations have largely remained understudied in biological and forensic anthropology.

Sex Estimation

The first objective of this study is to assess how the nonmetric visual sex assessment methods using the cranium, clavicle, humerus, and pelvis that were developed on individuals of African and European descent perform in classifying Japanese and Thai individuals of known sex. Further, the cranial and postcranial sex assessment methods will be refined to provide more accurate classification rates for individuals of East and Southeast Asian origin. Sex estimation is one of the most important components of biological profile method because it dictates the methods used later in the assessment of age, ancestry, and stature.

Homo sapiens is the least sexually dimorphic species of primates, with the sexes sharing about 95% of variation; however, detectable metric and morphological differences exist between female and male skeletons. Because females and males each represent roughly 50% of the population, identifying the sex of a skeleton within a forensic context excludes a significant portion of the population. Within bioarchaeological contexts, the accurate assessment of sex enables the establishment of demographic profiles. Therefore, sex determination has played an important role in biological and forensic anthropology, and numerous metric (Krogman and İşcan1986; Stewart 1979), morphological (Rogers 1999, 2005; Rogers *et al.* 2000; Walker 2005, 2008), and geometric morphometric (Garvin and Ruff 2012; Kimmerle *et al*. 2008) methods have been developed. As a result, nearly every skeletal element has been studied to determine if metric or morphological differences exist between females and males.

The emergence of sexually dimorphic features of the skeleton, which are considered secondary sex characteristics, coincides with the production of sex hormones during puberty and the adolescent growth spurt (Bogin 1999; Scheuer and Black 2004). In particular, the onset of puberty (~8 – 12 years in females; 9 – 14 years in males) is marked by a significant increase in gonadotropin-releasing hormone and gonadotropin secretion, which is maintained throughout puberty (Grumbach 2002). The timing of puberty is partly under genetic control, and certain regions of the body, such as the pelvis, are under more genetic control than others (Fazekas and Kosa 1978; Stinson 2012). However, because secondary sex characteristics occur relatively late in development, they are susceptible to environmental or extrinsic factors, including biomechanical loading, nutrition, and activity patterns (Bogin 1999; Solorzano and McCarthey 2010). For example, populations experiencing nutritional deficiencies exhibit slower maturation rates and reduced sexual dimorphism compared to populations with adequate nutrition (Stinson 1985, 2012). Gonadarche, or the timing of testicular enlargement in males, coincides with testicular androgen production and is followed by the masculinization of the musculoskeletal system (Solorzano and McCarthey 2010). Because males significantly diverge from females in the musculoskeletal form at this time, reduced nutrition can hinder the production of sex hormones and lead to the reduced male secondary sex characteristics. Further, females are better protected from extrinsic factors than males due to buffering, which is hypothesized to prepare females for the stresses and demands of childbirth (Charisi *et al*. 2011; Frayer and Wolpoff 1985; Stinson 1985). As such, populations may go through puberty at different times, and these differences can be attributed to differing ontogenic trajectories, population and individual health, time period, and secular change.

Generally, it is maintained that sex can be determined from the overall shape of the pelvis if the pelvis is actively fusing or fused, which occurs around 14 years (Scheuer and Black 2005). However, other features develop later. In particular, a precursor to the ventral arc can be seen as early as 14 years, but the actual ventral arc generally fully develops in the early 20s (Sutherland and Suchey 1991). While subadult methods for skeletal sex determination have been explored, their results are mostly negligible. As such, anthropologists generally agree that skeletal sex cannot be reliably determined prior to the onset of puberty (Baker *et al.* 2005).

Due to the reduced sexual dimorphism exhibited in modern humans, much overlap exists in morphological and metric features between females and males. Despite this, it is generally maintained that on average males are absolutely and relatively larger than females due to larger muscle mass and/or the longer duration of growth experienced by males (Janssen *et al.* 2000; Wood 2011). However, small males can be more consistent metrically or morphologically with females, while large females can be more consistent metrically and morphologically with males (Spradley and Jantz 2011; Walker 1995, 2005, 2008). Additionally, certain regions of the body may be more sexually dimorphic than others. For instance, the humeral and femoral head diameters can show 20 – 30% difference between females and males (Stewart 1979; Berg 2012). Other regions, such as the calcaneus, are less helpful in sex determination in certain populations (Spradley and Jantz 2011).

Metric sex estimation

Metric methods for determining sex are frequently used in anthropology because they are often derived from the standard cranial and postcranial measurements that researchers have been documenting since the inception of the discipline (Buikstra and Ubelaker 1994; Jantz 1994; Moore-Jansen *et al.* 1994). Metric estimation can be based on univariate statistics, where sectioning or cutoff points for single measurements can provide relatively quick and easy estimates of sex (Krogman and İşcan1986; Stewart 1979). Alternately, sex determination based on multiple measurements used in conjunction can be analyzed using multivariate statistics such as linear regression or discriminant function analysis (France 1998; Ousley and Jantz 2005; Slice and Ross 2009). As such, metric methods are amenable to statistical manipulation, are easy to teach and learn, and exhibit relatively low intra- and inter- observer error rates (Adams and Byrd 2002). Additionally, metric approaches to sex estimation are generally accompanied by accuracy rates, probabilities, and error rates that help to satisfy the *Daubert* criteria (U.S Supreme Court 1993).

Sex has been reliably determined from the cranium using multiple measurements and discriminant functions since the 1960s (Giles and Elliot 1963; Holland 1986; Ousley and Jantz 2005). Anthropologists have long believed that the cranium is the second best predictor of sex after the pelvis, despite evidence suggesting that postcranial measurements perform better than cranial analyses (Bass 2005; Byers 2002; France 1998; Pickering and Bachman 1997; Spradley and Jantz 2011). This may be partly attributed to the historic importance that anatomists and anthropologists placed on the cranium since the 1700s, which was codified by the influential founding members of forensic anthropology including Hrdlička (1939), Krogman and İşcan (1986), and Stewart (1979). Spradley and Jantz (2011) tested this long-held assumption on American Black and White females and males from the Forensic Data Bank (FDB) using standard cranial and postcranial anthropometrics to compare cranial and postcranial sex classification results. Individuals born after 1930 were chosen for the study to mitigate the issue of secular change, a process that has been documented in Black and White Americans during the last 150 years (Jantz 2001; Jantz and Meadows Jantz 2000). Discriminant function analyses of the cranium resulted in cross-validated correct classification rates between 90% and 91%, while those of the postcranium resulted in 92% to 94% correct classification rates (Spradley and Jantz 2011). Overall, measurements of the joint surface provided the best discrimination, and measurements of the calcaneus were the only ones that failed to discriminate. Further, Spradley and Jantz (2011) found that Black individuals exhibit greater sexual dimorphism compared to

White individuals. Thus, knowledge of the decedent's ancestry can improve the accuracy of sex estimation methods.

Traditional morphological sex assessment

While sex can be accurately determined through the measurement of numerous cranial and postcranial elements (France 1998; Spradley and Jantz 2011), sex is most often determined in relatively complete individuals through the visual assessment of robust or gracile features present on the pelvis (Buikstra and Ubelaker 1994; Phenice 1969). The pelvic traits that are useful in sex assessment are morphologically different between females and males due to the female capacity for childbirth (Bass 1995; Phenice 1969; White *et al.* 2012). Subsequent to puberty, the female pelvis expands to accommodate childbirth, while the male pelvis retains the pre-adolescent morphology, resulting in morphometric differences between females and males. These growth differences result in a wider and more flared pelvis in females, and a narrow and constricted pelvis in males. Additionally, the sacrum is wider with minimal anterior curvature in females, while in males the sacrum is narrower and exhibits more anterior curvature. Accordingly, females exhibit a relatively larger pelvic outlet, even though males may exhibit larger and more robust pelvic bones.

The most useful areas to determine sex in the pelvis were documented by Phenice (1969) in the anterior pubic area, and include the ventral arc, subpubic concavity, and ischiopubic ramus ridge. In his study of 275 females and males from the Terry Collection, Phenice found that females generally exhibit an angled ventral arc, a large subpubic concavity, and a narrow ischiopubic ramus ridge, while males generally exhibit a wide ischiopubic ramus ridge, a slightly raised and straight ridge instead of a ventral arc, and no subpubic concavity. Used together, Phenice found that the pubic traits exhibit 95% accuracy in determining sex, and each trait can be used individually with slightly decreased accuracy. While Phenice simply noted the presence or absence of the trait, Buikstra and Ubelaker (1994) present ordinal scoring systems for the Phenice traits from 1 (female) to 3 (male), with 2 representing an indeterminate category.

Numerous studies have tested the Phenice (1969) method on additional samples, and determined that the three traits perform well in predicting sex (Kelley 1978; Klales *et al.* 2012; Lovell 1989; Sutherland and Suchey 1987). While the scoring of the traits generally produces low intra- and inter-observer error rates regardless of experience level (Klales *et al.* 2012; Lovell 1989), the classification accuracies for these studies are somewhat lower compared to Phenice's results (Kelley 1978; Klales *et al.* 2012; Lovell 1989; Sutherland and Suchey 1987). Lovell (1989) attributes this to the possibly younger sample used by Phenice compared to other studies, though his age distributions are unknown. In particular, Lovell (1989) found that classification accuracy decreased in older individuals, and the ventral arc produced the most uncertainty due to irregular bone growth in the anterior pubic region that can characterize older individuals. Further, Kelley (1978) and Klales *et al*. (2012) argue that Phenice's present/absent scoring system fails to capture variation, as individuals can exhibit morphological intermediacy. In response, Klales *et al.* (2012) developed a five-point ordinal scoring system for each trait on 310 adult individuals from the Hamman-Todd and William M. Bass Donated Skeletal Collections. In testing their method, Klales and coauthors found that their ordinal scoring system and logistic regression equations correctly classified 86.2% of individuals. Moreover, probabilities can be calculated from their logistic regression equations, thereby satisfying *Daubert* requirements, which was not possible with Phenice's original method.

Two additional traits of the pelvis that are helpful in sex assessment include the sciatic notch and preauricular sulcus (Buikstra and Ubelaker 1994). The sciatic notch is related to the overall shape of the pelvic outlet; thus, the notch is typically open with a low width-to-depth ratio in females, while the notch is U-shaped and narrower with a high width-to-depth ratio in males (Walker 2005). The sciatic notch is scored from 1 (female) to 5 (male) based on diagrammatic representations presented in Buikstra and Ubelaker (1994). Accordingly, it has been traditionally held that a score of 3 represents an indeterminate morphology. However, Walker (2005) analyzed the sciatic notch scores of 296 individuals from the Hamman-Todd, Terry, and St. Brides collections and found that more males were observed with a score of 2, while around 90% of those with a score of 1 were female, and 90% those with a score of 3 or higher were male. As such, Walker suggests that a score of 2 indicates an "indeterminate" or a "probable male" classification depending on the amount of potential error the analyst is willing to introduce. When all individuals were included, Walker found that 80% of individuals were correctly classified using the sciatic notch alone. When individuals with a score of 2 were removed, however, the correct classification rate increased to 89%. Additionally, Walker found that English sciatic notches are wider than African and English born individuals living in America. Further, Walker found that sciatic notch scores and ages-at-death are correlated prior to approximately 50 years of age, especially in males. Individuals who died at a younger age typically had wider sciatic notches than those who died later in life.

The preauricular sulcus, a groove on the inferior margin of the auricular surface where the sacroiliac ligament attaches, is often wide and deep in females, and absent or small and narrow in males. A score of 0 indicates a lack of a preauricular sulcus, which is more commonly found in males, and scores of 1-4 indicate differing manifestations of the sulcus (Buikstra and Ubelaker 1994).

Although less reliable than the pelvis and long bone measurements, metric and nonmetric analyses of the cranium can be used to differentiate females and males, as males are generally robust compared to more gracile females (Buikstra and Ubelaker 1994; White *et al*. 2012). Sexual dimorphism of the cranium is attributed to the more intense and longer duration of cranial growth rate experienced by males, resulting in relatively and absolutely larger male skulls and features (Rogers 2005; Vidarsdottir and O'Higgins 2003; Vidarsdottir *et al.* 2003). While nearly 20 nonmetric features on the cranium have been shown to be sexually dimorphic (Rogers 2005; Williams and Rogers 2006), the features that have been found to be especially helpful in morphological sex assessment include the nuchal crest, mastoid processes, supra-orbital margins, glabella, and mental eminence (Acsadi and Nemeskeri 1970; Buikstra and Ubelaker 1994; Garvin *et al.* 2014; Stevenson *et al*. 2009; Walker 2008). Paul Broca first identified these five cranial traits in 1875 (Acsadi and Nemeskeri 1970; Garvin *et al.* 2014), and they are used in most sex assessment studies. Similar to the sciatic notch, sexually dimorphic features of the skull are normally assigned a score of 1 through 5, with 1 representing a typical female expression and 5 representing a typical male expression (Buikstra and Ubelaker 1994). In a perfect world, male crania exhibit a well-developed nuchal crest, large mastoid processes, blunt supraorbital margins, a protruding glabella, and a well-delineated mental eminence, while females exhibit a smoothened nuchal region, small mastoid processes, sharp supraorbital margins, a small glabella, and a smoothened mental eminence. However, in reality, much overlap exists in the expression of these traits.

In Walker's (2008) study of 304 African American, European American, and English-born individuals, he found that univariate statistics correctly classified individuals 69 – 83% of the time when the five cranial traits were applied independently. Generally, the mastoid process and glabella performed the best, while the nuchal crest and supraorbital margin exhibited reduced discriminatory power. However, population-specific logistic regression discriminant functions for pooled African and European Americans and ancient Native Americans resulted in 84 – 88% correct classification rates. Discriminant functions that incorporated multiple variables were superior to those that only incorporated two variables. Overall, this study demonstrates that ordinal scores for the five cranial traits achieve correct classification rates on par with metric analyses; however, population differences exist in the degree of sexual dimorphism expressed.

Garvin *et al.* (2014) applied Walker's scoring system to Arikara Native Americans, medieval Nubians, U.S. Blacks, and U.S. Whites to determine if population, body size (femoral head diameter and maximum femoral length), and age influence sexual dimorphism. Similar to Walker (2008), Garvin *et al.* 2014 found that the mastoid and glabellar regions provided the best univariate scores while the nuchal region performed less successfully. Overall, the individual traits provided correct classification rates of 63 – 79%. However, logistic regression discriminant function analyses increased the accuracy and produced correct classifications of 74 – 99% when the nuchal region was excluded. While age and body size are correlated with trait scores in Garvin *et al.*'s (2014) samples, these two variables do not significantly contribute to the logistic regression equations. However, population affiliation was found to significantly influence trait scores. Accordingly, Garvin and coauthors caution against using the arbitrarily defined indeterminate cutoff score of 3, as a significant proportion of each population would be incorrectly classified. This study further stresses the importance of developing population-specific sex assessment methods.

The pelvic and cranial scoring systems have been applied to numerous populations throughout the world; however, these methods were developed and tested largely on individuals of African and European descent (Rogers 2005; Rogers and Saunders 1994; Walker 2005, 2008; Williams and Rogers 2006). Further, significant differences in the degree of sexual dimorphism exist between populations, which affects the success of the scoring method (Garvin *et al.* 2014; Rogers and Saunders 1994). For instance, Walker (2005) found that the sciatic notch scores of English-born individuals differ significantly (more gracile) from Americans of African and European descent (more robust). Similarly, Walker (2008) found that the five sexually dimorphic skull traits correctly classified 88% of modern African American, European American, and English skulls, compared to 78% of ancient Native American skulls. However, it should be noted that Walker estimated the “correct” sex of the Native Americans through the assessment of pelvic features. Further, through the development of discriminant functions that use the visually assessed scores to identify the features and scores that best predict sex, Walker (2008) found that ancient Native Americans are less sexually dimorphic than modern African and European populations. Likewise, Guyomarc’h and Bruzek (2011) found that Thai individuals are less sexually dimorphic than French individuals when cranial measurements were analyzed with discriminant functions in FORDISC (Ousley and Jantz 2005). Further, İşcan *et al.* (1994, 1995) found that modern Japanese exhibit reduced sexual dimorphism compared to earlier Japanese populations based on cranial and tibial measurements, which they attribute to an increase in female size over time.

While it is clear that differences in sexual dimorphism exist between populations, little work has tested the efficacy of these pelvic and cranial nonmetric-scoring systems on Asian populations. Since sexual dimorphism in Asian populations is poorly understood, the use of current sex assessment methods may misclassify Asian individuals, thereby introducing error into later age, ancestry, and stature assessments. Therefore, it is critical for such methods to be rigorously tested and validated on additional populations.

Non-traditional morphological sex assessment

In the absence of the pelvis and cranium, skeletal biologists can examine the morphology of other postcranial elements to determine sex, including features on the clavicle and humerus. Importantly, these regions are often preserved in highly fragmentary and incomplete cases, including explosive mass fatality incidents (i.e., aircraft crashes), where the cranium and pelvis may be damaged. Rogers *et al.* (2000) examined whether a depression, or rhomboid fossa, on the medial clavicle can indicate sex in a sample of 344 Black and White clavicle pairs from the William F. McCormick Collection at the University of Tennessee in individuals who were 10 to 92 years old. The infero-medial clavicle serves as an attachment site for the costoclavicular or rhomboid ligament that connects the first rib to the clavicle and stabilizes the shoulder girdle. It is hypothesized that increased muscularity and mechanical usage can produce tubercles, depressions, and pitting on the clavicle where the costoclavicular ligament attaches. If no depression was present, or if there was a raised area of bone, Rogers and coauthors scored the fossa as absent. If pitting, grooving, or a small-large excavation was evident, the fossa was scored as present. Rogers *et al.* (2000) found that males exhibit a rhomboid fossa 36% of the time on the right and 31% of the time on the left clavicles, while females exhibit a fossa 8% of the time on the right and 3% of the time on the left clavicles. Additionally, they found that a rhomboid fossa on the left clavicle indicates male with a 92% posterior probability, while a fossa on the right indicates male with an 82% posterior probability. While age was not correlated with the presence of a rhomboid in all age groups, males 20 – 30 years old were more likely to display the largest fossae.

Rogers (1999) investigated whether morphological differences in the distal humerus can predict sex. It is thought that sex differences in the distal humerus are attributed to the lateral deviation of the forearm relative to the arm, or carrying angle in the living, whereby females exhibit a 20 – 25 degree angle and males exhibit a 10 – 15 degree angle (Rogers 1999; Vance *et al.* 2011). Accordingly, the carrying angle affects both soft and hard tissue structures. The ulnar collateral ligament, which originates on the medial epicondyle of the humerus and inserts on medial aspect of the coronoid process on the ulna, and the eccentric shape of the trochlea, alters the carrying angle during flexion to prevent misalignment (Rogers 1999; Vance *et al.* 2011). Therefore, Rogers (1999) examined the distal humeri of females and males from the Grant Collection at the University of Toronto and found four sexually dimorphic landmarks: trochlear constriction, trochlear asymmetry, olecranon fossa shape and depth, and angle of the medial epicondyle. Females exhibit a more constricted trochlea, a more symmetrical trochlea, a deep and oval olecranon fossa, and a raised medial epicondyle. Conversely, males exhibit a less constricted trochlea, an asymmetrical trochlea, a shallow and triangular olecranon fossa, and a flat medial epicondyle. Subsequently, Rogers scored each trait as “male-like” or “female-like” on 7 female and 28 male White individuals from the Documented Collection at the University of New Mexico and 19 female and 74 male White individuals from the William M. Bass Donated Skeletal Collection at the University of Tennessee. Together, the four distal humeral features had an accuracy of 92% in classifying individuals.

No work has tested the clavicular or humeral sex assessment methods on Asian populations; however, there is evidence to suggest that population differences exist in distal humerus morphology. Vance *et al.* (2011) refined Rogers’ (1999) method by removing trochlear constriction, which performed poorly, and adding an ordinal scoring system so that each of the three distal humeral features is scored 1 (typical male) through 5 (typical female). They found that these features correctly classified 75.5% of Black and White South Africans, which is significantly less than Rogers’ (1999) accuracy rate of 92%.

Additional validation studies of the Rogers’ (1999) distal humerus method on European collections indicate that the method performs fairly well. Further work by Rogers (2006) found that the distal humerus method resulted in correct classification rates of 80% for 49 adults from the Spitafields Collection in England, and 83% for 101 adults from the Lisbon Collection in Portugal. Additionally, Rogers (2009) demonstrated that the sexually dimorphic traits are also evident in adolescents. In her sample of 42 British and Portuguese individuals 11 – 20 years of age, Rogers found that the four distal humeral traits can be assessed once the trochlea begins to fuse with an accuracy of 81%. In testing the distal humerus method on 351 individuals from the St. Bride’s Church collection, London, Falys *et al.* (2005) found that Rogers’ (1999) scoring procedures failed to capture the variation expressed in their sample. Despite this, Falys and coauthors found that 79.1% of individuals were correctly classified, and therefore the method is relevant to forensic casework.

While several methods exist for visually assessing sex, the lack of testing on Asian populations may result in misclassification if such methods are applied to Asian individuals, thereby hindering identifications. The cranial and postcranial sex assessment methods highlighted here will be applied to Japanese and Thai skeletal collections to measure sexual dimorphism in these two groups and establish refined methods that can be cautiously applied to other Asian populations.

Ancestry Assessment

The second objective of this project is to determine how the cranial trait expressions and frequencies identified in pre-contact Native American skeletal remains perform in classifying contemporary Japanese and Thai individuals as "Asian" during the assessment of ancestry. Accordingly, the frequencies for cranial traits used in identifying Native Americans will be established for modern Japanese and Thai individuals. Subsequently, the Japanese and Thai trait frequencies will be compared to determine if inter-group variation exists between East and Southeast Asian individuals. Identifying similarities or differences in cranial trait features and expressions among Japanese, Native American, and Thai individuals allows anthropologists to more accurately determine the biogeographic origin, or ancestry, of unknown remains.

Ancestry assessment is often considered the most difficult, least accurate, and most subjective of the biological profile methods (Adams and Byrd 2008; Hefner 2009; Nakhaeizadeh *et al*. 2013). “Race” (i.e., Asian, Black, Latino/a, White) may indicate an individual’s sociocultural group membership, and is often reported through family members in missing-person’s reports. Conversely, the anthropological assessment of ancestry from skeletonized remains is a biogeographic estimate that reflects the genetic origin of population variation (Konigsberg *et al.* 2009; Relethford 2009). Group similarities and differences in cranial and postcranial morphometrics can be attributed to micro-evolutionary processes (i.e., genetic drift, gene flow, mutation, and selection) in human populations. However, this is a relatively modern view on population variation, and historical perspectives focused on categorizing groups of people into highly circumscribed typological races (AAPA 1996).

A brief history of race in physical anthropology

Prior to European transoceanic expeditions to explore and colonize new lands, the idea of inherent, biologically based racial differences was not common (Brace 1995; Graves 2003). Rather, the concept of race stemmed from the need to explain the existence, origins, and differences of the groups who came to inhabit the New World. Brace (1995) argues that the social barriers of the three main newly commingled groups that inhabited North America – Native American populations who came from Asia, European immigrants, and forcefully imported African populations – perpetuated the idea of three easily identifiable, discrete, disparate, and wholly unrelated populations, despite the occurrence of genetic and social exchange. The phenotypes expressed by the three groups came to represent social status; however, the continued intermixing of the groups broke down the discrete genetic and social barriers (Graves 2003). Despite the diminishing differences, Europeans used racial ideas to categorize people when it became politically, economically, and socially advantageous, such as during colonization activities (Graves 2003). While the race concept was born from a very specific and socially complex context, America's far-reaching influence exported racial ideas far and wide (Brace 1995).

Organizing life, including humans groups, into immutable categories stemmed from the Chain of Being during the Middle Ages, which ordered all living species created by God in a linear hierarchy from "Man" down to plants and ethereal matter (Bowler 1989). During the 1700s, Carl Linneaus further codified this hierarchy by developing taxonomic classifications (e.g., *genera* and *species*), which were considered static groupings created by God (Bowler 1989). Using this binomial nomenclature, Linneaus categorized humans into four distinct groups – *Homo sapiens americanus* (Native American), *europaeus* (European), *asiaticus* (Asian), and *afer* (African) – which greatly influenced future perspectives on human variation, concepts of race, and ancestry. Concurrently, scientists involved in classifying humans divided themselves into two primary groups: monogenists, who argued that all human groups were descended from the same ancestral stock; and polygenists, who argued that the major human groups descended from distinct and separate ancestors since time immemorial (Bowler 1989).

The primary way in which scientists proved the existence of typological racial categories was made possible by documenting differences in cranial size and shape (Brace 1996; Caspari 2009; Michael 1988). The focus on the skull stemmed from an interest in the brain, which was thought to be the origination of racial differences (Marks 1995). However, in the absence of significant numbers of brains, scientists utilized skulls as proxies and largely disregarded the postcranial skeleton. In the late-1700s, Johann Friedrich Blumenbach, a German monogenist who was arguably the father of European physical anthropology, first used skull morphology to classify humans into five racial categories including American, Caucasian, Ethiopian, Malay, and Mongolian; all of whom were descended/degenerated from Adam and Eve (Brace 1996). In the 1800s, Samuel George Morton, the father of American physical anthropology and a polygenist (Hrdlička 1919), continued Blumenbach's work by measuring the cranial capacities of the five "races" and ranking them from largest/most intelligent (Caucasian) to smallest/least intelligent (Ethiopian) (Michael 1988). Morton concluded that the ancient individuals interred in burial mounds throughout the eastern U.S. were represented by the extant Native Americans; thus, the present-day racial forms represented by differing cranial capacities originated independently and deep in history (Brace 2005). Other scientists used the cephalic index (relationship of cranial length to width), which was developed by Anders Retzius in 1842, to document racial differences thought to be heritable and unchanging (Marks 1995). The then-perceived scientifically proven existence and hierarchical organization of the five "races" became cemented in the American psyche, resulting in the justified subjugation of minority groups and helped shaped anthropological perspectives on human variation for the next 200 years (Veran 2012)

Physical anthropology's obsession with scientifically documenting racial differences continued with Paul Broca, a French polygenist who developed new methods to measure crania, and Aleš Hrdlička, a Czech-born immigrant to New York who was strongly influenced by Broca's work (Caspari 2009). Additionally, Hrdlička was swayed by the European anthropological school of thought, which maintained that behavior, intellect, psychological traits, and cultural traits were inherited alongside biological attributes (Lipphardt 2012). In particular, Hrdlička's racial typological studies, which were largely descriptive and devoid of theory, sought to address inequality in racial and sociopolitical issues (Caspari 2009). He attempted to document "pure" African American characteristics with craniometrics, and argued that European Americans represented a separate and distinctive subgroup of Caucasians (Blakely 1987). In the U.S., Hrdlička's influence was significant as he served as the curator in the Division of Anthropology at the National Museum of Natural History and founded the *American Journal of Physical Anthropology* in 1918 (Caspari 2009). Hrdlička (1915, 1920) also aligned himself with the eugenics movement, which sought to mitigate racial degradation by preventing less racially pure groups from mating with those considered more pure.

A discernable shift in anthropological perspectives of race occurred in the 1920s and 1930s with Ernest Hooton and Franz Boas, two academic anthropologists who focused on racial issues and trained numerous physical and cultural anthropologists. Hooton held the first full-time academic physical anthropology position in the U.S. while at Harvard, where he produced the first Ph.Ds. in physical anthropology beginning in 1925 (Brace 2005). Hooton (1936) believed in the typological race concept, and he divided humans into White, Negroid, and Mongoloid groups, each containing secondary and tertiary races. Additionally, he argued against racial hygiene, pure races, and the conflation of race with nationality, language, and culture (Brace 2005; Hooton 1936; Watkins 2012). However, Hooton (1939) attempted to correlate criminal activity with biometrics, and argued that some races are more likely to participate in criminal activity compared to others. Hooton was interested in studying polymorphic (within group) variation rather than solely focusing on polytypic (between group) variation that occupied his predecessors' research (Marks 1995). Moreover, Hooton argued that mixing is rather beneficial to groups based largely on the work of Harry Shapiro, his first Ph.D. student, who documented skeletal plasticity in the height of Hawaiian-born Japanese individuals (Anderson 2012). Further, Hooton advocated for the use of non-adaptive morphological features over cranial measurements or indices, and in the 1930s developed the first standardized forms to tabulate over 100 nonmetric observations (Brace and Hunt 1990; Brues 1991; Hefner 2009). Hooton influenced a myriad of physical anthropologists interested in cranial morphology and variation in subsequent years, as evidenced by the continued use of many of his nonmetric scoring systems (Brues 1990; Hefner 2009).

Like Hooton, Boas believed in slight biological differences between groups and argued adamantly against racial hierarchies. As a true four-field anthropologist, Boas situated physical anthropology within the larger field of anthropology by employing theory, statistics, and cultural relativism (Caspari 2009). Additionally, he taught at Columbia University and played a significant role in the formation of the *American Anthropological Association.* Boas was interested in the sources of variation within and between groups, and argued that immigration and race mixing had no deleterious effects on offspring (Anderson 2012). Namely, he documented changes in cranial form between generations of European immigrants; therefore, highlighting the issues of using cranial measurements to identify circumscribed racial groups (Boas 1912; Marks 1995). Boas (1912) documented that changes to the cranium can result from human behavior, such as cradle boarding, or the changing environment, and became the first to caution against using the cephalic index as a tool to identify races (Boas 1899). More importantly, Boas and other four-field anthropologists questioned the relevance of anthropometrics and race (Anderson 2012; Caspari 2009).

Despite the issues of utilizing cranial anthropometrics to identify discrete races, the notion that humans could be divided into major categories based on phenotypic expressions remained unchanged in certain circles. Carleton Coon, a student of Hooton's, argued that *Homo erectus* evolved into Australoid, Capoid, Caucasoid, Congoid, and Mongoloid groups in the five major geographic regions; however, they each evolved into modern humans at different times (Coon 1939, 1965; Coon *et al.* 1950). Not surprisingly, Coon argued that the Caucasoid and Mongoloid groups attained modern human status before the others (Coon 1965). Further, he argued that each of the groups were adapted to their environments, and that the concentrations of geographically congruent traits within a region indicates genetic relatedness. While each group could be considered a subspecies, Coon (1965) maintained that gene flow in areas of geographic overlap prevented complete speciation, but the traits of each group were maintained through endogamous mating practices.

The racial typological ideas adopted by anthropologists like Coon (1939, 1965) were challenged by scientists as early as 1951 with the United Nations Educational, Scientific and Cultural Organization's (UNESCO) "Statement on Race" drafted by 14 prominent anthropologists, biologists, geneticists, psychologists, and sociologists (Comas 1961; Marks 2010; Selcer 2012; UNESCO 1951). The statement argued that human biological diversity must be understood through a population perspective rather than a typological approach (Selcer 2012; UNESCO 1951). Importantly, the document argued that inherent genetic differences do not play a role in producing differences between cultures or achievements of people, and that there are no "pure" races, as groups have been mixing for a considerable amount of time (UNESCO 1951). Additional UNESCO statements were published in 1964 and 1967 (UNESCO 1969). Ashley

Montagu (1962), one of the UNESCO Statement's authors, specifically argued against Coon's (1965) polygenist ideas, and went on to say that "race is the witchcraft of our time" (Montagu 1974:23). Further, Montagu asserted that the concept of race should be abandon entirely since zoological terms (such as race) cannot be automatically applied to human populations (Montagu 1962, 1974).

The anti-typological sentiments were further echoed by proponents of the "new physical anthropology" movement (Washburn 1951), who advocated for exploring the mechanisms of evolutionary change, rather than focusing on racial typological approaches (Marks 1995; Relethford 2010; Veran 2012; Washburn 1951). The new physical anthropologists were concerned that the typological approach supported the superiority of Whites and the continued subjugation of non-Whites, which was exemplified by groups such as the Pioneer Fund who distributed Coon's work to universities throughout the South (Brace 2005; Relethford 2010). Sadly, the Pioneer Fund still exists and has supported the racist work of J. Philippe Rushton (1995), who argued until his death in 2012 that individuals of African ancestry are inherently less advanced than individuals of European ancestry. Namely, Rushton (1995) argued that compared to individuals of European ancestry, individuals of African descent exhibit less intelligence, law abidingness, sexual restraint, and social organizational skills, in part according to Rushton, because adaptation to cooler climates by Europeans required more advanced cognitive ability (Brace 1996; Brace 2005; Rushton 1995). While Rushton's perspective is infrequent and easily discredited by anthropologists, Marks (2012) argues that such scientific racism is considerably more detrimental than unscientific creationism, or so-called creation science, because it authoritatively uses the scientific method for support, which is alluring to racist people.

Despite the existence of marginalized racist holdouts such as Rushton, most biologists, biological anthropologists, and sociocultural anthropologists, abandoned the biological race concept by the 1970s or 1980s (Caspari 1998; Cartmill 1998). Namely, anthropologists largely agreed that race is a sociocultural construction, and that there is no genetic or morphological evidence to support the typological race concept (Brace 1996, 2005). This led the American Association of Physical Anthropologists to reiterate and revise UNESCO's (1951, 1969) statements in 1996 (AAPA 1996). Chiefly, the AAPA (1996) argued that biological differences are both hereditary and due to natural and social environments, and that there is no causal linkage between behavior and biology. However, as a result of adopting a no-race perspective, Relethford (1999) argues that anthropologists grew weary in addressing ancestry and population variation in general, and subscribed largely to a "no variation" perspective until the incorporation of genetic data. Similarly, Selcer (2012) argues that physical anthropology entered an existential crisis once race was delegitimized as a proper area of study. Interestingly, however, Veran (2012) notes that the evidence historically used by physical anthropologists to legitimate poor treatment, enslave, and render people lower status is now used to give power to marginalized groups through legitimating indigenous land claims, ancestry, and heritage.

The development of a modern perspective on cranial population variation

Where the early studies of morphological and metric human craniofacial form solely focused on documenting differences between geographical regions in order to establish racial typologies, later studies incorporated genetic evidence to explore population variation, structure, and history. This began as early as the 1930s and 1940s with crossbreeding mice to understand the inheritance of nonmetric traits (Gruneberg 1939, 1943, 1958). This early work demonstrated that nonmetric traits are not inherited by simple Mendelian genetics, as no consistent correlation existed between mice parents and offspring in trait expressions. As such, nonmetric traits came to be known as quasi-continuous epigenetic traits, whereby a genetic basis exists, but the trait's expression is discontinuous. That is, the expression and distribution of nonmetric traits are determined by the individuals' genetic propensity to develop a trait, in addition to environmental factors that occur during ontogeny (Berry and Berry 1967; Tyrrell 2000).

The early research on mice epigenetics was later applied to human crania with the work of Berry and Berry (1967), who argued that epigenetic traits are coded in the genotype, but their expression in the phenotype is mediated by environmental forces. Using multivariate statistics developed from mice data, Berry and Berry examined 585 adult crania from South America, North America, Burma, North India, Palestine, Nigeria, and Egypt in order to document epigenetic variability from disparate geographic regions. They found a low level of correlation between 30 epigenetic traits, suggesting that the variants are the result of many independent developmental processes. However, their findings indicated that epigenetic traits reveal differences between populations due to environment and disease, among other factors. As such, they advocated for the use of epigenetic traits in studying population variation because they are relatively easy to assess and were argued to be representative of genetic processes.

The work of Berry and Berry (1967) contributed to the polygenic theory of inheritance, which is intrinsic in modern studies of population variation. Accordingly, the phenotypic expression of craniofacial traits is due to multiple genes, rather than simple Mendelian inheritance. Each gene has a small individual affect, but they produce certain phenotypic traits when working together. Additionally, the traits that produce a certain phenotype are also pleiotropic (one gene contributes to multiple phenotypes). Polygenic traits are generally considered quantitative traits such as skin color, stature, and epigenetic traits of the cranium (i.e., nonmetric, quasi-continuous, discontinuous, discrete, or threshold traits), which arise from interactions between multiple genes and between genes and the environment. An individual expresses a particular trait by passing a genotypic threshold for a particular trait (Berry and Berry 1967; Hauser and DeStefano 1989; Tyrrell 2000). In theory, the distribution of quantitative traits within a particular population is normal (bell curved), and a certain proportion of the population exhibits the trait if they fall above the threshold, while the remainder fall under the threshold and do not exhibit the trait. An individual can pass the threshold through genetics alone, or through interactions between the genes and the environment.

Concurrent with developing ideas on epigenetic inheritance, biological anthropologists such as Livingstone (1962) emphatically argued that more variation was present within groups than between groups; therefore, arguing against the existence of biological races. Livingstone's argument that "there are no races, there are only clines" became famous, and was supported by the emerging field of genetics. For instance, Lewontin (1972) found genetic diversity between geographical groups (races) is approximately 8%, genetic diversity between populations within the groups is approximately 6%, and diversity between individuals is approximately 86%. This landmark study set the bar for studies of human variation, including craniofacial studies, as it demonstrated that genetic variation is minimal between populations, and set a baseline for population variation to be used in future genetic and craniofacial studies (Brown and Armelagos 2001). Moreover, Lewontin's study demonstrated that racial taxonomy is a poor way to explain population variation because race poorly fits the genetic data, which has been strongly reiterated in recent years (Long *et al.* 2009). Similarly, based on multivariate metric analysis of worldwide crania, Howells concluded, “there are no races, only populations” (1995:103).

The eventual technological advances in DNA studies in the 1980s and 1990s allowed researchers to systematically test the hypothesis that cranial morphology and metrics can be used as a proxy for genetic data (Cheverud 1988). While such studies have demonstrated that the entirety of human cranial morphological diversity cannot be explained by genetic inheritance alone, the vast majority of these studies indicate that there is a significant correlation between genetics and cranial morphology, and that it is indeed a scientifically sound approach to population studies (Carson 2006; Relethford 1994, 2001, 2002). In particular, craniofacial morphology is geographically patterned and can be used to document micro-evolutionary processes (Cheverud 1988; Kohn 1991; Patterson *et al.* 1993; Relethford 1994).

The work of Carson (2006), Cheverud (1982, 1988), Kohn (1991), Patterson *et al.* (1993), and Relethford (1994; 2001; 2002) demonstrate that human craniofacial morphology can be used as proxies for genetics, particularly in the absence of genetic data. Kohn (1991) argued that no major theory proposed by morphological studies have been usurped by genetic studies; all in all, morphological data is consistent with genetic data. Further, Cheverud (1998) argued that studies of human population variation and human evolution should not only rely on genetics, but also should incorporate craniofacial morphology. Moreover, in studying craniofacial metrics, Relethford (1994) found similar levels of variation as Lewontin’s (1972) genetic data. Relethford found that approximately 6% of craniofacial diversity is found between geographical regions, and the remainder of variation is found within populations. Thus, Relethford argues that craniofacial morphology demonstrates similar population variation as DNA polymorphisms and microsatellite data, and can therefore be applied to studies of human population variation. However, Relethford (2004a) does caution that craniometric variables do show some degree of cranial plasticity, but not enough to obscure population relationships.

Arguably, if craniofacial variation exhibited higher levels of variation than that found by Lewontin (1972) and other DNA researchers, then craniofacial morphology would not be suitable for population variation studies, as it would over-estimate variation. Additional craniometric studies have continued to demonstrate that craniofacial variability is similar to that of genetic variability (Hanihara 1996; Roseman and Weaver 2004). However, Devor (1987) cautions that environmental factors are almost as important as genetic factors in the expression of craniofacial dimensions. Regardless, craniometric variation is less affected by selection pressures compared to other adaptive traits, such as skin reflectance (Roseman and Weaver 2004). Furthermore, the population differences in craniofacial morphology develop prenatally or early postnatally and are modified during ontogeny (Vidarsdottir and O'Higgins 2003; Vidarsdottir *et al*. 2003).

Howells (1973, 1989, 1995) and Smith (2009) have shown that specific areas of the cranium are more correlated than others with genetic data. In particular, Smith's (2009) study examined the correlation of 83 digitized cranial landmarks and microsatellite data for 14 worldwide geographic regions. Of the cranial regions analyzed, including the basicranium, mandible, upper face, temporal bone, maxilla, and cranial vault, Smith found that the morphology of the entire cranium, basicranium, temporal region, and the upper face are more correlated with genetic data than other regions (particularly the neurocranium, mid-face, and masticatory regions). In particular, Smith's results support previous findings that the basicranium is largely free of external influences during development because of its endochondral ossification and the relatively early age of complete ossification. Conversely, the face and mandible are more prone to external factors. Therefore, Smith argues that future studies using craniofacial morphology to document genetic relationships should focus on the basicranium, temporal bone, morphology of the entire cranium, and the upper facial region. Other areas may reflect adaptation and natural selective pressures.

The finding that certain areas of the cranium are more correlated with genetics than other areas is related to the development of the cranium and follows the growing brain. The developing brain produces tension on the pericranial and endocranial surfaces of the neurocranium, causing an expansion of the neurocranium at the sutures, synchondroseal expansion in the basicranium, and bone drift in the neurocranium and basicranium through osteoblastic and osteoclastic activity (Lieberman *et al.* 2000). While the basicranium is believed to be independent of brain size, Lieberman and coauthors argue that the basicranium influences the neurocranium and potentially the face because the basicranium develops under endochondral ossification (from chondrocranium), and is the first area of the skull to develop and attain adult size at approximately 8 years of age. Conversely, the neurocranium and splanchnocranium develop through intramembranous ossification, and finish growth after the basicranium, at 10 and 18-20 years, respectively. Lieberman *et al.* (2000) analyzed adult crania from Europe, Africa, and Asia through measurements, radiographs, and ectocranial volume to determine if basicranial shape appreciably affects the neurocranium and splanchnocranium.

Lieberman *et al.* (2000) found that the neurocranial breadth is impacted by basicranial breadth and ectocranial volume. Additionally, the cranial base length and cranial flexion are independent of neurocranial length. As such, if the basicranium or ectocranial volume is narrow (dolichocephalic), the neurocranium will similarly be narrow and will grow posteriorly and vertically. If the basicranium or ectocranial volume is wide (brachycephalic), the neurocranium will also be wide. However, the relationship of the splanchnocranium to the neuro-basicranial complex is weak. That is, in individuals with a narrow cranial base and neurocranium, the face may be narrower and elongated; however, the trend was statistically weak. Consequently, they argue that although the basicranium and neurocranium are highly correlated during ontogeny, face shape is mostly determined through different processes, such as different ontogenetic trajectories and epigenetic interactions.

The work of Lieberman *et al.* (2000) has been supported by numerous studies. In fact, Howells (1973, 1989, 1995) hypothesized that the basicranium influenced the growth and shape of the cranium, though he largely lacked the data to test his hypothesis. Further, Hallgrímsson *et al.* (2007) used functional matrix theory to investigate how embryologically distinct regions of the cranium interact in mice. The functional matrix theory states that soft tissue and air-filled structures of the cranium (i.e., brain, eyes, mouth, esophagus, and sinuses) will guide the development of the surrounding skeletal structures (Vidarsdottir and O'Higgins 2003). Skeletal regions that grow through intramembranous ossification are argued to be more susceptible to epigenetic effects because the functional matrices guide these regions. Skeletal regions that grow through endochondral ossification are generally independent of the functional matrices. Hallgrímsson and coauthors (2007) found that the widths of the basicranium, neurocranium, and splanchnocranium co-vary; however, the splanchnocranium co-varies less than the other two regions. They also found that changes in one region of the skull through genetic perturbations cause changes in the other regions in a predictable manner.

Biological anthropologists have incorporated evolutionary and molecular theory into studies of craniofacial variation, many of which were not known or accepted during the time of the early studies on biological race. In particular, it has been demonstrated by Relethford (2004b) that population variation, both genetic and morphometric, can be partly explained by the isolation-by-distance model. This model states that increasing geographical distances between populations leads to an exponential decrease in migration and, therefore, gene flow between local and global populations (Relethford 2001, 2002, 2004b; Relethford and Blangero 1990). This has resulted in adaptive (Beals *et al.* 1994; Yokley 2009) and hereditary (Relethford 2009) differences that are detectable in genetics and craniofacial morphology. The isolation-by-distance model allows biological anthropologists to explain why differences exist between modern groups that originated from different continents. However, Hunley *et al.* (2009) demonstrated that isolation-by-distance models alone fail to explain the amount of variation observed within and between groups. Rather, Hunley and coauthors found that when using computer simulations of genetic data from 53 worldwide populations from seven geographic regions, serial fissions, regional bottlenecks, and gene flow also account for the observed variation.

Though race, which is based primarily on skin color in U.S. society, is a sociocultural concept, it is still a reality that has biological consequences. Edgar (2009) and Watkins (2012) show that changing historical definitions for White and Black over the last 100 years has, in turn, affected assortative mating practices. Biological characteristics identified in a particular group were used as support for anti-miscegenation regulation, which in many areas of society dictated who could marry and bear offspring (Edgar 2009). This led to the propagation of those identified biological traits due to endogamous mating. As such, the social construction of race and biology function together as a feedback loop. This feedback loop of population variation and sociocultural constructions of race has led to significant health consequences, whereby African American populations suffer the highest levels of morbidity and mortality for most chronic diseases (Gravlee 2009). Biological anthropology research in race and population variation can now be applied to biomedical issues, and shows that there are health disparities between the races, despite the fact that biological races do not exist.

While much of U.S. society uses skin color among other features to classify sociocultural races, biological anthropologists have incorporated more nuanced views of skin color and population variation into their research (Edgar and Hunley 2009). In particular, Relethford (2009) has demonstrated that skin color is atypical of human variation because unlike craniofacial morphology, skin color variation is greatest between regional populations than within populations. This is due to the fact that skin color is an adaptive trait from exposure to differing levels of ultraviolet radiation produced by the sun. It is well documented that skin color is correlated with latitude, so that individuals who live closer to the equator with more sun exposure will exhibit darker pigmentation that those who live in northern regions. While skin color does show significant differences between large geographical areas (particularly in Africa, Europe, Asia, and North American), there is overlap between populations, as skin color is clinal in its distribution. However, Relethford argues that skin color is discordant with other biologically variable traits, and as such, cannot be used as an explanation of population variation.

Adaptation and craniofacial form

In addition to epigenetics and ontogeny, researchers have long known that cranial variation is also related to natural selection and adaptation. The physical anthropologists of the early 19th and 20th centuries largely assumed that craniofacial form was the result of inherent, biological differences between typological races. Accordingly, populations have lived under different selection pressures, and this may be reflected in their skeleton. In the post-Darwin and Neo-Darwinian eras, all traits were argued to be the result of selective pressures, even if selective pressures could not be postulated for particular traits (Brace 1996).

Arguably, the primary selective force that is attributed to craniofacial variation is climactic adaptation. Numerous regions of the body are thought to be shaped in response to thermoregulation, including body mass, body build, nose shape, cranial size and shape, limb proportions, and brain size (Hall *et al.* 2004). According to Hall *et al.* (2004), adaption occurs through immediate, developmental, and long-term changes. For example, immediate adaptation to the cold includes biological (e.g., shivering and vasoconstriction) and cultural behavior (e.g., adding clothes and using fire). Developmental adaptation occurs through changes in body fat, increased metabolic rate, and less reliance on shivering. While both immediate and developmental adaptations operate on the individual, long-term adaptation operates on the population and includes longer trunks relative to the lower limb, wider shoulders and hips, increased crural and brachial indices, and changes in nasal form.

Concerning the cranium, Beals *et al.* (1984) and Guglielmino-Matessi *et al.* (1979) argue that neurocranial shape is attributed to thermodynamic regulation. Accordingly, brachycepalization (cranial width increase) and encephalization (cranial size increase) are found in cold, northern climates (Beals *et al.* 1984). Larger, rounded skulls have been shown to retain heat better than smaller, narrower skulls. Beals *et al.* (1984) found that there is a statistically significant difference in cranial form between individuals living in hot and cold environments. However, Kouchi (2000) found that brachycepalization is correlated with height in modern Japanese populations. Both height and cranial breadth have been increasing in modern Japanese individuals for the last 100 years. However, Kouchi attributes brachycepalization to environmental conditions rather than genetics, such as supine sleeping practices, which has changed to prone sleeping in more recent years.

Another area of the cranium arguably shaped by climate is nose form. It has long been observed that populations from northern climates exhibit fairly narrow noses that are tall, while individuals from southern climates exhibit shorter and wider noses (Hall *et al.* 2004; Yokley 2009). Yokley (2009) analyzed CT scans of clinical patients and found that seven out of the study's ten nasal measurements correlate with climate. That is, individuals from cold and cold-wet climates exhibit relatively longer and higher noses, which increases the amount of surface area in the nose to warm and moisten inspired air, while individuals from hot and hot-dry environments exhibit wider and shorter noses, which assists in heat dissipation. However, it has been postulated that the internal nasal structures are more important than the external nose, and the nasal indices on dry skeletal remains only document external nasal form. Yokley (2009) examined the cross-sections of nasal cavities to determine if there was a difference between

African and European Americans, and found that they do not correlate with the expected surface area to volume ratios. No statistically significant differences exist between African and European Americans. However, when the African American individuals were decongested as a response to physical activity or other environmental changes, statistically significant differences were observed. As such, Yokley argues that mucosal thickness is an important factor that determines the thermoregulatory ability of the nasal passages, which the traditional skeletal elements fail to capture. Yokley argues that different selection pressures (cold temperatures and physical activity in certain environments) contribute to nasal form. While there is considerable overlap in climate, and therefore selective forces between geographical areas, skeletal adaptation can also be used to examine population variation.

Metric analyses in forensic ancestry assessment

Ancestry has been determined from the cranium using multiple measurements and discriminant functions since the 1960s (Ayers *et al.* 1990; Giles and Elliot 1962). However, analyses in the FORDISC computer program presently serve as the primary metric analytical tool to determine ancestry from both the cranial and postcranial skeleton (Ousley and Jantz 2005). This program allows standard measurements from an unknown individual to be compared to mostly known individuals from FDB. The unknown individual is compared to up to 13 groups (born after 1930) using customized discriminant function analyses based on the available measurements. More reference groups exist for the cranial measurements and include American Black, American Indian, American White, Hispanic, and Japanese females and males, and Chinese, Guatemalan, and Vietnamese males. Additionally, the Howells cranial dataset, which is comprised of 28 worldwide groups (Howells 1973, 1989), is also included in FORDISC. The postcranial reference samples are represented only by Black and White females and males. FORDISC provides cross-validated correct classification rates and posterior and typicality probabilities based on the utilized measurements.

While FORDISC is flexible in that it allows for the analysis of varying numbers of measurements, the program will always place an unknown individual into one of the groups, even if the individual is not represented by the reference samples (Ousley and Jantz 2005). Therefore, the analyst must assess the likelihood that the unknown individual belongs to one of the groups included in the customized discriminant function analysis by assessing the posterior and typicality probabilities. Posterior probabilities represent the probability that the unknown individual belongs to each group included in the analysis, which all sum to 1. Posterior probabilities are calculated from the relative distances of the unknown individual to the centroid of each of the groups. The highest posterior probability classifies the unknown individual into that group. For example, a posterior probability of 0.85 indicates that the unknown individual has an 85% posterior probability of being from a particular group, assuming that the individual belongs to one of the reference groups. Typicality probabilities indicate how likely the unknown individual belongs to the groups included in the analysis. Typicality probabilities are calculated from the absolute distances of the individual from the reference groups. For example, a typicality probability of 0.33 indicates that 33% of the reference group’s individuals are expected to be as far or farther from the group’s centroid (Ousley and Jantz 2005). Generally, typicality probabilities above 0.05 are valid; however, if all typicality probabilities are very low, then it is likely that the individual does not belong to any of the groups included in analysis. It should be noted that while FORDISC is most often used to determine ancestry, sex can be determined in the context of ancestry by determining if the measurements of the unknown individual are closest to females or males in different populations.

While FORDISC is the most common discriminant function software program used in ancestry assessment for U.S. forensic cases, CRANID is most commonly used in Australian and European cases (Wright 1992). The CRANID program is similar to FORDISC in that it compares cranial measurements of an unknown individual to mostly known individuals from multiple worldwide locations using discriminant functions. Also similar to FORDISC, CRANID includes the Howells (1973) dataset, but the program is also augmented with data from Australia and Europe (Wright 1992). Because FORDISC and CRANID always place the individual into one of the reference groups, Guyomarc'h and Bruzek (2011) caution against using such software programs in forensic casework wherein the unknown individual's ancestry is not included in the reference samples.

Whereas FORDISC and CRANID utilize two-dimensional data to determine the sex and ancestry of unknown remains, other computer programs such as 3D-ID use three-dimensional size and shape data gathered from geometric morphometrics to classify unknown individuals (Kimmerle *et al.* 2008; Ross *et al.* 2015; Slice and Ross 2009). Similar to FORDISC, 3D-ID compares the cranial landmark data (up to 34 digitized landmarks) from the unknown individual with known individuals mainly of African, European, and Latin American descent, though some Asian individuals are included in the database (Slice and Ross 2009). Posterior and typicality probabilities and Mahalanobis squared differences are calculated based on comparisons of Cartesian coordinates between the unknown individual and reference samples.

The use of morphological traits in forensic anthropology

The use of nonmetric traits has a long history in the biological sciences and physical anthropology. Anatomists during the late 19th century noted the variable nature of human morphological traits, such as foramina number, sutural bones, and proliferative ossifications (Berry and Berry 1967; Hauser and DeStefano 1989; Hefner 2007). While many of these discrete, dichotomous, and discontinuous morphological traits proved useful in examining genetic relatedness and biological distances between and within populations, they lacked forensic application until the 1970s when Finnegan and McGuire (1979) found that cranial and postcranial discrete/epigenetic traits correctly classified individuals 50 – 80% of the time within a statistical framework. However in subsequent years, forensic anthropologists focused mainly on quasicontinuous cranial traits – or macromorphoscopic/morphoscopic traits according to Hefner (2009) – many of which are recognizable in soft tissue structures and are influenced by selective forces (Hefner *et al.* 2012). Many of these traits were adapted from Hooton's standardized trait lists and serve to align an unknown individual with one of three or four ancestral groups (e.g., African, Asian, European, Hispanic) based on morphological similarities, rather than determining the genetic relatedness or biological distances of skeletal assemblages.

The use of morphoscopic traits emerged as the primary way in which to determine ancestry with Gill and Rhine's (1990) edited volume, *Skeletal Attribution of Race: Methods in Forensic Anthropology*. In particular, Rhine (1990) provides lists and frequencies for 45 traits that are expected to be present in Anglo (n=53), Hispanic (n=15), Black (n=7), and Indian (n=12) skulls. Perhaps more influential than Rhine's trait frequencies are the diagrams he presents for typical American Caucasoid (grouped Anglo and Hispanic), Southwestern Mongoloid (pre-contact and modern Native Americans), and American Black crania, each with associated trait lists that are considered useful in ancestry assessment. Appendix A presents Rhine's (1990) traits that he argues as being useful in race determination, the scoring method, and associated groups for many of the traits that he considered useful. The traits presented in Rhine (1990), and others in the volume, were largely adapted from Hooton's extensive nonmetric trait lists developed for the purpose of standardization while at Harvard. Despite the meager sample sizes and lack of methodological application, these trait lists have been reproduced in numerous physical and forensic anthropology textbooks (Klepinger 2006; Burns 1999; Byers 2002). Similar trait lists appeared in the influential work of Bass (1995) and Gill (1998). The success and widespread adoption of morphoscopic traits can be attributed to their applicability to fragmentary and incomplete remains, the fact that measuring equipment is not required, and the deep-seated trend in anthropological training in stressing the importance of morphology (Brues 1990).

Fairly recently, anthropologists (i.e., Edgar 2005, 2013; Hefner 2007, 2009; Pilloud *et al.* 2014) started critiquing the nonmetric trait list method, largely in response to *Daubert* rulings in the U.S., which requires the methods used in the court-of-law to be scientifically assessed through peer review, be replicable, have known error rates, and be accepted in the scientific community (U.S. Supreme Court 1993). Arguably, this rulings are more applicable to evidence that would be used to make a positive identification (i.e., antemortem-postmortem radiographic analysis) or to document the circumstances of death (i.e., trauma analysis). However, these rulings sparked intense responses in the forensic anthropological community to ensure that all the methods employed be scientifically validated and held to the same standard (National Research Council 2009).

Hefner (2007, 2009) and Hefner and Ousley (2014) argue that the morphoscopic trait list approach proposed by Rhine (1990), Gill (1998), and Bass (1995) is neither a true method nor scientific. In particular, Hefner (2009) argues that morphological traits lists reduce population variation to typological race categories, and that the identification of such categories (i.e., Caucasoid, Mongoloid, Negroid) relies on the extreme expression of traits that are attributed to, or expected in, each of the groups. Hefner and Ousley (2014) argue that the process in which forensic anthropologists assess ancestry is a part of the problem: anthropologists traditionally analyze the overall gestalt of the cranium to form an initial impression, and then identify the traits that "worked" in a *post-hoc* manner once the cranium has been determined to be of a particular ancestry through positive identification. This is exemplified in a published letter written by George Gill and sent to a Wyoming crime lab in 1979 subsequent to the ancestry assessment of unknown skeletonized remains: "When the I.D. of this individual is pretty well confirmed please let me know. Each one of these identified ones helps us 'calibrate' our techniques" (in Gill 1984:339). As such, the forensic anthropologist is relying on a subjective assessment, where traits are not weighed equally and the assessment depends on the anthropologist's experience level and comfort in using a particular region of the cranium for ancestry attribution (Hefner and Ousley 2014). Until fairly recently, anthropological studies did not systematically identify trait frequencies within and between populations and explore which traits performed better than others. As such, no error rates were known for nonmetric traits due to a lack of in-depth statistical analyses aimed at understanding population variation.

In addition to the lack of error rates, morphoscopic traits have been demonstrated to be somewhat difficult to teach and depend on the anthropologist's experience level (Birkby *et al.*

2008; Hefner *et al.* 2012). Conversely, metric assessment relies on specific landmarks that are usually easy to identify, and require less skill. While considerable time is spent teaching students how to correctly take cranial and postcranial measurements, significantly less time is devoted to training students how to correctly score and assess nonmetric traits (Hefner *et al*. 2012). As a result, inter- and intra- observer error rates for morphoscopic traits can be quite high between individuals with varying experience levels. Despite some difficult measurements in the subtrochanteric and pubic regions (Adams and Byrd 2008), metrics are easily obtained and generally produce low levels of inter- and intra- observer error. Perhaps most importantly, metric traits are amenable to robust statistical analyses, while morphoscopic traits lacked statistical backing until recently due to the categorical nature of the data.

Despite the statistical and methodological problems associated with morphoscopic traits, forensic anthropologists have historically been successful in identifying the ancestral background of skeletonized remains (Birkby *et al.* 2008; Hurst 2012; Konnigsberg *et al.* 2009; Sauer 1992). Konnigsberg *et al.* (2009) attribute this, in part, to the fact that forensic anthropologists typically know some background of the case, and in particular, where the remains originated. Therefore, forensic anthropologists use *a priori* knowledge to narrow down the list of possible groups of people who live in a particular area where the remains were recovered. For an example, Konnigsberg and coauthors show how an individual recovered from Iowa was unlikely to be of Polynesian or African ancestry, in which the individual was metrically classified in FORDISC, due to the homogenous population structure of Iowa, which is dominated by individuals of European descent.

In 1992 Sauer posed the rhetorical question: "*If races do not exist, how are forensic anthropologists so good at identifying them*?" Sauer (1992) hypothesized that there is a correlation between skin color or sociocultural race and skeletal form. Additionally, he argued that the traditional race concept is not validated by the ability of forensic anthropologists to detect differences between populations because it is the forensic anthropologist's role to translate biological reality into meaningful sociocultural reality (Brace 2005). In their study of Black and White individuals from the FDB, Ousley *et al.* (2009) found that there is indeed a correlation between skin color (race) and craniofacial form. Ousley and coauthors were able to correctly classify modern crania into Black and White groups in excess of 90% of the time. They argue that differences between Black and White individuals exist despite gene exchange between these two groups for over 200 years. That is, differences that arose when ancestral populations were on different continents are still detectable in modern populations despite gene flow. Therefore, forensic anthropologists are capable of determining the ancestry of skeletal remains for these two groups with relatively high degrees of accuracy.

In response to legislative rulings and critiques of nonmetric trait lists, there has been a recent surge in re-assessing the anthropological methods used for ancestry estimation due to the lack of scientific vigor associated with these methods. In particular, anthropologists have reexamined cranial morphology (Hefner 2007, 2009; Hefner *et al.* 2014; Hefner and Ousley 2014; Hurst 2012; Klales and Kenyhercz 2014), dental morphology (Edgar 2005, 2013), and dental metrics (Pilloud *et al.* 2014) to develop population frequencies, known accuracy and error rates, and precision estimates within statistical frameworks. Notably, Hefner (2009) analyzed 11 of Rhine's (1990) often-used morphoscopic traits in African, European, East Asian, and Native

American samples, including anterior nasal spine (ANS), inferior nasal aperture (INA), interorbital breadth (IOB), malar tubercle (MT), nasal aperture width (NAW), nasal bone contour (NBC), nasal overgrowth (NO), postbregmatic depression (PBD), supranasal suture (SNS), transverse palatine suture (TPS), and zygomaticomaxillary suture (ZMS). Rather than relying on dichotomous, present or absent scores, Hefner developed ordinal scores and diagrammatic representations for the 11 traits. Hefner found that the range of frequencies exceeded expectations: most traits were found in all groups at varying levels (0.7 – 92.9%), indicating significant overlap between populations. This also shows that the trait lists long utilized by forensic anthropologist ignore within-group variation and simplifies traits into typological racial classifications.

Despite the overlap in morphoscopic trait expressions and frequencies, numerous traits correlate with the geographical groupings used by Hefner (2009), indicating that they can be used for ancestry assessment. However, Hefner argues that the traits need to be used within a statistical framework. Of the statistical methods Hefner used to analyze the traits (Bayesian, k-nearest neighbor, logistic regression), logistic regression performed the best and resulted in cross-validated correct classification rates over 90%, which is consistent with the correct classification rates for metric analyses (i.e., FORDISC). Additionally, intra- and inter- observer rates were low, which is attributed, in part, to more standardized descriptions and diagrammatic representations of the traits under analysis. Overall, this work demonstrates that morphoscopic traits can be used scientifically to determine ancestry, and in doing so, the typological race concept is not propagated as none of the traits exhibit frequencies of 100%.

Hefner and Ousley (2014) subjected the morphoscopic traits to several additional statistical tests in order to develop a usable methodological framework. In particular, after scoring the traits following Hefner (2009), Hefner and Ousley (2014) dichotomized the ordinal scores using the optimized summed scored attributes (OSSA) method to maximize the inter-group differences between American Black and White individuals. Accordingly, scores commonly observed in American Blacks were rescored as 0, and scores commonly observed in American Whites were rescored as 1. Using six morphological traits (ANS, INA, IOB, NAW, NBC, and PBD), an unknown cranium can be scored 0-6, with a score of 3 and below indicating American Black, and a score of 4 and above indicating American White. Hefner and Ousley found that artificial neural networks, OSSA, support vector machines, and random forest modeling produce correct classifications at least 85% of the time using morphoscopic traits. While these statistical methods are successful at classifying crania using nonmetric traits, the methods were limited to Americans of African and European descent.

Further work by Hefner (2015) demonstrates the utility of using morphoscopic traits in discriminant function equations in order to differentiate American Black, American White, and Hispanic individuals. Using seven traits, including ANS, INA, IOB, NAW, NBC, NO, and PBD, Hefner developed seven-, five-, and three-trait discriminant function equations for two- and three-group analyses. The seven-trait equation using three groups produced a cross-validated correct classification rate of 83.4%.

Subsequent research has further validated that the statistical application of morphoscopic traits can be used with high degrees of accuracy in different contexts. In particular, Klales and Kenyhercz (2014) found that Hefner's (2009) morphoscopic traits used with ordinal logistic regression statistics correctly classified African and European American individuals from the Hamman-Todd collection with high degrees of accuracy and low levels of intra- and inter-observer error. Further, Hurst (2012) used many of Hefner's (2009), Rhine's (1990), and Gill's (1998) morphoscopic traits to determine if such traits can differentiate Southwest Hispanics, African Americans, and European Americans. She found that eight traits correctly classified these three groups with relatively high accuracy and precision.

The success of morphoscopic traits in forensic ancestry assessment has been extended to dental remains. Edgar (2005, 2013, 2015) demonstrates that logistic regression and naïve Bayesian statistical frameworks can successfully differentiate African American, European American, and Hispanic American individuals with high levels of accuracy and known error rates. While Edgar (2013) found difficulty in differentiating Southwest Hispanics from South Florida Hispanics due to significant overlap in population variation, the dental morphoscopic methods work well to separate European Americans, African Americans, and Hispanic Americans with two-, three-, and four-trait combinations.

While many anthropologists utilize both metric and morphoscopic traits for ancestry estimation, it is unknown which method is better, or if one should be weighed more than the other. However, Hefner *et al.* (2014) found that metric and morphoscopic methods performed equally well in correctly classifying individuals. Further, the combined use of metric and morphoscopic methods using Random Forest Modeling resulted in even better classification rates than either method used on its own. Random Forest Modeling (RFM) represents a decision-tree data mining method wherein both morphological and metric data can be analyzed. As such, Hefner and coauthors advocate for the incorporation of RFM into future iterations of computer software packages such as FORDISC.

Postcranial ancestry assessment methods

While the majority of metric and morphological ancestry assessment methods have focused on the cranium and mandible, attempts have been made to ascertain if postcranial regions can also predict ancestry (DiBennardo and Taylor 1983). In particular, the proximal, diaphyseal, and distal femur has proved somewhat useful in population differentiation (Baker *et al.* 1990; Ballard 1999; Craig 1995; Gilbert and Gill 1990; Gill 1995; Gill 2001; Gill and Rhine 1990; McIlvaine and Schpartz 2015; Stewart 1979; Tallman 2015; Tallman and Winburn 2015; Walensky 1965; Wescott 2005). However, the femur's susceptibility to sex-related changes and biomechanical forces potentially complicate its use in forensic ancestry assessment (Shirley *et al.* 2015; Wescott 2006; Wescott and Srikanta 2008). Other postcranial regions used in ancestry assessment include the pelvis (Ayers *et al.* 1990; İşcan1983), spine (Duray *et al.* 1999; Marino 1997), and feet (Bidmos 2006; Kidd and Oxnard 2002). However, these methods produce rather equivocal results. Moreover, the postcranial ancestry assessment methods mainly differentiate individuals of African And European descent, or Native American from non-Native individuals only.

Spradley (2015) calculated discriminant functions from standard anthropometric measurements for individual and multiple postcranial elements in order to classify American Black, American White, and Hispanic individuals. Spradley's correct classification rates ranged from 17% to 75%, with the radius, ulna, and femur performing the best, and the os coxa and sacrum performing the worst. However, the cross-validated discriminant function classification rates based on multiple long bones were rather impressive: 72% for Hispanics, 85% for American Blacks, and 80% for American Whites. Spradley attributes the comparatively lower Hispanic correct classification rate to the variable Hispanic population histories, as the individuals comprising this group are from geographically separated countries, each with unique histories.

Shirley *et al.* (2015) provide geometric morphometrically derived discriminant function equations for the femur and tibia that were obtained from CT scans. While the CT scans provide a reliable and quick data acquisition method, Shirley and coauthors provide discriminant functions that are based on traditional and novel anthropometric measurements since CT scans are not ubiquitous. Shirley *et al.*'s cross-validated correct classification rates for the discriminant functions ranges from 72% to 83% for American Black and American White males.

Conclusions on ancestry

Biological anthropologists' search for differences in craniofacial morphology does not validate the biological race concept because of the incorporation of evolutionary theory, molecular theory and data, and advances in sociocultural constructions of race. All biological anthropologists understand that variation exists between populations. That variation is often patterned and can be identified genetically and morphologically. Forensic anthropologists document differences in cranial trait frequencies and craniofacial dimensions, particularly among the three major biogeographical ancestries currently living in the U.S., with comparatively advanced theories and knowledge in their tool kit compared to earlier researchers. The search for differences between these populations is useful in forensic anthropology because it is imperative in certain forensic contexts to scientifically assess the ancestral background for unknown remains (see Cox *et al.* 2006). While Konigsberg *et al.* (2009) found that the assessment of ancestry in a forensic case from Iowa was not helpful in contributing to a positive identification because of the homogeneous population structure of Iowa, the determination of ancestry is important in forensic contexts where diverse groups coexist (i.e., large urban areas, mass disasters, and military losses). For example, Cox *et al.* (2006) argue that the assessment of ancestry from skeletonized remains is crucial in New Zealand because the indigenous Maori have an intimate connection to their ancestors that requires the special treatment of Maori remains. Therefore, if forensic anthropologists refuse to assess ancestry and consequently fail to identify indigenous remains, they are placing their personal beliefs above those of the Maori, which causes undue harm. Thus, the work of Hefner (2009) and Edgar (2005, 2013, 2015) are important because these studies provide known error rates and correct classification rates for populations in which anthropologists work. These studies are very successful in correctly classifying the three major populations currently living in the U.S. because of the biological differences that arose on different continents under different selection pressures and population structures.

Conclusion: The Need for Revised Methods

The majority of biological profile methods, including the sex and ancestry assessment methods highlighted in this chapter were developed on African and European descended individuals. This is partly attributable to the demographics of the U.S. prior to circa 1950, and the lack of skeletal collections representing minority populations. However, the demographics of the U.S. are changing due to an influx of Hispanic, Asian, and Middle Eastern people. While anthropologists are addressing the need for revised biological profile methods for Hispanic populations (Birkby *et al.* 2008; Hefner 2015; Hurst 2012; Ross *et al*. 2015; Ross *et al.* 2004; Spradley *et al*. 2008), other minority populations, including Asian groups remain understudied. As more foreign skeletal collections become known and available to researchers, population-specific methods can be developed for many of the myriad groups that currently live in the U.S.

The paucity of biological profile methods developed from Asian populations is especially problematic in forensic contexts where Asian remains are likely to be recovered, including large western U.S. cities where significant populations of East and Southeast Asians reside. It is estimated that Asian groups make up 6% of the U.S. population, and are presently the fastest growing ancestral demographic in the U.S. (Hoeffel *et al*. 2012). The Asian classification includes a geographically and culturally diverse group, defined by the U.S. Census as Asian Indian, Bangladeshi, Bhutanese, Burmese, Cambodian, Chinese, Filipino, Hmong, Indonesian, Japanese, Korean, Laotian, Malaysian, Nepalese, Pakistani, Sri Lankan, Taiwanese, Thai, and Vietnamese (Jones 2012). Of these, East (Korean and Japanese) and Southeast (Vietnamese) Asian individuals make up approximately 26% of the Asians living in the U.S. (Hoeffel *et al.* 2012).

Approximately 75% all Asians living in the U.S. reside in just 10 states: California, New York, Texas, New Jersey, Hawaii, Illinois, Washington, Florida, Virginia, and Pennsylvania (Hoeffel *et al.* 2012). Further, of the 193 unidentified Asian individuals listed in the National Missing and Unidentified Persons System (https://www.namus.gov) as of 29 March 2014, 67% were recovered in New York, California, Texas, and Florida. Of these, California has the largest populations of Asian Indian, Chinese, Filipino, Japanese, Korean, and Vietnamese individuals (Hoeffel *et al.* 2012). Specifically, the L.A. County Coroner reports that Asian individuals represent approximately 7% of their cases (Molina *et al.* 2010), while the San Diego County Medical Examiner reports that 5.3% of their cases are represented by Asian individuals (Wagner 2012). Similarly, the King County Medical Examiner's Office in Seattle reports that Asian individuals represent approximately 7% of their cases (Fleming and Harruff 2011). Further, in Hawaii, Asian individuals make up approximately 32% of the homicide cases investigated by the Honolulu County Medical Examiner's Office (Goodhue 2011). As the population of Asian groups is increasing at a rate of 46%, forensic cases involving Asian individuals are also likely to increase (Hoeffel *et al.* 2012; Jones 2012).

Circumstances involving mass disaster forensic response further necessitate the development of Asian-specific biological profile methods. In particular, the December 2004 Southeast Asian tsunami resulted in the death of approximately 228,000 individuals from 58 countries (De Valck 2006). The vast majority of the victims were from Asian countries including Indonesia, Sri Lanka, India, and Thailand, which were among the hardest hit. Within two years of the disaster, more than 92% of the foreign nationals – mostly from Europe – were identified through antemortem dental records (Schuller-Gotzburg and Suchanek 2007). However, the identification rates were significantly lower for individuals from countries where dental care is less common. The lack of expedient dental identifications for local Southeast Asians led to the reliance on other identification methods, including fingerprints, DNA, and anthropological examination (De Valck 2006). As such, the lack of Asian-specific methods could misclassify individuals and ultimately hinder identifications.

A mass disaster in the U.S. could also result in a large number of Asian decedents. Of the 373 foreign nationals killed in the 11 September 2001 attacks, Interpol (http://www.interpol.int) reports that 4% were from an Asian country, and many more victims were Asian American individuals. Further, the identification of the 213 Korean nationals who died in the 6 August 1997 Korean Airlines 801 crash in Guam, a U.S. territory, was hindered by the inability to quickly obtain antemortem medical records, significant cultural differences, and the fact that entire families perished (Saul and Saul 2003). The extreme fragmentation, burning, and rapid decomposition of the remains further prolonged identification efforts and caused added stress to the decedents' loved ones. Therefore, the application of Asian-specific biological profile methods could expedite the identification of individuals in these contexts by narrowing the list of potential decedents.

The lack of population-specific methods available for use on individuals of Asian descent has led to the ongoing application of methods developed on non-Asian populations. In particular, metric and nonmetric data obtained from pre-contact Native American assemblages were assumed to represent Asian remains due to their shared genetic history. The use of Native Americans as biological proxies for Asians can be directly tied to the development of the theory that the New World was populated by groups who traveled from Northeast Asia, which was first postulated by Jose de Acosta in the 1590s (Bonnichsen and Steele 1994). As more sophisticated archaeological and genetic models were developed to explain the migration and dispersal of Asian populations into the New World, the shared population history and genetic relationship of Native Americans and Asians was cemented. Researchers found that most present-day Native

Americans belong to five mitochondrial DNA haplogroups, which are also observed in lineages throughout Asia (Gonzalez-Jose *et al.* 2008; Schurr *et al*. 1990).

Moreover, the morphological cranial trait expressions and frequencies shared between pre-contact Native Americans and Asians during the Late Pleistocene were grouped together to represent “Mongoloid” traits, despite the heterogeneous nature of these traits (Gonzalez-Jose *et al.* 2008). Subsequently, in the absence of modern Asian populations available for study, forensic anthropologists such as Rhine (1990) used only three modern and nine pre-contact Native American skulls to identify the typical morphological traits that are useful in identifying “Mongoloid” (i.e., Native American and Asian) individuals. Though this trait list has been used extensively in forensic anthropology casework to identify individuals of Asian descent, the assumption that *ancient* Native Americans can serve as biological proxies for *modern* Asians has not been systematically tested. Reliance on North American collections, which lack Asian individuals, has propagated the probable misapplication of methods developed on non-Asian populations in forensic contexts.

CHAPTER III: Population Histories Of Japan And Thailand

This chapter briefly discusses the population histories of Japan and Thailand, highlighting the major theories regarding the peopling of Japan and Southeast Asia using genetic, dental, archaeological, and skeletal evidence. While questions as to the origins of modern Japanese and Thai populations are beyond the purview of this study, the peopling hypotheses presented here importantly demonstrate that modern East and Southeast Asian populations have undergone significantly different population histories despite having distantly shared origins. Further, while considerably more is known about the population history of Japan compared to that of Southeast Asia, much debate surrounds the modern origins of both geographic regions. However, the major peopling models and debates for the two biogeographic populations are remarkably similar. That is, the majority of the debates situate models showing long-term continuity of populations since the late Pleistocene giving rise to modern populations against models that demonstrate gene flow from immigrant populations, resulting in entirely replaced or variably admixed modern populations. Also similar is the introduction and widespread adoption of wet-rice agriculture in Japan and Southeast Asia, which is central to modern identity constructions in both regions.

Japan

Scholarly interest in the peopling of Japan (Figure 3.1) emerged as early as the 1880s, when Tsuboi Shogoro established anthropology as an academic discipline in Japan and initiated the search for Japanese origins (Low 2012). While conservative and traditional thinkers argued

Figure 3.1. Japanese archipelago in relation to mainland Asia. Tokyo represents the location of the Jikei and Chiba University's collections used in the current research (see Chapter IV). (Map adapted from http://thefutureofeuropes.wikia.com).

for the homogeneity of the Japanese – a culture bound by by a single unique culture, language, and identity – Shogoro maintained that Japan represents a mixture of races. Japan was never colonized by European nations, and was itself a colonizing empire. In fact, the rise and expansion of the Japanese empire provided fieldwork opportunities for scholars to study Japan's origins, and included comparative body measurements of the different groups that were encountered during colonization activities. As a result, many Japanese political leaders used the results from anthropological studies to substantiate claims of Japanese superiority, nationalism, and homogeneity (Low 2012).

Prior to more modern models for the peopling of Japan, much debate existed as to the origins of the modern Japanese. The majority of the debates centered around three main theories: transformation theory, whereby modern Japanese descended from indigenous population *in situ* who were in Japan for thousands of years; replacement theory, whereby indigenous inhabitants of the Japanese archipelago were replaced by immigrants from mainland Asia; and the hybridization theory, whereby modern Japanese populations represent an admixture between indigenous populations who inhabited Japan for thousands of years, and more recent immigrants from mainland Asia (Brace *et al*. 1989; Low 2012; Hammer *et al*. 2006; Hanihara 1991; Nakashima *et al.* 2010). The prevailing idea up to the post-WWII era proffered that local, indigenous populations (the Jomon) gave rise to modern Japanese populations through long-term population continuity (Low 2012). Low (2012) argues that this idea was propagated through public policy and the work of Japanese physical anthropologists mainly because it idealized Japan as a homogenous country with a deep and important history in Asia.

The aftermath of WWII found Japan in political and economic turmoil, and a unifying theory of Japan as being made up of homogenous peace-loving agriculturalists arguably helped the collective Japanese psyche to reunite, rebuild, and move on (Low 2012). However, the Ainu, who were known as the indigenous inhabitants of the northern Hokkaido Island, presented a problem with the transformation theory. Collectively, the modern Japanese were unsure how the Ainu fit into the history of Japan, as they exhibit hirsutism, lighter skin tones, and different facial features compared to Japanese majority. As such, many Japanese physical anthropologists and politicians argued that the Ainu were a separate race of people originating from the Neolithic era who failed to evolve and achieve the great level of success that was characteristic of the modern Japanese empire. Additionally, some Japanese argued that the Ainu were Caucasoid (Brace *et al.* 1989). According to Low (2012), the Japanese became focused on studying the Ainu, which turned into a nationalistic pursuit aimed at identifying the origins of modern Japan. This led to the exploitation of the Ainu through the plundering of Ainu graves and corpses and the display of living Ainu in Japanese and world-wide expositions, including in the U.S (Low 2012). While some late 19th century Japanese physical anthropologists suspected that the Ainu were direct descendants of the Jomon, the primitive race idea prevailed, and the Japanese majority considered themselves largely to be descendants of the Jomon and wholly unrelated to the Ainu.

Hanihara (1991) was one of the first scholars who synthesized craniometric and dental studies to argue for a hybridized model of modern Japanese origins. This is called the Dual Structure Model (DSM) because he argued that the modern Japanese people were the product of admixture between the indigenous Jomon, who were hunter-gatherer-collectors that had lived throughout the Japanese archipelago for at least 13,000 years, and the Yayoi, mainland Asian immigrants who migrated to Japan approximately 2,300 years ago and brought with them wet-rice agriculture. While anthropologists had known of the Yayoi migration for a considerable amount of time, those who advocated for the transformation (long-term continuity) theory argued that no significant gene flow occurred between the Yayoi and the Jomon. Rather, they posited that the Yayoi migration resulted in a cultural transmission only, which eventually revolutionized agricultural practices throughout Japan. Hanihara (1991) argued that the Jomon migrated into Japan 20,000 – 13,000 years ago, when cold conditions during the Last Glacial Maximum connected island and mainland Asia through lowered sea levels. Following his theory, the Jomon originated from Southeast Asian populations who migrated northward and occupied the entirety of the Japanese archipelago, from Hokkaido in the north to the Ryukyu Islands in the south. Due to rising sea levels approximately 13,000 years ago, the Jomon were isolated from mainland Asia, resulting in an absence of gene flow for at least 10,000 years.

The Yayoi, according to Hanihara (1991), were advanced agriculturalists who migrated from the Korean peninsula due to environmental instability on the mainland, bringing with them rice paddy agriculture, metal working, and political systems that eventually evolved into the powerful Yamato political structure that came to dominate Japan and other parts of Asia (i.e., Korea and Taiwan). Accordingly, the Yayoi were argued to have originated from East/Northeast Asian populations. The modern Japanese, then, are considered genetically admixed between the Jomon and the Yayoi. The Ainu, he further argued, were descended directly from the Jomon, and therefore were relatively homogenous in their genetic and craniofacial structure, and were originally located throughout the archipelago. Similarly, the inhabitants of the Ryukyu Islands in the south were also considered to be related to the Ainu, and hence, descended from the Jomon.

Following this model, the Hokkaido Ainu and Ryukyuans did not exhibit Yayoi admixture because they occupied geographically isolated areas that prevented easy migration from the main island of Japan (Honshu). As such, the northern and southern extremes of Japan remained relatively untouched from mainland Asian populations until modern Japanese populations systematically colonized the north and south islands in the mid-1800s (Low 2012).

Hanihara's (1991) DSM primarily relies on craniometric and dental data. In particular, he cites Turner's (1990) findings that there are two distinct dental morphologies present in South and East/Northeast Asia. Turner found a generalized and primitive dental pattern of nonmetric dental traits in Southeast Asians (sundadont dental complex), and a more derived and advanced dental pattern in East and Northeast Asians and Native Americans (sinodont dental complex). According to Turner, the modern Japanese exhibit mostly sinodont dentition, reflecting considerable gene flow from East/Northeast Asian sinodant populations (from the Korean peninsula). Conversely, the Ainu exhibit sundadont dentition, which according to Hanihara (1991), directly links the Ainu with Southeast Asian, Polynesian, and Micronesian populations. Turner (1990) argues that the sundadont dentition arose early *in situ* in Southeast Asian prehistory, likely the result of northern (possibly Chinese) populations exchanging genes with, or replacing, local, Australo-Melanesians who occupied much of Southeast Asia. The Southeast Asian sundadonts (named after the Sunda shelf that connects mainland Asia and the Pacific Islands) migrated northward, and the sinodont dental pattern subsequently evolved from the sundadont morphology. Though the sinodant dental complex could have arisen from (unknown) selective forces, Turner argued that this pattern likely originated due to small effective population sizes, bottlenecks, and isolation during the migration northward.

Hanihara (1991) also demonstrates that the Yayoi are closely related to northern Asian populations (from Mongolia, Northeast China, and Siberia) based on craniofacial morphology, such as brachycephaly. Accordingly, the Yayoi are descended from cold-adapted populations. Hanihara used craniofacial morphology to argue that there are differential rates of Yayoi immigration throughout Japan. Due to its proximity to the Korean peninsula, the more southern island of Kyushu or southern Honshu would have likely represented the entry point for Yayoi groups migrating into Japan. Therefore, the Yayoi populations were significantly larger in the western part of Japan, and this is reflected in modern Japanese skeletal morphology: the Yayoi (northern Asian) morphology (i.e., brachycephaly) is seen in greater proportions than the Jomon (southern Asian) morphology. This proportion decreases moving east. That is, modern Japanese populations in the east exhibit less Yayoi morphological proportions. To further this assertion, Hanihara cites evidence from non-human species; namely, dog and mice lineages. Because dogs and mice are symbiotic with human populations, they exhibit similar population substructures as humans. Dog breeds and mice populations in western Japan exhibit genetic affiliations with northern Asian lineages (as they would have migrated with northern Yayoi), while dog breeds and mice populations in eastern Japan exhibit genetic affiliations with southern Asian lineages (as they would have migrated with southern Jomon). Hanihara further argues that this east-west dichotomy in human and non-human population substructures is also reflected in cultural characteristics including differences in dialect, burial practices, subsistence strategies, and food, all of which are still seen today. Therefore, he argues, that the DSM is ongoing in the modern era.

While Hanihara's (1991) DSM mainly incorporated craniofacial and odontological evidence to argue that modern Japanese are admixed between Yayoi (northern Asian) and Jomon (southern Asian) populations, subsequent models incorporating mtDNA, Y-chromosome, and skeletal evidence have variably supported, augmented, and refuted Hanihara's assertions. The majority of anthropologists believe that the modern Japanese are a hybridized population rather than a transformed or replaced population. However, most argue that Hanihara's (1991) model is too simplistic to explain Japanese population variability.

Largely in support of Hanihara's (1991) DSM, Fukase *et al*. (2012) argue that the Jomon indeed inhabited the entirety of the Japanese archipelago, and were relatively homogeneous throughout. However, Fukase and coauthors found that the Okinawa Jomon (in the Ryukyu Islands) exhibited flatter faces than the Honshu Jomon. They argue that a Jomon culture and biology inhabited the entirety of the Japanese archipelago and were mostly similar throughout. Therefore, the Ainu and the Ryukyuans are related and directly descended from the Jomon.

Using mtDNA D-loop data, Horai *et al.* (1996) found that the modern Japanese are the product of Jomon (approximately 35%) and Yayoi (approximately 65%) intermixing, further supporting the hybridization model. The modern Japanese show significant mtDNA similarities with mainland Asian populations, while the Ainu show significantly reduced mainland similarities. However, they argue that the Ainu and the Ryukyuans are unrelated. As such, the Ainu and the Ryukyuans were likely separate populations at the time of Yayoi immigration. This is also found with facial flatness studies (Dodo *et al*. 2000) and craniofacial nonmetrics (Dodo *et al.* 1998), which demonstrate that the Ainu/Jomon are not related to the Ryukyuans. However, based on metric and nonmetric morphological similarities, the Jomon and Ainu are related (Dodo and Kawakubo 2002; Kawakubo *et al.* 2009). Additionally, Dodo *et al.* (1998, 2000) argue that the Ryukyuans are more closely aligned with North Asian populations, including the Yayoi, Kofun, and Okhotsk populations.

Bannai *et al.* (2000) analyzed human leukocyte antigens (HLA) and found that the Ainu are closely aligned with the Tlingit (Alaska), and they are both intermediaries between East Asians and South American Amerindians. The genetic distances between the Ainu and all East Asian populations in this study were small, suggesting a relationship between the Ainu and East Asian populations. As such, this contradicts Hanihara's (1991) DSM. However, the Ainu and the modern Japanese do not share many alleles, suggesting that the modern Japanese are descended primarily from mainland Asian populations. Also using HLA data, Nakaoka *et al.* (2013) found that North Asian groups are situated between Jomon/Ainu and Native American populations, suggesting that Native American and Jomon lineages originated in Northeast Asia. Similarly, utilizing Y-chromosome data, Hammer *et al.* (2006) found that the Jomon/Ainu are more closely aligned with Central Asian populations, including populations from the Altai Mountain region in China and Tibet. They also found that the modern Japanese are the product of Jomon and Yayoi population admixture; however, the Yayoi contribute more to modern Japanese populations genetically. The major haplogroups seen in Japanese populations are C, D, N, and O (most common in Japan); however, the Ainu do not exhibit the O haplogroup. Also contradicting Hanihara's (1991) DSM, Hammer *et al.* (2006) found that the O haplogroup is found in high frequencies in Southeast Asia, suggesting that the Yayoi possibly originated from Southeast Asia.

The majority of the mtDNA and Y-chromosome evidence suggests that the Jomon, and therefore Ainu, originated from Central or North/Northeast Asian populations rather than from Southeast Asian populations (Nakashima *et al.* 2010). This is further supported by craniofacial metric studies conducted by Hanihara and Ishida (2009), Ishida *et al.* (2009), and Nakashima *et al.* (2010) who found that the Jomon/Ainu populations likely originated in the north and migrated southward. In particular, Ishida *et al.* (2009) found craniofacial similarities in the Ainu and Okhotsk group, indicating that the Okhotsk group likely migrated to Hokkaido and exchanged genes with the Ainu from more northern islands (Hanihara *et al.* 2008). Additionally, Ishida *et al.* (2009) found that the Okhotsk are morphologically similar to Artic groups, while the Jomon/Ainu group were similar to Siberian populations. However, Ishida *et al.* (2009) and Pietrusewsky (1999, 2004) found no relationship between the Ainu and the Ryukyuans, who exhibit East Asian morphological characteristics. Somewhat surprisingly, Ishida *et al*. (2009) found that the Yayoi exhibit minimal morphological variability, which they attribute to a founder effect, resulting from low effective population sizes. Hanihara and Ishida (2009) further argued for the Northeast Jomon/Ainu origin by demonstrating that they migrated in a north-to-south trajectory. They found that the Hokkaido Jomon/Ainu in the north exhibit significant craniofacial diversity, and that the populations south and east of Hokkaido exhibited continually decreasing craniofacial variability. This led them to conclude that the Jomon populations experienced bottlenecks, isolation, and small effective population sizes as they extended southward from Hokkaido. As such, they argue that the Jomon are from Northeast Asia rather than Southeast Asia, further suggesting that the Ainu, who are at least partially descended from the Jomon, are also of northern origin.

The mtDNA, Y-chromosome, and craniofacial evidence suggest that the peopling of Japan is significantly more complicated than the original DSM model proposed by Hanihara (1991). While much of the hybridization component holds up against newer evidence (i.e., Yamaguchi-Kabata *et al.* 2008), the majority of the studies indicate that the Ainu, who are at least partially descended from the Jomon, are from East/Northeast Asian populations. However, this is further complicated by the migrations of Okhotsk people into northern Hokkaido (Hanihara *et al*. 2008; Ishida *et al.* 2009) and potentially Yayoi migrations from northern Honshu into southern Hokkaido (Matsumura 2001). As such, the Ainu are not the homogenous, primitive race advocated by early 19th century physical anthropologists, or a relic southern population living in the north as advocated by Hanihara (1991). In fact, Low (2012) argues that nationalist scholars such as Hanihara propagate the notion that the Ainu are the remnants of a proto-Japanese culture that failed to evolve for 2,000 years. Further, modern Japanese populations are likely admixed or hybridized; however, considerable debate surrounds the origins of the contributing populations.

Southeast Asia and Thailand

Western interest in the origins of modern Thai (Figure 3.2) popuations emerged at least as early as the 16th and 17th centuries when Euorpeans first came into contact with people from the Kingdom of Siam (Highman 1996). However, like Japan, Thailand was never colonized by a European nation, and Thai scholars have been personally invested in searching for the origins of Thai people. Arguably, the purpose of much of this scholarly pursuit has been to preserve Thai ethnic identity and advance political agendas (Baker and Phongpaichit 2005). While Southeast

Figure 3.2. Thailand in relation to neighboring Southeast Asian countries. Khon Kaen and Chiang Mai represent the locations of skeletal collections used in the present study (see Chapter IV). (Map adapted from http://www.lahistoriaconmapas.com).

Asia’s history extends deep into antiquity, relatively few archaeological sites in Southeast Asia produce well preserved bone due to myriad taphonomic factors, thereby limiting bioarchaeological studies compared to Japan, Europe, and North America (Tayles and Oxenham 2006; Shackelford and Demeter 2012). As a result, considerable uncertainty exists regarding the peopling of Southeast Asia, which includes the modern countries of Myanmar, Thailand, Cambodia, Laos, Vietnam, Malaysia, Indonesia, and the Philippines.

Despite the paucity of skeletal evidence that allows for a clear picture regarding the peopling of Southeast Asia, two main models persist: the Two-Layer model and Regional Continuity model. Both models maintain that anatomically modern humans had settled regions of Southeast Asia by approximately 40,000 years ago, and a related indigenous Australo-Melanesian population occupied Southeast Asia during the late Pleistocene and early Holocene by at least 26,000 years ago (Anderson 1990; Highman 2002). The Australo-Melanesian population exhibited dolicocephalic crania, prominent glabellae, robust mandibles, large teeth, prognathism, and slender, long-limbed bodies (Matsumura 2006). Some modern hunter-gatherer-collector populations in Malaysia, the Andaman Islands, and the Philippines, who are often referred to as “Negritos,” also display these morphological characteristics, leading some to conclude that they represent populations directly descended from Australo-Melanesians (Matsumura 2006). Additionally, numerous skeletal remains recovered throughout Southeast Asia and dating to at least 10,000 years ago display morphological characteristics similar to indigenous Australo-Melanesians (Matsumura 2006).

Proponents of the Two-Layer model argue that Neolithic immigrants from North and/or East Asia either entirely replaced, or exchanged genes with, the indigenous Australo-Melanesian populations in Southeast Asia after their migration south, resulting in the modern Southeast Asian morphology (Matsumura and Hudson 2005; Matsumura 2006). In contrast to the Australo-Melanesian morphology, modern Southeast Asian populations exhibit brachiocephalic crania, gracile crania and postcrania, and reduced stature, leading proponents of the Two-Layer model to conclude that they are unlikely directly descended from Australo-Melanesian populations (Howells 1997). Following this model, the northern immigrants likely originated from the Yangzi Valley of China, where wet-rice agriculture developed approximately 8,000 years ago and was brought into Southeast Asia approximately 5,000 years ago with the northern immigrants (Brace *et al.* 1991; Howells 1997; Matsumura 2006).

The Two-Layer model is supported by archaeological findings (Bellwood 1993; Highman 1996, 2002), linguistics (Diamond and Bellwood 2003; Higham 2002), skeletal analyses (Brace *et al.* 1991; Brace and Tracer 1992; Matsumura and Hudson 2005; Matsumura 2001, 2006; Nakahashi 1993), and genetic studies (Letrit *et al.* 2008; Nakaoka *et al.* 2013; Tan 2001). In particular, mtDNA studies by Tan (2001) document genetic similarities between Chinese and Southeast Asian skeletal samples. Additionally, linguistic and archaeological studies demonstrate a Chinese/Taiwanese origin for wet-rice agriculture and Southeast Asian languages (Diamond and Bellwood 2003). Also telling, the arrival of wet-rice agriculture in Southeast Asia coincides with the arrival of large ceramic assemblages that lack ceramic precursors anywhere in Southeast Asia, and are consistent with ceramics found in China (Anderson 1990; Sorensen 1972).

Much of the support for the Two-Layer model derives from physical anthropological studies. In particular, Matsumura (2006) analyzed 21 nonmetric dental traits from 25 Southeast Asian archaeological sites to calculate population relationships. Accordingly, the Northeast

Asians (Mongolians, Chinese, and Japanese) cluster together and the pre-Neolithic and Neolithic Southeast Asians separately cluster with the Andaman Islanders and Australian Aborigines. The majority of the modern Southeast Asian populations occupy an intermediate position. Further, analyses of dental measurements indicate that modern Southeast Asian populations share similarities with Northeast Asians, suggesting that Northeast Asian populations contributed genetically to Southeast Asian populations (Matsumura 2001, 2006).

The Two-Layer theory is further supported by Matsumura and Oxenham (2014), who analyzed 21 nonmetric dental traits from 58 North and Southeast Asian populations, and found clinal distributions for 15 of the traits. Matsumura and Oxenham found similarities between Southeast Asians and Australo-Melanesians, and between Northeast Asians and Native Americans. Additionally, considerable heterogeneity exists in the Southeast Asian populations, and much overlap exists between the Southeast and Northeast Asian populations. The authors conclude that modern Southeast Asian populations are markedly heterogeneous and share many dental traits with modern Northeast Asian populations, which lends support to the Two-Layer model, whereby gene flow resulted from a demic agricultural migration from the north.

Following the Two-Layer model for the peopling of Southeast Asia, the northern geographic origin for Southeast Asian populations is likely China (Letrit *et al*. 2008; Matsumura 2006). Shackelford and Demeter (2012) found that cranial morphological characteristics found in China roughly 30,000 years ago are also observed in coastal and insular populations in Southeast Asia until the prehistoric period (around 6,000 years ago). As such, the authors argue that the continuous southern migration of populations from China into Southeast Asia was precipitated by climatic and environmental degradation in the north during the last glacial period.

Shackelford and Demeter also found that populations from inland Southeast Asia exhibit somewhat different morphological characteristics compared to those from the coastal and insular regions, indicating different migrations and/or routes from 30,000 years ago to roughly 1,200 years ago.

The Holocene-era southern migration from China hypothesis (Two-Layer model) is further supported by Letrit *et al.* (2008). Letrit and coauthors extracted mtDNA from 42 individuals recovered from two archaeological sites dating from 3,500 – 1,000 years ago in northeastern Thailand and compared the results to sequences obtained from 74 modern Thai individuals and populations north of Thailand. The authors found that the Southeast Asian groups largely cluster together, while the northern groups cluster together. Additionally, the Southeast Asia cluster is closest to modern individuals living in China. The prehistoric Thai populations are closely related to each other, and are very similar to a modern population living in northwestern Thailand. The authors argue that their findings support the hypothesis that groups migrated from southern China into what is now Thailand during the early second millennium. Subsequently, the populations living in Thailand intermixed with Khmer populations, who migrated into what is now Cambodia around 4,000 years ago, leading to the Khmer subjugation of Thai people during the 12th and 13th centuries.

In contrast to the Two-Layer model, proponents of the Regional Continuity model argue against a Neolithic expansion southward from China. Instead, they argue that Southeast Asian populations evolved *in situ* from late Pleistocene Australo-Melanesian populations who later migrated northward (Hanihara 2006; Turner 1987, 1990, 2006). As evidence, Turner (1987, 1990, 2006) cites the differences between the simple sundadont dental complex displayed by modern Southeast Asians since the late Pleistocene and the derived sinodont dental complex displayed by the North/East Asian populations. Following this theory, the sundadont dental complex developed locally in Southeast Asia and gave rise to the more derived sinodont dental complex exhibited by northern Asian populations as the southern populations migrated north (Hanihara 1991; Turner 1990). Turner (1990) hypothesizes that the evolution of the specialized sinodont dentition arose approximately 30,000 years ago due to small effective population sizes, isolation, and bottlenecks rather than selection pressures alone. The Sunda shelf, which connects mainland and island Asia, surfaced during the Last Glacial Maximum (21,000 – 18,000 years ago), which lowered sea levels 100 – 150 meters, thus allowing populations to migrate northward from Southeast Asia. Accordingly, Northeast Asian populations contributed genetically little to Southeast Asian populations, as this model places Southeast Asia as the origin for Northeast Asian populations. As further evidence, Turner (1990) cites the presence of the sundadont dental complex in the Japanese Jomon and Ainu populations, and argues that they retain the sundadont dental complex because they originated in Southeast Asia and were isolated for thousands of years after sea levels rose. Turner asserts that the sundadont and sinodont dental complexes remained distinct due limited gene flow between North/East and Southeast Asian populations.

To further investigate the peopling of Southeast Asia, Pietrusewsky (2006) measured archaeologically derived crania from Thailand, Laos, Vietnam, north China, and Japan and compared them to modern and near-modern individuals from Oceania, Australia, Southeast Asia, and East Asia. The minimum frontal breadth, nasion-bregma chord, maximum cranial breadth, and maximum cranial length contribute most to the differences documented between the groups. In Pietrusewky’s (2005, 2006) analyses, modern populations from East and Southeast Asia consistently form separate clusters with little to no overlap, indicating to him that there were separate origins for the two broad groups. Therefore, Pietrusewsky (2006) argues that the results support entirely separate origins for Southeast and East/North Asian populations. Further, the groups from the Pacific region (Australia, Tasmania, New Guinea, and Melanesia) are significantly different than groups from East Asia, Southeast Asia, Micronesia, and Polynesia. As such, Pietrusewsky argues that two separate lineages gave rise to these two broad groups. Additionally, a strong relationship exists between prehistoric and modern Southeast Asian crania, while little relationship exists between the East/North Asian and Southeast Asian groups. Accordingly, Pietrusewsky argues that the craniometric data support long-term evolution and subsequent population continuity in East/North Asia and Southeast Asia rather than complete displacement or admixture.

Positioned somewhat between the Two-Layer and Regional Continuity models, Hanihara's (2006) analysis of 34 cranial measurements on individuals from 103 population groups from Southeast Asia, Northeast Asia, South Asia, and the Middle East shows a clear distinction between the Australian/Melanesian, East/Southeast Asian, and Northeast Asian samples. Hanihara argues that because the East and Southeast Asian groups are not morphologically similar, a population from the north did not entirely replace the groups living in Southeast Asia. Rather, East/Northeast Asia and Southeast Asia likely form two phylogenetic units; however, some gene flow likely occurred between East/Northeast and Southeast Asians via multiple migrations of northern populations into Southeast Asia.

While the majority of studies advocate for the Two-Layer model, an early (late Pleistocene) northward migration of Southeast Asian populations is supported by Y-chromosome haplogroup studies. Shi *et al.* (2005) and Su *et al.* (1999) examined the O3-M122 haplogroup in 2,332 males, which is common in East Asian populations. The authors found that the Southeast Asian samples are more polymorphic than the Northeast Asian samples, suggesting a Southeast Asian origin for the O3-M122 haplogroup. Additionally, Shi and coauthors estimate that the haplogroup likely emerged 30,000 – 20,000 years ago, which coincides with a northward expansion. Shi *et al.*'s (2005) findings are, however, contradicted by Demeter's (2006) study of fossil remains dating from 67,000 to 1,200 years ago. Demeter's craniometric analysis of 44 fossil specimens and 100 modern individuals from East and Southeast Asia demonstrate that anatomically modern human populations inhabited East/Northeast Asia, including the Japanese archipelago, and Southeast Asia, including Thailand, by 67,000 years ago. These populations likely originated from Africa, following the Out of Africa hypothesis. Demeter argues that the northern population migrated south around 30,000 years ago due to environmental degradation in the north and extensively interbred with the populations living in the south. While gene flow occurred, the two populations also retained their distinct morphologies.

While less is known about the peopling of Southeast Asia compared to the Japanese archipelago, current archaeological, linguistic, skeletal, and genetic evidence suggests that Southeast Asia was settled due to an argriculturally demic expansion or migration into the region from a more northerly region during the Neolithic (Oxenham and Tayles 2006). The majority of the skeletal evidence largely supports the the Two-Layer model (out of China or Northeast Asia): Australo-Melanesians who inhabited Southeast Asia interbred with northern agriculturalists (likely from China's Yangtze Valley) who migrated southward (Matsumura 2006; Shackelford and Demeter 2012). Local populations who still live in Southeast Asia (i.e., "Negritos") retain much of the Australo-Melanesian form, indicating that the Australo-Malanesian populations and associated morphological characteristics were not entirely replaced. While proponents for the Regional Continuity model cite the craniometric and dental differences between East/Northeast and Southeast Asian populations as evidence for two distinct and largely unrelated populations (Pietrusewsky 2006; Turner 1990), Freas (2008) contends that the documented differences fail to sufficiently exclue the Two-Layer model, as both regions have undergone long-term population continuity into the modern era. As such, differences between East/Northeast and Southeast Asian populations are expected. Therefore, it is generally argued that modern Southeast Asian populations are admixed between Australo-Melanesians and the northern immigrants (Letrit *et al.* 2008; Matsumura 2006; Oxenham and Tayles 2006).

Conclusion

While the Japanese and Thai do not represent the entirety of morphological skeletal variation within Asia, they exemplify two geographically disparate populations from East and Southeast Asia who are distantly related, yet morphologically and genetically distinct (Brace *et al*. 2001; Demeter 2006; Hanihara and Ishida 2009; Letrit *et al.* 2008; Scott and Turner 1997). The majority of the studies suggest that anatomically modern human populations living in East/Northeast Asia migrated south during the late Pleistocene and interbred with indigenous Southeast Asian populations (Demeter 2006). Though present, less evidence indicates that Southeast Asian populations migrated into Northeast Asia (Shi *et al.* 2005). Despite these overlapping population histories during the late Pleistocene and possibly early Holocene, East/Northeast and Southeast Asia have subsequently divergent population histories shaped by biogeographically specific micro-evolutionary processes.

Both Japan and Thailand received immigrants from mainland East/Northeast Asia who exchanged genes with genetically and morphologically distinct indigenous populations living in East and Southeast Asia. In Japan, the Yayoi from the Korean peninsula likely migrated into the archipelago approximately 2,300 years ago and exchanged genes with the indigenous Jomon who arrived in Japan by approximately 13,000 years ago, resulting in the modern admixed Japanese population (Hanihara 1991). While some debate surrounds the origins of the Jomon and Yayoi populations, and subsequent migrations into Japan, it is likely that they stem, at least partly, from mainland East/Northeast Asia (Hammer *et al.* 2006; Karafet *et al*. 2001). Similarly, in Thailand, populations from south China likely migrated into insular and mainland Southeast Asia by at least 5,000 years ago, if not earlier, and exchanged genes with Australo-Melanesians who were in Southeast Asia by at least 26,000 years ago, resulting in the modern admixed Southeast Asian population (Brace *et al.* 1991; Howells 1997; Letrit *et al.* 2008; Matsumura 2006). While most studies conclude that populations living in China migrated south, the timing and subsequent migrations are heavily debated. Both of the east and south migrations not only brought new genes, but also cultural and technological traditions including wet-rice agriculture, which has been instrumental in narratives regarding the peopling, development, and advancement of modern Japan and Southeast Asian populations (Anderson 1990; Diamond and Bellwood 2003; Hanihara 1991; Sorensen 1972).

Based on the divergent population histories experienced in East and Southeast Asia, the Japanese and Thai skeletal collections present an appropriate opportunity to examine whether population differences exist in a way that is detectable with the assessment of nonmetric traits frequently used in forensic anthropology and bioarchaeology. It is expected that populations from East and Southeast Asia exhibit some metric and genetic differences due to differing micro-evolutionary processes; however, it is unclear if nonmetric traits are resolute enough to also detect differences in two populations living in the same broad geographic area (Asia).

CHAPTER IV: Skeletal Samples and Methods

This chapter describes the skeletal samples, data collection methods, and statistical analyses used to address the hypotheses presented in Chapter I. The sex and age composition of the four Japanese and Thai skeletal collections are discussed first. This is followed by a discussion of the cranial and postcranial nonmetric sex estimation scoring methods, and the cranial traits scored for nonmetric ancestry assessment. Lastly, this chapter concludes with a discussion of the statistical methods used to test and refine the cranial and postcranial sex assessment methods and those used in the establishment of cranial trait frequencies.

Skeletal Samples

In Japan, two skeletal collections from the greater Tokyo region representing urban and coastal east Japan were analyzed. The skeletal collection housed at Chiba University's (CU) Department of Bioenvironmental Medicine, Chiba City (Chiba prefecture), is comprised of over 200 known individuals whose bodies were acquired by CU during the late 19th and early 20th centuries. While very little is known of this collection, it comprised mainly of dissection cadavers and possibly incarcerated individuals (Matsuno pers. comm. 2014). The collection curated at Jikei University's (JU) School of Medicine, Tokyo (Tokyo prefecture), consists of almost 300 relatively complete and known individuals in addition to over 800 known skulls lacking postcrania. The JU collection is comprised of individuals who willed their bodies to the university's body donation program from the 1960s to the 1990s, in addition to dissection cadavers (Negishi pers. comm. 2014). See Figure 3.1 (Chapter III) for the samples' location in Japan.

In Thailand, two collections from the central and northern regions were analyzed. The collection housed at Khon Kaen University's (KKU) Faculty of Medicine, Khon Kaen, is comprised of more than 700 known individuals from the Issan region, Thailand's largest central region (Khon Kaen province) that borders Laos and Cambodia and consists of many small lowland agricultural villages. The KKU collection is composed of middle age to elderly individuals, Buddhist monks, prominent faculty, and some individuals with advanced cancer or trauma from vehicular accidents, all of who willed their bodies to the university through an ongoing body donation program (Mann 2013). The collection housed at Chiang Mai University's (CMU) Department of Forensic Osteology, Chiang Mai, consists of more than 400 known individuals from northern Thailand (Chiang Mai province), which is characterized by highlands, rainforest, and mountainous regions. Similar to KKU, the CMU collection is mainly comprised of middle age to elderly adults, Buddhist monks, and prominent faculty who willed their bodies to an ongoing body donation program (Mann 2013). While the Khon Kaen and Chiang Mai provinces significantly differ in topography, flora and fauna, and customs, Freas (2008) found that modern Thai subpopulations, including those from Bangkok, Chiang Mai, and Khon Kaen, are craniometrically homogenous. As such, the Khon Kaen and Chiang Mai skeletal collections are representative of modern Thai populations as a whole. See Figure 3.2 (Chapter III) for the Thai skeletal collections' locations.

As the cranial and postcranial sexually dimorphic traits develop skeletally during late adolescence (Scheuer and Black 2004; Sutherland and Suchey 1987), adults 17 years of age or older were analyzed. Individuals with pathological or traumatic defects impacting the areas of analysis were not included in the study. A total of 1,397 adult individuals 17-96 years of age were analyzed from the four skeletal collections (Table 4.1). Only 44 individuals lack known ages. As with the majority of anatomical collections, the Japanese and Thai skeletal collections have significantly more males (see Buikstra and Komar 2008; Hunt and Albanese 2004; Komar and Grivas 2008). The Japanese sample is comprised of 219 females and 562 males, while the Thai sample is comprised of 198 females and 418 males. The female:male sex ratio for the Japanese skeletal sample is 1:2.6, while the female:male sex ratio for the Thai skeletal sample is 1:2.1.

Table 4.1. Total number of individuals and age groups by collection included in study.

Collection/sex	**Age group (years)**								
	17-29	**30-39**	**40-49**	**50-59**	**60-69**	**70-79**	**80-96**	**Unknown**	**Total**
Chiba females	10	7	9	7	11	13	1	0	58
Chiba males	20	33	38	26	15	14	1	4	151
Jikei females	23	25	27	24	31	18	9	4	161
Jikei males	49	42	59	108	78	52	20	3	411
Japanese females	33	32	36	31	42	31	10	4	**219**
Japanese males	69	75	97	134	93	66	21	7	**562**
Khon Kaen females	3	3	21	34	36	29	10	13	149
Khon Kaen males	13	20	48	63	70	63	33	19	329
Chiang Mai females	3	2	4	7	12	14	7	0	49
Chiang Mai males	0	0	11	17	22	22	16	1	89
Thai females	6	5	25	41	48	43	17	13	**198**
Thai males	13	20	59	80	92	85	49	20	**418**
Total	121	132	217	286	275	225	97	44	**1397**

Descriptive statistics and Kolmogorov-Smirnov (K-S) significance values for the ages of the Japanese and Thai samples are presented in Table 4.2. Kolmogorov-Smirnov tests were calculated to determine if the ages for each sample are normally distributed. Based on a significance value of 0.078 ($\alpha = 0.05$), only the Thai female sample is normal. Additionally, the pooled female and male Thai ages are significantly higher than the pooled female and male Japanese ages (K-S sig. = 0.000). However, the Japanese female and male mean ages are similar (K-S sig. = 0.873), as are the mean ages for the Thai females and males (K-S sig. = 0.750). A two-sample K-S test is a nonparametric test that determines if the two samples come from the same distribution (Field 2009). A small significance value (less than 0.05) indicates that the samples have different distributions, and the samples differ in the mean, variability, and/or shape of the distributions. Overall, the sex ratios and age distributions are consistent with other anatomical skeletal collections used in skeletal biology research (Buikstra and Komar 2008; Hunt and Albanese 2004; Komar and Grivas 2008).

Table 4.2. Descriptive statistics for the Japanese and Thai ages (in years).

Group	N	Mean	Range	S.D.	S.E.	K-S Sig.
Japanese females	215	51.0	17-95	18.52	1.26	0.001*
Japanese males	555	51.0	17-90	18.88	0.72	0.016*
Thai females	185	61.5	20-94	14.36	1.10	0.078
Thai males	398	61.6	18-96	15.63	0.78	0.002*

* $\alpha = 0.05$

Data Collection

Sex assessment

The first objective of this study is to determine how the traditional and non-traditional cranial and postcranial nonmetric sex assessment methods developed on individuals of African and European descent perform when applied to Japanese and Thai individuals. The elements needed for this evaluation include the cranium, mandible, clavicles, humeri, and the pelvis. Complete elements from individuals who were free of pathological conditions were analyzed, and both sides were scored. A total of 15 nonmetric sexually dimorphic traits were assessed following Buikstra and Ubelaker (1994), Rogers *et al.* (2000), and Vance *et al.* (2011). Table 4.3 presents the sexually dimorphic traits assessed, unique ordinal scoring systems, and associated references. Data collection was conducted in the blind, meaning that the PI did not know the documented sexes of the individuals being scored. Additionally, the ordinal scores for each individual were input into a Microsoft Excel spreadsheet to allow for export into the IBM SPSS (version 23.0) statistical program for analysis.

The traditional sexually dimorphic regions of the skull and pelvis were scored according to conventional standards proposed by Buikstra and Ubelaker (1994) and Walker (2008), which include descriptions and diagrammatic representations of the trait expressions. The traits of the skull include the nuchal crest, mastoid process, supra-orbital margin, supra-orbital ridge/glabella, and the mental eminence (Figure 4.1). Generally, males exhibit more robust features with scores of 4 and 5 due to greater muscle mass compared to females with scores of 1 and 2, and the traits are scored according to their size relative to the surrounding structures.

Table 4.3. Cranial and postcranial sexually dimorphic traits, ordinal scoring systems, and associated references assessed in the present study.

Trait	Ordinal scoring system	References
Nuchal crest Mastoid process Supraorbital margin Supraorbital ridge/glabella Mental eminence	0=undetermined sex; 1=female; 2=probable female; 3=ambiguous sex; 4=probable male; 5=male	Buikstra and Ubelaker 1994; Garvin *et al.* 2014; Walker 1995, 2008
Ventral arc Subpubic concavity Ischiopubic ramus ridge	0=undetermined sex; 1=female; 2=ambiguous sex; 3=male	Buikstra and Ubelaker 1994; Kelley 1978; Klales 2016; Klales *et al.* 2012; Lovell 1989; Phenice 1969; Sutherland and Suchey 1987
Greater sciatic notch	1-5; 1=wide (female); 5=constricted (male)	Buikstra and Ubelaker 1994; Walker 2005
Preauricular sulcus	0=absent (male); 1=wide and deep (female); 2=wide and shallow; 3=well-defined but narrow; 4=narrow, shallow and smooth walled	Buikstra and Ubelaker 1994
Rhomboid fossa	0=absent; 1=small fossa; 2=large fossa; 3=shallow groove; 4=deep groove; 5=pitting/porosity 0=absent; 1=present (large/small fossa, groove, or pitting/porosity	Rogers *et al.* 2000; Singh and Singh 2009
Angle of medial epicondyle Olecranon fossa shape/depth Trochlear extension Trochlear constriction	1=clearly male; 2=cautiously male; 3=ambiguous sex; 4=cautiously female; 5=female Composite: 3-8=male; 9=ambiguous; 10-15=female	Falys *et al*. 2005; Rogers 1999, 2006; Vance *et al.* 2011

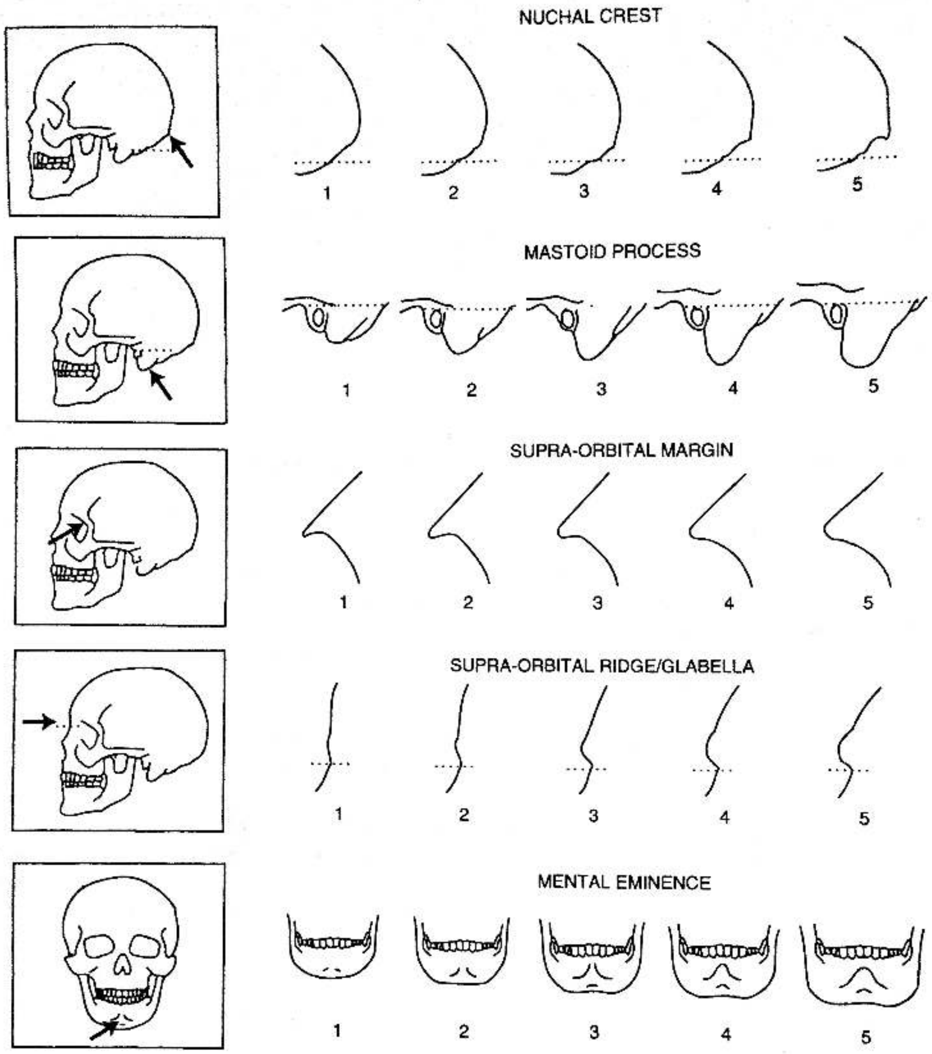

Figure 4.1. Visual scoring systems for the sexually dimorphic cranial traits (diagram in Buikstra and Ubelaker 1994:20).

The pelvic traits that were used to evaluate sexual dimorphism include the Phenice (1969) traits of the pubic bone (ventral arc, subpubic concavity, and ischiopubic ramus ridge). These pubic bone traits were assigned an ordinal scored based on their form, where females typically exhibit a ventral arc, large subpubic concavity, and sharp ischiopubic ramus ridge (Figure 4.2). Generally, a score of 1 indicates female, a score of 2 is indeterminate, and a score of 3 indicates male (Buikstra and Ubelaker 1994).

The greater sciatic notch was assigned an ordinal score based on its constriction following Buikstra and Ubelaker (1994) (Figure 4.3). For the sciatic notch, a score of 1 indicates a wide notch that is consistent with female morphology, while the higher numbers indicate narrower notches that are consistent with male morphology.

The preauricular sulcus was assigned an ordinal score based on its presence and form following Buikstra and Ubelaker (1994) (Figure 4.4). A score of 0 signifies an absence of a sulcus and usually indicates male, while scores of 2-4 signify varying expressions of the sulcus and generally indicate female.

Concerning the non-traditional sex assessment methods, the rhomboid fossa of the medial clavicle was assigned an ordinal score based on the presence or absence and degree of expression following Rogers *et al*. (2000). While Rogers *et al*. (2000) found that an ordinal scoring system based on the size of the fossa had less discriminatory power compared to scoring for the presence or absence of a fossa, the present study scores this region ordinally and converts the scores to a dichotomous score. A score of 0 signifies an absence of a fossa (either a flattened area or a raised tubercle), a score of 1 indicates a small excavated fossa, 2 indicates a large excavated fossa, 3 signifies a small linear groove, 4 signifies a large linear groove, and a 5 signifies pitting or porosity (Figure 4.5). Dichotomously, a score of 0 indicates an absence of a fossa, while a score of 1 indicates the presence of a fossa in any form. Rogers *et al.* (2000) hypothesized that rhomboid fossae may develop at the attachment site for the costoclavicular ligament in males due to greater muscle mass and/or increased physical activity compared to females.

A second non-traditional sex assessment method examines the distal humerus morphology. The sexually dimorphic traits of the distal humerus include trochlear constriction, trochlear symmetry, olecranon fossa shape and depth, and angle of the medial epicondyle (Rogers 1999). The differences between females and males of the distal humerus is attributed to the different carrying angles, whereby males exhibit a 10 – 15 degree carrying angle while females exhibit a 20 – 25 degree carrying angle (Rogers 1999). Typically, males exhibit a slightly constricted and asymmetrical trochlea, a shallow and triangular olecranon fossa, and a flat or slightly raised medial epicondyle, while females exhibit a more constricted, spool-shaped, and symmetrical trochlea, deep and oval olecranon fossa, and a distinctly raised medial epicondyle (Rogers 1999). The distal humerus features were ordinally and composite scored following Vance *et al.* (2011) based on their "male-like" or "female-like" expression. Vance *et al*. (2011) discarded Rogers' (1999) trochlear constriction, as it perform poorly in their South African sample. As such, each of the three remaining traits were scored as clearly male (1), cautiously male (2), ambiguous (3), cautiously female (4), or clearly female (5) (Figure 4.6). Composite scores of 3 – 8 indicate male, a score of 9 is indeterminate, and scores of 10 – 15 indicate female.

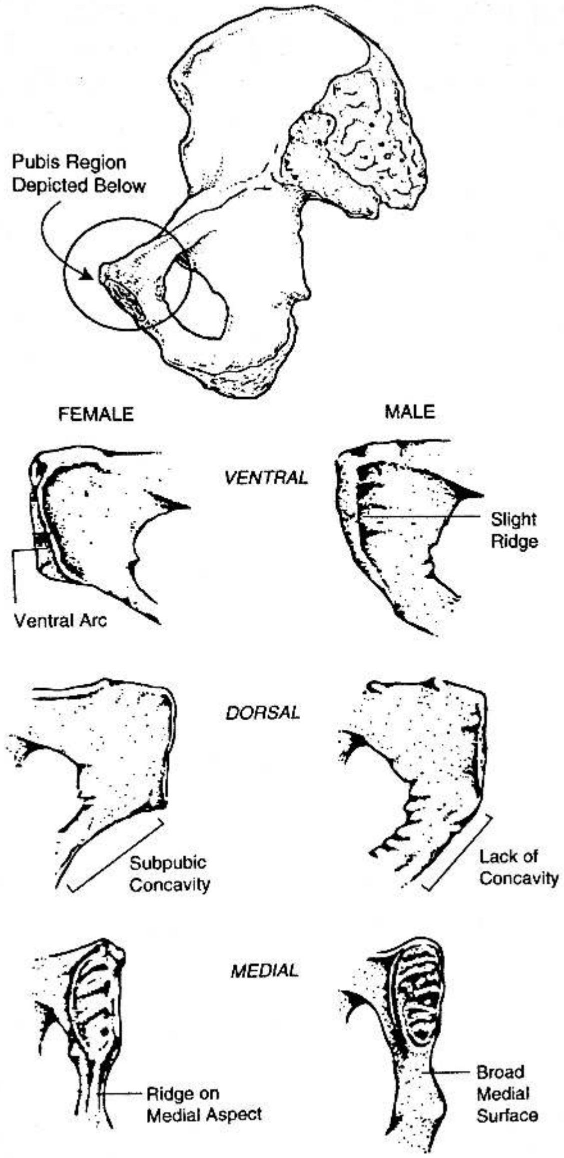

Figure 4.2. Sexually dimorphic differences of the pubic region (diagram in Buikstra and Ubelaker 1994:17).

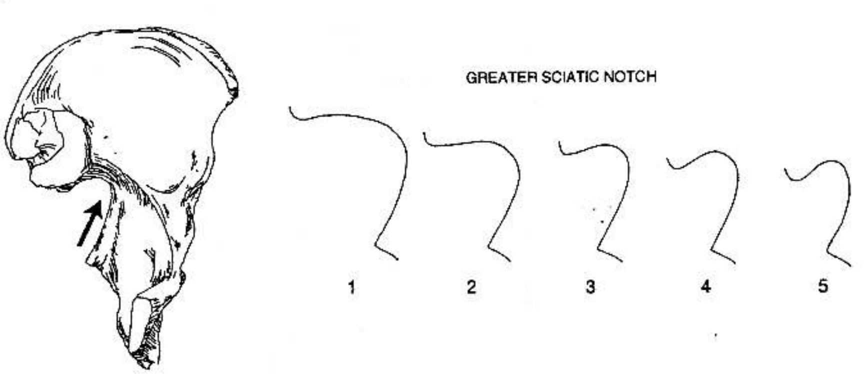

Figure 4.3. Visual scoring system for the sciatic notch (diagram in Buikstra and Ubelaker 1994:18).

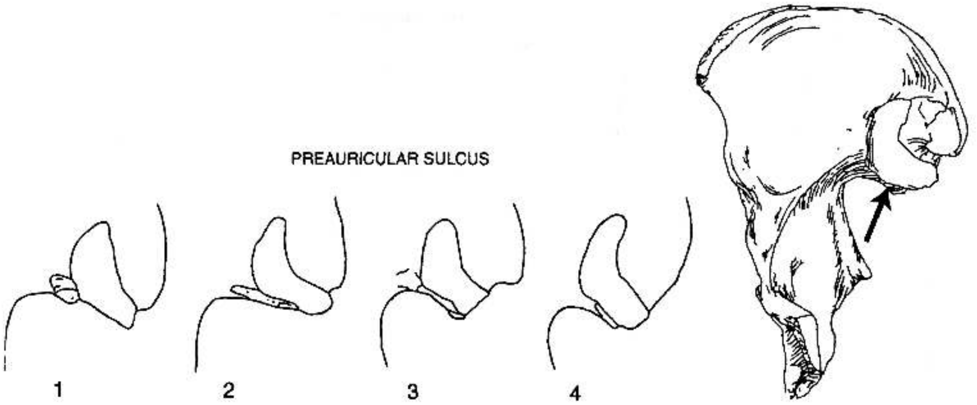

Figure 4.4. Visual scoring system for the preauricular sulcus (diagram in Buikstra and Ubelaker 1994:19).

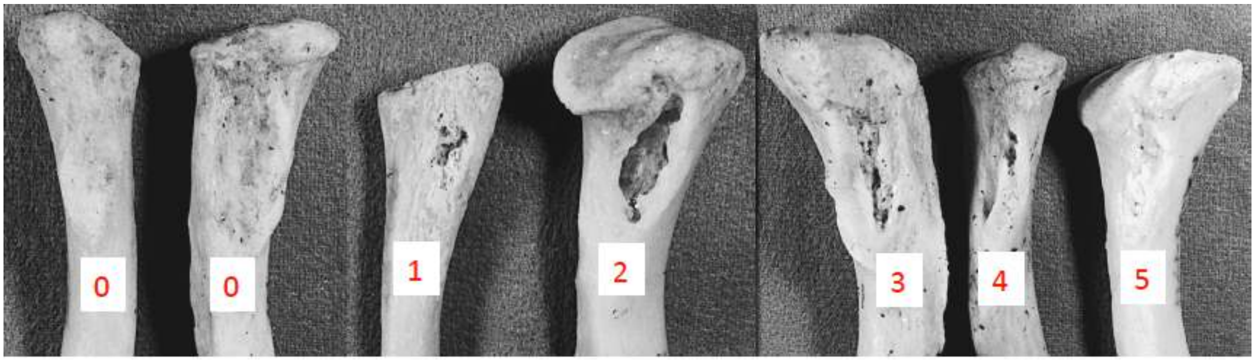

Figure 4.5. Variation in rhomboid fossa form: 0 = fossa absent (raised tubercle or impression), 1 = small fossa; 2 = large fossa; 3 = shallow groove; 4 = deep groove; 5 = porosity/pitting (photographs adapted from Rogers *et al.* 2000:63-64).

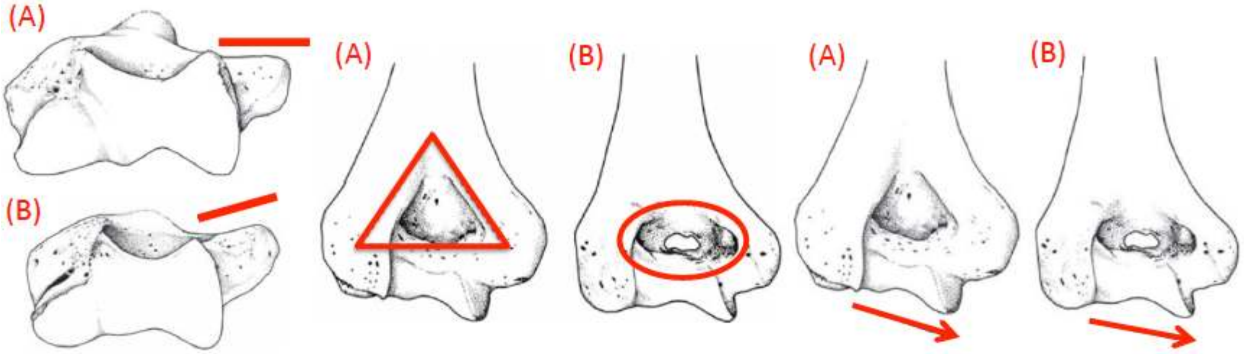

Figure 4.6. Variation in distal humerus morphology: (A) demonstrates a flat medial epicondyle, triangular olecranon fossa, and an asymmetrical trochlea as seen in males; (B) demonstrates an angled medial epicondyle, circular olecranon fossa, and a more symmetrical trochlea as seen in females (diagrams adapted from Vance *et al*. 2011:711).

Cranial trait frequencies

The second objective of this study is to establish cranial trait frequencies for Japanese and Thai individuals so that they can be compared to each other and published data on Native Americans. The elements needed for this analysis included complete or partial crania and mandibles that were free of pathological conditions.

Sixteen cranial traits originally proposed by Rhine (1990) and adapted by Hefner (2009, 2012) were ordinally scored: anterior nasal spine, inferior nasal aperture, interorbital breadth, malar tubercle form, nasal aperture shape, nasal aperture width, nasal bone contour, nasal bone shape, nasal overgrowth, nasofrontal suture, orbital shape, postbregmatic depression, posterior zygomatic tubercle, supranasal suture, zygomaticomaxillary suture, and transverse palatine suture. Hefner (2009, 2012) provides descriptions and diagrammatic representations in order to facilitate the ordinal scoring of each trait, and a unique ordinal scoring system is provided for each trait. Two of Hefner's (2009) ordinal scoring systems (malar tubercle and nasal bone contour) were altered by adding an additional ordinal score to each. All of the assessment methods require direct observation of the bony region, except for the scoring of the nasal bone contour, which requires the use of a contour gauge. With the contour gauge positioned perpendicular to the orbits, it was pressed gently on the nasal bones, approximately one centimeter inferior to nasion. The shape of the impression in the contour gauge was then assessed. Additionally, six of Rhine's (1990) cranial traits not included in Hefner's (2009) study were ordinally scored, and include keeling, suture form, the presence of wormian bones, zygomatic projection, prognathism, and dental arcade shape.

In addition to Hefner's (2009, 2012) and Rhine's (1990) cranial traits, mandibular traits were scored Parr (2005, 2006). Parr's (2005, 2006) traits include chin shape, mandibular border shape, ascending ramus shape, ascending ramus profile, gonial angle flare, and posterior ramus inversion, location of inversion, presence of mandibular tori, gonial muscle attachment ridging, mylohyoid bridging, the presence of accessory mandibular foramen, degree chin prominence, and number of mental foramen. Similar to Hefner (2009, 2012), Parr (2005, 2006) provides unique ordinal scoring systems for each trait.

Two additional nonmetric traits identified by the PI during the initial analysis of the CU skeletal collection were added, along with ordinal scoring systems. The type of occlusion exhibited by the maxillary and mandibular anterior (incisor) dentition was assessed as normal occlusion (dentition slightly in front of lower dentition) or malocclusion (upper dentition far in front of lower dentition, lower dentition far in front of upper dentition, or edge-to-edge contact). Additionally, the orientation of the maxillary incisors was assessed as vertical, slightly anteriorly projected, or markedly anteriorly projected. However, due to the advanced age and poor dental health of many of the collection's individuals, the scoring of these traits was infrequent.

Table 4.4 presents the 37 cranial and mandibular nonmetric traits assessed, along with the unique ordinal scoring systems, and associated references. The number following each trait corresponds with the location of the trait presented on Figures 4.7 and 4.8.

Lastly, a random sample of 120 analyzed individuals (8.6% of the sample) were re-scored by the PI in order to determine the degree of intraobserver error in the scoring of nonmetric sex and cranial traits.

Table 4.4. Cranial traits, ordinal scoring systems, and associated references assessed in the present study.

Trait	Scoring system	References
Anterior nasal spine (1)	1=slight; 2=moderate; 3=marked	Gill 1998; Hefner 2009, 2012; Rhine 1990
Inferior nasal aperture (2)	1=smooth transition; 2=sloping, angular transition; 3=right angle; 4=weak vertical ridge; 5=pronounced sill	Gill 1998; Hefner 2009, 2012; Rhine 1990
Interorbital breadth (3)	1=narrow; 2=intermediate; 3=broad	Bass 1995; Hefner 2009, 2102; Rhine 1990
Malar tubercle form (4)	0=no projection; 1=trace; 2=medium; 3=pronounced; 4=double	Hauser and De Stefano 1989; Hefner 2009, 2012; Rhine 1990
Nasal aperture shape (5)	1=teardrop shaped; 2=bell shaped; 3=bowed	Hefner 2012; Rhine 1990
Nasal aperture width (6)	1=narrow; 2=medium; 3=broad	Bass 1995; Hefner 2009, 2012; Rhine 1990
Nasal bone contour (7)	0=low and rounded; 1=oval with high walls; 2=steep walls with broad plateau; 3=steep walls with narrow plateau; 4=triangular cross-section; 5=flat	Brues 1990; Hefner 2009, 2012; Rhine 1990
Nasal bone shape (8)	1=no nasal pinch; 2=superior pinch with minimal lateral bulging; 3=superior pinch with pronounced lateral bulging; 4=triangular-shaped	Hefner 2012; Rhine 1990
Nasofrontal suture (9)	1=rounded; 2=square; 3=triangular; 4=irregular/jagged	Hefner 2012; Rhine 1990
Nasal overgrowth (10)	0=absent; 1=present	Hefner 2009, 2012; Rhine 1990
Supranasal suture (11)	0=obliterated; 1=open; 2=closed but visible	Hauser and De Stefano 1989; Hefner 2009, 2012; Rhine 1990
Orbital shape (12)	1=rounded; 2=rectangular; 3=rhombic	Hefner 2012; Rhine 1990
Postbregmatic depression (13)	0=absent; 1=present	Bass 1995; Hefner 2009, 2012; Rhine 1990
Posterior zygomatic tubercle (14)	0=absent; 1=weak; 2=moderate; 3=marked	Hefner 2012; Rhine 1990

Table 4.4, continued.

Trait	**Scoring system**	**References**
Zygomaticomaxillary suture (15)	0=no angles and greatest lateral projection is at inferior margin; 1=one angle and greatest lateral projection is near midline; 2=two or more angles and variable lateral projection; 3=obliteration	Gill 1998; Hauser and DeStefano 1989; Hefner 2009; Rhine 1990
Transverse palatine suture (16)	1=straight; 2=anterior bulging; 3=M-shaped; 4=posterior bulging	Gill 1998; Hauser and DeStefano 1989; Hefner 2009, 2012; Rhine 1990
Keeling (17)	0=absent; 1=slight; 2=marked	Rhine 1990
Suture form (18)	1=simple; 2=moderate; 3=complex	Mann *et al.* 2015; Rhine 1990
Wormian bones (19)	0=absent; 1=present	Rhine 1990
Zygomatic projection (20)	1=retreating; 2=vertical; 3=marked projection	Rhine 1990
Prognathism (21)	0=absent; 1=moderate; 2=significant	Rhine 1990
Dental arcade shape (22)	1=narrow/tapering; 2=wide and smoothly curving; 3=rectangular	Rhine 1990
Mandibular ramus inversion (23)	0=absent; 1=slight; 2=moderate; 3=extreme	Angel and Kelley 1990; Berg 2008; Parr 2005, 2006; Rhine 1990
Location of inversion, if present (24)	1=low; 2=medium; 3=high	Parr 2005, 2006
Gonial eversion (25)	0=absent; 1=slight; 2=moderate; 3=extreme flare	Berg 2008; Parr 2005, 2006; Rhine 1990
Mandibular border shape (26)	1=straight; 2=undulating; 3= rocker	Berg 2008; Parr 2005, 2006; Rhine 1990
Gonial muscle attachment ridging (27)	0=absent; 1=minimal ridging; 2=moderate ridging; 3=extreme ridging	Parr 2005, 2006
Mylohyoid bridging (28)	0=absent; 1=present	Parr 2005, 2006
Accessory mandibular foramen (29)	0=absent; 1=present	Parr 2005, 2006
Chin prominence (30)	0=recessive; 1=blunt/vertical; 2=prominent	Parr 2005, 2006; Rhine 1990
Chin shape (31)	1=rounded; 2=pointed; 3=square/bilobate	Berg 2008; Parr 2005, 2006; Rhine 1990

Table 4.4, continued.

Trait	Scoring system	References
Number of mental foramen (32)	0=none; 1=one; 2=two; 3=three	Parr 2005, 2006
Ascending ramus shape (33)	1=pinched; 2=wide	Berg 2008; Rhine 1990
Ascending ramus profile (34)	1=straight; 2=medium; 3=slanted	Berg 2008; Rhine 1990
Mandibular tori (35)	0=absent; 1=slight; 2=moderate; 3=extreme	Hassett 2006; Hauser and DeStefano 1989; Ossenberg 1978; Parr 2005, 2006; Rhine 1990
Occlusion (36)	1=normal (maxillary incisors slightly in front of mandibular incisors); 2=malocclusion (maxillary incisors far in front of mandibular incisors, “overbite”); 3=malocclusion (mandibular incisors far in front of maxillary incisors, “underbite”); 4=edge-to-edge contact	
Maxillary incisor orientation (37)	1=vertical; 2=slight anterior projection; 3=marked anterior projection	

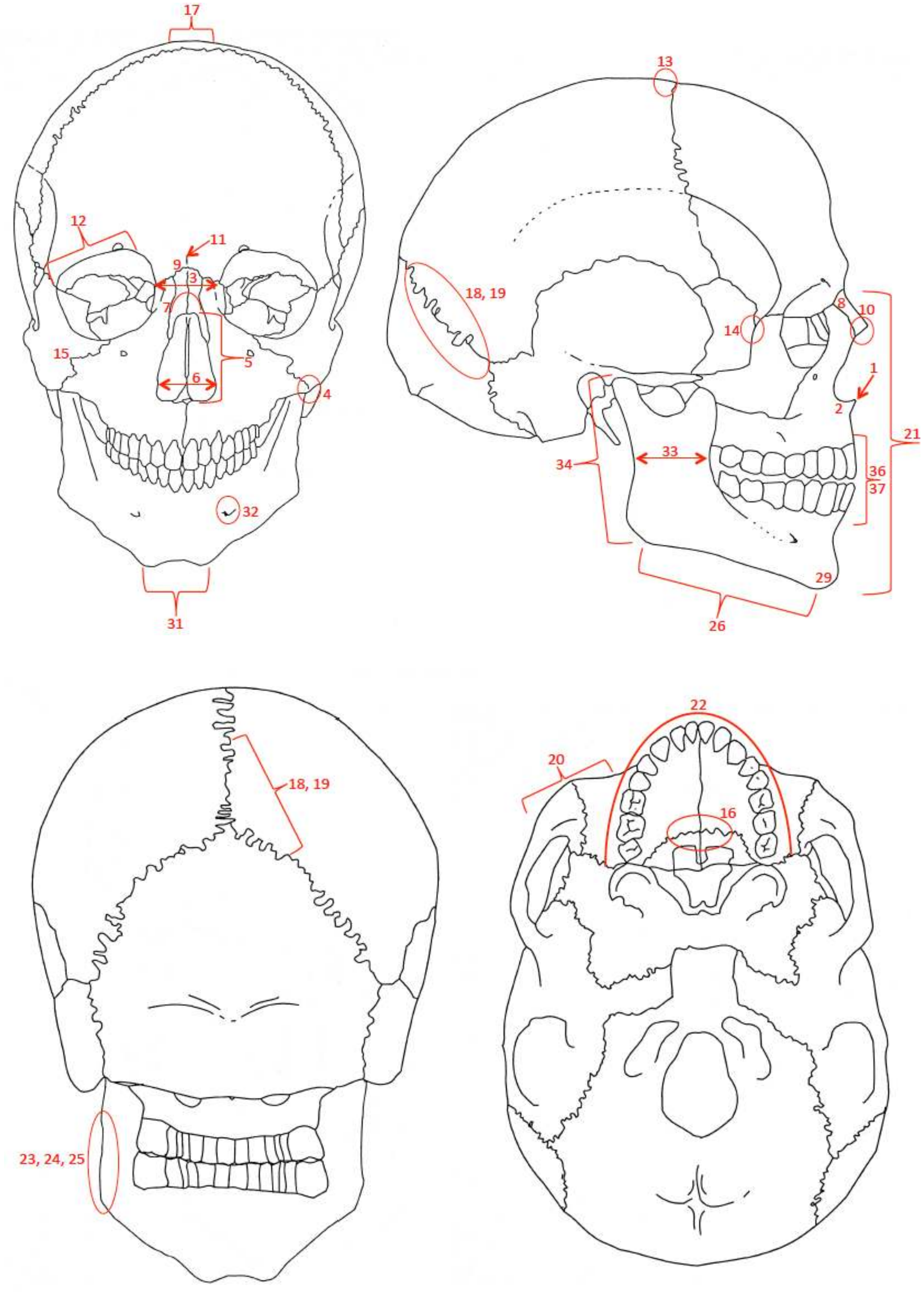

Figure 4.7. Anterior, lateral, posterior, and inferior regions of the cranium analyzed following Hefner (2009, 2012), Rhine (1990), and Parr (2005, 2006). Numbers correspond to ordinal scoring systems presented in Table 4.4 (diagram adapted from Buikstra and Ubelaker 1994).

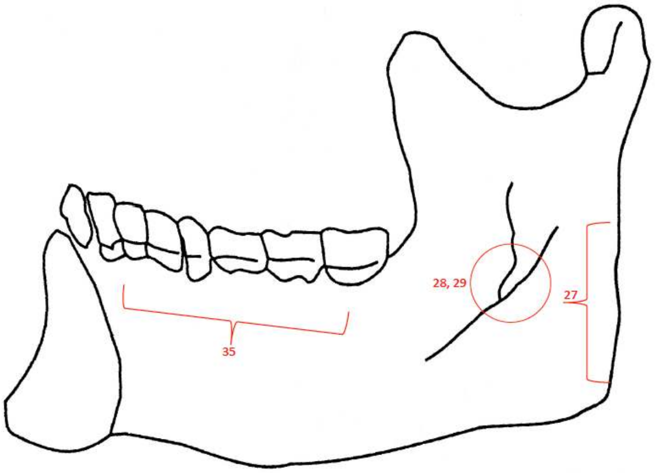

Figure 4.8. Medial aspect of the mandible analyzed following Parr (2005, 2006). Numbers correspond to ordinal scoring systems presented in Table 4.4 (diagram adapted from Buikstra and Ubelaker 1994).

Statistical Analyses

All statistical analyses were conducted in IBM SPSS (version 23.0). Because this study uses non-continuous categorical (i.e., ordinal) variables, which are inherently not normally distributed, statistical tests that do not assume a normal distribution or utilize means in analyses were primarily employed (i.e., nonparametric). First, Pearson chi-square analyses were performed to determine if there are statistically significant side differences in the scoring of nonmetric traits. A Pearson chi-square analysis compares the observed frequencies in specific categories to the frequencies expected in those categories by chance alone (Field 2009). As such, it is a test of independence to determine if there is an association between two independent categorical variables (Field 2009). Chi-square analyses are well suited for large datasets because the sampling distribution of the test statistic has an approximate chi-square distribution. In large samples, the approximation is close enough to reality to be accurate. However, in small sample sizes, as indicated by frequencies over 20% of the SPSS cells having values below five, the significance value of the Pearson chi-square statistic is rendered inaccurate. In these circumstances, the significance value for the Fisher's exact test of the chi-square statistic was reported, as is it calculates the exact, rather than approximate, probability. Accordingly, the null hypothesis states that there is no association between trait scores for the right and left sides. If the significance value is smaller than 0.05, then the hypothesis that the variables are independent is rejected, and the right and left sides are somehow related. If there was an association between trait scores on the right and the left sides, the left side was used in future analyses, with the right side substituted when the left was missing. Subsequent to chi-square tests, Phi and Cramer's V tests were calculated to determine the strength of the association between side and trait score. Phi and Cramer's V tests are *post-hoc* tests that produce values ranging from 0 (no association) to 1 (strong association) (Field 2009). Phi tests measure the strength of association between two categorical variables with two categories based on Fisher's exact tests (i.e., 2 x 2 table), while Cramer's V tests the strength of association between variables with more than two categories based on Pearson tests (i.e., 2 x. 3 or more table).

Sex assessment statistics

Chi-square analyses were also calculated to determine if differences exist in the cranial and pelvic nonmetric trait scores between females and males for each group. The null hypothesis states that there is no association between cranial and pelvic trait scores and sex. If the significance value fell below 0.05, the null hypothesis was rejected, as sex affects the trait scores.

As such, this test determines if the traits are indeed sexually dimorphic. Pearson chi-square tests were also calculated to determine if differences exist between the Japanese and Thai groups (i.e., population differences). The null hypothesis states that there is no association between group membership and cranial or pelvic trait scores. If the significance value fell below 0.05, the null hypothesis was rejected, as group membership affects traits scores. Accordingly, this test indicates population differences in the expression of sexually dimorphic nonmetric traits.

While the majority of the Japanese and Thai individuals come from modern populations, the CU collection was established during the late 19th and early 20th centuries, thus representing a more historic population, which can be compared to the modern JU individuals. Chi-square analyses were used to test the hypothesis that the scoring of traits is independent of the era in which the individuals died. If the significance values fell below 0.05, the null was rejected, and significant differences exist in the expression of traits between historic (CU) and modern (JU) Japanese individuals. Therefore, the chi-square statistic used in this context will determine if secular change has occurred in the expression of traits among individuals from the greater Tokyo area.

In order to determine how the cranial and pelvic nonmetric sex assessment methods developed on non-Asian populations perform when applied to Japanese and Thai individuals, the data were statistically analyzed following the procedures of Walker (2005, 2008). First, the percentage of females and males each with a particular nonmetric score within each group (Japanese and Thai) were calculated. Next, probabilities were calculated for each of the nonmetric traits within each group (Japanese females, Japanese males, Thai females, and Thai males) to determine which scores indicate male, female, or indeterminate sex. The trait-by-trait probabilities were calculated using the following equations:

$$P_m = \% \text{ males with trait} / (\% \text{ males with trait} + \% \text{ females with trait})$$

$$P_f = \% \text{ females with trait} / (\% \text{ females with trait} + \% \text{ males with trait})$$

P_m and P_f are the probabilities of being male and female, respectively, for each particular trait. The % male and % female are the proportions of individuals assigned a particular score. Individuals with a P_m greater than 0.50 are likely to be male, while individuals with a P_f greater than 0.50 are likely to be female. The univariate probabilities determined which trait(s) perform best for each group.

Based on the calculated P_m and P_f probabilities, cutoff points for each trait were established for each group by determining if proportionately more females or males exhibited each ordinal score. For instance, if the probabilities associated with ordinal scores of 1, 2, and 3 for a particular trait each have female probabilities over 0.50, and scores of 4 and 5 each have male probabilities over 0.50, then the cutoff point for that trait is between 3 and 4. Statistically, more individuals with scores of 1, 2, and 3 are female, while more individuals with scores of 4 and 5 are male. Since the majority of the scoring methods for the sexually dimorphic nonmetric traits have a sexually indeterminate category (i.e., 2 for traits scored 1 – 3, and 3 for traits scored 1 – 5), establishing population-specific cutoff points will determine if the indeterminate category is necessary.

Based on the probabilities and cutoff points, the correct classification rates when using each nonmetric trait separately to determine sex were calculated for each group (Japanese females, Japanese males, Thai females, and Thai males). The sex bias for each trait was calculated by subtracting the % of females correctly classified from the % of males correctly classified. As such, a negative sex bias indicates that the traits perform better in classifying females, while a positive sex bias indicates that the traits perform better in classifying males (Walker 2008).

Spearman's rank-order correlation coefficients (rho) were calculated for each trait and each group to determine if an association exists between age-at-death and nonmetric scores. The Spearman's rho is a nonparametric test that assesses the strength of a relationship between two ranked variables (Field 2009). If the significance value is less than 0.05, then a statistically significant relationship exists between a nonmetric trait score and age, and therefore age may have an affect on the expression of a trait. A positive Spearman's rho score indicates a positive (increasing) relationship, while a negative Spearman's rho score indicates a negative (decreasing) relationship. The ages for the 1,353 individuals with known ages were grouped into seven age categories: 17-29 years, 30-39 years, 40-49 years, 50-59 years, 60-69 years, 70-79 years, and 80-96 years (see Table 4.1, above).

If a Spearman's rho correlation was found between age and the expression of a trait, a Kruskal-Wallis and associated *post-hoc* tests were conducted to determine which age categories statistically significantly differed in mean trait score ranks. A Kruskal-Wallis test, which is the non-parametric equivalent of a one-way analysis of variance (ANOVA) test, ranks the mean or median values for three or more groups and determines if differences exist in their distributions (Field 2009). The Kruskal-Wallis test produces a value (H), which is based on the chi-square statistic. If the significance (p) value associated with H falls below 0.05, statistically significant differences exist in trait score ranks between at least two age groups. If statistically significant differences were found between the age groups, a *post-hoc* pairwise test was used to identify which age groups statistically differed.

Spearman's rho were also used to determine if the nonmetric traits co-vary, wherein a positive or negative change in one trait is associated with a positive or negative change in another trait(s). Inter-trait correlations determined from Spearman's rho can ascertain which traits are most correlated and how the traits interact (Hauser and DeStefano 1989).

Using the cranial nonmetric scores for each of the four Asian groups, several of Walker's (2008) discriminant function equations were tested to determine the utility of the equations when they are applied to Japanese and Thai individuals. Walker (2008) developed population-specific discriminant function equations for pooled African American, European American, and English born individuals (six equations) and Native American individuals (three equations) using three-trait and two-trait combinations. Of the four discriminant function equations investigated (linear, logistic, quadratic, and k-nearest neighbor), Walker found that logistic regression equations performed the best, resulting in relatively high correct classification rates and low sex biases. Additionally, three of Garvin *et al.'s* (2014) canonical discriminant function equations were tested, including equations for pooled U.S. Black, pooled U.S. White, and Arikara individuals. The cranial trait scores were input into the discriminant function equations, and 0 was used as the sectioning point to distinguish males and females; scores less than 0 indicate male, while scores greater than 0 indicate female for both Walker's (2008) and Garvin *et al.*'s (2014) equations.

Subsequent to testing Walker's (2008) and Garvin *et al.'s* (2014) discriminant functions, population-specific binary logistic regression equations were calculated for the Japanese, Thai, and pooled Japanese and Thai samples using the Forward Wald function in IBM SPSS. Logistic regression analysis predicts the probability that an observation (individual) will fall into a dichotomous category (female or male) based on categorical or continuous independent variables (ordinal nonmetric scores) (Field 2009). The Wald statistic determines if the coefficients (nonmetric traits) significantly contribute to the prediction and outcome; the higher the Wald statistic, the more the independent variable contributes to the dichotomous classification. As such, binary logistic regression equations will predict the sex of an unknown individual based on the different combinations of cranial trait scores available for that individual. The group (female/male) was used as the dependent variable, and the five cranial and five pelvic traits were used as the covariates. As such, equations using five, four, three, two, and one variables were calculated for each of the groups, and only the traits that were statistically significant were included in the equations. The logistic regression equation cutoff point to determine if an individual is male or female was 0.50, with scores below 0.50 indicating male and scores of 0.50 and above indicating female. Additionally, sex biases for each of the equations was calculated based on the correct classification rates of the logistic regression equations. Logistic regression equations were used over linear, quadratic, and k-nearest neighbor discriminant functions because: they are designed for variables that have two values (female/male); a linear relationship between the dependent and independent variables is not necessary; multivariate normality of the independent variables is not required; and it does not assume homoscedasticity (equal variance) (Hosmer and Lemeshow 1989; Walker 2008).

An additional benefit of using binary logistic regression analyses, especially in forensic casework, is that probabilities can be calculated from the logistic equation scores (Klales *et al.* 2012; Walker 2008). Though not used in the present study, individual probabilities are calculated as follows: $P_f = 1/(1 + e^{\text{logistic equation score}})$; $P_m = 1 - P_f$. Therefore, an unknown individual is classified as female or male based on the greater probability.

A second, exploratory multivariate classification analysis was used to predict sex for the Japanese and Thai samples. The Chi Square Automatic Interaction Detection (CHAID) decision tree is a nonparametric test that predicts group membership of a dependent variable based on the chi-square statistic of the independent variables (IMB 2011). The dependent and independent variables can be nominal, scale, or ordinal. The CHAID analyzes the interactions of the variables, using only those independent variables that best predict the outcome, and produces a growing tree. The tree is represented by a parent or root node, branches leading to internal nodes, internal nodes, branches leading to leaves, and terminal nodes or leaves. The independent variables used in the decision tree are ranked, so that the first independent variable (internal node) stemming from the root node is the one that contributes most to predicting the outcome. Depending on the distribution of scores, branches leading to terminal nodes will stem off of the internal nodes. Chi-square statistics are provided for each variable used in the tree. Each terminal node is associated with outcome probabilities, and the decision tree produces correct classification rates and resubstitution risk values to assess model performance. Additionally, cross-validated risk values can concurrently be computed, which measures the predictive performance of the models. Most importantly, CHAID analysis is easy to use, largely free of ambiguity, good at predicting variables, and is robust even with missing variable values (Song and Lu 2015).

To determine if sex can be predicted based on the presence or absence of a rhomboid fossa on the clavicle, the data were analyzed following Rogers *et al.* (2000). The percentage of females and males with each ordinal score (0-5) were calculated for both left and right clavicles. The ordinal scores were also dichotomized so that a score of 0 indicates an absence of a rhomboid fossa, and a score of 1 indicates the presence of a rhomboid fossa (originally scored 1-5). Subsequently, probabilities were calculated for the ordinal and dichotomous scores. Statistics for the left and right clavicles were calculated separately as Rogers *et al.* (2000) found side differences and subsequently developed probabilities for each antimere. Pearson chi-square tests were calculated to determine if rhomboid fossae are sexually dimorphic, and if population differences exist between Japanese and Thai individuals in the expression of a fossa. Spearman's rho were calculated to determine if age and the presence of a rhomboid fossa are associated. Further, binary logistic regression analysis was performed to determine if age, sex, and/or group predicts the presence of a rhomboid fossa. As such, sex served as the dependent variable, and age, sex, and group (Japanese and Thai) served as the independent variables.

To determine if distal humerus morphology predicts sex, the ordinal scores were analyzed following Rogers (1999) and Vance *et al.* (2011). The percentage of females and males with each ordinal score (1-5 following Vance *et al.* 2011) were calculated on the left humerus for the angle of the medial epicondyle, olecranon fossa shape, trochlear extension, and trochlear symmetry. Subsequently, probabilities and correct classification rates were calculated based on the probability predictions. Also based on the probabilities, cutoff points were established to determine which traits best indicate female and male. Using the new population-specific cutoff points, correct classification rates and sex biases were calculated. Following Vance *et al.* (2011), the individuals classified as male (composite scores of 3-8), ambiguous (composite score of 9), and female (composite score of 10-15) were calculated with trochlear symmetry excluded. Based on the percent correctly and incorrectly classified, the sectioning points were altered to better classify Japanese and Thai individuals. Pearson chi-square tests were conducted to determine if statistically significant differences exist between females and males and between Japanese and Thai individuals. Spearman's rho were calculated to determine if age and distal humerus morphology traits are associated. Binary logistic regression equations were developed to determine if they are superior to univariate probabilities in predicting sex. As such, the sex of the individuals served as the dependent variable, and the four distal humerus traits served as the independent variables. Lastly, CHAID decision tree analyses were conducted to determine which distal humerus traits best predict sex using chi-square statistics.

The univariate probabilities, chi-square significance, binary logistic regression statistics, and decision trees test the hypothesis that cranial and postcranial nonmetric sex assessment methods developed on individuals of African and European descent perform poorly in classifying Japanese and Thai individuals of known sex. Further, the statistical analyses provide error rates and probabilities for the sex assessment methods, thereby fulfilling an important requirement of the *Daubert* ruling. Additionally, the statistical analyses test the hypothesis that Japanese and Thai individuals exhibit inter-group differences in sexual dimorphism.

Cranial and mandibular trait statistics

Analyses of the nonmetric cranial trait data were similar to the statistical procedures used to explore sexual dimorphism. Accordingly, the percentage of each ordinal trait score within each group was calculated. These frequency distributions were then compared to those presented in Hefner (2009) and Rhine (1990). Pearson chi-square analyses and Fisher's exact tests were calculated to determine if differences exist between males and females and between the pooled Japanese and Thai groups. The chi-square null hypothesis states that there is no association between cranial and mandibular trait scores and group membership. If the significance value falls below 0.05, the null hypothesis is rejected, and group membership affects cranial and mandibular trait scores. Chi-square analyses also determined if differences exist in the expression of cranial and mandibular traits between historic and modern Japanese individuals. Thus, significance values below 0.05 reject the hypothesis that cranial and mandibular traits are independent of the era of death. Additionally, Spearman's rho were calculated to determine if age and cranial trait scores are correlated. Spearman's rho also ascertained if certain cranial traits were more correlated than others, and whether correlations work better at classifying the Japanese and Thai groups than individual traits alone. Binary logistic regression equations were developed to determine if they could be used to discriminate between Japanese and Thai individuals. As such, the group (Japanese and Thai) was used as the dependent variable, and the traits that are statistically significant were used as the independent variables. The logistic regression cutoff point to determine if an individual is Japanese or Thai was 0.50, with scores below 0.50 indicating Japanese and scores of 0.50 and above indicating Thai. Lastly, CHAID decision tree analyses were conducted to determine which cranial and mandibular traits best predict group membership based on the chi-square statistic.

The frequency distributions and statistical analyses were used to test the hypothesis that Japanese and Thai individuals exhibit statistically significantly different cranial trait expressions and frequencies. Accordingly, separate cranial trait frequencies were established for Japanese and Thai individuals, and models were developed to differentiate the two groups. Secondly, while no Native American individuals were analyzed in the present study, the cranial and mandibular trait frequencies were used to test the hypotheses that Japanese and Thai individuals exhibit different cranial trait expressions and frequencies compared to Native Americans. This determined if the cranial traits traditionally used to classify Native Americans following Rhine (1990) and presented in Table 2.1 are useful in classifying Japanese and/or Thai individuals.

Intraobserver error

Lastly, intraobserver error was assessed on 120 individuals (8.6%), who were scored on two separate occasions by the PI, using Cohen's kappa statistic, which analyzes the degree of agreement/disagreement in categorical data between two observations (Hefner 2009). This analysis produces a kappa (k) value that can range from -1 to +1, and demonstrates the level of agreement above chance alone (Field 2009). The level of agreement based on the k value is assessed as follows: < 0 (poor agreement); 0.0 – 0.20 (slight agreement); 0.21 – 0.40 (fair agreement); 0.41 – 0.60 (moderate agreement); 0.61 – 0.80 (substantial agreement); and 0.81 – 1.0 (almost perfect agreement) (Landis and Koch 1977).

CHAPTER V: Results

This chapter presents the results of the nonmetric analyses conducted on the Chiba (CU), Jikei (JU), Khon Kaen (KKU), and Chiang Mai (CMU) University collections discussed in Chapter IV. While the entire sample is robust (n=1,397), not every individual was complete and therefore some nonmetric scores for the 15 sexually dimorphic traits and 37 cranial/mandibular traits are lacking for some individuals. This is particularly true for the scoring of occlusion and the maxillary incisor orientation, which required observations on incisors in the mandibular and/or maxillary alveoli. A significant proportion of the sample lacked incisors due to antemortem and postmortem tooth loss. However, the maximum number of individuals with each score was used for statistical analyses.

The first section of this chapter presents the results for the 15 sexually dimorphic nonmetric traits. The second section of this chapter presents the results for the 37 nonmetric cranial and mandibular traits. All analyses were conducted in IBM SPSS (version 23.0).

Sexually Dimorphic Traits

The first objective of this study is to determine if the Japanese and Thai individuals are different from non-Asian populations and each other in the expression of sexually dimorphic nonmetric traits present on the cranium, mandible, clavicle, humerus, and pelvis. Prior to determining if differences exist, chi-square analyses were used to ascertain if side differences exist in the scoring of the sexually dimorphic traits. To determine if population differences exist, univariate probabilities, chi-square statistics, Spearman's rank order correlation coefficients, binary logistic regression equations, and chi-square automatic detection (CHAID) decision trees were calculated separately for Japanese females and males and Thai females and males. Each region of the body is presented separately.

Side differences

Chi-square analyses were conducted on the cranial and postcranial nonmetric traits that were scored on both the right and left sides to test the null hypothesis that there is no association in the scoring of traits and side. The significance values associated with each of the chi-square values are all significant at the 0.001 level, and therefore the null hypothesis is rejected, indicating that an association exists between the scoring of nonmetric traits and side (Table 5.1). Further, the Cramer's V/Phi values indicate that the association between side and nonmetric score is robust. Because no statistically significant side differences exist, the left side was used in all subsequent analyses, with scores on the right substituted when the left was missing.

Table 5.1. Chi-square analyses testing the association of side and the scoring of sexually dimorphic traits.

Trait	N	Chi-square value	Cramer's V/ Phi
Mastoid process	1304	3969.030	0.872
Supraorbital margin	1307	3944.939	0.869
Ventral arc	986	1686.001	0.925
Subpubic concavity	1015	2030.000	1.000
Ischiopubic ramus ridge	1002	1954.003	0.987
Sciatic notch	1031	3379.630	0.905
Preauricular sulcus	1029	1514.672	0.848
Rhomboid fossa	978	184.556	0.434
Medial epicondyle angle	1011	3861.417	0.977
Olecranon fossa shape	1011	2532.783	0.791
Trochlear extension	1009	3177.672	0.887
Trochlear constriction	1012	3458.991	0.924

Cranial trait sexual dimorphism

The number of individuals with each cranial trait within each group, the percentages, and probabilities of being female or male are presented in Table 5.2. In general, females exhibit lower trait scores, while males exhibit higher trait scores. Males show more variation in cranial trait scores compared to females, as evidenced by males exhibiting all ordinal scores. Females exhibit less variation in cranial trait scores, as evidenced by the lack of females with scores of 5 for the glabella and mental eminence.

Based on the frequencies and probabilities presented in Table 5.2, population-specific cutoff points were established for the Japanese and Thai samples, and are presented in Table 5.3. Ordinal scores with male probabilities above 0.50 indicate individuals with those scores are likely male, while ordinal scores with female probabilities above 0.50 indicate that individuals with those scores are likely female. The Japanese and Thai samples exhibit the same cutoff points for the supraorbital margin (between 2 and 3), glabella (between 1 and 2), and mental eminence (between 2 and 3). However, they differ in nuchal crest and mastoid process cutoff points. The Japanese nuchal crest cutoff point is between 3 and 4, while the Thai cutoff point is between 2 and 3. Both Japanese females and males with mastoid process ordinal scores of 3 have probabilities of 0.50, indicating an indeterminate category. Conversely, the mastoid process cutoff point for the Thai sample is between 3 and 4.

Table 5.2. Cranial trait score frequencies and probabilities for Japanese females and males and Thai females and males.

Trait	Group	N	Score				
			1	2	3	4	5
Nuchal crest	Japanese females	204	20 (9.8%)	76 (37.3%)	77 (37.7%)	29 (14.4%)	2 (1.0%)
	Probability		0.73	0.71	0.52	0.33	0.06
	Japanese males	517	19 (3.7%)	80 (15.5%)	183 (35.4%)	148 (28.6%)	87 (16.8%)
	Probability		0.27	0.29	0.48	0.67	0.94
	Thai females	190	34 (17.9%)	99 (52.1%)	48 (25.3%)	8 (4.2%)	1 (0.5%)
	Probability		0.74	0.62	0.39	0.20	0.10
	Thai males	401	26 (6.3%)	130 (32.5%)	159 (39.8%)	69 (17.3%)	17 (4.3%)
	Probability		0.26	0.38	0.61	0.80	0.90
	Pooled females	394	54 (13.7%)	175 (44.4%)	125 (31.7%)	37 (9.4%)	3 (0.8%)
	Probability		0.74	0.66	0.46	0.28	0.07
	Pooled males	918	45 (4.9%)	210 (22.9%)	342 (37.3%)	217 (23.6%)	104 (11.3%)
	Probability		0.26	0.34	0.54	0.72	0.93
Mastoid process	Japanese females	209	18 (8.6%)	59 (28.2%)	72 (34.4%)	33 (15.8%)	27 (12.9%)
	Probability		0.88	0.74	0.50	0.34	0.35
	Japanese males	513	6 (1.2%)	50 (9.7%)	177 (34.5%)	155 (30.2%)	125 (24.4%)
	Probability		0.12	0.26	0.50	0.66	0.65
	Thai females	191	4 (2.1%)	43 (22.5%)	97 (50.5%)	25 (13.1%)	22 (11.5%)
	Probability		0.88	0.81	0.61	0.27	0.30
	Thai males	375	1 (0.3%)	20 (5.3%)	120 (32.0%)	132 (35.2%)	102 (27.2%)
	Probability		0.12	0.19	0.39	0.73	0.70
	Pooled females	400	22 (5.5%)	102 (25.5%)	169 (42.3%)	58 (14.5%)	49 (12.3)
	Probability		0.87	0.76	0.56	0.31	0.32
	Pooled males	888	7 (0.8%)	70 (7.9%)	297 (33.4%)	287 (23.3%)	227 (25.6%)
	Probability		0.13	0.24	0.44	0.69	0.68
Supraorbital margin	Japanese females	205	31 (15.1%)	99 (48.3%)	63 (30.7%)	11 (5.4%)	1 (0.5%)
	Probability		0.86	0.68	0.46	0.16	0.05
	Japanese males	515	13 (2.5%)	117 (22.7%)	184 (35.7%)	149 (28.9%)	52 (10.1%)
	Probability		0.14	0.32	0.54	0.84	0.95
	Thai females	191	33 (17.3%)	111 (58.1%)	39 (20.4%)	7 (3.7%)	1 (0.5%)
	Probability		0.81	0.63	0.36	0.16	0.13
	Thai males	402	16 (4.0%)	139 (34.6%)	155 (38.6%)	78 (19.4%)	14 (3.5%)
	Probability		0.19	0.37	0.65	0.84	0.87

Table 5.2, continued.

Trait	Group	N	Score				
			1	2	3	4	5
Supraorbital margin, cont.	Pooled females	396	64 (16.2%)	210 (53.0%)	102 (25.8%)	18 (4.5%)	2 (0.5%)
	Probability		0.84	0.66	0.41	0.15	0.06
	Pooled males	917	29 (3.2%)	256 (27.9%)	339 (37.0%)	227 (24.8%)	66 (7.2%)
	Probability		0.16	0.34	0.59	0.85	0.94
Glabella	Japanese females	205	184 (89.9%)	15 (7.3%)	6 (2.9%)	0 (0.0%)	0 (0.0%)
	Probability		0.76	0.14	0.13	0	0
	Japanese males	515	145 (28.2%)	227 (44.1%)	104 (20.2%)	36 (7.0%)	3 (0.6%)
	Probability		0.23	0.86	0.87	1.0	1.0
	Thai females	192	180 (93.8%)	7 (3.6%)	2 (1.0%)	3 (1.6%)	0 (0.0%)
	Probability		0.77	0.08	0.05	0.14	0
	Thai males	402	112 (27.9%)	171 (42.5%)	69 (17.2%)	40 (10.0%)	10 (2.5%)
	Probability		0.23	0.92	0.95	0.86	1.0
	Pooled females	397	364 (91.7%)	22 (5.5%)	8 (2.0%)	3 (0.8%)	0 (0.0%)
	Probability		0.77	0.11	0.10	0.09	0.00
	Pooled males	917	257 (28.0%)	398 (43.4%)	173 (18.9%)	76 (8.3%)	13 (1.4%)
	Probability		0.23	0.89	0.90	0.91	1.00
Mental eminence	Japanese females	194	40 (20.6%)	103 (53.1%)	46 (23.7%)	5 (2.6%)	0 (0.0%)
	Probability		0.77	0.59	0.34	0.20	0
	Japanese males	507	32 (6.3%)	187 (36.9%)	231 (45.6%)	53 (10.5%)	4 (0.8%)
	Probability		0.23	0.41	0.66	0.80	1.0
	Thai females	183	16 (8.7%)	87 (47.5%)	69 (37.7%)	11 (6.0%)	0 (0.0%
	Probability		0.81	0.65	0.41	0.23	0
	Thai males	388	8 (2.1%)	101 (26.0%)	209 (53.9%)	60 (15.5%)	10 (2.6%)
	Probability		0.19	0.35	0.59	0.72	1.0
	Pooled females	377	56 (14.9%)	190 (50.4%)	115 (30.5%)	16 (4.2%)	0 (0.0%)
	Probability		0.77	0.61	0.38	0.25	0.00
	Pooled males	895	40 (4.5%)	288 (32.2%)	440 (49.2%)	113 (12.6%)	14 (1.6%)
	Probability		0.23	0.39	0.62	0.75	1.00

Table 5.3. Population-specific cutoff points for the cranial nonmetric traits.

		Cutoff points				
Trait	**Group**	**1**	**2**	**3**	**4**	**5**
Nuchal crest	Japanese	Female			Male	
	Thai	Female		Male		
Mastoid process	Japanese	Female		Indeterminate	Male	
	Thai	Female			Male	
Supraorbital margin	Japanese	Female		Male		
	Thai	Female		Male		
Glabella	Japanese	Female	Male			
	Thai	Female	Male			
Mental eminence	Japanese	Female		Male		
	Thai	Female		Male		

Using the population-specific cutoff points for each of the cranial traits presented in Table 5.3 (above), all individuals were rescored. Table 5.4 shows the number of individuals correctly classified using each of the five traits separately for each sample, along with the sex biases for each trait, in comparison to Walker's (2008) American/English sample. Correct classification rates using the population-specific cutoff points range from 45.5% (nuchal crest, Japanese males) to 94.8% (glabella, Thai females). Concerning the total individuals correctly classified, the mastoid process performed the best, followed by glabella, supraorbital margin, mental eminence, and, lastly, the nuchal crest. Because the mastoid process score of 3 is indeterminate for the Japanese sample, removing those individuals from analysis improves the mastoid process correct classification rates (note that both correct classification rates including and excluding individuals with mastoid process scores of 3 are presented in Table 5.4). The nuchal crest performed particularly poor for the males (45.5 – 61.2%), while the glabella classified females well (89.8 – 94.8%). If the pooled cutoff point for the nuchal crest is used (between 2 and 3), which is the same as the Thai cutoff point, the Japanese female correct classification rate changes from 84.3% to 47.1% (96/204), and Japanese male correct classification changes from 45.5% to 80.9% (418/517). Similarly, if the pooled cutoff point for the mastoid process is used (between 3 and 4), which is the same as the Thai cutoff point, the Japanese female correct classification rate changes from 74.2% to 71.3% (149/209), and the Japanese male correct classification rate changes from 89.0% to 54.6% (280/513). The cranial traits show significant sex bias, with biases ranging from -38.8% (nuchal crest, Japanese) to 15.6% (mental eminence, Thai). The majority of the cranial traits better classify Japanese and Thai females, as evidenced by most traits showing significant negative sex biases. The sex biases are significantly larger than those presented in Walker's (2008) study, which documented sex biases ranging from -19.9% to 3.4%. The individual and combined univariate cranial traits do not perform particularly well among the Japanese and Thai samples, as indicated by few correct classification rates above 80%.

All cranial traits are indeed sexually dimorphic for the Japanese and Thai samples, and several traits differ between the Japanese and Thai samples, indicating that population differences exist in the expression of the sexually dimorphic cranial traits (Table 5.5). Chi-square analyses were conducted to test the null hypothesis that there is no association between the scoring of cranial traits and sex. All significance values fell below 0.05 for the Japanese and Thai samples, indicating that sex is associated with the scoring of the cranial nonmetric traits (i.e., sexual dimorphism is present). Further, chi-square analyses were conducted to test the null hypothesis that there is no association between the scoring of cranial traits and population. Significance values fell below 0.05 for the nuchal crest, mastoid process, glabella, and mental eminence scores for the Japanese and Thai females, indicating that population is associated with

Table 5.4. Correct classification rates and sex biases for the sexually dimorphic cranial traits compared to Walker's (2008) results.

Trait	Group	N	Correct/ Walker's Correct	Sex Bias	Walker's Sex Bias
Nuchal crest	Japanese females	204	172 (84.3%)/82.1% 96 (47.1%)*	-38.8%	-19.9% 33.8%*
	Japanese males	517	235 (45.5%)/62.2% 418 (80.9%)*		
	Thai females	190	133 (70.0%)/82.1%	-8.8%	
	Thai males	399	244 (61.2%)/62.2%		
	Total	1310	784 (59.8%)/71.4% 891 (68.0%)*		
Mastoid process	Japanese females	205/128	95 (46.3%/74.2%)/78.6% 149 (71.3%)*	13.4%/14.8%	0.1% -16.7%*
	Japanese males	514/345	307 (59.7%/89.0%)/78.7% 280 (54.6%*		
	Thai females	190	166 (87.4%)/78.6%	-22.2%	
	Thai males	399	260 (65.2%)/78.7%		
	Total	1308/1062	828 (63.3%/78.0%)/78.6% 855 (65.4%)*		
Supraorbital margin	Japanese females	205	130 (63.4%)/67.9%	11.4%	1.7%
	Japanese males	515	385 (74.8%)/69.5%		
	Thai females	191	144 (75.4%)/67.9%	-14.0%	
	Thai males	402	247 (61.4%)/67.9%		
	Total	1313	906 (69.0%)/68.8%		
Glabella	Japanese females	205	184 (89.8%)/80.7%	-18.0%	3.4%
	Japanese males	515	370 (71.8%)/84.1%		
	Thai females	192	180 (94.8%)/80.7%	-22.7%	
	Thai males	402	290 (72.1%)/84.1%		
	Total	1314	1024 (77.9%)/82.6%		
Mental eminence	Japanese females	194	143 (73.7%)/78.6%	-16.8%	-3.6%
	Japanese males	506	288 (56.9%)/75.0%		
	Thai females	183	103 (56.3%)/78.6%	15.6%	
	Thai males	388	279 (71.9%)/75.0%		
	Total	1271	813 (64.0%)/76.6%		
Combined traits	Japanese females	936	724 (77.4%)	-11.3%	
	Japanese males	2398	1585 (66.1%)		
	Thai females	946	726 (76.7%)	-10.4%	
	Thai males	1990	1320 (66.3%)		
	Total	6270	4355 (69.5%)		

*Pooled cutoff points used to determine frequencies and sex biases.

the scoring of these sexually dimorphic nonmetric cranial traits. Further, significance values fell below 0.05 for the nuchal crest, supraorbital margin, and mental eminence scores for the Japanese and Thai males, also indicating that population is associated with the scoring of these sexually dimorphic nonmetric cranial traits.

To determine if age affects the expression and scoring of the sexually dimorphic cranial traits, Spearman's rank order (rho) correlation coefficients were calculated to assess the relationship between age and cranial trait scores for each group (Table 5.6). The majority of the traits are unaffected by age. However, a slight positive correlation exists between the nuchal crest scores and age for Japanese and Thai males. As age increases, the nuchal crest becomes more robust. Additionally, a slight negative correlation exists between mental eminence scores and age for Japanese and Thai females. As age increases, the mental eminence scores decrease. As such, age has a minimal affect on the expression of the sexually dimorphic cranial traits.

To further explore how age affects nuchal crest and mental eminence scores, Kruskal-Wallis analyses were conducted with the seven age groups as the independent variables and the nuchal crest scores (males) and mental eminence scores (females) as the dependent variables. The results of the nuchal crest Kruskal-Wallis for Japanese males indicate that a statistically significant difference exists in the mean ranks of at least two age groups ($H = 26.089$; $df = 6$; $p = 0.001$). A *post-hoc* pairwise test shows that the youngest Japanese males (17-29 years) have lower nuchal crest scores compared to males 30-39 years ($p = 0.019$), 40-49 years ($p = 0.000$), 50-59 years ($p = 0.002$), 60-69 years ($p = 0.003$), and 70-79 years ($p = 0.001$). Additionally, the results of the nuchal crest Kruskal-Wallis for Thai males indicate that a statistically significant difference exists in the mean ranks of at least two age groups ($H = 17.305$; $df = 6$; $p = 0.008$). A

Table 5.5. Chi-square values between all groups to explore the affects of sex and population for the sexually dimorphic cranial traits.

Trait	Group	Japanese females	Japanese males	Thai females
Nuchal crest	Japanese males	84.592*	--	
	Thai females	25.167*	182.681*	--
	Thai males	8.683	76.602*	69.565*
Mastoid process	Japanese males	187.253*	--	
	Thai females	17.821*	148.855*	--
	Thai males	205.305*	6.971	175.085*
Supraorbital margin	Japanese males	124.271*	--	
	Thai females	6.981	167.135*	--
	Thai males	53.768*	34.973*	85.134*
Glabella	Japanese males	224.865*	--	
	Thai females	8.847**	242.791*	--
	Thai males	209.392*	9.395	226.005*
Mental eminence	Japanese males	66.999*	--	
	Thai females	18.178*	11.411**	--
	Thai males	132.094*	28.267*	51.005*

*significant at the 0.001 level; **significant at the 0.05 level.

Table 5.6. Age affects on sexually dimorphic cranial scores for each group.

Trait	Group	N	Spearman's rho
Nuchal crest	Japanese females	200	0.046
	Japanese males	510	0.151*
	Thai females	178	-0.027
	Thai males	390	0.186*
Mastoid process	Japanese females	201	-0.062
	Japanese males	507	0.007
	Thai females	185	0.079
	Thai males	389	-0.007
Supraorbital margin	Japanese females	201	0.034
	Japanese males	508	0.078
	Thai females	179	0.110
	Thai males	392	0.021
Glabella	Japanese females	201	-0.112
	Japanese males	508	-0.011
	Thai females	180	0.076
	Thai males	392	-0.096
Mental eminence	Japanese females	190	-0.234*
	Japanese males	500	-0.057
	Thai females	171	-0.154**
	Thai males	379	0.039

*significant at the 0.01 level (2-tailed); **significant at the 0.05 level (2-tailed).

post-hoc pairwise test shows that males 80-96 years have lower nuchal crest scores compared to males 40-49 years (p = 0.019). The results of the mental eminence Kruskal-Wallis for Japanese females indicate that no statistically significant differences exist in the mean ranks for any of the seven age groups (H = 17.662; df = 6; p = 0.007). Similarly, the mental eminence Kruskal-Wallis for the Thai females indicates that no statistically significant differences exist in the mean ranks for any of the seven age groups (H = 7.236; df = 6; p = 0.300).

While age is minimally correlated with two cranial traits, all sexually dimorphic cranial traits are positively correlated with each other, as indicated by statistically significant Spearman's rho values (Table 5.7). As such, an increase in the ordinal score of one trait is correlated with a slight to moderate increase in the ordinal scores for all other traits.

Walker's (2008) nine published discriminant function equations developed on his American/English and Native American (Arikara) samples were tested on the Japanese and Thai samples (Table 5.8). While many of the discriminant functions produced relatively high correct classification rates in excess of 85%, many have significant associated sex biases. The correct classification rates range from 26.3% (Thai females) to 97.4% (Thai males), with sex biases ranging -63.1 – 71.1%. Walker's correct classifications range from 69.5% (Arikara males) to 86.6% (American/English males), with associated sex biases ranging -13.4 – 4.5%. Several of Walker's American/English discriminant function equations performed better on the whole compared to those developed on the Arikara. Generally, Walker (2008) achieved better correct classification rates and lower sex biases, compared to when his equations are applied to the Japanese and Thai samples.

Table 5.7. Spearman's rho correlation coefficients for the sexually dimorphic cranial traits.

	Nuchal crest	**Mastoid process**	**Supraorbital margin**	**Glabella**
Mastoid process	0.302*	--		
Supraorbital margin	0.307*	0.330*	--	
Glabella	0.329*	0.446*	0.432*	--
Mental eminence	0.125*	0.222*	0.190*	0.242*

*significant at the 0.01 level (2-tailed).

Additionally, Garvin *et al.*'s (2014) published discriminant function equations developed on their pooled U.S. White, pooled U.S. Black, and Arikara samples were applied to the Japanese and Thai samples (Table 5.9). The correct classification rates range from 30.6% (Thai males) to 97.6% (Japanese females), with sex biases ranging -67.3 – 9.9%. Both of Garvin *et al.'s* pooled U.S. White and U.S. Black discriminant function equations produced extreme negative sex biases in the Japanese and Thai samples, with the equations greatly favoring females. Their Arikara discriminant function equation performed better on the whole, with correct classification rates of 74.9 – 88.4% and positive sex biases of 9.9 – 13.5%. However, on the whole, Garvin and coauthors achieved better total correct classification rates, compared to when their equations are applied to the Japanese and Thai samples. Like Walker's (2008) equations, Garvin *et al.*'s (2014) discriminant function equations exhibit reduced discriminatory power at predicting the sex of Japanese and Thai individuals.

Table 5.8. Walker's (2008) cranial discriminant function equations applied to the Japanese and Thai samples.

Walker's Sample	Discriminant Function	Group	N	Correct (%)	% Walker's Correct	% SB	% Walker's SB
American/ English	GLA(-1.375) + MP(-1.185) + ME(-1.151) + 9.128	Japanese females	192	174 (90.6)	86.4	-20.1	2.0
		Japanese males	491	346 (70.5)	88.4		
		Japanese total	683	520 (76.1)			
		Thai females	179	155 (86.6)	86.4	-5.1	
		Thai males	378	308 (81.5)	88.4		
		Thai total	557	463 (83.1)			
	GLA(-1.568) + MP(-1.459) + 7.434	Japanese females	200	177 (88.5)	82.9	-14.8	2.5
		Japanese males	513	378 (73.7)	85.4		
		Japanese total	713	555 (77.8)			
		Thai females	190	175 (92.1)	82.9	-15.2	
		Thai males	398	306 (76.9)	85.4		
		Thai total	588	481 (81.8)			
	GLA(-1.525) + ME(-1.485) + 7.372	Japanese females	192	178 (92.7)	82.1	-37.7	4.5
		Japanese males	493	271 (55.0)	86.6		
		Japanese total	685	449 (65.5)			
		Thai females	181	166 (91.7)	82.1	-28.2	
		Thai males	381	242 (63.5)	86.6		
		Thai total	562	408 (72.6)			
	ME(-1.629) + MP(-1.415) + 7.382	Japanese females	192	86 (44.8)	83.6	47.5	-3.7
		Japanese males	492	454 (92.3)	79.9		
		Japanese total	684	540 (78.9)			
		Thai females	179	47 (26.3)	83.6	71.1	
		Thai males	378	368 (97.4)	79.9		
		Thai total	557	415 (74.5)			
	SOM(-1.007) + ME(-1.1850) + 6.018	Japanese females	192	105 (54.7)	77.9	29.9	0.2
		Japanese males	492	416 (84.6)	78.1		
		Japanese total	684	521 (76.2)			
		Thai females	180	80 (44.4)	77.9	42.8	
		Thai males	381	336 (88.2)	78.1		
		Thai total	561	416 (74.2)			

Table 5.8, continued.

Walker's Sample	Discriminant Function	Group	N	Correct (%)	% Walker's Correct	% SB	% Walker's SB
	NC(-0.7) + MP(-1.559) + 5.329	Japanese females	201	80 (39.8)	82.9	54.6	-6.1
		Japanese males	514	485 (94.4)	76.8		
		Japanese total	715	565 (79.0)			
		Thai females	190	60 (31.6)	82.9	64.9	
		Thai males	399	385 (96.5)	76.8		
		Thai total	589	445 (75.6)			
Native American	SOM(-0.499) + ME(-0.606) + 3.414	Japanese female	192	182 (94.8)	77.9	-59.9	0.2
		Japanese males	493	172 (34.9)	78.1		
		Japanese total	685	354 (51.7)			
		Thai females	180	168 (93.3)	77.9	-63.1	
		Thai males	381	115 (30.2)	78.1		
		Thai total	561	283 (50.4)			
	ME(-0.576) + MP(-1.136) + 4.765	Japanese females	192	146 (76.0)	72.7	1.2	1.4
		Japanese males	492	380 (77.2)	74.1		
		Japanese total	684	526 (76.9)			
		Thai females	179	112 (62.6)	72.7	23.9	
		Thai males	378	327 (86.5)	74.1		
		Thai total	557	439 (78.8)			
	GLA(-0.797) + MP(-1.085) + 5.025	Japanese females	205	171 (83.4)	82.9	-18.3	-13.4
		Japanese males	513	334 (65.1)	69.5		
		Japanese total	718	505 (70.3)			
		Thai females	188	160 (85.1)	82.9	-12.7	
		Thai males	399	289 (72.4)	69.5		
		Thai total	587	449 (76.5)			

GLA=glabella; MP=mastoid process; SOM=supraorbital margin; ME=mental eminence; SB=sex bias

Table 5.9. Garvin *et al.*'s (2014) cranial discriminant function equations applied to the Japanese and Thai samples.

Garvin's Sample	Discriminant Function	Group	N	% Correct	% Garvin's Correct	% Sex Bias
Pooled U.S. White	MP(0.360) + SOM(0.275) + GLA(0.939) – 4.141	Japanese females	205	200 (97.6)	86.1	-66.0
		Japanese males	512	162 (31.6)		
		Japanese total	717	362 (50.5)		
		Thai females	190	186 (97.9)		-67.3
		Thai males	399	122 (30.6)		
		Thai total	589	308 (52.3)		
Pooled U.S. Black	MP(0.586) + GLA(0.704) + MEN(0.359) – 4.153	Japanese females	192	179 (93.2)	81.0	-27.9
		Japanese males	490	320 (65.3)		
		Japanese total	682	499 (73.2)		
		Thai females	179	167 (93.3)		-18.7
		Thai males	378	282 (74.6)		
		Thai total	557	449 (80.6)		
Arikara	MP(0.772) + SOM(0.477) + GLA(0.399) + ME(0.368) – 4.911	Japanese females	192	144 (75.0)	89.7	9.9
		Japanese males	490	416 (84.9)		
		Japanese total	682	560 (82.1)		
		Thai females	179	134 (74.9)		13.5
		Thai males	378	334 (88.4)		
		Thai total	557	468 (84.0)		

MP=mastoid process; SOM=supraorbital margin; GLA=glabella; MEN=mental eminence

The lackluster performance of Walker's (2008) and Garvin *et al.*'s (2014) discriminant function equations when applied to the Japanese and Thai samples is evident when comparing their correct classification rates and sex biases in Tables 5.8 and 5.9 (above). The overall poor performance of these equations when applied to Japanese and Thai individuals is due to reduced sexual dimorphism, significant overlap in ordinal scores between females and males, and the significant variation exhibited by males in the Japanese and Thai samples. Thus, the application of these discriminant function equations to Japanese and Thai individuals is not appropriate.

Population-specific binary logistic regression equations were calculated for the Japanese, Thai, and pooled Japanese and Thai samples using the Forward Wald function in IBM SPSS (Table 5.10). Equations using five, four, three, two, and one variables were calculated for each of the groups. All of the equations presented in Table 5.10 are statistically significant, and all of the traits within each equation are also statistically significant. However, the glabella scores performed the best at predicting sex, followed by mastoid process, mental eminence, nuchal crest, and, lastly, the supraorbital margin in all five-trait combinations. Correct classification rates for the binary logistic regression equations ranged from 72.8% to 91.3% for the Japanese, with associated sex biases ranging from -18.0% to 18.4%; 71.8% to 89.7% for the Thai samples, with associated sex biases from -18.0% to 12.6%; and 67.8.8% to 91.7% for the pooled Japanese and Thai samples, with associated sex biases from -19.7% to 23.9%. The single-trait logistic regression equations performed the worst, while the five-trait logistic regression equations performed the best, producing the highest total correct classification rates. However, the two-trait logistic regression equations using the glabella and mastoid process produced relatively high female and male correct classification rates, high total correct classification rates, and relatively low sex biases. Generally, the pooled Japanese and Thai logistic regression equations produced larger sex biases compared to the population-specific Japanese and Thai equations. The addition of age did not contribute to any of the equations, and the population did not contribute to the pooled Japanese and Thai equations.

A binary logistic regression equation with the five sexually dimorphic cranial traits and population as the independent variables and sex as the dependent variable was conducted on 1,239 individuals to determine if the population affects the prediction of sex. The Wald statistic for the population (2.245) was small and not statistically significant (p = 0.134), compared to the Wald statistics for the glabella (91.485), mastoid process (80.378), mental eminence (24.483), nuchal crest (17.667), and supraorbital margin (15.243), which were all statistically significant (p = 0.000). Similarly, a CHAID decision tree with sex as the dependent variable and the five cranial traits and population as the independent variables was conducted to test the affect of population on the prediction of sex. The decision tree eliminated population and nuchal crest as predictors, correctly classifying 66.2% of females and 92.1% of males using the glabella, mastoid process, mental eminence, and supraorbital margin. Thus, population does not affect the prediction of sex when using the cranial traits.

A CHAID decision tree analysis was conducted for the Japanese cranial traits for 736 individuals (Figure A.1). Accordingly, the glabella and mastoid process performed the best, correctly classifying 77.3% of females and 85.8% of males, with a total correct classification rate of 83.4%. The inclusion of age did not contribute to the tree’s performance. The resubstitution and cross-validated risks associated with this tree are 0.166 (S.E. = 0.014). The probabilities for each of the terminal nodes are presented in Table A.1.

Table 5.10. Population-specific cranial binary logistic regression equations for Japanese, Thai, and pooled Japanese and Thai samples.

Group	Coefficients						% Correctly Classified			% SB
	NC	MP	SOM	GLA	ME	CON	F	M	T	
Japanese[1]	--	-0.907	--	-2.054	--	4.948	78.0	84.8	82.9	6.8
	--	--	--	-2.36	--	2.540	89.8	71.8	76.9	-18.0
		-0.931	--	-1.957	-0.739	6.602	75.0	90.4	86.1	15.4
	--	-0.927	--	-1.941	-0.750	6.598	74.9	90.4	86.0	15.5
	-0.466	-0.838	-0.349	-1.667	-0.69	8.033	74.9	91.0	86.5	16.1
	-0.505	-0.867	--	-1.831	-0.754	7.773	72.8	91.3	86.0	18.4
Thai[2]	--	-1.198	--	-1.995	--	6.164	82.1	86.8	85.3	4.7
	--	-1.112	--	-1.949	-0.639	7.507	79.9	87.8	85.3	7.9
	-0.382	-1.082	-0.505	-1.732	-0.563	8.888	78.8	89.2	85.8	10.4
	--	-1.071	-0.526	-1.794	-0.605	8.353	77.1	89.7	85.6	12.6
	--	--	--	-2.360	--	2.540	89.8	71.8	76.9	-18.0
Pooled Japanese Thai[3]	--	-1.002	--	-2.052	--	5.406	80.0	85.7	84.0	5.7
	--	-0.929	-0.516	01.771	-0.579	7.541	75.9	89.7	85.3	14.8
	--	--	--	-2.435	--	2.703	91.7	72.0	77.9	-19.7
	-0.452	-0.893	-0.435	-1.697	-0.599	8.371	75.1	90.8	86.1	15.7
	-0.513	-0.921	--	-1.868	-0.639	7.847	73.5	91.0	85.8	17.5
	--	-0.970	--	-1.986	-0.0632	6.771	67.8	91.7	84.6	23.9

[1] Models used 682 individuals (87.3%) to build equations

[2] Models used 557 individuals (90.4%) to build equations

[3] Models used 1239 individuals (88.7%) to build equations

NC=nuchal crest; MP=mastoid process; SOM=supraorbital margin; GLA=glabella; ME=mental eminence; CON=constant; F=female; M=male; T=total; SB=sex bias

A CHAID decision tree analysis was conducted for the Thai cranial traits on 603 individuals (Figure A.2). Accordingly, the glabella and mastoid process performed the best, correctly classifying 81.4% of females and 86.6% of males, with a total correct classification rate of 84.9%. The inclusion of age did not contribute to the tree's performance. The resubstitution and cross-validated risks associated with this tree are 0.151 (S.E. = 0.015). The probabilities for each of the terminal nodes are presented in Table A.2.

A CHAID cranial decision tree analysis was conducted for the combined Japanese and Thai samples for 1,339 individuals (Figure A.3). Accordingly, the glabella, mastoid process, and supraorbital margin performed the best, correctly classifying 68.8% of females and 91.8% of males, with a total correct classification rate of 84.9%. The inclusion of age and population did not contribute to the tree's performance. The resubstitution risk associated with this tree is 0.151 (S.E. = 0.010), while the cross-validated risk is 0.163 (S.E. = 0.01). The probabilities associated with each of the terminal nodes are presented in Table A.3.

Pelvic trait sexual dimorphism

The number of individuals with each pelvic trait within each group, the percentages, and probabilities of being female or male are presented in Table 5.11. The highest probability was achieved with the Japanese female sample that has a probability of 0.99 of being female with a preauricular sulcus score of 1. For the males, the highest probability is 0.95 of being male with a subpubic concavity score of 3.

Based on the frequencies and probabilities presented in Table 5.11, population-specific cutoff points were established for the Japanese and Thai samples, and are presented in Table

5.12. Ordinal scores with male probabilities above 0.50 indicate individuals with those scores are likely male, while ordinal scores with female probabilities above 0.50 indicate that individuals with those scores are likely female. Cutoff points differ between the Japanese and Thai in the ventral arc (between 1 and 2 for the Japanese; between 2 and 3 for the Thai), and sciatic notch (between 2 and 3 for the Japanese; between 3 and 4 for the Thai). Japanese and Thai cutoff points are the same for the subpubic concavity (between 2 and 3), ischiopubic ramus ridge (between 2 and 3), and preauricular sulcus (between 0 and 1).

Using the population-specific cutoff points for each of the pelvic traits presented in Table 5.12, all individuals were rescored. Table 5.13 shows the number of individuals correctly classified using each of the five traits separately for each sample, along with the sex biases for each trait. Correct classification rates using the population-specific cutoff points range from 65.5% (sciatic notch, Japanese females) to 97.5% (sciatic notch, Japanese males). Additionally, no scores are distributed "normally" whereby scores of 2 (in three ordinal scores) or 3 (in five ordinal scores) indicate indeterminate sex. Concerning the total correctly classified, the subpubic concavity performed the best, followed by ischiopubic ramus ridge, preauricular sulcus, ventral arc, and lastly, the sciatic notch. The sex biases are all toward the males, with a range of 0.4 – 32.0%. Overall, the univariate pelvic traits perform better than the cranial traits. In particular, the subpubic concavity and the ischiopubic ramus ridge perform the best with high correct classification rates and relatively low sex biases. The subpubic concavity has a correct classification rate of 91.3 – 95.8%, with sex biases at 0.4% (Thai) and 4.0 (Japanese). The ischiopubic ramus ridge has a correct classification rate of 89.4 – 94.8%, with sex biases of 0.5% (Thai) to 4.0% (Japanese). The sciatic notch performs the worst, with relatively low correct

Table 5.11. Pelvic trait score frequencies and probabilities for Japanese females and males and Thai females and males.

Trait	Group		Score					
		N	0	1	2	3	4	5
Ventral arc	Japanese females	101	--	79 (78.2%)	11 (10.9%)	11 (10.9%)	--	--
	Probability			0.89	0.41	0.13		
	Japanese males	334	--	33 (9.9%)	52 (15.6%)	249 (74.6%)	--	--
	Probability			0.11	0.59	0.87		
	Thai females	192	--	114 (59.4%)	36 (18.6%)	42 (21.9%)	--	--
	Probability			0.95	0.78	0.19		
	Thai males	405	--	13 (3.2%)	22 (5.4%)	370 (91.4%)	--	--
	Probability			0.05	0.22	0.81		
	Pooled females	293	--	193 (65.9%)	47 (16.0%)	53 (18.1%)	--	--
	Probability			0.91	0.62	0.18		
	Pooled males	739	--	46 (6.2%)	74 (10.0%)	619 (83.8%)	--	--
	Probability			0.09	0.38	0.82		
Subpubic concavity	Japanese females	115	--	101 (87.8%)	4 (3.5%)	10 (8.7%)	--	--
	Probability			0.98	0.56	0.08		
	Japanese males	338	--	7 (2.1%)	9 (2.7%)	322 (95.3%)	--	--
	Probability			0.02	0.44	0.92		
	Thai females	191	--	173 (90.6%)	9 (4.7%)	9 (4.7%)	--	--
	Probability			0.96	0.87	0.05		
	Thai males	405	--	14 (3.5%)	3 (0.7%)	388 (95.8%)	--	--
	Probability			0.04	0.13	0.95		
	Pooled females	306	--	274 (89.5%)	13 (4.2%)	19 (6.2%)	--	--
	Probability			0.97	0.72	0.06		
	Pooled males	743	--	21 (2.8%)	12 (1.6%)	710 (95.6%)	--	--
	Probability			0.03	0.28	0.94		
Ischiopubic ramus ridge	Japanese females	113	--	90 (79.6%)	11 (9.7%)	12 (10.6%)	--	--
	Probability			0.96	0.80	0.10		
	Japanese males	330	--	11 (3.3%)	8 (2.4%)	311 (94.2%)	--	--
	Probability			0.04	0.20	0.90		

Table 5.11, continued.

Trait	Group	N	Score					
			0	1	2	3	4	5
Ischiopubic ramus ridge, cont.	Thai females	193	--	163 (84.5%)	19 (9.8%)	11 (5.7%)	--	--
	Probability			0.96	0.83	0.06		
	Thai males	406	--	13 (3.2%)	8 (2.0%)	385 (94.8%)	--	--
	Probability			0.04	0.17	0.94		
	Pooled females	306	--	253 (82.7%)	30 (9.8%)	23 (7.5%)	--	--
	Probability			0.96	0.82	0.07		
	Pooled males	736	--	24 (3.3%)	16 (2.2%)	696 (94.6%)	--	--
	Probability			0.04	0.18	0.93		
Sciatic notch	Japanese females	116	--	36 (31.0%)	40 (34.4%)	20 (17.2%)	11 (9.5%)	9 (7.8%)
	Probability			0.98	0.93	0.40	0.17	0.23
	Japanese males	339	--	2 (0.6%)	8 (2.4%)	88 (26.0%)	153 (45.1%)	88 (26.0%)
	Probability			0.02	0.07	0.60	0.83	0.77
	Thai females	196	--	58 (29.6%)	85 (43.4%)	42 (21.4%)	11 (5.6%)	0 (0.0%)
	Probability			0.98	0.94	0.53	0.11	0.0
	Thai males	409	--	3 (0.7%)	12 (2.9%)	79 (19.3%)	192 (46.9%)	123 (30.0%)
	Probability			0.02	0.06	0.47	0.89	1.0
	Pooled females	312	--	94 (30.1%)	125 (40.1%)	62 (19.9%)	22 (7.1%)	9 (2.9%)
	Probability			0.98	0.94	0.47	0.13	0.09
	Pooled males	748	--	5 (0.7%)	20 (2.7%)	167 (22.3%)	345 (46.1%)	211 (28.2%)
	Probability			0.02	0.06	0.53	0.87	0.91
Preauricular sulcus	Japanese females	116	18 (15.5%)	26 (22.4%)	30 (25.9%)	18 (15.5%)	24 (20.7%)	--
	Probability		0.14	0.99	0.98	0.96	0.80	
	Japanese males	339	316 (92.2%)	1 (0.3%)	2 (0.6%)	2 (0.6%)	18 (5.3%)	--
	Probability		0.86	0.01	0.02	0.04	0.20	

Table 5.11, continued.

Trait	Group	N	Score					
			0	1	2	3	4	5
Preauricular sulcus, cont.	Thai females	196	36 (18.4%)	43 (21.9%)	44 (22.4%)	28 (14.3%)	45 (23.0%)	--
	Probability		0.17	0.98	0.98	0.95	0.81	
	Thai males	409	380 (92.9%)	2 (0.5%)	2 (0.5%)	3 (0.7%)	22 (5.4%)	--
	Probability		0.83	0.02	0.02	0.05	0.19	
	Pooled females	312	54 (17.3%)	69 (22.1%)	74 (23.7%)	46 (14.7%)	69 (22.1%)	--
	Probability		0.16	0.98	0.98	0.95	0.81	
	Pooled males	748	696 (93.0%)	3 (0.4%)	4 (0.5%)	5 (0.7%)	40 (5.3%)	--
	Probability		0.84	0.02	0.02	0.05	0.19	

Table 5.12. Population-specific cutoff points for the sexually dimorphic pelvic nonmetric traits.

Trait	Group	Cutoff points					
		0	1	2	3	4	5
Ventral arc	Japanese	--	Female	Male		--	--
	Thai	--	Female		Male	--	--
Subpubic concavity	Japanese	--	Female		Male	--	--
	Thai	--	Female		Male	--	--
Ischiopubic ramus ridge	Japanese	--	Female		Male	--	--
	Thai	--	Female		Male	--	--
Sciatic notch	Japanese	--	Female		Male		
	Thai	--	Female			Male	
Preauricular sulcus	Japanese	Male	Female				--
	Thai	Male	Female				--

correct classification rates for Japanese females (65.5%) and Thai males (77.0%), and high associated sex biases of 17.4% (Thai) and 32.0% (Japanese). Using the pooled cutoff point for the ventral arc (between 2 and 3), the Japanese female correct classification rate changes from 77.2% to 89.1% (90/101), and the Japanese male correct classification rate changes from 90.1% to 74.6% (249/334). Using the pooled cutoff point for the sciatic notch (between 2 and 3), the Thai female correct classification changes from 94.4% to 73.0% (143/196), and the Thai male correct classification rate changes from 77.0% to 96.3% (394/409). The Japanese and Thai correct classification rates are somewhat lower than Phenice's findings that the three traits in combination correctly classify 95% of his sample.

All pelvic traits are sexually dimorphic for the Japanese and Thai samples, and two of the traits differ between the Japanese and Thai samples, indicating that population differences exist in the expression of the sexually dimorphic pelvic traits (Table 5.14). Chi-square analyses were conducted to test the null hypothesis that there is no association between the scoring of pelvic traits and sex. All significance values fell below 0.001 for the Japanese and Thai samples, indicating that sex is associated with the scoring of the pelvic nonmetric traits (i.e., sexual dimorphism exists). Further, chi-square analyses were conducted to test the null hypothesis that there is no association between the scoring of pelvic traits and population. Significance values fell below 0.001 for the ventral arc for the Japanese and Thai females and males, and the sciatic notch for the Japanese and Thai females.

Table 5.13. Correct classification rates and sex biases for the sexually dimorphic pelvic traits.

Trait	Group	N	Correct	Sex Bias
Ventral arc	Japanese females	101	78 (77.2%)/ 90 (89.1%)*	12.1% -14.5%*
	Japanese males	334	301 (90.1%)/ 249 (74.6%)*	
	Thai females	192	150 (78.1%)	13.2%
	Thai males	403	368 (91.3%)	
	Total	1029	897 (87.2%) 857 (83.3%)*	
Subpubic concavity	Japanese females	115	105 (91.3%)	4.0%
	Japanese males	338	322 (95.3%)	
	Thai females	194	185 (95.4%)	0.4%
	Thai males	406	389 (95.8%)	
	Total	1053	1001 (95.1%)	
Ischiopubic ramus ridge	Japanese females	113	101 (89.4%)	4.8%
	Japanese males	330	311 (94.2%)	
	Thai females	192	181 (94.3%)	0.5
	Thai males	405	384 (94.8%)	
	Total	1040	977 (93.9%)	
Sciatic notch	Japanese females	116	76 (65.5%)	32.0%
	Japanese males	399	389 (97.5%)	
	Thai females	196	185 (94.4%)/ 143 (73.0%)*	17.4% 23.3%*
	Thai males	409	315 (77.0%)/ 394 (96.3%)*	
	Total	1120	965 (86.2%) 1002 (89.5%)*	
Preauricular sulcus	Japanese females	116	98 (84.5%)	8.7%
	Japanese males	339	316 (93.2%)	
	Thai females	196	160 (81.6%)	11.3%
	Thai males	409	380 (92.9%)	
	Total	1060	954 (90.0%)	
Combined traits	Japanese females	561	458 (81.6%)	12.4%
	Japanese males	1740	1639 (94.2%)	
	Thai females	970	861 (88.8%)	1.6%
	Thai males	2032	1836 (90.4%)	
	Total	5303	4794 (90.4%)	

*Pooled cutoff points used to determine frequencies and sex biases.

Table 5.14. Chi-square values between all groups to explore the affects of sex and population for the sexually dimorphic pelvic traits.

Trait	Group	Japanese females	Japanese males	Thai females
Ventral arc	Japanese males	193.807*	--	
	Thai females	10.530*	168.132*	--
	Thai males	323.362*	38.282*	308.046*
Subpubic concavity	Japanese males	352.616*	--	
	Thai females	2.231	445.729*	--
	Thai males	382.871*	5.478	490.237*
Ischiopubic ramus ridge	Japanese males	305.443*	--	
	Thai females	2.541	409.171*	--
	Thai males	356.789*	0.196	470.335*
Sciatic notch	Japanese males	224.628*	--	
	Thai females	18.594*	328.494*	--
	Thai males	252.057*	5.194	371.254*
Preauricular sulcus	Japanese males	288.474*	--	
	Thai females	0.995	319.903*	--
	Thai males	323.795*	0.275	357.550*

*significant at the 0.01 level.

To determine if age affects the expression and scoring of the sexually dimorphic pelvic traits, Spearman's rho correlation coefficients were calculated to assess the relationship between age and pelvic trait scores for each group (Table 5.15). Most of the groups' pelvic ordinal scores are unaffected by age. However, a positive correlation exists between age and ischiopubic ramus ridge scores in Thai males. That is, as age increases, ischiopubic ramus ridge scores also increase. Likewise, positive correlations exist between age and sciatic notch scores for Japanese and Thai males, so that as age increases, sciatic notch scores also increase, therefore becoming more constricted.

To further explore the associations between ischiopubic ramus ridge and sciatic notch scores and age, Kruskal-Wallis analyses were conducted with the seven age groups as the independent variables and the ischiopubic ramus ridge (Thai males) and sciatic notch scores

Table 5.15. Age affects on the sexually dimorphic traits for all groups.

Trait	Group	N	Spearman's rho
Ventral arc	Japanese females	100	0.074
	Japanese males	330	-0.045
	Thai females	179	-0.085
	Thai males	386	0.009
Subpubic concavity	Japanese females	114	-0.024
	Japanese males	334	0.103
	Thai females	181	0.103
	Thai males	387	0.067
Ischiopubic ramus ridge	Japanese females	112	0.001
	Japanese males	325	0.031
	Thai females	182	0.031
	Thai males	387	0.122*
Sciatic notch	Japanese females	116	0.075
	Japanese males	335	0.192**
	Thai females	182	0.78
	Thai males	390	0.104*
Preauricular sulcus	Japanese females	116	-0.178
	Japanese males	335	-0.076
	Thai females	183	0.049
	Thai males	391	0.019

*significant at the 0.05 level; **significant at the 0.01 level

(Japanese and Thai males) as the dependent variables. The results of the ischiopubic ramus ridge Kruskal-Wallis indicate that a statistically significant difference exists in the mean rank scores of at least two age groups (H = 25.871; df = 6; p = 0.001). A *post-hoc* pairwise test shows that the youngest Thai males (17-29 years) have lower ischiopubic ramus ridge scores compared to males 40-49 years (p = 0.011), 50-59 years (p = 0.003), 60-69 years (p = 0.000), 70-79 years (p = 0.001), and 80-96 years (p = 0.010). Additionally, the sciatic notch Kruskal-Wallis analysis for the Japanese and Thai males also indicates that that a statistically significant difference exists in the mean rank scores of at least two age groups (H = 24.079; df = 6; p = 0.001). A *post-hoc* pairwise test shows that the youngest males (17-29 years) have lower sciatic notch scores compared to males 50-59 years (p = 0.027), 60-69 years (p = 0.033), 70-79 years (p = 0.004), and 80-96 years (p = 0.012). Additionally, males 40-49 years have lower sciatic notch scores compared to males 70-79 years. However, the youngest Japanese and Thai males do not exhibit statistically significant differences in mean sciatic notch scores compared to males 30-49 years old.

While age is minimally correlated with two pelvic traits, all sexually dimorphic pelvic traits are moderately correlated with each other, as indicated by statistically significant Spearman's rho values (Table 5.16). All traits except for the preauricular sulcus are positively correlated with each other. As such, an increase in the ordinal score of one trait is correlated with an increase in the ordinal scores for all other traits. The preauricular sulcus deviates from this trend because the ordinal scoring of this trait is not scaled from gracile-robust like the other pelvic traits. A preauricular sulcus score of 0 indicates a lack of a sulcus, which is typically associated with males, while a score of 1 indicates a wide and deep sulcus, which is associated with females. Accordingly, the preauricular sulcus exhibits a strong negative correlation with all other traits.

Table 5.16. Spearman's rho correlation coefficients for the sexually dimorphic pelvic traits.

	Ventral arc	**Subpubic concavity**	**Ischiopubic ramus ridge**	**Sciatic notch**
Subpubic concavity	0.702*	--		
Ischiopubic ramus ridge	0.666*	0.938*	--	
Sciatic notch	0.481*	0.676*	0.672*	--
Preauricular sulcus	-0.521*	-0.727*	-0.716*	-0.554*

*significant at the 0.01 level (2-tailed).

Population-specific binary logistic regression equations were calculated for the Japanese, Thai, and pooled Japanese and Thai samples using the Forward Wald function in IBM SPSS (Table 5.17). Equations using five, four, three, two, and one variables were calculated for each of the groups. All of the equations presented in Table 5.17 are statistically significant, and all of the traits within each equation are also statistically significant. For the Japanese, the subpubic concavity contributed most to the equations, followed by the preauricular sulcus, ventral arc, sciatic notch, and lastly, the ischiopubic ramus ridge. For the Thai, the subpubic concavity contributed most to the equations, followed by the ischiopubic ramus ridge, sciatic notch, ventral arc, and, lastly, preauricular sulcus. For the pooled Japanese and Thai samples, the subpubic concavity contributed most to the equations, followed by ventral arc, sciatic notch, ischiopubic ramus ridge, and, lastly, the preauricular sulcus. Correct classification rates for the binary logistic regression equations ranged from 72.3% to 98.2% for Japanese, with associated sex biases ranging from 2.2% to 24.4%; 89.0% to 97.0% for the Thai samples, with associated sex biases from 1.7% to 5.9%; and 78.5% to 97.3% for the pooled Japanese and Thai samples, with associated sex biases from 4.5% to 10.0%. All logistic regression equations better classified males for all three groups, and the inclusion of age had no affect on the prediction of sex for any of the groups. Additionally, the inclusion of population in the pooled Japanese and Thai logistic equations did not contribute significantly to the determination of sex. Overall, the binary logistic regression equations performed best on the Thai sample, producing high correct classification rates and low associated sex biases. The single-trait logistic regression equations performed the worst, while the two-, three-, and four-trait logistic regression equations performed the best, producing the highest total correct classification rates.

Table 5.17. Population-specific pelvic binary logistic regression equations for Japanese, Thai, and pooled Japanese and Thai samples.

	Coefficients						% Correctly Classified			
Group	VA	SPC	IPR	SN	PAS	CON	F	M	T	% SB
Japanese[1]	--	3.043	--	--	--	-5.645	86.0	98.2	95.3	12.2
	--	2.788	--	--	-0.521	-4.587	89.0	98.2	96.0	2.2
	0.710	2.338	--	--	-0.555	-5.010	89.0	92.0	96.0	2.2
	0.832	1.964	--	0.516	-0.528	-6.177	89.0	98.2	96.0	2.2
	0.590	0.590	--	--	--	-5.835	88.0	97.3	95.2	9.3
	1.831	--	--	1.271	--	-6.616	72.3	96.7	91.0	24.4
	.626	1.991	.780	--	--	-6.337	89.0	98.2	96.0	9.2
	.619	2.659	--	--	--	-6.066	88.0	97.6	95.3	9.6
	--	3.043	--	--	--	-5.645	86.0	98.2	95.3	12.2
Thai[2]	--	3.116	--	--	--	-5.807	90.6	96.5	94.6	5.9
	--	2.387	--	0.984	--	-7.295	93.7	96.8	95.8	3.1
	--	1.595	0.973	0.907	--	-7.445	94.8	96.5	96.0	1.7
	--	2.076	1.221	--	--	-6.215	93.3	96.3	95.3	3.0
	--	--	2.243	1.237	--	-7.920	91.8	97.0	95.3	5.2
	.625	1.777	1.154	--	--	-6.909	93.2	96.3	95.3	3.1
	--	3.119	--	--	--	-5.810	90.6	96.5	94.6	5.9
	--	2.074	1.217	--	--	-6.198	93.2	96.3	95.3	3.1
Pooled Japanese Thai[3]	3.088	--	--	--	--	-5.748	89.0	97.3	94.9	8.3
	2.567	--	--	0.738	--	-6.983	91.8	97.3	95.7	5.5
	0.653	2.196	--	0.767	--	-7.730	91.8	97.3	95.7	5.5
	0.662	2.025	--	0.669	-0.349	-6.708	92.8	97.3	96.0	4.5
	0.599	2.737	--	--	--	-6.307	91.1	96.9	95.2	5.8
	1.776	--	--	--	-0.818	-2.201	78.5	88.5	85.6	10.0
	.588	1.931	.969	--	--	-6.666	91.8	97.0	95.3	5.2
	--	3.089	--	--	--	-5.750	89.0	97.3	94.9	8.3
	--	2.227	1.008	--	--	-6.083	91.9	97.0	95.5	5.1

[1] Models used 428 individuals (54.8%) to build equations

[2] Models used 594 individuals (96.4%) to build equations

[3] Models used 1022 individuals (73.2%) to build equations

VA=ventral arc; SPC=subpubic concavity; IPR=ischiopubic concavity; SN=sciatic notch; PAS=preauricular sulcus; CON=constant; F=female; M=male; T=total; SB=sex bias.

A binary logistic regression equation with the five sexually dimorphic pelvic traits and population as the independent variables and sex as the dependent variable was conducted on 1,022 individuals to determine if the population affects the determination of sex. The Wald statistic for the population (0.052) was small and not statistically significant (p = 0.820), compared to the Wald statistics and significance values for the subpubic concavity (26.374; p = 0.000), sciatic notch (13.077; p = 0.000), ventral arc (8.427; p = 0.004), and preauricular sulcus (6.961; p = 0.008). The ischiopubic ramus ridge also did not impact the prediction of sex (Wald = 3.595; p = 0.058). As such, population does not affect the prediction of sex when using the pelvic traits within binary logistic regression.

A CHAID pelvic trait decision tree analysis was conducted for the Japanese sample on 456 individuals (Figure A.4). Accordingly, the subpubic concavity performed the best, correctly classifying 91.5% of females and 95.0% of males, with a total correct classification rate of 94.1%. The resubstitution error associated with this tree is 0.059 (S.E. = 0.011), while the cross-validated error is 0.066 (S.E. = 0.012). The inclusion of age did not contribute to the tree's predictive success. The associated probabilities for the terminal nodes are presented in Table A.4.

A CHAID pelvic trait decision tree analysis was conducted for the Thai sample on 606 individuals (Figure A.5). Accordingly, the subpubic concavity and ventral arc performed the best, correctly classifying 95.4% of females and 94.9% of males, with a total correct classification rate of 95.0%. The resubstitution and cross-validated risk associated with this tree is 0.050 (S.E. = 0.009). The inclusion of age did not contribute to the tree's classification rate. The associated probabilities for the terminal nodes are presented in Table A.5.

A CHAID pelvic trait decision tree analysis was conducted for the combined Japanese and Thai samples on 1,062 individuals (Figure A.6). Accordingly, the subpubic concavity and preauricular sulcus performed the best, correctly classifying 93.9% of females and 94.9% of males, with a total correct classification rate of 94.6%. The resubstitution and cross-validated risk associated with this tree is 0.054 (S.E. = 0.007). The inclusion of age and population did not affect the tree's classification rate. The probabilities associated with each of the terminal nodes are presented in Table A.6.

Rhomboid fossa sexual dimorphism

The number of individuals with each rhomboid fossa score (0-5) within each group, the percentages, and probabilities of being female or male are presented in Table 5.18. The majority of Japanese and Thai individuals lack a rhomboid fossa, with scores of 0 ranging 56.9 – 91.7%. Proportionately more Japanese individuals exhibit a rhomboid fossa compared to Thai individuals. For all groups, the presence of a rhomboid fossa is more common on the right clavicle compared to the left. If a fossa was present, the majority of individuals were scored as a 1 or 2 (small and large fossae). Only a few Japanese individuals exhibit scores of 3 (shallow groove) and 4 (deep groove), while no Thai individuals exhibited scores of 3 and 4. Likewise, few Japanese and Thai individuals were scored as a 5 (porosity or pitting). As such, scoring fossa by type or size fails to assist in classification rates. Additionally, the scores of 3 and 4 were difficult to identify and distinguish, and many were likely placed into scores of 1 or 2.

Table 5.18. Rhomboid fossa score frequencies and probabilities for Japanese females and males and Thai females and males.

Group	Side	N	Rhomboid Fossa Score/Probability (P)					
			0	1	2	3	4	5
Japanese females	Left	116	106 (91.4%) P=0.56	5 (4.3%) P=0.17	0 (0.0%)	0 (0.0%)	0 (0.0%)	5 (4.3%) P=0.30
	Right	113	92 (81.4%) P=0.59	10 (8.8%) P=0.33	1 (0.9%) P=0.09	0 (0.0%)	0 (0.0%)	10 (8.8%) P=0.39
Japanese males	Left	304	217 (71.4%) P=0.44	44 (20.3%) P=0.83	11 (5.1%) P=1.00	1 (0.3%) P=1.00	1 (0.3%) P=1.00	30 (9.9%) P=0.70
	Right	304	173 (56.9%) P=0.41	55 (18.1%) P=0.67	29 (9.5%) P=0.91	4 (1.3%) P=1.00	1 (0.3%) P=1.00	42 (13.9%) P=0.61
Thai females	Left	190	185 (97.4%) P=0.57	3 (1.6%) P=0.09	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (1.1%) P=0.15
	Right	193	183 (94.8%) P=0.60	5 (2.6%) P=0.11	1 (0.5%) P=0.06	0 (0.0%)	0 (0.0%)	1 (0.5%) P=0.06
Thai males	Left	401	297 (74.1%) P=0.43	66 (16.5%) P=0.91	14 (3.5%) 1.00	0 (0.0%)	0 (0.0%)	24 (6.0%) P=0.85
	Right	406	262 (64.5%) P=0.40	82 (20.2%) P=0.89	31 (7.6%) P=0.94	0 (0.0%)	0 (0.0%)	31 (7.6%) P=0.94

The rhomboid fossa scores of 1-5 were collapsed into 1 (present) to simplify probabilities, and are presented in Table 5.19. For the Japanese sample, a rhomboid fossa on the left clavicle has a probability of 0.77 (77%) of being male, while a fossa on the right has a probability of 0.70 (70%) of being male. For the Thai sample, a rhomboid fossa on the left or the right clavicle has a probability of 0.91 (91%) of being male. As such, the presence of a rhomboid fossa is better able to identify Thai males, as the Thai sample exhibits greater difference between females and males in the presence/absence of a rhomboid fossa. For the pooled Japanese and Thai samples, a fossa on the right clavicle indicates male with 0.81 probability (81%), whereas a fossa on the left indicates male with 0.85 probability (85%). While proportionately more females lack a rhomboid fossa, the absence of a fossa is not indicative of female, as considerable proportions of Japanese and Thai males also lack rhomboid fossae. Rogers *et al.* (2000) found that a rhomboid fossa on the left clavicle has a 92.2% probability of being male, while one on the right indicates male with an 81.7% probability in their modern American Black and White samples.

The condensed rhomboid fossa scores show sex and population differences for the Japanese and Thai samples (Table 5.20). Chi-square analyses were conducted to test the null hypothesis that there is no association between the scoring of the rhomboid fossa and sex for the left and right clavicles. All significance values fell below 0.05 for the Japanese and Thai samples, indicating that sex is associated with the scoring of the rhomboid fossa (i.e., sexual dimorphism is present). Further, chi-square analyses were conducted to test the null hypothesis that there is no association between the scoring of the rhomboid fossa and population.

Table 5.19. Condensed rhomboid fossa score frequencies and probabilities for Japanese females and males and Thai females and males.

Group	Side	N	Rhomboid fossa score/probability (P)	
			0 (Absent)	1-5 (Present)
Japanese females	Left	116	106 (91.4%) P=0.56	10 (8.6%) P=0.23
	Right	113	92 (81.4%) 0.59	21 (18.6%) P=0.30
Japanese males	Left	304	217 (71.4%) P=0.44	87 (28.6%) P=0.77
	Right	304	173 (56.9%) P=0.41	131 (43.1%) P=0.70
Thai females	Left	190	185 (97.4%) P=0.57	5 (2.6%) P=0.09
	Right	193	183 (94.8%) P=0.60	7 (3.6%) P=0.09
Thai males	Left	401	297 (74.1%) P=0.43	104 (25.9%) P=0.91
	Right	406	262 (64.5%) P=0.40	144 (35.5%) P=0.91
Pooled Japanese and Thai Females	Left	306	291 (95.1%) P=0.57	15 (4.9%) P=0.15
	Right	306	275 (89.9%) P=0.59	28 (9.2%) P=0.19
Pooled Japanese and Thai males	Left	705	514 (72.9%) P=0.43	191 (27.1%) P=0.85
	Right	710	435 (61.3%) P=0.41	275 (38.7%) P=0.81

Table 5.20. Chi-square values between all groups to explore the affects of sex and population for the left and right rhomboid fossae.

Side	Group	N	Japanese females	Japanese males	Thai females
Right clavicle	Japanese females	112	--		
	Japanese males	304	20.915*	--	
Left clavicle	Japanese females	115	--		
	Japanese males	304	18.615*	--	
Right clavicle	Thai females	193	14.290*	89.492*	--
	Thai males	406	11.303*	4.258**	62.825*
Left clavicle	Thai females	190	5.634**	52.101*	--
	Thai males	401	15.432*	0.630	46.543*

*significant at the 0.01 level; **significant at the 0.05 level.

Significance values fell below 0.05 for the left and right rhomboid fossa scores for the Japanese and Thai females, and for the right rhomboid fossa scores for Japanese and Thai males, indicating that population is associated with the scoring of the rhomboid fossa. Proportionately more Japanese females exhibit rhomboid fossae on the left and right clavicles compared to Thai females. Similarly, proportionately more Japanese males exhibit rhomboid fossae on the right compared to Thai males. Rogers *et al*. (2000) found no population differences in rhomboid fossa scores between Black and White individuals.

Binary logistic regression analyses were conducted for the dichotomous left and right rhomboid fossa scores to determine the affects of age, sex, and population on fossa expression. The presence or absence of a fossa served as the dependent variable, and age, sex, and population were covariates. For the left and right clavicles, the models indicate that sex has the largest statistically significant affect on the presence or absence of a rhomboid fossa, while age has no statistically significant affect on the expression of a rhomboid fossa (Table 5.21). Additionally, the population affects the fossa score for the right clavicle only. As with the univariate probabilities, the left rhomboid fossa is better at predicting sex than the right.

Table 5.21. The affects of age, sex, and population on the expression of left and right rhomboid fossae.

Side	Covariate	Wald statistic	Sig.	Chi-square	Correctly classified
Left (n=977)	Age	1.201	0.201	81.573; p=0.000	79.6%
	Sex	48.266	0.000		
	Population	1.722	0.189		
Right (n=980)	Age	0.002	0.969	100.441; p=0.000	69.8%
	Sex	66.928	0.000		
	Population	9.263	0.002		

Age has a minimal affect on the expression of rhomboid fossa scores for the Japanese and Thai samples (Table 5.22). All age groups exhibit scores of 1 (small fossa), 2 (large fossa), and 5 (pitting/porosity). A slight statistically significant positive correlation exists between age and right rhomboid fossa score for the Japanese females. Conversely, a statistically significant slight negative correlation exists between age and left rhomboid fossa score for the Thai males. Rogers *et al*. (2000) found that in those with fossae, younger individuals tended to have larger fossae (scores of 2) compared to older individuals, indicating that age had an affect on the expression of rhomboid fossae in their American Black and White sample.

To further investigate the affects of age, Kruskal-Wallis analyses were calculated with the rhomboid fossa score (0-5) as the dependent variable and age as the independent variable. For the Japanese females, the results indicate that a statistically significant difference exists in the mean right rhomboid fossa rank scores for at least two age groups (H = 19.933; df = 6; p = 0.002). A *post-hoc* pairwise test shows that females 30-39 years have lower rhomboid fossa scores than females 70-79 years (p = 0.036), and females 40-49 years also have lower fossa scores compared to females 70-79 years (p = 0.011). For the Thai males, the results of the Kruskal-Wallis test indicate that a statistically significant difference exists in the left mean rank scores for at least two age categories (H = 14.822; df = 6; p = 0.019). A *post-hoc* pairwise test shows that males 40-49 years have higher rhomboid fossa scores than males 70-79 years (p = 0.027) only.

Spearman’s rho correlation coefficients indicate that the left and right rhomboid fossa scores are moderately correlated for both ordinal (rho = 0.446) and dichotomous (rho = 0.434) scoring systems. Both correlations are significant at the 0.01 level (2-tailed).

Table 5.22. Age affects on the expression of right and left rhomboid fossae for all groups.

Rhomboid fossa	Group	N	Spearman's rho
Right (0-5)	Japanese females	112	0.204*
	Japanese males	300	-0.063
	Thai females	182	-0.029
	Thai males	386	0.001
Left (0-5)	Japanese females	115	0.188*
	Japanese males	301	-0.039
	Thai females	179	0.047
	Thai males	382	-0.117*
Right (0-1)	Japanese females	112	0.190*
	Japanese males	300	-0.074
	Thai females	182	-0.029
	Thai males	386	0.025
Left (0-1)	Japanese females	115	0.183
	Japanese males	301	-0.050
	Thai females	179	0.046
	Thai males	382	-0.119*

*significant at the 0.05 level (2-tailed).

Distal humerus sexual dimorphism

The number of individuals with each distal humerus trait score within each group, the percentages, and probabilities of being female or male are presented in Table 5.23. The correct classifications range from 13.9% (trochlear constriction, Thai females) to 84.7% (medial epicondyle angle, Japanese males). The trait scores are all biased towards males, with associated sex biases ranging 16.4 – 64.3%. The angle of medial epicondyle performs the best, followed by trochlear extension, olecranon fossa shape, and lastly, trochlear constriction. However, each trait when used alone performs rather poorly. Vance *et al*. (2011) also found that trochlear constriction performed poorly, which led them to remove this feature from their subsequent analyses.

Based on the frequencies and probabilities presented in Table 5.23, distal humerus population-specific cutoff points were established for the Japanese and Thai samples, and are presented in Table 5.24. Ordinal scores with male probabilities above 0.50 indicate individuals with those scores are likely male, while ordinal scores with female probabilities above 0.50 indicate that individuals with those scores are likely female. Cutoff points for the distal humerus traits are between 2 and 3 for all traits and groups, except for Thai trochlear constriction, which is between 1 and 2.

Using the new population-specific cutoff points, the Japanese and Thai female correct classification rates increased, while the Japanese and Thai male correct classification rates mostly remained the same (Table 5.25). This is because the indeterminate scores of 3 were added to the female classification since proportionately more individuals with scores of 3 were female. However, the Thai male correct classification rate decreased for trochlear constriction because

Table 5.23. Distal humerus trait score frequencies and probabilities for Japanese females and males and Thai females and males.

Trait	Group	N	Score (%)					CC (%)	SB (%)
			1	2	3	4	5		
Medial epicondyle angle	Japanese females	123	11 (8.9)	22 (7.9)	6 (4.9)	32 (26.0)	52 (42.3)	84 (68.3)	16.4
	Prob.		0.14	0.22	0.59	0.80	0.88		
	Japanese males	326	185 (56.7)	91 (27.9)	11 (3.4)	21 (6.4)	18 (5.5)	276 (84.7)	
	Prob.		0.86	0.78	0.41	0.20	0.12		
	Thai females	195	40 (20.5)	29 (14.9)	25 (12.8)	38 (19.5)	63 (32.3)	101 (51.8)	29.6
	Prob.		0.29	0.32	0.66	0.76	0.85		
	Thai males	413	207 (50.1)	129 (31.2)	27 (6.5)	26 (6.3)	24 (5.8)	336 (81.4)	
	Prob.		0.71	0.68	0.34	0.24	0.15		
	Pooled females	318	51 (16.0)	51 (16.0)	31 (9.7)	70 (22.0)	115 (36.2)	185 (58.2)	28.7
	Prob.		0.23	0.35	0.66	0.77	0.86		
	Pooled males	739	392 (53.0)	220 (29.8)	38 (5.1)	47 (6.4)	42 (5.7)	642 (86.9)	
	Prob.		0.77	0.65	0.34	0.23	0.14		
Olecranon fossa shape	Japanese females	123	17 (13.8)	40 (32.5)	36 (29.3)	21 (17.1)	9 (7.3)	30 (24.4)	44.6
	Prob.		0.32	0.45	0.69	0.60	0.53		
	Japanese males	326	98 (30.0)	127 (39.0)	43 (13.2)	37 (11.3)	21 (6.4)	225 (69.0)	
	Prob.		0.68	0.55	0.31	0.40	0.47		
	Thai females	195	29 (14.9)	61 (31.3)	47 (24.1)	46 (23.6)	12 (6.2)	58 (29.7)	50.2
	Prob.		0.27	0.44	0.65	0.82	0.77		
	Thai males	412	167 (40.5)	162 (39.3)	54 (13.1)	21 (5.1)	8 (1.9)	329 (79.9)	
	Prob.		0.73	0.56	0.35	0.18	0.23		
	Pooled females	318	46 (14.5)	101 (31.8)	83 (26.1)	67 (21.1)	21 (6.6)	88 (27.7)	47.4
	Prob.		0.29	0.45	0.67	0.73	0.63		
	Pooled males	738	265 (35.9)	289 (39.2)	97 (13.1)	58 (7.9)	29 (3.9)	554 (75.1)	
	Prob.		0.71	0.55	0.33	0.27	0.37		
Trochlear extension	Japanese females	123	13 (10.6)	25 (20.3)	24 (19.5)	28 (22.8)	33 (26.8)	61 (49.6)	30.4
	Prob.		0.19	0.37	0.64	0.81	0.88		
	Japanese males	325	148 (45.5)	112 (34.5)	36 (11.1)	17 (5.2)	12 (3.7)	260 (80.0)	
	Prob.		0.81	0.63	0.36	0.19	0.12		
	Thai females	194	28 (14.4)	39 (20.1)	31 (16.0)	34 (17.5)	62 (32.0)	96 (49.5)	35.7
	Prob.		0.20	0.43	0.71	0.78	0.90		

Table 5.23, continued.

Trochlear extension, cont.	Thai males	413	241 (58.4)	111 (26.9)	27 (6.5)	20 (4.8)	14 (3.4)	352 (85.2)	
	Prob.		0.80	0.57	0.29	0.22	0.10		
	Pooled females	317	41 (12.9)	64 (20.2)	55 (17.4)	62 (19.6)	95 (30.0)	157 (49.5)	33.4
	Prob.		0.20	0.40	0.67	0.80	0.90		
	Pooled males	738	389 (52.7)	223 (30.2)	63 (8.5)	37 (5.0)	26 (3.5)	612 (82.9)	
	Prob.		0.80	0.60	0.33	0.20	0.10		
Trochlear constriction	Japanese females	122	24 (19.7)	42 (34.4)	27 (22.1)	20 (16.4)	9 (7.4)	29 (23.8)	53.8
	Prob.		0.32	0.49	0.60	0.72	0.86		
	Japanese males	326	137 (42.0)	116 (35.6)	48 (14.7)	21 (6.4)	4 (1.2)	253 (77.6)	
	Prob.		0.68	0.51	0.40	0.28	0.14		
	Thai females	194	57 (29.4)	74 (67.5)	36 (18.6)	17 (8.8)	10 (5.2)	27 (13.9)	64.3
	Prob.		0.38	0.69	0.57	0.59	0.78		
	Thai males	413	198 (47.9)	125 (30.3)	59 (14.3)	25 (6.1)	6 (1.5)	323 (78.2)	
	Prob.		0.62	0.31	0.43	0.41	0.22		
	Pooled females	316	81 (25.6)	116 (36.7)	63 (19.9)	37 (11.7)	19 (6.0)	56 (17.7)	60.2
	Prob.		0.36	0.53	0.58	0.65	0.81		
	Pooled males	739	335 (45.3)	241 (32.6)	107 (14.5)	46 (6.2)	10 (1.4)	576 (77.9)	
	Prob.		0.64	0.47	0.42	0.35	0.19		

Table 5.24. Population-specific cutoff points for the sexually dimorphic distal humerus traits.

Trait	Group	Cutoff points				
		1	2	3	4	5
Medial epicondyle angle	Japanese	Male		Female		
	Thai	Male		Female		
Olecranon fossa shape	Japanese	Male		Female		
	Thai	Male		Female		
Trochlear extension	Japanese	Male		Female		
	Thai	Male		Female		
Trochlear constriction	Japanese	Male		Female		
	Thai	Male	Female			

the cutoff point was moved between 1 and 2. If the pooled cutoff point for trochlear constriction is used (between 1 and 2), which is the same as the Thai cutoff point, the Japanese male correct classification rate decreases from 77.6% to 42.0% (137/326), while the female correct classification increases from 45.9% to 80.3% (98/122). The total correct classification rates ranged 61.0 – 78.1%, with associated sex biases ranging -22.7 – 31.7%. The four distal humerus traits better classify the Japanese sample compared to the Thai sample.

The individuals classified as male, with Vance *et al.* (2011) composite scores of 3-8, ambiguous, with a composite score of 9, and female, with composite scores of 10-15 were tallied for each group for the medial epicondyle angle, olecranon fossa shape, and trochlear extension (Table 5.26). The three composite traits performed better than the individual traits, with correct classification rates ranging from 56.7% (Thai females) to 94.2% (Thai males). However, the sex biases are high.

Because the individual distal humerus scores were heavily skewed towards males, and new sectioning points were calculated for each trait, the Vance *et al.* (2011) composite scoring method was adjusted to improve the correct classification rates for the Japanese and Thai samples (Table 5.27). Proportionately more Japanese and Thai females exhibited the ambiguous scores, and were therefore added to the female correct classification. As such, scores of 3-8 indicate male, and scores 9-15 indicate female. The correct classification rate for Japanese females improved 14.6%, while the correct classification rate for the Thai females improved 11.3%. Additionally, the sex bias for the adjusted scoring system decreased significantly from 29.7% to 15.1% for Japanese, and from 37.5% to 26.2% for Thai. However, more females are wrongly classified as male, than are males wrongly classified as females.

Table 5.25. Correct classification rates and sex biases for the sexually dimorphic distal humerus traits.

Trait	Group	N	Correctly classified	Sex Bias
Medial epicondyle angle	Japanese females	123	90 (73.2%)	11.5%
	Japanese males	326	276 (84.7%)	
	Thai females	195	124 (63.6%)	17.8%
	Thai males	413	336 (81.4%)	
	Total	1057	826 (78.1%)	
Olecranon fossa shape	Japanese females	123	66 (53.7%)	15.3%
	Japanese males	326	225 (69.0%)	
	Thai females	195	105 (53.8%)	26.1%
	Thai males	412	339 (79.9%)	
	Total	1056	735 (69.6%)	
Trochlear extension	Japanese females	123	85 (69.1%)	10.9%
	Japanese males	325	260 (80.0%)	
	Thai females	194	127 (65.5%)	19.7%
	Thai males	413	352 (85.2%)	
	Total	1055	824 (78.1%)	
Trochlear constriction	Japanese females	122	56 (45.9%) 98 (80.3%)*	31.7% -38.3*
	Japanese males	326	253 (77.6%) 137 (42.0%)*	
	Thai females	194	137 (70.6%)	-22.7%
	Thai males	413	198 (47.9%)	
	Total	1055	644 (61.0%)	
Combined traits	Japanese females	368	297 (80.7%)	2.9%
	Japanese males	1304	1014 (77.8%)	
	Thai females	778	493 (63.4%)	10.8%
	Thai males	1651	1225 (74.2%)	
	Total	4101	3029 (73.9%)	

*Pooled cutoff points used to determine frequencies and sex biases

Table 5.26. Vance *et al*. (2011) composite system correct classification rates and sex biases.

Group	N	Vance *et al.* (2011) Score			Sex bias
		3-8 (Male)	9 (Ambiguous)	10-15 (Female)	
Japanese females	123	30 (24.4%)	18 (14.6%)	75 (61.0%)	29.7%
Japanese males	322	292 (90.7%)	16 (5.0%)	14 (4.3%)	
Thai females	194	62 (32.0%)	22 (11.3%)	110 (56.7%)	37.5%
Thai males	412	388 (94.2%)	6 (1.5%)	18 (4.4%)	
Pooled females	317	92 (29.0%)	40 (12.6%)	185 (58.4%)	34.2%
Pooled males	734	680 (92.6%)	22 (3.0%)	32 (4.4%)	

Table 5.27. Adjusted distal humerus composite scoring system correct classification rates and sex biases.

Group	N	Adjusted composite scores and probabilities (P)		Sex bias
		3-8 (Male)	9-15 (Female)	
Japanese females	123	30 (24.4%) P=0.21	93 (75.6%) P=0.89	15.1%
Japanese males	322	292 (90.7%) P=0.79	30 (9.3%) P=0.11	
Thai females	194	62 (32.0%) P=0.25	132 (68.0%) P=0.92	26.2%
Thai males	412	388 (94.2%) P=0.75	24 (5.8%) P=0.08	
Pooled females	317	92 (29.0%) P=0.24	225 (71.0%) P=0.91	21.6%
Pooled males	734	680 (92.6%) P=0.76	54 (7.4%) P=0.09	

Chi-square analyses were conducted to determine if the four distal humerus traits are sexually dimorphic and show population differences (Table 5.28). Based on significance values below 0.001 for the Japanese and Thai, the null hypothesis that distal humeral trait scores are not related to sex is rejected. As such, all distal humerus traits are sexually dimorphic. Further, population differences exist in medial epicondyle angle between Japanese and Thai females, as indicated by significance values below 0.05. More Japanese females are "male-like" in their medial epicondyle morphology, as proportionately more Japanese females have higher ordinal scores compared to Thai females. Additionally, population differences exist in olecranon fossa shape and trochlear constriction between Japanese and Thai males, as indicated by significance values below 0.05. Thai males exhibit more "female-like" morphology in olecranon fossa shape and trochlear constriction, as more Thai males exhibit lower ordinal scores compared to Japanese males.

Figure 5.28. Chi-square values between all groups to explore the affects of sex and population for the distal humerus traits.

Trait	Group	Japanese females	Japanese males	Thai females
Medial epicondyle angle	Japanese males	157.230**	--	
	Thai females	15.137*	136.513**	--
	Thai males	168.872**	5.762	135.233**
Olecranon fossa shape	Japanese males	26.450**	--	
	Thai females	2.540	34.173**	--
	Thai males	61.438**	23.998**	87.073**
Trochlear extension	Japanese males	115.798**	--	
	Thai females	3.129	132.296**	--
	Thai males	157.098**	13.858*	181.818**
Trochlear constriction	Japanese males	36.456**	--	
	Thai females	7.856	14.401*	--
	Thai males	46.028**	3.123	23.124**

*significant at the 0.05 level; **significant at the 0.001 level.

Spearman's rho correlation coefficients were calculated to determine if age affects the distal humerus scores (Table 5.29). Overall, age and the distal humerus traits are not statistically significantly associated, except for the medial epicondyle (Thai females and males) and trochlear constriction (Japanese males). As age increases in the Thai sample, the medial epicondyle angle scores decrease, as indicated by the low negative correlations between age and trait score. As age increases in Japanese males, the trochlear constriction scores also increase, as indicated by the low positive correlation between age and trait score.

To further explore the affects of age, Kruskal-Wallis analyses were calculated with the medial epicondyle angle (Thai females and males) and trochlear constriction (Japanese males) as the dependent variables and age as the independent variable. For the Thai females, no statistically significant differences in medial epicondyle angle mean rank scores were found for

Table 5.29. Age affects on the distal humerus traits.

Trait	Group	N	Spearman's rho
Medial epicondyle angle	Japanese females	123	-0.122
	Japanese males	326	-0.085
	Thai females	194	-0.163*
	Thai males	393	-0.242**
Olecranon fossa shape	Japanese females	123	0.088
	Japanese males	325	0.026
	Thai females	185	0.079
	Thai males	392	0.026
Trochlear extension	Japanese females	123	0.152
	Japanese males	325	0.010
	Thai females	185	0.095
	Thai males	393	0.058
Trochlear constriction	Japanese females	123	-0.154
	Japanese males	326	0.131*
	Thai females	181	-0.026
	Thai males	393	0.011

*significant at the 0.05 level (2-tailed); **significant at the 0.01 level (2-tailed).

any of the age group (H = 9.892; df = 6; p = 0.121). For the Thai males, the results of the Kruskal-Wallis indicate that a statistically significant difference exists in the mean medial epicondyle angle rank scores and at least two age groups (H = 32.537; df = 6; p = 0.000). A *post-hoc* pairwise test shows that males 30-39 years have higher medial epicondyle angle scores than males 60-69 years (p = 0.002), 70-79 years (p = 0.033), and 80-96 years (p = 0.001). Additionally, males 40-49 years have higher medial epicondyle scores than males 60-69 years (p = 0.014) and 80-96 years (p = 0.010). For the Japanese males, the results of the Kruskal-Wallis show no significant difference in mean trochlear constriction rank scores for any age groups (H = 9.296; df = 6; p =0.157).

All sexually dimorphic distal humerus traits are minimally-moderately correlated with each other, as indicated by statistically significant Spearman's rho values (Table 5.30). As such, an increase in the ordinal score of one trait is correlated with an increase in the ordinal scores for all other traits. All correlations are significant at the 0.01 level (2-tailed).

Table 5.30. Spearman's rho correlation coefficients for the sexually dimorphic distal humerus traits.

	Medial epicondyle angle	**Olecranon fossa shape**	**Trochlear extension**
Olecranon fossa shape	0.113	--	
Trochlear extension	0.329	0.221	--
Trochlear constriction	0.185	0.186	0.091

Population-specific binary logistic regression equations were calculated for the Japanese, Thai, and pooled Japanese and Thai samples using the Forward Wald function in IBM SPSS (Table 5.31). Equations using five, four, three, two, and one variables were calculated for each of the groups. All of the equations presented in Table 5.31 are statistically significant, and all of the traits within each equation are also statistically significant. In a regression equation using all four distal humerus traits, the olecranon fossa shape performed the worst (not statistically significant) for the Japanese sample, while trochlear constriction performed the worst (not statistically significant) for the Thai sample. For the pooled Japanese and Thai sample, trochlear constriction performed the worst; however, all traits in the pooled sample were statistically significant. For the Japanese and pooled Japanese/Thai samples, medial epicondyle angle contributed most to the binary logistic regression equations. For the Thai sample, trochlear extension performed the best and contributed most to the logistic regression equations. Correct classification rates for the binary logistic regression equations ranged from 68.0% to 94.4% for Japanese, with associated sex biases ranging from 19.3% to 26.4%; 49.5% to 92.2% for the Thai samples, with associated sex biases from 23.9% to 42.5%; and 49.4% to 94.0% for the pooled Japanese and Thai samples, with associated sex biases from 25.1% to 42.2%. All logistic regression equations better classified males for all three groups. The inclusion of age into the logistic regression analyses for all three groups had no affect on the prediction of sex. Overall, the binary logistic regression equations performed best on the Japanese sample, producing higher correct classification rates and lower associated sex biases compared to the Thai sample. Additionally, the logistic regression equations performed similarly to the adjusted composite scoring method.

Table 5.31. Population-specific distal humerus logistic regression equations for Japanese, Thai, and pooled Japanese and Thai samples.

	Coefficients					% Correctly Classified			
Group	MEA	OFS	TE	TC	CON	F	M	T	% SB
Japanese[1]	-0.967	--	--	--	3.569	68.9	88.2	82.9	19.3
	-0.841	--	-0.718	--	5.030	68.0	94.4	87.2	26.4
	-0.775	--	-0.767	-0.528	6.116	70.5	94.4	87.9	23.9
Thai[2]	--	--	-0.908	--	2.924	49.5	91.7	78.2	42.5
	-0.557	--	-0.794	--	4.049	63.4	90.8	82.0	27.4
	-0.553	-0.609	-0.735	--	5.273	68.6	92.2	84.6	23.6
Pooled Japanese and Thai[3]	--	--	-0.905	--	3.064	49.4	91.6	78.9	42.2
	-0.670	--	-0.766	--	4.435	63.0	93.1	84.0	30.1
	-0.673	-0.428	-0.716	--	5.334	68.4	93.5	85.9	25.1
	-0.644	-0.392	-0.721	-0.248	5.698	68.0	94.0	86.2	26.0

[1] Models used 445 individuals (57.0%) to build equations

[2] Models used 605 individuals (98.2%) to build equations

[3] Models used 1050 individuals (75.2%) to build equations

MEA=medial epicondyle angle; OFS=olecranon fossa shape; TE=trochlear extension; TC=trochlear constriction; CON=constant; F=female; M=male; T=total; SB=sex bias.

A binary logistic regression analysis with the four distal humeral traits in addition to the population as the independent variables and the sex as the dependent variable for 1,050 individuals was conducted to test the affect of population on the prediction of sex. While ranked last based on the Wald statistic, the population (Wald = 8.434; p = 0.004) does contribute to the prediction of sex, along with the medial epicondyle angle (112.584; p = 0.000), trochlear extension (117.407; p = 0.000), olecranon fossa shape (28.662; p = 0.000), and trochlear constriction (9.209; p = 0.002).

A CHAID distal humerus decision tree analysis was conducted for the Japanese sample for 450 individuals (Figure A.7). The angle of the medial epicondyle performed the best, correctly classifying 68.3% of the females and 88.1% of the males, with a total correct classification rate of 82.7%. The resubstitution risk associated with the tree is 0.173 (S.E. =

0.018), while the cross-validated risk is 0.182 (S.E. = 0.018). The associated probabilities for the decision tree terminal nodes are presented in Table A.7.

A CHAID distal humerus decision tree analysis was conducted for the Thai sample on 608 individuals (Figure A.8). The trochlear extension and olecranon fossa shape performed the best, correctly classifying only 53.3% of females and 94.4% of males, with a total correct classification rate of 81.3%. The resubstitution risk associated with the tree is 0.188 (S.E. = 0.016), while the cross-validated risk is 0.214 (S.E. = 0.017). The inclusion of age did not contribute to the decision tree. The associated probabilities for the decision tree terminal nodes are presented in Table A.8.

A CHAID distal humerus decision tree analysis was conducted for the combined Japanese and Thai samples on 1058 individuals (Figure A.9). The trochlear extension, medial epicondyle angle, and olecranon fossa shape performed the best, correctly classifying 75.8% of females and 85.4% of males, with a total correct classification rate of 81.9%. The resubstitution risk associated with this tree is 0.181 (S.E. = 0.012), while the cross-validated risk is 0.198 (S.E. = 0.012). The associated probabilities for the decision tree terminal nodes are presented in Table A.9.

Secular change in the sexually dimorphic traits for the Japanese sample

Chi-square analyses were conducted on the sexually dimorphic traits for the CU and JU collections to test the hypothesis that the scoring of traits is not influenced by the century of death (see Appendix C). Based on chi-square significance values below 0.05, four traits show differences between the historic and modern samples for the females (nuchal crest, preauricular sulcus, right rhomboid fossa, and trochlear extension), and eight traits show differences in the males (all cranial traits, ventral arc, sciatic notch, and right rhomboid fossa). In general, the modern individuals (JU) are more gracile than the historic individuals (CU).

Intraobserver error in the sexually dimorphic traits

Intraobserver error rates were calculated on the 15 cranial and postcranial sexually dimorphic traits for 120 individuals of the Japanese and Thai sample. Table 5.32 presents the Cohen's kappa (k) value for each trait, along with the level of agreement following Landis and Koch (1977). All Cohen's k values were statistically significant at the 0.001 level. Overall, the scoring of the sexually dimorphic traits on two separate occasions are in a fair to almost perfect level of agreement. The pelvic traits exhibit the lowest error, while the distal humeral traits exhibit the highest error.

Table 5.32. Intraobserver error analysis for the 15 cranial and postcranial sexually dimorphic traits.

Trait	Cohen's k	Agreement
Nuchal crest	0.629	Substantial
Mastoid process	0.574	Moderate
Supraorbital margin	0.537	Moderate
Glabella	0.621	Substantial
Mental eminence	0.445	Moderate
Ventral arc	0.814	Almost perfect
Subpubic concavity	0.900	Almost perfect
Ischiopubic ramus ridge	0.973	Almost perfect
Sciatic notch	0.640	Substantial
Preauricular sulcus	0.605	Moderate
Rhomboid fossa	0.878	Almost perfect
Medial epicondyle angle	0.371	Fair
Olecranon fossa shape	0.433	Moderate
Trochlear extension	0.334	Fair
Trochlear constriction	0.236	Fair

Cranial Nonmetric Variation

The second objective of this study is to establish frequencies for the cranial and mandibular traits that are often used in biogeographic ancestry assessments, and determine if they differ between the Japanese and Thai samples. Prior to determining if differences exist, chi-square analyses were used to ascertain if side differences exist in the scoring of the cranial and mandibular traits. To determine if population differences exist, chi-square statistics, Spearman's rank order correlation coefficients, and binary logistic regression equations were calculated for the Japanese and Thai samples.

Side differences

Pearson chi-square analyses were calculated on the cranial and mandibular nonmetric traits that were scored on both the right and left sides to test the null hypothesis that there is no association in the scoring of traits and side. The significance values associated with each of the Pearson chi-square values are all significant at the 0.001 level, and therefore the null hypothesis is rejected, indicating that an association exists between the scoring of nonmetric traits and side (Table 5.33). Further, the Cramer's V and Phi values indicate that the association between side and nonmetric score is robust. Because no statistically significant side differences exist, the left side was used in all subsequent analyses, with scores on the right substituted when the left was missing.

Table 5.33. Chi-square analyses testing the association of side and the scoring of cranial and mandibular traits.

Trait	N	Chi-square	Phi/ Cramer's V
Malar tubercle	1294	2824.863	0.739
Zygomaticomaxillary suture	1222	2590.659	0.841
Orbit shape	1299	2331.458	0.947
Zygomatic posterior tubercle	1297	1723.570	0.666
Ramus inversion	1276	2230.939	0.763
Location of inversion	426	626.724	0.905
Gonial eversion	1275	1172.141	0.697
Mandibular border	1277	1646.647	0.841
Mandibular tori	1272	1491.683	0.882
Gonial muscle attachment	1276	2487.711	0.806
Mylohyoid bridging	1274	79.207	0.742
Accessory mandibular foramen	1274	266.373	0.578
Number of mental foramen	1271	126.872	0.446
Ascending ramus shape	1274	954.017	0.865
Ascending ramus profile	1275	2487.969	0.988

Cranial and mandibular trait frequencies

The number of individuals with each of the 37 cranial and mandibular traits within each group, and the percentages are presented in Tables 5.34 through 5.70. The frequencies range from 0.0% to 97.0%; however, the majority of groups display all ordinal scores for each trait in varying frequencies. Only Japanese or Thai females have frequencies of 0.0% for some ordinal scores for 10 traits. The Japanese and Thai males do not exhibit 0.0% trait frequencies. No individuals exhibit frequencies of 100%. If available, comparable frequency data from Hefner (2009), Parr (2005), and Rhine (1990) are presented in Tables A.10 – A.41 (Appendix D).

Table 5.34. Anterior nasal spine (ANS) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
ANS	**Females (N=200)**	**Males (N=511)**	**Total (N=711)**	**Females (N=191)**	**Males (N=399)**	**Total (N=590)**
1	108 (54.0%)	235 (46.0%)	343 (48.2%)	74 (38.7%)	94 (23.6%)	168 (28.5%)
2	71 (35.5%)	198 (38.7%)	269 (37.8%)	94 (49.2%)	218 (54.6%)	312 (52.9%)
3	21 (10.5%)	78 (15.3%)	99 (13.9%)	23 (12.0%)	87 (21.8%)	110 (18.6%)

Table 5.35. Inferior nasal aperture (INA) shape frequencies in the Japanese and Thai groups.

	Japanese			Thai		
INA	**Females (N=205)**	**Males (N=513)**	**Total (N=718)**	**Females (N=192)**	**Males (N=400)**	**Total (N=590)**
1	7 (3.4%)	33 (6.4%)	40 (5.6%)	20 (10.4%)	64 (16.0%)	84 (14.2%)
2	42 (20.5%)	92 (17.9%)	134 (18.7%)	48 (25.0%)	126 (31.5%)	174 (29.5%)
3	92 (44.9%)	228 (44.4%)	320 (44.6%)	90 (46.9%)	161 (40.3%)	251 (42.5%)
4	46 (22.4%)	109 (21.2%)	155 (21.6%)	19 (9.9%)	28 (7.0%)	47 (8.0%)
5	18 (8.8%)	51 (9.9%)	69 (9.6%)	15 (7.8%)	21 (5.3%)	36 (6.1%)

Table 5.36. Interorbital breadth (IOB) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
IOB	**Females (N=201)**	**Males (N=509)**	**Total (N=710)**	**Females (N=190)**	**Males (N=399)**	**Total (N=589)**
1	25 (12.4%)	68 (13.4%)	93 (13.1%)	28 (14.7%)	48 (12.0%)	76 (12.9%)
2	129 (64.2%)	321 (63.1%)	450 (63.4%)	137 (72.1%)	285 (71.4%)	422 (71.6%)
3	47 (23.4%)	120 (23.6%)	167 (23.5%)	25 (13.2%)	66 (16.5%)	91 (15.4%)

Table 5.37. Malar tubercle (TUB) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
TUB	**Females (N=204)**	**Males (N=510)**	**Total (N=714)**	**Females (N=192)**	**Males (N=402)**	**Total (N=594)**
0	27 (13.2%)	47 (9.2%)	74 (10.4%)	22 (11.5%)	21 (5.2%)	43 (7.2%)
1	98 (48.0%)	212 (41.6%)	310 (43.4%)	78 (40.6%)	141 (35.1%)	219 (36.9%)
2	63 (30.9%)	149 (29.2%)	212 (29.7%)	84 (43.8%)	182 (45.3%)	266 (44.8%)
3	7 (3.4%)	71 (13.9%)	78 (10.9%)	8 (4.2%)	56 (13.9%)	64 (10.8%)
4	9 (4.4%)	31 (6.1%)	40 (5.6%)	0 (0.0%)	2 (0.5%)	2 (0.3%)

Table 5.38. Nasofrontal suture (NFS) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
NFS	Females (N=204)	Males (N=510)	Total (N=714)	Females (N=192)	Males (N=401)	Total (N=593)
1	87 (42.6%)	265 (52.0%)	352 (49.3%)	74 (38.5%)	226 (56.4%)	300 (50.6%)
2	67 (32.8%)	172 (33.7%)	239 (33.5%)	84 (43.8%)	140 (34.9%)	224 (37.8%)
3	8 (3.9%)	9 (1.8%)	17 (2.4%)	3 (1.6%)	8 (2.0%)	11 (1.9%)
4	42 (20.6%)	64 (12.5%)	106 (14.8%)	31 (16.1%)	27 (6.7%)	58 (9.8%)

Table 5.39. Nasal aperture shape (NAS) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
NAS	Females (N=205)	Males (N=510)	Total (N=715)	Females (N=190)	Males (N=398)	Total (N=588)
1	85 (41.5%)	298 (58.4%)	383 (53.6%)	46 (24.2%)	142 (35.7%)	188 (32.0%)
2	89 (43.4%)	117 (22.9%)	206 (28.8%)	96 (50.5%)	198 (49.7%)	294 (50.0%)
3	31 (15.1%)	95 (18.6%)	126 (17.6%)	48 (25.3%)	58 (14.6%)	106 (18.0%)

Table 5.40. Nasal bone shape (NBS) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
NBS	Females (N=201)	Males (N=512)	Total (N=713)	Females (N=190)	Males (N=398)	Total (N=588)
1	112 (55.7%)	272 (53.1%)	384 (53.9%)	101 (53.2%)	223 (56.0%)	324 (55.1%)
2	75 (37.3%)	182 (35.5%)	257 (36.0%)	70 (36.8%)	134 (33.7%)	204 (34.7%)
3	13 (6.5%)	47 (35.5%)	60 (8.4%)	19 (10.0%)	39 (9.8%)	58 (9.9%)
4	1 (0.5%)	11 (2.1%)	12 (1.7%)	0 (0.0%)	2 (0.5%)	2 (0.3%)

Table 5.41. Nasal aperture width (NAW) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
NAW	Females (N=204)	Males (N=511)	Total (N=715)	Females (N=189)	Males (N=399)	Total (N=588)
1	14 (6.9%)	51 (10.0%)	65 (9.1%)	5 (2.6%)	11 (2.8%)	16 (2.7%)
2	118 (57.8%)	316 (61.8%)	434 (60.7%)	107 (56.6%)	228 (57.1%)	335 (57.0%)
3	72 (35.3%	144 (28.2%)	216 (30.2%)	77 (40.7%)	160 (40.1%)	237 (40.3%)

Table 5.42. Nasal bone contour (NBC) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
NBC	Females (N=202)	Males (N=511)	Total (N=713)	Females (N=190)	Males (N=398)	Total (N=588)
0	116 (57.4%)	177 (34.6%)	293 (41.1%)	136 (72.7%)	249 (62.7%)	385 (65.5%)
1	50 (24.8%)	250 (48.9%)	300 (42.1%)	14 (7.5%)	107 (27.0%)	121 (20.6%)
2	1 (0.5%)	9 (1.8%)	10 (1.4%)	0 (0.0%)	4 (1.0%)	4 (0.7%)
3	7 (3.5%)	29 (5.7%)	36 (5.0%)	1 (0.5%)	7 (1.8%)	8 (1.4%)
4	13 (6.4%)	38 (7.4%)	51 (7.2%)	23 (12.3%)	23 (5.8%)	46 (7.8%)
5	15 (7.4%)	8 (1.6%)	23 (3.2%)	13 (7.0%)	7 (1.8%)	20 (3.4%)

Table 5.43. Nasal overgrowth (NO) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
NO	Females (N=201)	Males (N=507)	Total (N=708)	Females (N=142)	Males (N=340)	Total (N=482)
0	155 (77.1%)	363 (71.6%)	518 (73.2%)	46 (32.4%)	142 (41.8%)	188 (39.0%)
1	46 (22.9%)	144 (28.4%)	190 (26.8%)	96 (67.6%)	198 (58.2%)	294 (61.0%)

Table 5.44. Postbregmatic depression (PBD) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
PBD	Females (N=192)	Males (N=477)	Total (N=669)	Females (N=191)	Males (N=404)	Total (N=595)
0	162 (84.4%)	407 (85.3%)	569 (85.1%)	173 (90.6%)	357 (88.4%)	530 (89.1%)
1	30 (15.6%)	70 (14.7%)	100 (14.9%)	18 (9.4%)	47 (11.6%)	65 (10.9%)

Table 5.45. Supranasal suture (SNS) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
SNS	Females (N=204)	Males (N=509)	Total (N=713)	Females (N=192)	Males (N=402)	Total (N=594)
0	138 (67.6%)	144 (28.3%)	282 (39.6%)	156 (81.3%)	125 (31.1%)	281 (47.3%)
1	32 (15.7%)	48 (9.4%)	80 (11.2%)	11 (5.7%)	14 (3.5%)	25 (4.2%)
2	34 (16.7%)	317 (62.3%)	351 (49.2%)	25 (13.0%)	263 (65.4%)	288 (48.5%)

Table 5.46. Transverse palatine suture (TPS) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
TPS	**Females (N=201)**	**Males (N=474)**	**Total (N=675)**	**Females (N=174)**	**Males (N=328)**	**Total (N=502)**
1	115 (57.2%)	304 (64.1%)	419 (62.1%)	50 (28.7%)	92 (28.0%)	142 (28.3%)
2	42 (20.9%)	102 (21.5%)	144 (21.3%)	92 (52.9%)	159 (48.5%)	251 (50.0%)
3	23 (11.4%)	39 (8.2%)	62 (9.2%)	22 (12.6%)	54 (16.5%)	76 (15.1%)
4	21 (10.4%)	29 (6.1%)	50 (7.4%)	10 (5.7%)	23 (7.0%)	33 (6.6%)

Table 5.47. Zygomaticomaxillary suture (ZMS) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
ZMS	**Females (N=198)**	**Males (N=461)**	**Total (N=659)**	**Females (N=191)**	**Males (N=399)**	**Total (N=590)**
0	157 (79.3%)	349 (75.7%)	506 (76.8%)	131 (68.6%)	205 (51.4%)	336 (56.9%)
1	22 (11.1%)	77 (16.7%)	99 (15.0%)	58 (30.4%)	152 (38.1%)	210 (35.6%)
2	19 (9.6%)	31 (6.7%)	50 (7.6%)	2 (1.0%)	5 (1.3%)	7 (1.2%)
3	0 (0.0%)	4 (0.9%)	4 (0.6%)	0 (0.0%)	37 (9.3%)	37 (6.3%)

Table 5.48. Sagittal keeling (KLN) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
KLN	**Females (N=192)**	**Males (N=477)**	**Total (N=669)**	**Females (N=191)**	**Males (N=399)**	**Total (N=590)**
0	132 (68.8%)	240 (50.3%)	372 (55.6%)	156 (81.7%)	263 (65.9%)	419 (71.0%)
1	55 (28.6%)	189 (39.6%)	244 (36.5%)	35 (18.3%)	124 (31.1%)	159 (26.9%)
2	5 (2.6%)	48 (10.1%)	53 (7.9%)	0 (0.0%)	12 (3.0%)	12 (2.1%)

Table 5.49. Suture complexity (SC) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
SC	**Females (N=165)**	**Males (N=375)**	**Total (N=540)**	**Females (N=148)**	**Males (N=313)**	**Total (N=461)**
1	50 (30.3%)	109 (29.1%)	159 (29.4%)	23 (15.5%)	51 (16.3%)	74 (16.1%)
2	83 (50.3%)	162 (43.2%)	245 (45.4%)	95 (64.2%)	186 (59.4%)	281 (61.0%)
3	32 (19.4%)	104 (27.7%)	136 (25.2%)	30 (20.3%)	76 (24.3%)	106 (22.9%)

Table 5.50. Wormian bone (WB) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
WB	**Females (N=161)**	**Males (N=369)**	**Total (N=530)**	**Females (N=146)**	**Males (N=311)**	**Total (N=457)**
0	85 (52.8%)	144 (39.0%)	229 (42.2%)	40 (27.4%)	66 (21.2%)	106 (23.2%)
1	76 (47.2%)	225 (61.0%)	301 (56.8%)	106 (72.6%)	245 (78.8%)	351 (76.8%)

Table 5.51. Orbit shape (OS) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
OS	**Females (N=205)**	**Males (N=514)**	**Total (N=719)**	**Females (N=192)**	**Males (N=401)**	**Total (N=593)**
1	134 (65.4%)	227 (44.2%)	361 (50.2%)	96 (50.5%)	151 (37.7%)	247 (41.7%)
2	44 (21.5%)	185 (36.0%)	229 (31.9%)	86 (44.8%)	232 (57.9%)	318 (53.6%)
3	27 (13.2%)	102 (19.8%)	129 (17.9%)	10 (5.2%)	18 (4.5%)	28 (4.7%)

Table 5.52. Zygomatic/maxillary projection (ZMP) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
ZMP	**Females (N=203)**	**Males (N=508)**	**Total (N=711)**	**Females (N=190)**	**Males (N=394)**	**Total (N=584)**
1	31 (15.3%)	77 (15.2%)	108 (15.2%)	15 (7.9%)	23 (5.8%)	38 (6.5%)
2	128 (63.1%)	286 (56.3%)	414 (58.2%)	153 (80.5%)	320 (81.2%)	473 (81.0%)
3	44 (21.7%)	145 (28.5%)	189 (26.6%)	22 (11.6%)	51 (12.9%)	73 (12.5%)

Table 5.53. Zygomatic posterior tubercle (ZPT) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
ZPT	**Females (N=204)**	**Males (N=515)**	**Total (N=719)**	**Females (N=191)**	**Males (N=401)**	**Total (N=592)**
0	20 (9.8%)	22 (4.3%)	42 (5.8%)	30 (15.7%)	23 (5.7%)	52 (9.0%)
1	72 (35.3%)	137 (26.6%)	209 (29.1%)	62 (32.5%)	92 (22.9%)	154 (26.0%)
2	89 (43.6%)	220 (42.7%)	309 (43.0%)	86 (45.0%)	210 (52.4%)	296 (50.0%)
3	23 (11.3%)	136 (26.4%)	159 (22.1%)	13 (6.8%)	76 (19.0%)	89 (15.0%)

Table 5.54. Prognathism (PRG) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
PRG	**Females (N=205)**	**Males (N=513)**	**Total (N=718)**	**Females (N=191)**	**Males (N=400)**	**Total (N=591)**
0	74 (36.1%)	179 (34.9%)	253 (35.2%)	132 (69.1%)	289 (72.3%)	421 (71.2%)
1	87 (42.4%)	206 (40.1%)	293 (40.8%)	55 (28.8%)	98 (24.5%)	153 (25.9%)
2	44 (21.5%)	128 (25.0%)	172 (24.0%)	4 (2.1%)	13 (3.3%)	17 (2.9%)

Table 5.55. Dental arcade shape (DAS) frequencies in the Japanese and Thai samples.

	Japanese			Thai		
DAS	**Females (N=202)**	**Males (N=506)**	**Total (N=708)**	**Females (N=189)**	**Males (N=399)**	**Total (N=588)**
1	7 (3.5%)	21 (4.2%)	28 (4.0%)	11 (5.8%)	8 (2.0%)	19 (3.2%)
2	174 (86.1%)	430 (85.0%)	604 (85.3%)	155 (82.0%)	341 (85.5%)	496 (84.4%)
3	21 (10.4%)	55 (10.9%)	76 (10.7%)	23 (12.2%)	50 (12.5%)	73 (12.4%)

Table 5.56. Occlusion (OCC) frequencies in the Japanese and Thai samples.

	Japanese			Thai		
OCC	**Females (N=88)**	**Males (N=224)**	**Total (N=312)**	**Females (N=58)**	**Males (N=127)**	**Total (N=185)**
1	9 (10.2%)	32 (14.3%)	41 (13.1%)	28 (48.3%)	74 (58.3%)	102 (55.1%)
2	76 (86.4%)	186 (83.0%)	262 (84.0%)	28 (48.3%)	44 (34.6%)	72 (38.9%)
3	2 (2.4%)	1 (0.4%)	3 (1.0%)	0 (0.0%)	2 (1.6%)	2 (1.1%)
4	1 (1.1%)	5 (2.2%)	6 (1.9%)	2 (3.4%)	7 (5.5%)	9 (4.9%)

Table 5.57. Maxillary incisor orientation (MIO) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
MIO	**Females (N=89)**	**Males (N=232)**	**Total (N=321)**	**Females (N=65)**	**Males (N=139)**	**Total (N=204)**
1	18 (20.2%)	82 (35.3%)	100 (31.2%)	36 (55.4%)	103 (74.1%)	139 (68.1%)
2	50 (56.2%)	119 (51.3%)	169 (52.6%)	24 (36.9%)	30 (21.6%)	54 (26.5%)
3	21 (23.6%)	31 (13.4%)	52 (16.2%)	5 (7.7%)	6 (4.3%)	11 (5.4%)

Table 5.58. Posterior ramus inversion (PRI) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
PRI	**Females (N=197)**	**Males (N=510)**	**Total (N=707)**	**Females (N=184)**	**Males (N=389)**	**Total (N=573)**
0	106 (53.8%)	341 (66.9%)	447 (63.2%)	76 (41.3%)	263 (67.6%)	339 (59.2%)
1	63 (32.0%)	127 (24.9%)	190 (26.9%)	72 (39.1%)	93 (23.9%)	165 (28.8%)
2	25 (12.7%)	33 (6.5%)	58 (11.4%)	26 (14.1%)	28 (7.2%)	54 (9.4%)
3	3 (1.5%)	9 (1.8%)	12 (1.7%)	10 (5.4%)	5 (1.3%)	15 (2.6%)

Table 5.59. Location of ramus inversion (LRI) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
LRI	**Females (N=91)**	**Males (N=169)**	**Total (N=260)**	**Females (N=108)**	**Males (N=125)**	**Total (N=233)**
1	37 (40.7%)	33 (19.5%)	70 (26.9%)	7 (6.5%)	6 (4.8%)	13 (5.6%)
2	47 (51.6%)	103 (60.9%)	150 (57.7%)	101 (93.5%)	117 (93.6%)	218 (93.6%)
3	7 (7.7%)	44 (19.5%)	51 (19.6%)	0 (0.0%)	2 (1.6%)	2 (0.9%)

Table 5.60. Gonial eversion (GE) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
GE	**Females (N=198)**	**Males (N=510)**	**Total (N=708)**	**Females (N=185)**	**Males (N=389)**	**Total (N=574)**
0	114 (57.6%)	195 (38.2%)	309 (43.6%)	128 (69.2%)	198 (50.9%)	326 (56.8%)
1	69 (34.8%)	236 (46.3%)	305 (43.1%)	52 (28.1%)	140 (36.0%)	192 (33.4%)
2	13 (6.6%)	66 (12.9%)	79 (11.2%)	4 (2.2%)	43 (11.1%)	47 (8.2%)
3	2 (1.0%)	13 (2.5%)	15 (2.1%)	1 (0.5%)	8 (2.1%)	9 (1.6%)

Table 5.61. Mandibular border shape (MBS) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
MBS	**Females (N=198)**	**Males (N=510)**	**Total (N=708)**	**Females (N=185)**	**Males (N=389)**	**Total (N=574)**
1	61 (30.8%)	130 (25.5%)	191 (27.0%)	119 (64.3%)	251 (64.5%)	370 (64.5%)
2	106 (53.5%)	306 (60.0%)	412 (58.2%)	27 (14.6%)	119 (30.6%)	146 (25.4%)
3	31 (15.7%)	74 (14.5%)	105 (14.8%)	39 (21.1%)	19 (4.9%)	58 (10.1%)

Table 5.62. Mandibular tori (MT) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
MT	**Females (N=197)**	**Males (N=510)**	**Total (N=707)**	**Females (N=184)**	**Males (N=385)**	**Total (N=569)**
0	146 (74.1%)	392 (76.9%)	538 (76.1%)	115 (62.5%)	208 (54.0%)	323 (57.8%)
1	47 (23.9%)	104 (20.4%)	151 (21.4%)	44 (23.9%)	123 (31.9%)	167 (29.3%)
2	4 (2.0%)	13 (2.5%)	17 (2.4%)	15 (8.2%)	41 (10.6%)	56 (9.8%)
3	0 (0.0%)	1 (0.2%)	16 (2.3%)	10 (5.4%)	13 (3.4%)	19 (3.3%)

Table 5.63. Gonial muscle attachment ridging (GMA) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
GMA	**Females (N=197)**	**Males (N=510)**	**Total (N=707)**	**Females (N=184)**	**Males (N=389)**	**Total (N=573)**
0	8 (4.1%)	13 (2.5%)	21 (3.0%)	8 (4.1%)	6 (1.5%)	14 (2.4%)
1	77 (39.1%)	134 (26.3%)	211 (29.8%)	37 (20.1%)	19 (4.9%)	56 (9.8%)
2	89 (45.2%)	243 (47.6%)	243 (34.4%)	97 (52.7%)	109 (28.0%)	206 (36.0%)
3	23 (11.7%)	120 (23.5%)	143 (20.2%)	47 (25.5%)	255 (65.6%)	302 (52.7%)

Table 5.64. Mylohyoid bridging (MHB) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
MHB	**Females (N=198)**	**Males (N=510)**	**Total (N=708)**	**Females (N=184)**	**Males (N=389)**	**Total (N=573)**
0	192 (97.0%)	494 (86.9%)	686 (96.9%)	175 (95.1%)	353 (90.7%)	528 (92.1%)
1	6 (3.0%)	16 (3.1%)	22 (3.1%)	9 (4.9%)	36 (9.3%)	45 (7.9%)

Table 5.65. Accessory mandibular foramen (AMF) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
AMF	**Females (N=196)**	**Males (N=509)**	**Total (N=705)**	**Females (N=184)**	**Males (N=389)**	**Total (N=573)**
0	179 (91.3%)	465 (91.4%)	644 (91.3%)	166 (90.2%)	346 (88.9%)	512 (89.3%)
1	17 (8.7%)	44 (8.6%)	61 (8.7%)	18 (9.8%)	43 (11.1%)	61 (10.7%)

Table 5.66. Chin prominence (CP) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
CP	**Females (N=201)**	**Males (N=510)**	**Total (N=711)**	**Females (N=183)**	**Males (N=389)**	**Total (N=574)**
0	1 (0.5%)	2 (0.4%)	3 (0.4%)	1 (0.5%)	2 (0.5%)	3 (0.5%)
1	145 (72.1%)	387 (75.0%)	532 (74.8%)	156 (85.2%)	332 (88.0%)	488 (85.0%)
2	55 (27.4%)	121 (23.7%)	176 (24.8%)	26 (14.2%)	52 (13.4%)	78 (13.6%)

Table 5.67. Chin shape (CS) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
CS	**Females (N=198)**	**Males (N=510)**	**Total (N=708)**	**Females (N=183)**	**Males (N=386)**	**Total (N=569)**
1	143 (72.2%)	320 (62.7%)	463 (65.3%)	124 (67.8%)	202 (52.3%)	326 (57.3%)
2	28 (14.1%)	41 (8.0%)	69 (9.7%)	30 (16.4%)	10 (2.6%)	40 (7.0%)
3	27 (13.6%)	149 (29.2%)	176 (24.9%)	29 (15.8%)	174 (45.1%)	203 (35.7%)

Table 5.68. Number of mental foramina (NMF) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
NMF	**Females (N=199)**	**Males (N=510)**	**Total (N=709)**	**Females (N=184)**	**Males (N=385)**	**Total (N=569)**
0	0 (0.0%)	3 (0.6%)	3 (0.4%)	1 (0.5%)	1 (0.3%)	2 (0.4%)
1	188 (94.5%)	456 (89.4%)	644 (90.8%)	169 (91.8%)	354 (91.9%)	523 (91.9%)
2	11 (5.5%)	48 (9.4%)	59 (8.3%)	13 (7.1%)	25 (6.5%)	38 (6.7%)
3	0 (0.0%)	3 (0.6%)	3 (0.4%)	1 (0.5%)	4 (1.0%)	5 (0.9%)
4	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.3%)	1 (0.2%)

Table 5.69. Ascending ramus shape (ARS) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
ARS	**Females (N=198)**	**Males (N=510)**	**Total (N=708)**	**Females (N=185)**	**Males (N=389)**	**Total (N=574)**
1	28 (14.1%)	80 (15.7%)	108 (15.3%)	35 (18.9%)	147 (37.8%)	182 (31.7%)
2	170 (85.9%)	430 (84.3%)	600 (84.7%)	150 (81.1%)	242 (62.2%)	392 (68.3%)

Table 5.70. Ascending ramus profile (ARP) frequencies in the Japanese and Thai groups.

	Japanese			Thai		
ARP	**Females (N=198)**	**Males (N=510)**	**Total (N=708)**	**Females (N=185)**	**Males (N=389)**	**Total (N=574)**
1	57 (28.8%)	193 (37.8%)	250 (35.3%)	67 (36.2%)	214 (55.0%)	281 (49.0%)
2	80 (40.4%)	215 (42.2%)	295 (41.7%)	95 (51.4%)	149 (38.3%)	244 (42.5%)
3	61 (30.8%)	102 (20.0%)	163 (23.0%)	23 (12.4%)	26 (6.6%)	49 (8.5%)

Sex affects on the cranial and mandibular traits

Chi-square tests were conducted to determine if an association exists between sex and the expression of nonmetric cranial and mandibular traits for the Japanese and Thai samples (Table 5.71). Numerous traits have chi-square significance values below 0.05, thereby rejecting the null hypothesis and indicating that sex is associated with the expression and scoring of these traits. For the Japanese, 16 (43.2%) of the cranial and mandibular traits are affected by sex and show moderate associations between sex and trait scores, as evidenced by statistically significant Phi or Cramer's V values ranging 0.123 – 0.416. For the Thai, 19 (51.4%) of the cranial and mandibular traits are affected by sex and show moderate associations between sex and trait scores, as indicated by statistically significant Phi or Cramer's V values of 0.101 – 0.493.

While both the Japanese and Thai female and male samples exhibit considerable overlap in the expression of many traits (see Tables 5.34 – 5.70, above), sex differences are also present in the groups. Table 5.72 presents the statistically significant population proportion differences in trait expressions between females and males for the Japanese and Thai samples.

Table 5.71. Sex affects on the cranial and mandibular nonmetric traits for the Japanese and Thai samples.

Trait	Japanese		Thai	
	Chi-square	Phi/Cramer's V	Chi-square	Phi/Cramer's V
Anterior nasal spine	4.656	0.081	17.780*	0.174
Inferior nasal aperture	3.215	0.067	8.829	0.122
Interorbital breadth	0.1224	0.013	1.693	0.054
Malar tubercle	19.214*	0.164	20.582*	0.186
Nasofrontal suture	11.788**	0.128	22.724*	0.196
Nasal aperture shape	30.152*	0.205	13.458*	0.151
Nasal bone shape	3.905	0.074	1.526	0.051
Nasal aperture width	4.385	0.078	0.025	0.007
Nasal bone contour	57.066*	0.283	45.288*	0.278
Nasal overgrowth	2.231	0.056	1.195	0.046
Postbregmatic depression	0.097	0.012	0.651	0.033
Supranasal suture	123.660*	0.416	144.247*	0.493
Transverse palatine suture	6.275	0.096	1.1831	0.060
Zygomaticomaxillary suture	6.338	0.098	26.642*	0.212
Keeling	22.503*	0.183	18.058*	0.175
Suture complexity	4.498	0.091	1.113	0.049
Wormian bones	8.662**	0.128	2.127	0.068
Orbit shape	26.472*	0.192	9.024*	0.123
Zygomatic/maxillary projection	3.712	0.072	1.032	0.042
Zygomatic posterior tubercle	26.614*	0.192	32.965*	0.236
Prognathism	0.991	0.037	1.701	0.054
Dental arcade shape	0.224	0.018	5.972*	0.101
Occlusion	3.461	0.105	3.884	0.145
Maxillary incisor orientation	9.171**	0.169	7.150*	0.187
Ramus inversion	13.230*	0.137	39.248*	0.262
Location of inversion	16.083*	0.249	2.022	0.093
Gonial eversion	23.336*	0.182	23.656*	0.203
Mandibular border	2.646	0.061	45.164*	0.281
Mandibular tori	1.486	0.046	6.407	0.106
Gonial muscle attachment ridging	18.967*	0.164	88.762*	0.394
Mylohyoid bridging	0.005	0.003	3.286	0.076
Accessory mandibular foramen	0.000	0.000	0.212	0.019
Chin prominence	1.301	0.043	0.575	0.032
Chin shape	21.334*	0.174	68.534*	0.347
Mental foramen number	5.340	0.087	1.172	0.045
Ascending ramus shape	0.263	0.019	20.617*	0.190
Ascending ramus profile	10.654*	0.123	18.923*	0.182

*significant at the 0.001 level; **significant at the 0.05 level.

Table 5.72. Morphological differences in the cranial and mandibular traits between females and males for the Japanese and Thai samples.

Trait	Japanese		Thai	
	Female	**Male**	**Female**	**Male**
Anterior nasal spine	--	--	Small	Large
Malar tubercle	Absent; trace	Pronounced; double	Small	Large
Nasofrontal suture	Rounded	Triangular; jagged	Square; jagged	Rounded; triangular
Nasal aperture shape	Bell-shaped	Teardrop-shaped	Rounded	Teardrop-shaped
Nasal bone contour	Low; flat	Oval; rounded; steep and narrow	Low; triangular; flat	Oval; rounded; steep and narrow
Supranasal suture	Open; completely obliterated	Closed but visible	Open; completely obliterated	Closed but visible
Zygomaticomaxillary suture	--	--	Greatest lateral extent at inferior end	Greatest lateral extent in middle; two or more angles
Keeling	Absent	Slight; pronounced	Absent	Slight; pronounced
Wormian bones	Absent	Present	--	--
Orbit shape	Rounded	Rectangular; rhombic	Rounded; rhombic	Rectangular
Zygomatic posterior tubercle	Absent	Marked	Absent; weak; moderate	Marked
Dental arcade shape	--	--	Narrow and tapering	Wide and smoothly curving
Maxillary incisor orientation	Slight projection; marked projection	Vertical	Slight projection	Vertical
Ascending ramus inversion	Slight; moderate	Absent	Slight; moderate; extreme	Absent
Location of inversion	Low	Medium; high	--	--
Gonial eversion	Absent; slight	Moderate; extreme	Absent	Slight; moderate; extreme
Mandibular border	--	--	Rocker	Undulating
Gonial muscle attachment ridging	Absent; minimal	Moderate; extreme	Absent	Extreme
Chin shape	Rounded; pointed	Square; bilobate	Rounded; pointed	Square; bilobate
Ascending ramus shape	--	--	Wide	Pinched
Ascending ramus profile	Slanted (obtuse)	Straight (acute)	Slanted (obtuse)	Straight (acute)

Age affects on the cranial and mandibular traits

Spearman's rho correlation coefficients were calculated to determine if age is associated with the cranial and mandibular trait scores for each group (Table 5.73). Numerous cranial and mandibular traits exhibit statistically significant Spearman's rho values, indicating that age is slightly to moderately correlated with some traits. In particular, 17 traits (45.9%) show a correlation with age for the Japanese sample, while nine traits (24.3%) show a correlation with age for the Thai sample.

To further investigate the affects of age on the expression of the cranial traits, Kruskal-Wallis tests were calculated with the traits that showed a correlation with age. As such, the trait scores served as the dependent variables and age category served as the independent variable. A Kruskal-Wallis test for the anterior nasal spine showed that there was no statistically significant difference between mean trait score ranks for any Thai age group (H = 9.296; df = 6; p = 0.148). Similarly, a Kruskal-Wallis test for nasal aperture shape showed that there were no statistically significant differences between mean trait score ranks for any Japanese age groups (H = 4.830; df = 6; p = 0.569). A Kruskal-Wallis test for nasal aperture width showed that a statistically significant difference in mean trait score ranks exists between at least two age groups (H = 21.027; df = 6; p = 0.001). A *post-hoc* pairwise test showed that Japanese individuals 17-29 years old had lower nasal aperture width scores compared to 70-79 year old individuals (p = 0.005). A Kruskal-Wallis test for postbregmatic depression showed that were no statistically significant differences in mean rank scores for any Japanese age groups (H = 9.028; df = 6; p = 0.167). A Kruskal-Wallis test for nasal aperture width scores showed that there were statistically significant differences between mean rank scores for at least two Japanese age groups (H =

Table 5.73. Age affects on the cranial and mandibular nonmetric traits for the Japanese and Thai samples.

Trait	Group	N	Spearman's rho
Anterior nasal spine	Japanese	700	-0.040
	Thai	560	-0.103**
Inferior nasal aperture	Japanese	707	0.009
	Thai	562	0.005
Interorbital breadth	Japanese	699	0.043
	Thai	560	-0.033
Malar tubercle	Japanese	703	0.065
	Thai	564	-0.051
Nasofrontal suture	Japanese	703	0.065
	Thai	563	0.015
Nasal aperture shape	Japanese	704	0.075**
	Thai	558	-0.055
Nasal bone shape	Japanese	702	0.027
	Thai	558	-0.026
Nasal aperture width	Japanese	704	0.153*
	Thai	559	0.029
Nasal bone contour	Japanese	702	0.019
	Thai	555	-0.047
Nasal overgrowth	Japanese	697	-0.009
	Thai	548	0.110
Postbregmatic depression	Japanese	659	-0.113**
	Thai	567	-0.044
Supranasal suture	Japanese	702	0.073
	Thai	564	-0.064
Transverse palatine suture	Japanese	664	-0.117**
	Thai	475	-0.056
Zygomaticomaxillary suture	Japanese	648	0.007
	Thai	561	-0.021
Keeling	Japanese	659	-0.053
	Thai	562	-0.055
Suture complexity	Japanese	530	-0.056
	Thai	435	-0.080
Wormian bones	Japanese	520	-0.046
	Thai	432	0.007
Orbit shape	Japanese	708	-0.003
	Thai	563	0.084**
Zygomatic/maxillary projection	Japanese	700	-0.051
	Thai	554	0.123**
Zygomatic posterior tubercle	Japanese	708	-0.053
	Thai	562	-0.107
Prognathism	Japanese	707	-0.084**
	Thai	561	-0.199*
Dental arcade shape	Japanese	697	0.080**
	Thai	560	-0.100**

Table 5.73, continued.

Trait	Group	N	Spearman's rho
Occlusion	Japanese	304	-0.021
	Thai	169	0.026
Maxillary incisor orientation	Japanese	313	0.045
	Thai	187	-0.161**
Mandibular ramus inversion	Japanese	698	-0.101**
	Thai	554	0.107**
Location of inversion	Japanese	257	0.182**
	Thai	225	0.026
Gonial eversion	Japanese	699	-0.207*
	Thai	555	0.026
Mandibular border	Japanese	699	-0.307*
	Thai	555	-0.080
Mandibular tori	Japanese	698	0.154*
	Thai	551	0.038
Gonial muscle attachment ridging	Japanese	698	0.125*
	Thai	554	0.076
Mylohyoid bridging	Japanese	699	-0.034
	Thai	554	-0.006
Accessory mandibular foramen	Japanese	696	-0.085**
	Thai	554	0.065
Chin prominence	Japanese	698	0.100**
	Thai	551	0.134**
Chin shape	Japanese	699	0.141*
	Thai	551	0.020
Number of mental foramen	Japanese	700	0.054
	Thai	551	-0.088**
Ascending ramus shape	Japanese	699	-0.159*
	Thai	555	0.061
Ascending ramus profile	Japanese	699	-0.135*
	Thai	555	0.044

*statistically significant at the 0.001 level; **statistically significant at the 0.05 level.

21.027; df = 6; p = 0.001). A *post-hoc* pairwise test showed that Japanese individuals 17-29 years old had lower nasal aperture width scores compared to 70-79 year old individuals (p = 0.005). A Kruskal-Wallis test for postbregmatic depression showed that were no statistically significant differences in mean rank scores for any Japanese age groups (H = 9.028; df = 6; p = 0.167). A Kruskal-Wallis test for transverse palatine suture showed that there were statistically significant differences between mean rank scores for at least two Japanese age groups (H = 14.799; df = 6; p = 0.021). A *post-hoc* pairwise test showed that the youngest Japanese individuals (17-29 years) had higher transverse palatine scores compared to 70-79 year olds (p = 0.018). A Kruskal-Wallis test for orbit shape showed that there were no statistically significant differences between mean rank scores and any Thai age groups (H = 8.243; df = 6; p = 0.224). A Kruskal-Wallis for zygomatic projection showed that there were no statistically significant differences between mean rank scores for any Thai age group (H = 11.234; df = 6; p = 0.082). A Kruskal-Wallis test for prognathism showed that there were statistically significant differences in mean rank scores for at least two Thai age groups (H = 23.798; df = 6; p = 0.001). Thai individuals 40-49 years old have higher scores compared to 70-79 year olds (p = 0.012) and 80-96 year olds (p = 0.006). Conversely, a Kruskal-Wallis test for prognathism showed that there were no statistically significant differences in mean rank scores for any Japanese age groups (H = 10.082; df = 6; p = 0.124). A Kruskal-Wallis test for dental arcade shape showed that there were no statistically significant differences in mean rank scores between any Japanese age groups (H = 10.389; df= 6; p = 0.112). Similarly, a Kruskal-Wallis test for dental arcade shape showed that there were no statistically significant differences in mean trait scores for any Thai age groups (H = 11.149; df = 6; p = 0.083). A Kruskal-Wallis test for maxillary incisor orientation showed that there were no statistically significant differences in mean trait score ranks for any Thai age groups (H = 7.498; df = 6; p = 0.275).

To further investigate the affects of age on the expression of the mandibular traits, Kruskal-Wallis tests were calculated with the traits that showed a correlation with age. As such, the trait scores served as the dependent variables and age category served as the independent variable. A Kruskal-Wallis test for mandibular ramus inversion showed that there were no statistically significant differences in mean trait score ranks for any Thai age groups (H = 9.830; df = 6; p = 0.125). Conversely, a Kruskal-Wallis test for mandibular ramus inversion showed that there were statistically significant differences in mean trait score ranks for at least two Japanese age groups (H = 15.858; df = 6; p = 0.014). A *post-hoc* pairwise test showed that individuals 40-49 years old had higher scores compared to 80-96 year olds (p = 0.014). A Kruskal-Wallis test for the location of mandibular inversion showed that there were no statistically significant differences in mean trait score ranks for any Japanese age groups (H = 13.319; df = 6; p = 0.037). A Kruskal-Wallis test for gonial eversion showed that there were statistically significant differences in mean trait score ranks for at least two Japanese age groups (H = 32.488; df = 6; p = 0.000). A *post-hoc* pairwise test showed that Japanese individuals 17-29 years old have higher gonial eversion scores than individuals 60-69 years old (p = 0.001), 70-79 years (p = 0.004), and 80-96 years (p = 0.017). Additionally, Japanese 40-49 years old have higher gonial eversion scores than 60-69 year olds (p = 0.036). A Kruskal-Wallis test for mandibular border form showed that there were statistically significant differences in mean trait score ranks for at least two Japanese age groups (H = 69.360; df = 6; p = 0.000). A *post-hoc* pairwise test showed that Japanese individuals 17-29 years old, 30-39 years old, and 40-49 years old have higher scores than individuals 60-69 years old (p = 0.000 – 0.001), 70-79 years old (p = 0.000), and 80-96 years old (p = 0.000 – 0.001). Additionally, individuals 50-59 years old have higher scores than individuals 70-79 years old (p = 0.013) and 80-96 years old (p = 0.030). A Kruskal-Wallis test for mandibular tori showed that there were statistically significant differences in mean trait score ranks for at least two Japanese age groups (H = 21.018; df = 6; p = 0.001). A *post-hoc* pairwise test showed that individuals 17-29 years had lower scores than individuals 60-69 years old (p = 0.011) and 80-96 years old (p = 0.010). A Kruskal-Wallis test for gonial muscle attachment ridging showed that there were statistically significant differences in mean trait score ranks for at least two Japanese age groups (H = 27.172; df = 6; p = 0.000). A *post-hoc* pairwise test showed that individuals 17-29 years old and 40-49 years old have lower scores compared to individuals 70-79 years old (p = 0.009 – 0.050) and 80-96 years old (p = 0.002 – 0.009). Additionally, individuals 50-59 years old and 60-69 years old have lower scores compared to individuals 80-96 years old (p = 0.020 – 0.025). A Kruskal-Wallis test for accessory mandibular foramen showed that there were no statistically significant differences in mean trait score ranks for any Japanese age groups (H = 8.675; df = 6; p = 0.187). Kruskal-Wallis tests for chin prominence showed that there were no statistically significant differences in mean trait score ranks for any Japanese (H = 11.393; df = 6; p = 0.076) or Thai (H = 10.957; df = 6; p = 0.089) age groups. A Kruskal-Wallis test for chin shape showed that there were no statistically significant differences in mean trait score ranks for any Japanese age groups (H = 18.602; df = 6; p = 0.004). A Kruskal-Wallis test for number of mental foramen showed that there were no statistically significant differences in mean trait score ranks for any Thai age groups (H = 6.058; df = 6; p = 0.413). A Kruskal-Wallis test for ascending ramus shape showed that there were statistically significant differences in mean trait score ranks for at least two Japanese age groups (H = 24. 998; df = 6; p = 0.000). A *post-hoc* pairwise test showed that individuals 17-29 years, 30-39 years, 40-49 years, and 50-59 years have higher scores than individuals 80-96 years of age (p = 0.003 – 0.015). Lastly, a Kruskal-Wallis for ascending ramus profile showed that there are statistically significant differences in mean trait score ranks for at least two Japanese groups (H = 21.025; df = 6; p = 0.002). A *post-hoc* pairwise test showed that individuals 17-29 years and 40-49 years have higher scores than individuals 70-79 years old (p = 0.022 – 0.024).

Population differences in cranial and mandibular morphology

Additionally, chi-square analyses were conducted to determine if population has an affect on the expression and scoring of cranial and mandibular traits. As such, the null hypothesis states that there is no association between population and trait score. However, chi-square significance values for 32 of the cranial and mandibular traits fall below 0.05, thereby rejecting the null hypothesis and indicating that population differences exist in the expression and scoring of the traits (Table 5.74). Only nasal bone shape, dental arcade shape, accessory mandibular foramen, and number of mental foramen show no population differences, with chi-square significance values above 0.05. Further, the majority of the Phi and Cramer's V values indicate the cranial and mandibular trait scores and population are moderately associated.

While both the Japanese and Thai samples exhibit all trait expressions and considerable overlap in the expression of many traits (see Tables 5.34 – 5.70, above), population differences are also present between the groups. Table 5.75 presents the statistically significant population proportion differences in trait expressions between the Japanese and Thai samples.

Table 5.74. Population affects on the cranial and mandibular nonmetric traits.

Trait	Pearson Chi-square	Phi/Cramer's V
Anterior nasal spine	52.897*	0.202
Inferior nasal aperture	85.936*	0.256
Interorbital breadth	13.846*	0.103
Malar tubercle	55.185*	0.205
Nasofrontal suture	8.841**	0.082
Nasal aperture shape	72.113*	0.235
Nasal bone shape	6.404	0.070
Nasal aperture width	31.279*	0.155
Nasal bone contour	97.582*	0.274
Nasal overgrowth	18.836*	0.121
Postbregmatic depression	4.491**	0.060
Supranasal suture	24.390*	0.137
Transverse palatine suture	148.438*	0.355
Zygomaticomaxillary suture	129.781*	0.322
Keeling	41.790*	0.182
Suture complexity	31.151*	0.176
Wormian bones	43.836*	0.211
Orbit shape	89.556*	0.261
Zygomatic/maxillary projection	77.132*	0.244
Zygomatic posterior tubercle	17.506*	0.116
Prognathism	202.523*	0.393
Dental arcade shape	1.287	0.032
Occlusion	109.609*	0.470
Maxillary incisor orientation	69.741*	0.364
Ramus inversion	3.082**	0.049
Location of inversion	84.867*	0.415
Gonial eversion	22.008*	0.131
Mandibular border	185.489*	0.380
Mandibular tori	81.524*	0.253
Gonial muscle attachment ridging	168.925*	0.363
Mylohyoid bridging	14.392*	0.106
Accessory mandibular foramen	1.454	0.034
Chin prominence	22.587*	0.133
Chin shape	18.517*	0.120
Mental foramen number	3.498	0.052
Ascending ramus shape	49.025*	0.196
Ascending ramus profile	54.527	0.204

*significant at the 0.001 level; **significant at the 0.05 level.

Table 5.75. Morphological differences in cranial and mandibular traits between the Japanese and Thai samples.

Trait	Japanese	Thai
Anterior nasal spine	Slight	Moderate; marked
Inferior nasal aperture	Right angled; weak vertical ridge; pronounced sill	Smooth, curved transition; sloping
Interorbital breadth	Broad	Intermediate
Malar tubercle	No protrusion; trace protrusion; double tubercle	Medium – marked protrusion
Nasofrontal suture	Irregular (jagged)	
Nasal aperture shape	Teardrop-shaped	Bell-shaped
Nasal aperture width	Narrow	Broad
Nasal bone contour	Oval; rounded; steep and narrow	Low and rounded
Nasal overgrowth	Absent	Present
Postbregmatic depression	Present	Absent
Supranasal suture	Open	Completely obliterated
Transverse palatine suture	Straight	Anterior bulging; M-shaped
Zygomaticomaxillary suture	Greatest lateral extent near inferior end of suture; two or more angles	Greatest lateral extent near midpoint of suture; obliterated
Keeling	Slight – significant	Absent
Suture complexity	Simple	Medium
Wormian bones	Absent	Present
Orbit shape	Circular; rhombic	Rectangular
Zygomatic/maxillary projection	Retreating; projecting	Moderate
Zygomatic posterior tubercle	Weak; marked	Absent; moderate
Prognathism	Moderate – large	Absent
Occlusion	Mandibular dentition far in front of maxillary dentition	Normal; edge-to-edge
Maxillary incisor orientation	Slight – marked anterior projection	Vertical
Ramus inversion	Absent	Slight – extreme
Location of inversion	Low; high	Medium
Gonial eversion	Slight – extreme	Absent
Mandibular border	Undulating; “rocker”	Straight
Mandibular tori	Absent	Slight – extreme
Gonial muscle attachment ridging	Minimal	Extreme
Mylohyoid bridging	Absent	Present
Chin projection	Prominent	Blunt/vertical
Chin shape	Rounded; pointed	Square/bilobate
Ascending ramus shape	Wide	Pinched

Inter-trait correlations

Spearman's rho were calculated to determine if the cranial and mandibular traits co-vary (Tables A.42 – A.45, Appendix E). The majority of the traits are correlated with at least one other trait. Generally, the traits are correlated by region for the neurocranium, nasal region, mandible, and mid-face. The strongest correlations are seen amongst the following traits: suture complexity and presence of wormian bones; occlusion, prognathism, and maxillary incisor orientation; gonial muscle attachment ridging, occlusion, and maxillary incisor orientation; gonial muscle attachment ridging and mandibular border form; chin shape and chin prominence; and ascending ramus profile and gonial muscle attachment ridging. The traits that are poorly correlated with other traits include orbit shape, dental arcade shape, accessory mandibular foramen, mylohyoid bridging, number of mental foramen, and postbregmatic depression.

Binary logistic regression equations for the cranial and mandibular traits

Binary logistic regression equations were calculated for the cranial and mandibular traits to determine which traits perform best in distinguishing between the Japanese and Thai samples. When all 24 cranial traits were entered into the equation, nine contributed significantly to the equation, and correctly classified a total of 84.4% of the sample (Table 5.76). Additionally, age contributed significantly to the equations, while sex had no affect. The equations all favor the Japanese individuals with correct classification rates up to 90.5%.

When Hefner's (2009) 11 traits were entered into the binary logistic regression analysis, seven traits contributed significantly to the equation and correctly classified a total of 68.0% of the sample (Table 5.77). However, when age was added as a coefficient, the correct classification rates improved slightly, indicating that age affects the classification.

When the 13 mandibular traits were entered into the binary logistic regression analysis, six traits contributed significantly to the equation and correctly classified a total of 75.4% of the sample (Table 5.78). Additionally, when age and sex were added as coefficients they significantly contributed to the equations and slightly increased the correct classification rates. As such, both sex and age have an affect on the expression of some of the mandibular traits, which influences the classification of Japanese and Thai individuals. Sex and age affect the expression of mandibular traits.

When the cranial and mandibular traits were combined into the binary logistic regression equations, seven traits contributed significantly to the equations and correctly classified up to 79.4% of the sample (Table 5.79). Age was also a significant coefficient.

Table 5.76. Binary logistic regression equations using the cranial traits for the Japanese and Thai groups.

Coefficients*											% Correct		
ANS	**INA**	**NAS**	**ZMS**	**WB**	**ZPT**	**PRG**	**OCC**	**MIO**	**AGE**	**CON**	**J**	**TH**	**T**
.684	-.871	.749	.735	1.314	-.509	-1.386	-7.729	-.935	--	2.952	89.5	75.0	84.4
--	-.665	.754	--	2.000	-.665	-1.372	-.736	-1.137	.076	.290	90.5	75.9	85.6
--	-.661	.850	--	1.869	-.645	-1.433	--	-1.273	.077	-.860	90.0	70.4	83.4
.607	-.758	.860	--	1.886	-.625	-1.345	-.741	-1.095	.075	-.776	90.0	74.1	84.6
0.883	-.821	0.406	0307	1.051	--	-1.484	--	--	--	0.094	74.7	73.2	73.9
0.896	-.820	0.398	0.282	1.073	--	-1.303	--	--	0.043	-2.553	79.2	75.8	77.6

*Models with OCC and MIO used 357 (25.6%) individuals to build equations; all other equations used 917 (65.6%) individuals; ANS=anterior nasal spine; INA=inferior nasal aperture; NAS=nasal aperture shape; ZMS=zygomaticomaxillary suture; WB=wormian bones; ZPT=zygomatic posterior tubercle; PRG=prognathism; OCC=occlusion; MIO=maxillary incisor orientation; CON=constant; J=Japanese; TH=Thai; T=total

Table 5.77. Binary logistic regression equations using Hefner's (2009) traits for the Japanese and Thai groups.

Coefficients*									% Correct		
ANS	INA	NAW	NBC	NO	TPS	ZMS	AGE	CON	J	TH	T
.765	-.573	.623	-.124	-.483	.515	.444	--	-2.212	74.6	60.5	68.0
.768	-.584	.642	--	-.474	.512	.440	--	-2.338	73.1	62.6	68.2
.757	-.591	.647	--	--	.520	.442	--	-2.426	74.7	63.6	69.6
.833	-.602	.555	--	--	.576	.446	.041	-4.779	75.7	66.4	71.5
.848	-.591	.557	--	-.600	.568	.449	.042	-4.765	76.5	65.3	71.4
.844	-.579	.536	-.139	-.620	.569	.454	.042	-4.643	75.2	66.8	71.4

*All models used 1039 individuals (74.4%) to build equations; ANS=anterior nasal spine; INA=inferior nasal aperture; NAW=nasal aperture width; NBC=nasal bone contour; NO=nasal overgrowth; TPS=transverse palatine suture; ZMS=zygomaticomaxillary suture; CON=constant; J=Japanese; TH=Thai; T=total

Table 5.78. Binary logistic regression equations using the mandibular traits for the Japanese and Thai samples.

Coefficients*										% Correct		
GE	MB	MT	GMA	CP	CS	ARS	SEX	AGE	CON	J	TH	T
-.591	-.980	1.012	1.035	-.647	--	-.748	--	--	1.452	81.0	69.0	75.4
--	-.948	.929	1.089	-.912	.369	-.596	-1.328	.046	-1.385	80.0	76.9	78.6
-.404	-.932	.947	1.126	-.933	.379	-.651	-1.255	.045	-1.181	80.4	76.0	78.4
--	-.956	.936	1.107	-.905	.388	--	-1.299	0.047	-2.605	78.4	76.5	77.5
-.577	-.984	1.031	1.027	--	--	-.701	--	--	.586	78.3	70.3	74.5
-.537	-.995	1.036	1.042	--	--	--	--	--	-.700	79.8	66.8	73.7

*Models with AGE used 476 individuals (34.1%) to build equations; the remaining models used 487 individuals (34.9%); GE=gonial eversion; MB=mandibular border; MT=mandibular tori; GMA=gonial muscle attachment ridging; CP=chin prominence; ARS=ascending ramus shape; CON=constant; J=Japanese; TH=Thai; T=total

Table 5.79. Binary logistic regression equations using the cranial and mandibular traits for the Japanese and Thai samples.

Coefficients*										% Correct		
INA	NAS	PRG	WB	GMA	MT	CP	SEX	AGE	CON	J	TH	T
-.669	.389	-1.273	1.184	1.005	.613	-.816	-.850	.034	-1.693	81.2	77.1	79.3
-.721	--	-1.283	1.170	1.000	.598	-.818	-.923	.035	-.886	81.2	77.1	79.3
-.704	--	-1.274	1.168	.995	.624	--	-.920	.032	-1.733	79.1	76.1	77.7
-.664	--	-1.229	1.068	.832	.593	--	--	.032	-2.049	79.1	75.1	77.3
-.662	.461	-1.357	.988	.953	.653	-.639	--	--	-.467	78.4	76.1	77.3
-.646	.460	-1.347	.997	.956	.664	--	--	--	-1.286	76.9	75.1	76.1
-.674	--	-1.356	.983	.936	.642	--	--	--	-.347	76.1	75.1	75.6

*Models with AGE used 871 individuals (62.3%) to build equations; models without AGE used 891 individuals (63.8%); INA=inferior nasal aperture; NAS=nasal aperture shape; PRG=prognathism; WB=wormian bones; GMA=gonial muscle attachment ridging; MT=mandibular tori; CON=constant; J=Japanese; TH=Thai; T=total

CHAID decision tree analysis on the cranial and mandibular traits

A CHAID cranial trait decision tree analysis was conducted for the Japanese and Thai samples using 1,327 individuals (Figure A.10). Maxillary incisor orientation, occlusion, suture complexity, and wormian bones were excluded from the model due to the high number of individuals missing these values (over 10%). Prognathism, transverse palatine suture, nasal aperture shape, anterior nasal spine, and zygomaticomaxillary suture performed the best, correctly classifying 79.0% of the Japanese and 68.1% of the Thai, with a total correct classification rate of 74.1%. The resubstitution risk associated with this tree is 0.259 (S.E. = 0.012), while the cross-validated risk is 0.305 (S.E. = 0.013). The associated probabilities for the terminal nodes are presented in Table A.46.

A CHAID decision tree analysis was conducted for Hefner's (2009) 11 cranial traits on 1,326 Japanese and Thai individuals (Figure A.11). The transverse palatine suture, zygomaticomaxillary suture, nasal bone contour, and anterior nasal spine performed the best, correctly classifying 74.3% of the Japanese and 70.1% of the Thai, with a total correct classification rate of 72.4%. The resubstitution risk associated with this tree is 0.276 (S.E. = 0.012), while the cross-validated risk is 0.326 (S.E. = 0.013). The associated probabilities for each of the terminal nodes are presented in Table A.47.

A CHAID mandibular trait decision tree analysis was conducted for the Japanese and Thai samples on 1,283 individuals (Figure A.12). One trait (location of ramus inversion) was omitted from the model due to the high number of individuals missing this trait (64.7%). The mandibular border, gonial muscle attachment ridging, mandibular tori, ascending ramus shape, and gonial eversion performed the best, correctly classifying 78.1% of the Japanese and 68.1%

of the Thai, with a total correct classification rate of 73.7%. The resubstitution risk associated with this tree is 0.263 (S.E. = 0.012), while the cross-validated risk is 0.264 (S.E. = 0.012). The associated probabilities for the terminal nodes are presented in Table A.48.

A CHAID decision tree analysis including 31 cranial and mandibular traits was conducted for the Japanese and Thai samples on 1,389 individuals (Figure A.13). Suture complexity, wormian bones, maxillary incisor orientation, occlusion, location of ramus inversion, and transverse palatine suture were not included in the model due to their high missing values (over 10% of individuals). Prognathism, gonial muscle attachment ridging, supranasal suture form, mandibular border shape, zygomaticomaxillary suture shape, and nasal bone contour performed the best, correctly classifying 85.5% of the Japanese and 62.7% of the Thai, with a total correct classification rate of 75.6%. The resubstitution risk associated with this tree is 0.244 (S.E. = 0.012), while the cross-validated risk is 0.279 (S.E. = 0.012). The associated probabilities for each of the terminal nodes are presented in Table A.49.

Intraobserver error analysis

Cranial and mandibular trait intraobserver error rates were assessed on 120 individuals of the Japanese and Thai sample. Table 5.80 presents the Cohen's kappa (k) values for each trait and the level of agreement following Landis and Koch (1977). All Cohen's kappa values are statistically significant at the 0.001 level.

Table 5.80. Intraobserver error analysis for the 37 cranial and mandibular traits.

Trait	Cohen's k	Agreement
Anterior nasal spine	0.768	Substantial
Inferior nasal aperture	0.474	Moderate
Interorbital breadth	0.637	Substantial
Malar tubercle	0.650	Substantial
Nasofrontal suture	0.616	Substantial
Nasal aperture shape	0.625	Substantial
Nasal bone shape	0.614	Substantial
Nasal aperture width	0.624	Substantial
Nasal bone contour	0.666	Substantial
Nasal overgrowth	0.792	Substantial
Postbregmatic depression	0.641	Substantial
Supranasal suture	0.765	Substantial
Transverse palatine suture	0.820	Almost perfect
Zygomaticomaxillary suture	0.716	Substantial
Keeling	0.639	Substantial
Suture complexity	0.373	Fair
Wormian bones	0.695	Substantial
Orbit shape	0.692	Substantial
Zygomatic/maxillary projection	0.457	Moderate
Zygomatic posterior tubercle	0.680	Substantial
Prognathism	0.426	Moderate
Dental arcade shape	0.436	Moderate
Occlusion	0.896	Almost perfect
Maxillary incisor orientation	0.702	Substantial
Ramus inversion	0.689	Substantial
Location of inversion	0.158	Slight
Gonial eversion	0.593	Moderate
Mandibular border	0.594	Moderate
Gonial muscle attachment ridging	0.509	Moderate
Mylohyoid bridging	1.000	Perfect
Accessory mandibular foramen	0.701	Substantial
Chin prominence	0.461	Moderate
Chin shape	0.584	Moderate
Number of mental foramen	0.526	Moderate
Ascending ramus shape	0.451	Moderate
Ascending ramus profile	0.753	Substantial

Secular change in cranial and mandibular traits for the Japanese sample

Chi-square analyses were conducted on the cranial and mandibular traits for the CU (historic) and JU (modern) collections to test the hypothesis that the scoring of traits is not related to the century of death (see Appendix G). Based on chi-square significance values below 0.05, numerous traits show differences between the historic and modern individuals for both sexes. For the females, 16 traits (43.2%) are significantly different, while the males show significant differences in 19 traits (51.4%). Females and males share differences between the historic and modern individuals, including: transverse palatine suture (CU have straighter sutures); suture complexity (JU have more complex sutures); orbit shape (JU are more rectangular, while the CU are more rounded); prognathism (JU are less prognathic); ramus inversion (JU are less inverted); location of inversion (JU has low or medium placement, while CH has higher placement); and ascending ramus profile (JU are straighter, while the CH are more slanted).

CHAPTER VI: Discussion

This chapter discusses the results presented in Chapter V for the nonmetric sexual dimorphism and cranial trait variation observed in the Japanese and Thai collections. As such, this chapter will first address whether the four hypotheses proposed in Chapter I are supported by the results. Further, this chapter will discuss the affects of sex, age, secular change, intraobserver error, and inter-trait correlations on the expression of nonmetric traits used in sex and biogeographic ancestry assessment.

A total of 15 nonmetric features considered to be sexually dimorphic and 37 cranial/mandibular traits frequently used in ancestry assessment were scored on 1,397 individuals, 17 to 96 years of age, from four documented modern or historic skeletal collections in Japan and Thailand. Multiple statistical analyses highlighted four broad findings concerning Japanese and Thai nonmetric trait variability, and the application of nonmetric traits to sex and ancestry assessment: 1) Population-specific sex assessment methods perform better in classifying Japanese and Thai individuals than those developed on non-Asian populations; 2) Differences exist in the expression of nonmetric traits between the Japanese and Thai such that they can be differentiated from one another, and therefore, the Japanese and Thai should not be considered homogenous; 3) The Japanese and Thai differ from Native Americans in the expression of nonmetric traits due to unique population histories, and thus, Native Americans should not be used as biological proxies for Asian populations; and 4) Many nonmetric traits are affected by sex, age, intraobserver error, inter-trait correlations, and population, and exhibit secular change, thereby complicating their use in biological profiles.

Population-Specific Sex Assessment Methods

Hypothesis 1 states that differences in the nonmetric expression of sexual dimorphism exist between the Asian groups (Japanese and Thai individuals) and non-Asian groups such that the sex assessment methods developed on individuals of African or European descent and Native Americans will not accurately classify Japanese or Thai individuals. Based on the results presented in Chapter V, this hypothesis is supported. In particular, the total correctly classified for each cranial trait was lower for the Japanese and Thai samples compared to Walker's (2008) and Garvin *et al.*'s (2014) American/English and Native American samples. Accordingly, when the methods are refined for the Japanese and Thai individuals, their accuracies increase. In general, Japanese and Thai individuals are less sexually dimorphic than non-Asian groups (including Native Americans), as evidenced by the reduced performance of the sex assessment methods (including probabilities and cutoff points) developed on non-Asian populations.

While the Japanese and Thai individuals generally exhibit robust nuchal crests, supraorbital margins, and mastoid processes, these two groups exhibit somewhat reduced cranial sexual dimorphism compared to non-Asian groups. For univariate sex assessment, the nuchal crest, glabella, and mastoid process performed less well in the Japanese and Thai compared Walker's (2008) American sample. However, the supraorbital margin performed better in the Japanese and Thai groups, while the mastoid process performed comparably to the American sample. The application of Walker's (2008) and Garvin *et al.'s* (2014) discriminant function equations to the Japanese and Thai individuals correctly classified 26.3 – 97.4% of the individuals and produced very large sex biases. While the sex biases decreased when population-specific logistic regression equations were created for the Japanese and Thai samples, many of the correct classification rates remained under 80%. The somewhat low correct classification rates and high sex biases indicate that there is considerable overlap in the expression of certain traits.

Somewhat surprising is the finding that the subpubic concavity performed the best in classifying Japanese and Thai females and males in univariate statistics, logistic regression equations, and Chi Square Automatic Interaction Detection (CHAID) decision tree analyses. Generally, previous researchers have found that the ventral arc performs the best in classifying individuals, followed by the subpubic concavity, and ischiopubic ramus ridge (Klales *et al.* 2012; Lovell 1987; Phenice 1969). In particular, Klales *et al.'s* (2012) study of the Phenice (1969) method in Black, White, Hispanic, Japanese, Mexican, and Asian individuals found that the ventral arc correctly classified 88.5%, the subpubic concavity correctly classified 86.6%, and the ischiopubic ramus ridge correctly classified 75.8%. It should be noted that their Asian and Japanese sample consists of two individuals, and all biogeographic ancestries were grouped for their analyses. Additionally, Klales and couthers devised and utilized an expanded five-point ordinal scoring system for Phenice's (1969) traits.

Differences between Asian and non-Asian groups in sciatic notch form are also evident. Proportionately less Japanese and Thai females were scored as female (1), and more Japanese and Thai females were scored as indeterminate (3) compared to Walker's (2005) African American, European American, and English females. Likewise, proportionately fewer Japanese and Thai males were scored as female (1 and 2), and more Japanese and Thai males were scored as probable male (4) compared to Walker's (2005) sample. As such, the Japanese and Thai individuals generally exhibit higher (more constricted) sciatic notch scores compared to

Walker’s (2005) non-Asian groups. Further, Walker found that scores of 2 are sexually indeterminate for the non-Asian groups due to the significant amount of overlap shared between females and males. Conversely, scores of 2 indicate female with a 0.93 probability for the Japanese and 0.94 probability for the Thai.

Slight differences in the frequencies of rhomboid fossae are found between Asian and non-Asian groups. Rogers *et al.* (2000) found that Black and White females exhibit a rhomboid fossa on the left clavicle 3% of the time, and one on the right 8% of the time. While these results are consistent with the Thai female frequencies (left = 2.6%, right = 3.6%), the Japanese females display higher frequencies of fossae on the left and right clavicles (left = 8.6%, right = 18.6%). The Japanese males show slightly higher frequencies of fossae on the right clavicle (43.1%) compared to Black and White males (36%), but similar frequencies on the left (Japanese = 28.6%, Black/White = 31%). Additionally, the probability that a Japanese individual with a rhomboid fossa on the right clavicle is male is 70%, and a fossa on the left indicates male with a 77% probability. This is somewhat lower than the Black and White male probabilities (left = 92.2%, right = 81.7%) found by Rogers *et al.* (2000). This can be attributed to the relatively higher frequencies of rhomboid fossae observed in Japanese females, resulting in less difference between females and males. However, the Thai sample exhibits higher male probabilities for the left and right clavicles (both 91%).

The frequencies of rhomboid fossae observed in the Japanese and Thai individuals are remarkably lower than those found in modern Indian individuals. Singh and Singh (2009) report that out of 343 paired clavicles obtained from modern autopsy cases, 92% of males show medium to large fossae, while 86% of females show small to medium fossae. While the majority of individuals in their sample exhibited a rhomboid fossa, the size of the fossa was significantly different between females and males, thus allowing for its use in forensic casework. Singh and Singh (2009) hypothesize that modern Indian populations experience more strenuous activity patterns compared to modern Americans. Following the hypothesis that rhomboid fossae develop in response to biomechanical stresses and muscle mass, the Japanese and Thai individuals likely experienced less activity induced stress on the infero-medial clavicle compared to Indian individuals.

Differences between Asian and non-Asian individuals can also be seen in distal humerus morphology. When using Vance *et al.*'s (2011) composite scoring method (1-8 = male; 9 = indeterminate; 10-15 = female) for the angle of the medial epicondyle, olecranon fossa shape, and trochlear extension, the Japanese and Thai females are poorly classified (Japanese = 61.0%; Thai = 56.7%) compared to Black and White South African females (77%). This is because proportionately more Japanese and Thai females were wrongly scored as male. However, this composite method performed better on Japanese and Thai males (Japanese = 90.7%; Thai = 94.2%) compared to Black and White South African males (74%). As such, the adjusted distal humerus scoring system presented here is superior at predicting the sex of Japanese and Thai individuals compared to Vance *et al.'s* (2011) scoring system.

Differences in distal humerus morphology are also seen between the Asian groups and White Americans. Rogers (1999) found that the four distal humerus features correctly classified the sex of White individuals 69 – 88% of the time, which is somewhat better than those for the Japanese and Thai individuals (45.9 – 84.7%) when used in a non-composite scoring system. Both studies found that the angle of the medial epicondyle is the single best predictor of sex, while trochlear constriction was the least effective indicator. Rogers (1999) argued that in indeterminate cases, more weight should be placed on the olecranon fossa shape, as it proved to be less ambiguous than the other traits in her American sample. However, the determination of oval/rounded (“female-like”) or triangular (“male-like”) in the Japanese and Thai was not particularly clear-cut during the scoring of this trait for the Japanese and Thai individuals. The olecranon fossa shape failed to produce correct classification rates in excess of 80% in the present study.

It is clear that population differences exist between the Asian (Japanese and Thai) groups and non-Asian groups in cranial morphology, pelvic morphology, rhomboid fossa presence, and distal humerus morphology. Therefore, the application of univariate cutoff points, logistic regression equations, and composite scoring systems developed on non-Asian populations leads to reduced correct classification rates for the Japanese and Thai individuals, which can skew aggregate demographic information and hinder identifications. The revised, population-specific cranial, pelvic, rhomboid fossa, and distal humerus morphology methods presented here improves the prediction of sex for Japanese and Thai individuals.

The potential reasons for sexually dimorphic differences between the Japanese and Thai and non-Asian populations are numerous. Every population has a unique history, each with different genetics, environments, selection pressures, and migratory events, leading to interacting biological and cultural differences in modern populations. In particular, nutritional intake between populations is quite varied, and can impact the development of secondary sex characteristics (Bogin 1999; Stinson 1985, 2012). It is important to remember that the majority of biological profile methods were developed on collections in North America (Komar and

Buikstra 2008), which is considered epidemiologically to be an obesogenic environment due to overnutrition (Chopra *et al*. 2002). The availability of low-cost, high-fat, and refined foods in developed countries like the U.S. has led to 66.8% of the U.S. being classified as overweight or obese, and in particular, 74% of males being classified as overweight or obese (NIH 2016). While the rates for obesity are presently at an all-time high, this epidemic started during the early 20th century in the U.S. (Komlos and Brabec 2010). Many of the collections used to develop biological profile methods were established well after the start of increasing obesity (Komar and Buikstra 2008). Economic inequality, which is problematic in the U.S., has been shown to be a primary cause for over- and under-nutrition (Subramanian *et al.* 2007). As obesity is associated with accelerated growth during puberty (Solorzano and McCarthey 2010), overnutrition, particularly in males, may account for some of the difference observed in sexual dimorphism between Asian and non-Asian individuals.

Differences Between Japanese and Thai Individuals

Hypotheses 2 and 3 state that differences in the nonmetric expression of the traits used in sex assessment (hypothesis 2) and ancestry (hypothesis 3) exist between Japanese and Thai individuals. The results presented in Chapter V largely support these hypotheses; however, the degree of population variation is trait dependent. While the sexually dimorphic differences between the Japanese and Thai are rather small, significant differences were observed in the cranial and mandibular traits that are used in ancestry assessment.

Sexually dimorphic traits

For the sexually dimorphic cranial and pelvic traits, chi-square analyses indicate that there are population differences in the expression of several traits between the Japanese and Thai individuals. In particular, the Japanese exhibit more robust nuchal regions, supraorbital margins, and glabellae compared to the Thai. The Thai exhibit more robust mastoid processes and mental eminences compared to the Japanese. Additionally, the Japanese exhibit more gracile ventral arc morphology than the Thai, and Japanese females are more robust in sciatic notch morphology compared to Thai females.

While statistically significant differences exist in cranial and pelvic morphology between the Japanese and Thai individuals, the binary logistic regression total correct classification rates for the pooled Japanese and Thai samples are very similar to the individual total correct classification rates for the Japanese and Thai. This suggests that the cranial and pelvic sexually dimorphic differences between the Japanese and Thai are minimal. Moreover, logistic regression equations and CHAID decision trees eliminated population from the independent variables that predict sex. Thus, while differences exist in the expression of cranial and pelvic traits at the univariate level, the population does not appreciably affect the statistical models that incorporate multiple variables to warrant separate sex assessment methods.

For the rhomboid fossa, chi-square analyses indicate that population differences exist in the expression of fossae between the Japanese and Thai individuals. Proportionately more Japanese females exhibit rhomboid fossae on the left and right clavicles compared to Thai females. Similarly, proportionately more Japanese males exhibit rhomboid fossae on the right compared to Thai males. As such, the Japanese are less sexually dimorphic than the Thai, resulting in significantly different probabilities associated with the prediction of sex based on the expression of a rhomboid fossa. The probability of being male when a rhomboid fossa is observed on the left or right clavicle for the Thai individuals is 0.91, which is higher than the Japanese probabilities (left = 0.77, right = 0.70), and the pooled Japanese and Thai probabilities (left = 0.85, right = 0.81). Moreover, a logistic regression analysis indicates that the population affects the expression of a rhomboid fossa for the right clavicle. This suggests that the population affects the expression of rhomboid fossae, and separate Japanese and Thai probabilities are appropriate.

For the distal humerus, chi-square analyses indicate that there are population differences between the Japanese and Thai individuals. In particular, more Japanese females are "male-like" in their medial epicondyle morphology, while Thai males exhibit more "female-like" morphology in olecranon fossa shape and trochlear constriction. The population-specific binary logistic regression equations show that the Japanese are more often correctly classified (68.0 – 94.0%) than the Thai (49.4 – 92.2%) and the pooled Japanese and Thai (49.4 – 94.0%) individuals. Further, logistic regression analysis shows that the population contributes to the prediction of sex when using the distal humerus. Therefore, separate distal humerus univariate probabilities and logistic regression equations should be maintained for the Japanese and Thai individuals.

While population differences exist between the Japanese and Thai individuals for many traits, the cranial and pelvic sexually dimorphic traits do not exhibit significant population differences. Therefore, the pooled univariate cranial and pelvic probabilities and pooled cranial and pelvic logistic regression equations presented in Chapter V can be utilized on Japanese and

Thai individuals. However, the rhomboid fossa expression and distal humerus morphology do show population differences, and as such, the population-specific univariate probabilities, composite scoring methods, and logistic regression equations should be used over the pooled methods.

Cranial and mandibular traits

Perhaps most importantly, the results presented in Chapter V indicate that the Japanese and Thai can be differentiated using nonmetric traits within a statistical framework, such as binary logistic regression analyses and CHAID decision trees, with a fair amount of statistical certainty. Although the majority of trait expressions and frequencies are observed in all groups, and considerable variability exists in the expression of most traits, 32 of the 37 cranial and mandibular traits show statistically significant chi-square values between the Japanese and Thai individuals, indicating that population differences exist.

The binary logistic regression equations for the cranial traits, mandibular traits, and the combined cranial and mandibular traits identified the best predictor variables for differentiating between Japanese and Thai individuals, while producing total correct classification rates of 68.0 – 85.6%. In all logistic regression analyses, the Japanese were more accurately classified compared to the Thai. Anterior nasal spine projection, inferior nasal aperture shape, nasal aperture shape, and the degree of prognathism performed the best for the cranial traits, while the gonial muscle attachment ridging, expression of mandibular tori, and chin projection performed the best for the mandibular traits. The cranial traits performed the best, while Hefner's (2009) 11 traits and the 13 mandibular traits exhibited reduced discriminatory power when analyzed separately. The inclusion of maxillary incisor orientation and occlusion increased the correct classification rates; however, the logistic regression models incorporating these two coefficients were computed from significantly smaller sample sizes than the other models due to the infrequency of incisors. Values for maxillary incisor orientation were missing in 872 individuals (62.4%), while values for occlusion were missing in 900 individuals (64.4%). As such, models utilizing these two predictor variables should be cautiously employed.

The CHAID results also indicate that the Japanese and Thai individuals can be differentiated based on chi-square interactions between the independent variables. While on the whole, the CHAID decision trees were less effective at differentiating the two groups compared to the binary logistic regression analyses, their correct classification rates ranged from 62.7% to 85.5%, further indicating that detectible differences exist in the nonmetric expression of cranial and mandibular traits. Generally, the CHAID analyses identified fewer traits that contributed to differentiating the two groups compared to the binary logistic regression analyses, which often included numerous traits. Like the binary logistic regression analyses, the CHAID decision trees better classified the Japanese individuals.

The binary logistic regression analyses and the CHAID decision trees both identified many of the same traits that are useful in differentiating the Japanese and Thai. For the cranial traits, both statistical approaches found that the anterior nasal spine, nasal aperture shape, prognathism, and zygomaticomaxillary suture performed the best. When using Hefner's (2009) 11 traits exclusively, both statistical approaches identified four traits that performed the best: anterior nasal spine, nasal bone contour, transverse palatine suture, and zygomaticomaxillary suture. For the mandibular traits, both statistical approaches identified gonial eversion, mandibular border shape, mandibular tori, gonial muscle attachment ridging, and ascending ramus shape as the best predictive traits. Lastly, when the cranial and mandibular traits were combined, both statistical approaches identified prognathism and gonial muscle attachment ridging as the best predictors.

Variable selection was also dependent on the statistical model used, resulting in the binary logistic regression analyses and CHAID decision trees incorporating different variables. Binary logistic regression analyses utilize the Wald statistic to determine which trait or traits contribute most to the model. The Wald statistic tests they hypotheses that the predictor variables are equal to zero (Field 2009). The variables that are equal to zero are removed from the equation, and those that are more than zero are added to the equation. The Wald statistic is based on a chi-square distribution, and is calculated by the value of the regression coefficient divided by the associated standard error, which is very similar to a t-test (Field 2009). The CHAID decision trees use chi-square analyses to ascertain how the predictor variables combine and interact to predict the outcome (IBM 2009). Unless specific commands are used in binary logistic regression analyses, the equations do not test interactions between the predictor variables, but instead determine how each predictor performs individually when added to the equation.

Clearly, the nasal region is important in distinguishing the Japanese and Thai individuals. In general, the Japanese have smaller nasal spines, narrower nasal apertures, and less nasal overgrowth than the Thai. The Japanese also have more angled or silled inferior nasal apertures compared to the rounded inferior nasal apertures observed in the Thai. The Japanese exhibit more teardrop-shaped nasal apertures, while the Thai exhibit more bell-shaped nasal apertures.

Lastly, the Japanese display steeper and narrower nasal bones compared to the low and rounded nasal bones typically seen in the Thai.

While subtle, the morphological differences observed in the nasal region between the Japanese and the Thai individuals may be due to adaptive responses to different climatic environments that have been retained from ancestral populations adapted to cooler, drier environments in the north and warmer, moister environments in the south. While some debate surrounds the origins of Northeast and Southeast Asian populations during the late Pleistocene (see Chapter III), the proximate ancestors of the modern Japanese likely migrated from northern mainland Asia, particularly the Korean peninsula, beginning at least 2,000 years ago (Hanihara 1991). These populations had been living in the north for a considerable amount of time and would have been adapted to cooler, temperate climates (i.e., narrower and higher nasal apertures, steeper nasal bones; Guglielmino-Matessi *et al.* 1979). Conversely, the proximate ancestors for the modern Thai populations likely migrated from southern China and exchanged genes with local populations already living in Southeast Asia approximately 5,000 years ago (Brace *et al.* 1991; Howells 1997; Matsumura 2006). These populations would have been adapted to more hot and dry and hot and wet environments (i.e., wider nasal apertures, low and rounded nasal bones; Guglielmino-Matessi *et al.* 1979). As such, these ancestral differences may have been retained and may be reflected in modern Japanese and Thai populations.

The mandible represents another region where morphological differences are observed between Japanese and Thai individuals. In general, the Japanese show less posterior ramus inversion and more gonial eversion compared to the Thai. Japanese mandibular borders are more often undulating or somewhat curved (“rocker”) compared to the more straight Thai mandibular borders. The Thai tend to have slight to extreme mandibular tori, while the Japanese show less frequencies of tori. Similarly, the Thai typically exhibit more gonial muscle attachment ridging than the Japanese. The Japanese more often display pointed or rounded chins that are prominent, while the Thai exhibit blunt or vertical chins that are square or bilobate. The ascending rami in the Japanese individuals are typically wide, while the rami in Thai are typically pinched. Lastly, mylohyoid bridging is seen more frequently in the Thai individuals.

Like the differences seen in the nasal region, the differences in mandibular morphology between the Japanese and Thai individuals are subtle. However, because the mandible is sensitive to biomechanical loading, the differences observed between the two groups may be related to differences in mastication (Coqueugniot and Minugh-Purvis 2003; Mays 2015; Paschetta *et al.* 2010; Weijs 1989). During mastication, the mandible acts as a lever, and is subjected to shearing, bending, and torsional forces (Weijs 1989). The alveolus, tempero-mandibular joint, and muscle attachment sites, including the zygomatic arch, malar, and gonial angle, bear the brunt of the stresses. Sites of bony reinforcement include the symphysis, condylar neck, and gonial angle. Generally, individuals with larger mastication muscle volume more often exhibit concomitant bony responses at the landmarks where they attach (Kita *et al*. 2002). The medial gonial angle serves as an insertion point for the medial pterygoid muscle, which originates from the pterygoid fossa and process of the sphenoid (Moore *et al.* 2014). As the medial pterygoid muscle is involved in the elevation, protrusion, and lateral excursion of the mandible, the marked gonial muscle attachment ridging and slight to extreme posterior ramus inversion observed in the Thai individuals may indicate increased masticatory stress compared to the Japanese.

Additionally, while mandibular tori have been attributed to bruxism, genetic factors, and biomechanical stress (Hassett 2006; Ossenberg 1978), the relatively high occurrence in Thai individuals (42.5%) versus the Japanese individuals (26.0%) positively co-varies with the gonial muscle attachment ridging (rho = 0.110; p = 0.001), suggesting they may be related to masticatory stress. Hassett (2006) found that the expression of mandibular tori is correlated with dental attrition, and therefore argues that mandibular tori are not solely the product of genetic inheritance. Instead, she posits that mandibular tori, like many of nonmetric cranial traits used in biogeographic ancestry assessment, are threshold (i.e., epigenetic) traits that have a genetic basis, but their expression is also regulated by environmental factors. Mann and Hunt (2005) attribute mandibular tori to developmental anomalies arising from the cortical plate, which increase in size with advancing age.

If indeed the Thai experienced increased and/or different masticatory stresses compared to the Japanese, these stresses may have also affected the architecture of the dental arcade, maxilla, malar, occlusion, maxillary incisor orientation, transverse palatine suture, and other features of the mandible (i.e., mandibular border, chin projection and shape, and ascending ramus shape). However, because this study did not examine familial inheritance and biodistance, or include dental morphology or metrics, genetic inheritance cannot be ruled out as a possible contributing factor for many of these traits.

While some trait expressions of the cranium may reflect adaptive responses (e.g., nasal region) and biomechanical stresses (e.g., mandible, maxilla, and dentition), others likely reflect purely genetic inheritance. For instance, the presence of mylohyoid bridging is generally argued to be the result of familial inheritance, and has been used extensively in biodistance and population studies (Jidoi *et al.* 2000; Sawyer and Kiely 1987; Turan-Ozdemir and Sendemir 2006). However, the etiologies of other traits are more ambiguous. Namely, suture complexity has been attributed to growth and development, mastication stresses, sex, stature, and genetics (Rao *et al.* 2009). Mann *et al.* (2015) found that suture complexity statistically significantly varies between populations. In particular, American White individuals display more complex sutures than American Black, Japanese, and Thai individuals. Additionally, wormian bones are often considered to be normal variants that indicate genetic inheritance (Hauser and DeStefano 1989); however, they are also associated with skeletal dysplasia, including osteogenesis imperfect (Cremin *et al.* 1982; Selmer *et al.* 2010). Other features, such as orbit shape and mental eminence shape, have been used as indicators for sex and ancestry (Rhine 1990; Rogers 2005; White *et al.* 2005).

The exact etiology of many of the cranial and mandibular traits is unknown and beyond the purview of this study; however, the results presented here indicate that nonmetric traits can be used within a statistical framework to differentiate between Japanese and Thai individuals. The ancestral differences can be attributed the unique population histories of Japan and Thailand. The results also demonstrate that certain traits perform better than others in differentiating the two groups. Where traditional biological distance and population studies mainly rely on traits that are believed to reflect genetics, the forensic anthropological assessment of biogeographic ancestry can incorporate traits that are also the result of adaptation and biomechanical stresses (Gonzalez-Jose *et al.* 2005). This is because the aims of the two approaches are inherently different. Biodistance studies examine if and to what degree populations are related by using nonmetric traits to approximate genetic data. Conversely, the forensic approach seeks to identify what population an individual is most similar to by using consistencies in morphometric variables. In fact, Pink (2015) demonstrated that multiple models incorporating the nonmetric traits regularly used in biological distance studies correctly identified the ancestry of modern individuals from the Terry collection in just over 50% to approximately 80% of individuals. The present study demonstrates that the inclusion of possibly adaptive and biomechanically mediated traits can improve classification rates (in excess of 80%) for certain groups. While populations with similar environmental or biomechanical stresses may show similar trait expressions and therefore complicate ancestry assessment (Gonzales-Jose *et al.* 2005), the use of multiple traits within statistical models that were developed from large datasets is key in mitigating this issue.

Differences Between the Japanese/Thai and Native American Individuals

Hypothesis 4 states that differences in the nonmetric expression of cranial traits exist between the Japanese/Thai individuals and Native American individuals such that the traits used to identify pre-contact Native Americans will not accurately classify contemporary Japanese/Thai individuals. While the Japanese and Thai do share some morphological similarities with the Native Americans, the results presented in Chapter V largely support the hypotheses that the modern Asian individuals are different from pre-contact Native American individuals. Additionally, as this study demonstrates that there are detectable morphological differences between the Japanese and Thai – two groups who are presumably more closely related than either are to the Native Americans – it is not surprising that differences exist between the Japanese/Thai and Native Americans.

Rhine's (1990) Southwestern Mongoloid trait list and skull diagram have come to represent the traits that should be present in Native American and Asian groups within the field of forensic anthropology, despite his statement that "this sample represents only a small fragment of the continuum of variability which makes up the Mongoloid group" (13). However, in using the term "Mongoloid", Rhine categorizes Asian and Native Americans under the same broad population group, which implicitly states that despite intra-population variation the two are expectedly and relatively similar. The use of Rhine's trait list and diagram is problematic, even when identifying Native American individuals, because they are based on frequencies obtained from a meager sample size. Rhine relies on only three modern and nine pre-contact male Native American skulls to establish the trait frequencies, in addition to 53 Anglo females and males, 15 Hispanic females and males, five Black males, and two Black male casts. Moreover, the Amerindian sample sizes for many of the cranial and mandibular frequencies he presents include only three individuals. Rhine fully concedes that the sample sizes are small, especially for Amerindians, and suggests that his study be viewed as a preliminary assessment of the traits that are often used in nonmetric ancestry assessment. However, in the immediate years following Rhine's (1990) publication, no thorough study emerged to replace or augment the preliminary results, and the trait lists presented therein became codified.

Though Rhine's (1990) trait descriptions are somewhat difficult to interpret and are not entirely consistent with Hefner's (2009) and Parr's (2005) terminology or scoring methods, many of the trait frequencies can be compared. Interestingly, discrepancies exist between what Rhine (1990) reports as being useful in his diagrams for identifying Southwestern Mongoloid individuals and the actual trait frequencies. Even though Rhine found discrepancies between the expected and actual frequencies for several traits, the diagrams and associated expected trait lists for American Caucasoid, American Black, and Southwestern Mongoloid came to represent the traits that should be present in the three groups, and have been used extensively in forensic casework.

While Native American nonmetric cranial data were not statistically analyzed in this study, the trait frequencies documented in the Japanese and Thai are significantly more variable than Rhine's Native American (1990) trait frequencies. This can be attributed to significantly different populations (Native Americans vs. East/Southeast Asians) used in the two studies with associated disparate population histories. Additionally, the present study's significantly larger sample size, which is 116 times larger than Rhine's, surely captures more variation in cranial and mandibular morphology. Further, the scoring criteria utilized in the present study, which is based on Hefner's (2009) and Parr's (2005) scoring procedures, is more nuanced and captures more variation compared to Rhine's scoring criteria, which is largely based on the presence or absence of traits. On the whole, the cranial frequencies observed among the Japanese and Thai are slightly more consistent with Hefner's (2009) Asian cranial trait frequencies than Rhine's Native American frequencies. However, Hefner's Asian sample is composed of only 15 contemporary Japanese individuals and 59 19th century Chinese individuals. Again, the significantly larger sample size of the present study, which is approximately 24 times larger than Hefner's, likely captures more cranial nonmetric variation.

In general, the Japanese and Thai do show some consistencies with Rhine's (1990) Native American cranial frequencies, though due to his small sample size these similarities should be cautiously interpreted. Namely, the Japanese and Thai share with Native Americans inferior nasal apertures that lack a distinct ridge or sill (referred to as blurring by Rhine); malar tubercles, though the Japanese and Thai show higher frequencies; an absence of postbregmatic depressions; the presence of wormian bones; high frequencies of zygomatic posterior tubercles; wide and smoothly curving dental arcade shapes (referred to as elliptic by Rhine); blunt chins (referred to as vertical by Rhine) that are rounded; and wide ascending mandibular rami.

Conversely, the Japanese and Thai differ from Native Americans in several key traits. Rhine (1990) lists a small nasal spine as a Native American trait (66.7%), though 58.1% of Japanese and 75.1% of Thai have moderate to large nasal spines. Native Americans supposedly display nasal openings that are flared at the base (wide); however, 69.8% of Japanese and 59.7% of Thai have narrow or medium nasal aperture widths. Rhine lists tented nasals that are wide and slightly concave as a Native American trait (66.7%), though only 1.3% of Japanese and 3.4% of Thai display tented nasals. Rhine found that 100% (n=2) of his Native American sample exhibits moderate prognathism. While 64.8% of Japanese display moderate to significant prognathism, 71.2% of Thai lack prognathism. Rhine lists a straight mandibular border as a Native American trait (66.7%), which is consistent with the Thai (64.5%), but different from the Japanese (27.0%). Rhine lists a vertical ascending mandibular ramus profile as a Native American trait (66.7%), though only 35.3% of Japanese and 49.0% of Thai have vertical (straight) profiles.

The Japanese and Thai also differ from Native Americans for the traits in which Rhine (1990) presents contradictory information. Despite 100% of Rhine’s Native American sample lacking nasal overgrowth, Rhine lists nasal overgrowth as a Native American trait. The Japanese (73.2%) and Thai (61.0%) generally lack nasal overgrowth. Though 50% of his Native Americans exhibit straight palatine sutures and 50% show (anterior) bulging palatine sutures, Rhine lists straight palatine sutures as a Native American trait. While the majority of Japanese (62.1%) have straight palatine sutures, only 28.3% of Thai exhibit straight sutures. Also peculiar, Rhine lists sagittal keeling as a Native American trait, though 100% of his sample lacks keeling. The Japanese lack keeling 55.6% of the time, while the Thai lack keeling 71.0% of the time. Though Rhine's three Native American individuals show rounded, rectangular, and sloping orbit shapes in equal proportions, he lists rounded orbits as a Native American trait. The Japanese exhibit rectangular or rhombic orbits 49.8% of the time, while the Thai exhibit rectangular or rhombic orbits 58.3% of the time. Two Native American individuals (66.7%) show retreating zygomatics, and one individual (33.3%) shows projecting zygomatics, though Rhine lists projecting zygomatics as a Native American trait. Only 26.6% of Japanese and 12.5% of Thai display projecting zygomatics. Complex sutures are also listed as a Native American trait, though 66.7% of his sample exhibits simple cranial sutures. Only 25.2% of the Japanese and 22.9% of the Thai exhibit complex cranial sutures. Lastly, Rhine lists gonial eversion as a Native American trait; however, he found that one individual exhibited an everted gonial angle and the other individual exhibited a straight gonial angle. The Japanese display everted gonial angles most frequently (56.4%), though the Thai display eversion somewhat less (43.2%).

Hefner's (2009) Native American sample includes significantly more individuals (n = 220 – 262) compared to Rhine's (1990) sample (n = 12 at the most), allowing for more appropriate trait frequency comparisons with the Japanese and Thai individuals in the current study. In so doing, divergent frequencies are evident between the Japanese/Thai and the Native Americans for the majority of traits. In fact, the Japanese/Thai and Native Americans display somewhat similar frequencies for only two traits. The Native American and Thai samples share similar rates of nasal overgrowth (Native American = 55.9%; Thai = 61.0%) compared to the Japanese (26.6%). Additionally, the Native American (92.9%), Japanese (85.1%), and Thai (89.1%) individuals generally lack postbregmatic depressions.

The Japanese and Thai individuals differ in frequencies from Hefner's (2009) Native American individuals in the nasal and malar regions. Hefner's (2009) Native American sample exhibited smaller nasal spines (67.9%) compared to the Japanese (48.2%) and Thai (28.5%) samples. The Native Americans displayed less silled inferior nasal apertures (0.4%) compared to the Japanese (9.6%) and Thai (6.1%) individuals, while Native Americans more frequently displayed right-angled inferior nasal apertures (56.9%) compared to the Japanese (44.6%) and Thai (42.5%) individuals. Native Americans also exhibited markedly narrower interorbital breadths (59.2%) compared to the Japanese (13.1%) and Thai (12.9%). The Native Americans more frequently lacked a malar tubercle (40.8%) compared to the Japanese (10.4%) and Thai (7.2%). Native American individuals also displayed significantly lower frequencies of wide nasal apertures (13.7%) compared to the Japanese (30.2%) and Thai (40.3%) individuals. Only 11.5% of Native Americans exhibit low and rounded nasal bones compared to the Japanese and Thai, with frequencies of 41.1% and 65.5%, respectively. Additionally, the Native Americans displayed higher frequencies of nasal bones that are steep and broad (24.8%) or steep and narrow (34.4%) compared to the Japanese (steep and broad = 1.4%; steep and narrow = 5.0%) and Thai (steep and broad = 0.7%; steep and narrow = 1.4%). Native Americans displayed higher frequencies of open supranasal sutures (31.3%) compared to the Japanese (11.2%) and Thai (4.2%). Lastly, Native Americans exhibited low frequencies of zygomaticomaxillary sutures that lack angles and the greatest lateral extent is at the inferior margin of the malar (2.9%) compared to the Japanese (74.8%) and Thai (56.9%). The Native American individuals exhibited significantly higher frequencies of zygomaticomaxillary sutures with two ore more angles (52.6%) compared to the Japanese (7.6%) and Thai (1.2%).

Based on the cranial trait frequencies, it is clear that the Japanese and Thai are different from the limited data on Native Americans, wherein the application of Native American cranial trait frequencies and expectations may misclassify Asian individuals or confound biogeographic ancestry analyses. The inability of methods developed on Native American individuals to accurately classify Asian individuals is similarly echoed in postcranial methods. Tallman and Winburn (2015) and Tallman (2015) found that the femur subtrochanteric sectioning points established on Native Americans to differentiate Native Americans/Asians from non-Asians misclassified significant numbers of Chiba Japanese and Khon Kaen Thai individuals because these two Asian groups are less platymeric than Native Americans (Gill and Rhine 1990; Wescott 2005). As such, they propose amended platymeric index ranges and anterior-posterior/medial-lateral sectioning points to better classify Asian individuals. The growing body of data emerging on the differences between Asian populations and Native Americans strongly indicates that forensic anthropologists should develop and apply population-specific methods for numerous Asian populations rather than rely on those derived from Native American data.

The cranial and mandibular differences between Asian populations, including Japanese and Thai individuals, and Native Americans are due to significantly different population histories. The ancestors of Native Americans began migrating from Asia into North America by at least 15,000 years ago, if not earlier (Brace *et al.* 2001; Gonzalez *et al.* 2008; Reich *et al.* 2012). While the exact number, timing, and route of the migrations are heavily debated, at least two major migratory events occurred (Brace *et al.* 2001; Goebel *et al.* 2008; Gonzalez *et al.* 2008; Reich *et al.* 2012; Szathmary and Ossenberg 1979). Because the major entry route into North America required that populations live for generations in Siberia and Beringia, the populations entering North America were cold adapted (Hall *et al.* 2004). East and Southeast Asia never experienced the cold temperature extremes characteristic of Beringia. Subsequently, as global temperatures warmed and the North American inhabitants moved south, cold adaptation became less important over time. Additionally, sea levels rose significantly at the end of the Last Glacial Maximum around 12,000 years ago, which submerged Beringia and effectively isolated the populations living in North, Central, and South America (Brace *et al.* 2001). Thus, Old World Asian populations and New World Asian-derived populations have undergone separate population histories for thousands of years with no gene flow between the two continents. Therefore, the grouping of Native Americans and Asians into one broad ancestral category, and the use of Native Americans as biological proxies for modern Asian individuals, are fundamentally flawed at best and scientifically invalid at worst.

Factors Affecting the Expression of Nonmetric Traits

Age and sex affects

The large sample size with known ages of 17 to 96 years in this study presents a perfect opportunity to examine how age affects the expression of nonmetric traits. Numerous cranial and mandibular traits that show Spearman's rho correlations between trait score and age failed to show statistically significant differences in ranked mean trait scores for the seven age groups when using Kruskal-Wallis analyses. This is because the two statistical tests are calculated entirely differently and have different assumptions. A Spearman's correlation is a non-parametric assessment of statistical dependence between two ranked variables, and it assumes a monotonic relationship between the two variables (Field 2009). That is, as one value increases, the other value will either increase or decrease. As such, it assesses the overall trend in the relationship of the two variables. Conversely, Kruskal-Wallis analyses differences and variation in ranked mean or median scores between more than two groups, which is similar to a Mann-Whitney *U* test (Field 2009). While the Kruskal-Wallis test does not assume normality of data, it does assume homoscedasticity. If ranked differences are found, pairwise *post-hoc* tests are useful at identifying where the differences are and how they change from group to group. Accordingly, Kruskal-Wallis tests and their associated *post-hoc* tests are useful at pinpointing where differences occur in the relationship, which can, for example, identify how traits change between the age groups.

As the results in Chapter V indicate, age minimally affects the expression of sexually dimorphic cranial and pelvic traits. However, age and nuchal crest scores are correlated in Japanese and Thai males. Nuchal crests become increasingly better defined and larger with advancing age from 17 years to approximately 50 years. Subsequently, the nuchal crests become more gracile from approximately 50 years to approximately 80 years. The nuchal region serves as an origin for multiple large neck and back muscles, including occipitalis, splenius capitis, trapezius, and sternocleidomastoid (Moore *et al.* 2014). Increased muscle development and activity with advancing age may produce robust nuchal lines at muscle attachment sites. Conversely, as individuals age, testosterone decreases, which can result in decreased muscle mass (Moore *et al.* 2014). Over time, the muscle attachment sites may diminish and the male skeleton can become more gracile. Interestingly, this trend was not seen with the mastoid process, a muscle attachment site for splenius capitis, longissimus capitis, posterior belly of digastric, and sternocleidomastoid (Moore *et al.* 2014). However, Garvin *et al.* (2014) also found that age did not influence the mastoid process in African, Native American, U.S. Black, and U.S. White individuals.

Concerning the sexually dimorphic pelvic traits, the ischiopubic ramus ridge is correlated with age in Thai males. In particular, the ridge becomes broadened and more robust with advancing age from 17 years to approximately 40 years of age. The ischiopubic ramus ridge serves as an attachment site for the obturator internus posteriorly, and the adductor magnus, adductor brevis, and gracilis anteriorly (Moore *et al.* 2014). As such, increased muscle mass or activity between 17 and 40 years of age could account for the more robust rami observed in older Thai males.

Interestingly, the sciatic notch is correlated with age in Japanese and Thai males. The sciatic notch is wider in younger individuals, and becomes increasingly constricted from approximately 17 years to 60 years. The increasing constriction seen in sciatic notch morphology of Japanese and Thai males with advancing age is consistent with Walker's (2005) findings that younger Americans of African and European ancestry and English-born individuals under 50 years of age exhibit wider sciatic notches than older individuals. Walker observed this trend in females and males; however, the trend was stronger in males. Additionally, this trend was also stronger in 19th century English-born individuals compared to modern Americans of African and European ancestry, who were much more similar to each other than to the English-born individuals. This led Walker to conclude that an environmental disturbance, such as rickets or osteomalacia, which were common in 18th and 19th century England, may have weakened the pelvis, making it more susceptible to biomechanical forces generated from walking and supporting the body. While it is highly unlikely that the Japanese and Thai individuals experienced significant vitamin-D deficiency, it is possible that sciatic constriction is a product of the biomechanical stresses associated with bipedal walking. However, this trend was not observed in Japanese or Thai females, suggesting that female pelves may be less susceptible to the stresses.

While there seems to be a correlation between the expression of a rhomboid fossa and age for Japanese females and Thai males, the nature of the correlations are ambiguous. The Thai males 40-49 years old show higher rhomboid fossa scores than males 70-79 years old. Conversely, the Japanese females 40-49 years of age show lower rhomboid fossa scores than females 70-79 years old; however, the 0-5 rhomboid fossa scoring system is not ordinal and oriented from least to greatest, or greatest to least. Rather, the system is more categorical, whereby scores of 1 and 2 indicate small and large fossae, 3 and 4 indicate small and large grooved fossae, and 5 indicates pitting or porosity following Rogers *et al*. (2000). While Rogers *et al*. (2000) found that the largest fossae were more likely to be observed in younger individuals, no research has demonstrated how rhomboid fossae develop and change with advancing age. Additionally, Singh and Singh (2009) found that rhomboid fossae were more likely to occur in modern Indian individuals who were 30 years of age or older rather than younger individuals. The infero-medial clavicle serves an attachment site for the costoclavicular (rhomboid) ligament, which anchors the clavicle to the first rib (Moore *et al.* 2014). Presumably, increased activity and muscle mass may create a depression at the site of the ligament attachment (Rogers *et al*. 2000).

Like any muscle or ligament attachment site, it may be affected by age due to increasing muscle mass, activity patterns, or decreasing muscle mass and activity.

An interesting association between age and angle of the medial epicondyle was seen in Thai males. Specifically, males 30-49 years old have higher medial epicondyle angle scores that are more “female-like” compared to older individuals that are more “male-like.” Thus, younger individuals have more posteriorly oriented medial epicondyles, which become more flattened with advancing age. The medial epicondyle serves as an attachment site for the ulnar collateral ligament, pronator teres, and the common flexor tendon for flexor carpi radialis, flexor carpi ulnaris, flexor digitorum superficialis, and palmaris longus (Moore *et al.* 2014). As the flexors are on the anterior forearm and biomechanical forces associated with flexing would be focused proximally on the medial epicondyle, over time biomechanical forces may be pulling the medial epicondyle anteriorly in males, which would present as a more flattened epicondyle.

While somewhat minimal, the correlation of age and the expression of sexually dimorphic cranial, pelvic, clavicular, and humeral traits has important implications for sex determination. Walker (1995) has previously documented that age-related changes occur with most of the sexually dimorphic cranial traits in over 300 modern American and English females and males; however, the changes are most pronounced in the supraorbital ridge/glabella. In particular, he found that younger males showed less developed ridges compared to older individuals. Because the sexually dimorphic cranial traits develop until approximately 30 years of age, the crania of males under 30 may appear more gracile, which can skew demographic profiles (Walker 1995). Conversely, female crania generally become more robust in individuals over 45 years, thus resulting in older females being classified as male. Therefore, age-related changes of sexually dimorphic traits can increase or decrease the sexual dimorphism and sex bias documented from skeletal remains, and lead to misclassifications in forensic and bioarchaeological contexts.

The results of this study also suggest that population differences may exist in the way in which age affects the sexually dimorphic traits. Walker (1995) found that the supraorbital ridge/glabella is the trait that is most affected by age in modern English and American individuals. No age-related changes were found in the supraorbital ridge/glabella of the Japanese or Thai individuals. In fact, this trait is very gracile in both females and males, whereby a score of 1 indicates female with a 0.77 pooled probability, and a score of 2 indicates male with a 0.89 pooled probability. However, it appears that the nuchal crest is the trait most affected by age in Japanese and Thai males. While the nuchal crest is the least reliable indicator of sex in Japanese and Thai individuals, younger individuals may show more gracile nuchal crests and could be classified as female, especially with small glabellae.

The finding that age is correlated with some sexually dimorphic traits is consistent with other studies (Garvin *et al.* 2014; Walker 1995, 2005, 2008). In particular, Garvin *et al.* (2014) found that age-related changes occurred with most sexually dimorphic cranial traits in African, Native American, U.S. Black, and U.S. White individuals. However, the correlated changes were not particularly pronounced, and the inclusion of age into logistic regression models failed to improve their classification results. Accordingly, Garvin *et al*. (2014) concluded that age, along with body size parameters, do not need to be included in sex estimation models for these four ancestral groups. Similarly, the inclusion of age into Japanese and Thai logistic regression equations and CHAID decision trees did not prove useful in differentiating between females and males.

Many of the cranial and mandibular traits analyzed in this study for the purpose of potential biogeographic ancestry assessment are also influenced by sex and age-related changes. As these traits are largely assumed to be the product of genetics and/or adaptation, they are often assumed to be free of sex or age influences (Cosseddu *et al.* 1979; Perizonius 1979). In fact, Hefner's (2009, 2014) research into cranial nonmetric variability of African, American Indian, Asian, and European individuals did not include correlation analyses of sex or age, and as such, cranial trait expressions were not considered to be affected by these important factors. Additionally, Cosseddu *et al.* (1979) found that sex only minimally affects the expression of the 33 epigenetic traits analyzed in their Sardinian sample. However, 43.2% of the cranial and mandibular traits are influenced by sex for the Japanese individuals, while 51.4% are influenced by sex for the Thai individuals. Similarly, 49.5% of the traits are correlated with age for the Japanese, and 23.4% are correlated with age for the Thai. Like the sexually dimorphic traits, the influence of sex and age can impact biogeographic assessments by increasing bias.

The mandibular traits seem to be more affected by age-related changes compared to the cranial traits, and the Japanese show more age-related changes than the Thai. However, younger Japanese individuals (17-39 years) had narrower nasal apertures compared to older individuals (70-79 years). Additionally, Thai individuals who were 40-49 years old were more prognathic than individuals who were 70-79 years old. As Japanese individuals age, the mandibular border straightens, inversion and eversion decrease, mandibular tori and gonial muscle attachment ridging increase, mandibular rami become more pinched, and the mandibular profile becomes more acute.

While age did not improve sex estimation correct classification rates when included in statistical models for the Japanese and Thai, age – and sex to a lesser extent – improved biogeographic ancestry correct classification rates when added to the logistic regression models. In particular, age improved classification rates when using cranial, mandibular, and combined cranial and mandibular traits to differentiate the two groups. The addition of sex improved logistic regression models using mandibular traits. As such, age should be considered when estimating the biogeographic ancestry of skeletonized remains, by incorporating age into statistical models. Further, if the mandible is going to be used extensively in biogeographic ancestry assessments, sex should be included in statistical models.

Secular change

Overall, Japanese males exhibit more traits that have changed over time compared to females. In particular, the cranium has become more gracile over time for all male traits, while only the nuchal crest has become more gracile in females. Conversely, the male sciatic notch and ventral arc have become more "male-like" over time. However, as previously discussed, age affects the expression of many traits. Namely, the sciatic notch becomes more constricted with advancing age in males. The mean age for the historic CU males (n = 147) is 45.4 years, and the mean age for the modern JU males (n = 408) is 52.9 years, which are significantly different (p = 0.000) based on the independent sample t-test. Accordingly, the increasing sciatic notch constriction may be an artifact of age-related change in the modern Japanese sample, rather than resulting from secular change. Similarly, the nuchal crest becomes more gracile in males over 50 years, and this may be confounding the secular change trend. Lastly, the differences seen in mandibular morphology between the historic and modern samples may also be attributable to age. Mandibular ramus inversion decreases and the ascending ramus becomes more pinched over time in females and males. However, ramus inversion decreases and ascending rami become more pinched with advancing age. Therefore, the older JU males may be driving this trend. However, the mean age for the historic CU females ($n = 58$) is 51.6 years, and the mean age for the modern JU females ($n = 157$) is 50.8 years, which are not significantly different ($p = 0.772$). Therefore, the differences observed in the female mandible may be due to secular change. However, the relatively small sample size for the CU collection, and particularly the females, may be contributing to the historic-modern differences due to sampling error.

The issue of secular change is important because the inclusion of historic samples in biological profile method development can produce biased results when those methods are applied to modern individuals in forensic contexts (Dirkmaat *et al.* 2008). Numerous studies have documented secular change in cranial morphology, limb proportions, and stature (Jantz 2001; Jantz and Meadows Jantz 2000; Meadows and Jantz 1995; Meadows Jantz and Jantz 1999; Ousley and Jantz 2005). While an efficient way to assess the presence of secular change involves regressing the nonmetric variables on birth year (see Jantz 2001; Jantz and Meadows Jantz 2000), the birth and death years were unknown for the Japanese sample. Despite this, significant differences were found between the historic and modern samples, indicating that secular change has likely occurred. Klales (2016) similarly documented secular change in the Phenice (1969) traits using the Hamman-Todd (historic) and William M. Bass Donated (modern) collections, whereby gracilization occurred over time in females for all traits and in males for the subpubic concavity and ventral arc. Despite the presence of secular change, Klales (2016) argues that the Klales *et al.* (2012) method for the Phenice traits, which incorporated historic samples, works well in correctly classifying modern individuals. Thus, according to Klales (2016), secular change does not significantly impact logistic regression classifications, and historic skeletal collections, such as Hamman-Todd, are still relevant in biological profile method development.

Inter-trait correlations

The sexually dimorphic traits of the cranium, pelvis, clavicle, and humerus are mostly moderately correlated, indicating that changes in one trait within a region are associated with changes to the other traits within that region. The pelvic traits are most correlated, with rho values from 0.481 (ventral arc and sciatic notch) to 0.938 (subpubic concavity and ischiopubic ramus ridge); followed by the left and right rhomboid fossa (0.446); cranial traits with rho values from 0.125 (nuchal crest and mental eminence) to 0.446 (glabella and mastoid process); and lastly the humeral traits with rho values of 0.091 (trochlear extension and trochlear constriction) to 0.329 (medial epicondyle angle and trochlear extension). The cranial correlations observed here are consistent with Garvin *et al.*'s (2014) rho range of 0.16 – 0.41; however, they found that the glabella and supraorbital margin are most correlated.

Though less correlated than the sexually dimorphic traits, the cranial and mandibular traits also show minimal-moderate correlations. In particular, nasal aperture shape and nasal aperture width are strongly correlated (rho = 0.404), as are suture complexity and wormian bones (rho = 0.267) and maxillary incisor orientation and occlusion (rho = 0.438). Interesting correlations are seen between gonial muscle attachment ridging and occlusion (rho = -0.217) and gonial muscle attachment ridging and maxillary incisor orientation (rho = -0.216). It appears that when gonial muscle attachment ridging increases, alveolar prognathism decreases and occlusion improves.

The nonmetric correlations documented in the present study indicate that the traits should not be viewed as independent variables existing in isolation (Hauser and DeStefano 1989; Key and Jantz 1990). Because of the inter-trait correlations, sex and biogeographic ancestry assessment methods that incorporate multiple traits will likely work better than methods that rely on a couple of traits. This is particularly true for the traits used in biogeographic ancestry assessment – many of which work well together to classify individuals, but have traditionally been viewed as independently functioning variables (Bass 1995; Gill 1998; Rhine 1990). This is echoed by Relethford (2009) who, after analyzing the Howells dataset, concluded that classification accuracies will be high as long as geographical distances between clusters or populations is greater than within populations, and if many traits are used. It is not surprising that many cranial traits are correlated, as the cranium is one of the most integrated structures within the human body (Cheverud 1982; Hallgrímsson *et al.* 2007; Hauser and DeStefano 1989; Liebermann *et al.* 2000). Therefore, the sexually dimorphic and biogeographic ancestral traits should be viewed holistically, as the traits often interact with each other, as well as with other variables such as age, sex, population, environment, activity patterns, and secular change.

Intraobserver error in nonmetric traits

The cranial, pelvic, and rhomboid fossa intraobserver error rates ranged from moderate to almost perfect, indicating that the standardized scoring methods following Hefner (2009, 2012), Buikstra and Ubelaker (1994), and Rogers *et al.* (2000) are adequate at producing reliable agreement from the same observer on two occasions. Similar to Stevenson *et al*. (2009), Walker (2008), and Williams and Rogers (2006), this study found that of the cranial traits, the glabella performed the best in intraobserver error assessment. The present study found that the mental eminence performed the worst in agreement (moderate). Conversely, Garvin *et al.* (2014) found that the mastoid process performed the best, while the nuchal crest performed the worst in intraobserver error tests. Assessing the mental eminence requires observation and palpation following Buikstra and Ubelaker (1994); however, the scoring method (small to massive projection) fails to accommodate the range of variation seen in Japanese and Thai mental eminence morphology. Likewise, Williams and Rogers (2006) found that of the Walker (2008) cranial traits analyzed, the mental eminence performed the worst. The results of the intraobserver error analysis indicate that the cranial traits are not equal in their reliability. As such, Garvin *et al.* (2014) recommend weighing more heavily the traits that have high levels of agreement, such as glabella.

The pelvic traits agree moderately to almost perfectly, with the three Phenice (1969) traits being in almost perfect agreement. The results of this analysis indicate that the Phenice traits are particularly reliable. In comparison, Klales *et al.* (2012) found that the three Phenice traits were in moderate to substantial agreement when intraobserver error was assessed on their mixed ancestry sample. The different levels of agreement in the Phenice traits between Klales *et al.*

(2012) and the present study may be due to the expanded ordinal scoring system (5 scores) developed and employed by Klales and coauthors. In fact, all of the sexually dimorphic traits in which more than 3 ordinal scores are used produced lower levels of intraobserver agreement in the present study. Therefore, while the addition of ordinal scores may better capture nonmetric variability, they allow for more intra- and interobserver error. This is echoed by Walker (2005), who found that sciatic notch scores with extreme female (1) or male (5) morphologies exhibited lower intraobserver error rates compared to those with more intermediate morphologies (2-4). Overall, Walker's (2005) intraobserver error rates for the sciatic notch ranged from k = 0.22 to k = 1.00, while the level in agreement in the present study is k = 0.640. Additionally, Rogers and Saunders (1994) found that the preauricular sulcus and ischiopubic ramus shape were the most problematic, while the ventral arc was very reliable.

The rhomboid fossa agrees almost perfectly, while the distal humerus traits achieve only a fair to moderate level of agreement. This suggests that the standardized scoring methods proposed by Vance *et al.* (2011) are not particularly reliable. As the PI had difficulty in assessing the olecranon fossa shape (rounded versus triangular) in the Japanese and Thai individuals, it is surprising that of the four humeral traits the olecranon fossa shape performed the best (k = 0.433; moderate). Further, the difficulty in scoring the olecranon fossa is particularly noteworthy because Rogers (1999, 2006) advocates for its use when the other humeral traits are equivocal. Additionally, the differences between females and males in distal humerus morphology as presented in Vance *et al.*'s (2011) diagrams (see Figure 4.6) are rather slight and often challenging to identify. Therefore, the use of the distal humerus sex assessment method should be limited to cases where other more sexually diagnostic indicators are absent, or where other sexually dimorphic regions are ambiguous.

The cranial and mandibular traits exhibited slight to perfect agreement; however, the majority of the traits agreed moderately to substantially. The present study displayed less agreement compared to Hefner's (2009) in the scoring of his 11 traits. Hefner found that the 11 traits produced intraobserver agreement rates from k = 0.422 to k = 1.00, while the present study had intraobserver agreement from k = 0.474 to k = 0.820. Hefner found that the anterior nasal spine produced the most error (k = 0.422), which he attributed to the difficulty in assessing the length of the spine relative to the face. The present study achieved a substantial level of agreement (k = 0.768) with the anterior nasal spine, but a moderate level of agreement (k = 0.474) for the inferior nasal aperture. Conversely, Hefner achieved an almost perfect level of agreement (k = 0.964) for the inferior nasal aperture. This feature has five ordinal scores, and while the extremes are easy to identify, the intermediate morphologies are more vague. The two traits used exclusively in this study performed well in the intraobserver analysis. Maxillary incisor orientation agreed substantially (k = 0.702), while occlusion agreed almost perfectly (k = 0.896). While they were relatively infrequent in the Japanese and Thai due to the antemortem and postmortem absence of incisors, these traits are ultimately reliable. Additionally, occlusion and maxillary incisor orientation performed well in differentiating the Japanese and Thai, further highlighting the usefulness of these traits in ancestry assessment. The location of posterior ramus inversion produced the most error (k = 0.158) because the location of gonial inversion was usually intermediate and difficult to assess. Lastly, suture complexity performed only fairly (k =

0.373) in intraobserver error analysis, likely due to the subjective assessment of rating simplicity to complexity.

CHAPTER VII: Conclusions

The purpose of this study was to statistically test and refine the cranial and postcranial nonmetric sex assessment methods developed from individuals of African and European descent on documented Japanese and Thai individuals, and to determine if the nonmetric cranial trait expressions and frequencies useful in identifying Native Americans are present and useful in identifying and distinguishing Japanese and Thai individuals. This study contributes valuable information to the field of anthropology by providing important and much needed data and associated statistical analyses on nonmetric skeletal variation for two understudied Asian populations representing East and Southeast Asia. Further, the results highlighted four broad findings concerning Japanese and Thai nonmetric trait variability: 1) Population-specific sex assessment methods perform better in classifying Japanese and Thai individuals than those developed on non-Asian populations; 2) Differences exist in the expression of nonmetric traits between the Japanese and Thai such that they can be differentiated from one another; 3) The Japanese and Thai differ from Native Americans in the expression of nonmetric traits due to unique population histories; and 4) Many nonmetric traits are affected by sex, age, intraobserver error, inter-trait correlations, and population, and exhibit secular change, thereby complicating their use in biological profiles.

The results involving the 15 sexually dimorphic cranial and postcranial traits indicate that differences in the nonmetric expression of sexual dimorphism do indeed exist between the Japanese/Thai and non-Asian groups, such that the sex assessment methods developed on individuals of African, European and Native American descent do not accurately classify

Japanese or Thai individuals. Further, in testing and refining the nonmetric sex assessment methods, it became clear that differences in the nonmetric expression of sexual dimorphism exist between Japanese and Thai individuals. While the differences are most pronounced in the clavicle and humerus, the differences are not particularly significant for the cranium or pelvis. As such, both population-specific and pooled sex assessment methods were established for the cranium, pelvis, clavicle, and humerus. Further, while age was correlated with many of the sexually dimorphic trait scores, it did not significantly impact statistical models developed to discriminate between females and males.

The results involving the 37 cranial and mandibular traits used for biogeographic ancestry assessment indicate that differences in the nonmetric trait expression and frequencies exist between Japanese and Thai individuals. As inter-group variation was observed, the Japanese and Thai are not homogenous, and cranial trait frequencies were maintained separately for the two groups. Additionally, sex and age influenced the expression of many of the cranial and mandibular traits, potentially complicating their use in forensic biogeographic ancestry assessments. Moreover, comparisons of the Japanese and Thai cranial trait frequencies to published data on Native Americans indicates that differences exist between Japanese/Thai and Native American individuals such that the traits used to identify pre-contact Native Americans may not accurately classify modern Japanese and Thai individuals. However, the Japanese and Thai do share some nonmetric cranial and mandibular traits with pre-contact Native Americans.

Perhaps most importantly, this study demonstrates that the use of pre-contact Native Americans, or any other non-Asian group, as biological proxies for modern Asians – particularly the Japanese and Thai – is largely unfounded, inaccurate, and simply bad science. As more

Asian-derived skeletal and anatomical collections become known and available to researchers, the onus is on anthropologists who occasionally or frequently encounter remains of possible Asian ancestry to develop specific research questions that can assist in their skeletal analyses and forensic casework. While Western researchers have only recently come to know about large Asian skeletal collections, the use of Native Americans as biological proxies for modern Asians is akin to using immediate descendants of Neolithic African or European populations as biological proxies for modern Americans. Clearly, modern anthropological perspectives would not be amenable to this notion.

The geographically and genetically disparate populations that are classified as Asian no doubt exhibit significant phenotypic skeletal variation. Some of this variation was observed in the present study within and between the Japanese and Thai samples. However, the sex assessment methods and cranial trait frequencies established in the present study for the Japanese and Thai may be useful in determining biological profiles for other Asian groups that are not yet represented by documented skeletal collections. Such refined methods for two disparate Asian populations can be cautiously applied to other Asian populations and subsequently refined as additional skeletal assemblages become available.

Nonmetric Traits and Daubert

The continued refinement of nonmetric sex and ancestry assessment methods is of utmost importance in the current judicial climate, which requires rigorous testing of scientific methods. Currently, the admissibility of scientific testimony in the court of law is dictated by the *Daubert* ruling of 1993, which requires methods used by expert witnesses to be empirically tested, peer reviewed, maintained by operation standards, accepted by the scientific community, and have known error rates (National Research Council 2009; U.S. Supreme Court 1993). Though the methods that provide a positive identification (i.e., antemortem-postmortem radiographic comparisons) or contribute to the cause and manner of death (i.e., trauma analysis) are the main focus of the *Daubert* ruling, all forensically significant methods including nonmetric assessments should be held to these standards. However, due to their historically subjective nature, which has traditionally relied on the observer's experience, many traditional nonmetric methods are not testable or falsifiable, and lack known error rates or probabilities, therefore failing to meet the *Daubert* criteria.

Despite their shortcomings, skeletal biologists still frequently employ nonmetric methods. This is partly attributable to the traditional anthropological training of skeletal biologists, which has historically emphasized the importance of morphology (Brues 1990). Additionally, nonmetric traits do not require specialized equipment, and are useful in determining biological profiles for fragmentary or incomplete remains (Gill 1998). Thus, the results of this study contribute to the larger movement in anthropology involving the development of more quantifiable, replicable, and accurate biological profile methods needed in the current judicial climate, which demands the employment of rigorously tested and scientifically accepted methods (Christensen 2006; Hefner 2009; Klales *et al.* 2012).

Specifically, the results of this study provide revised statistical methods, accuracy rates, and probabilities for the sex and biogeographic ancestry assessment methods needed to satisfy the *Daubert* criteria when dealing with Asian-derived remains in a forensic context. Establishing scientifically and judicially accepted methods for sex, age, ancestry, and stature estimation that are already used in forensic anthropology is an important first step. This is especially true for understudied populations, such as Asians groups, who currently represent the fastest growing ancestral demographic in the U.S. (Hoeffel *et al*. 2012).

Future Directions

As with any in-depth anthropological study, the findings and implications found here highlight several avenues of future research that could not be accommodated under the current study parameters. In particular, it is anticipated that future research will incorporate additional Asian populations as they become known and accessible. The incorporation of multiple Asian populations will allow for more in-depth studies of nonmetric variability within the broad classification of Asian, thereby demonstrating the diversity within this immense group. Likewise, Native American data will be incorporated in order to statistically test Asian and Native American similarities and differences and develop statistical models to distinguish the two broad groups. In particular, Ordinal Summed Scored Attributes (OSSA) represents a somewhat straightforward method to distinguish between Asian and Native American groups, in addition to Asian and Americans of African and European descent, which have yet been calculated (Hefner 2014). Future research would also benefit from the inclusion of metric and/or geometric morphometric data to further investigate population differences and assess the affects of age, sex, and other variables on the expression of nonmetric traits. Lastly, the incorporation of older samples with known birth dates will allow for an expanded time depth in order to explore how nonmetric traits – both in sexual dimorphism and in biogeographic ancestry assessment – change over time for Asian populations. At present, few studies have addressed how nonmetric traits are affected by secular change.

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APPENDICES

APPENDIX A: Rhine's (1990) useful traits, their scoring methods, and group membership associated with the traits.

Trait	Scoring method	Associated group (Rhine's terminology)
Keeling	Present	Southwestern Mongoloid
	Absent	
Postbregmatic depression	Present	American Black
	Absent	
Inion hook	Present	American Caucasoid
	Absent	
Longus capitis depression	Present	American Caucasoid
	Absent	
Base chord	Short	Southwestern Mongoloid
	Long	American Caucasoid; American Black
Base angle	High	Southwestern Mongoloid
	Low	American Black
Venous markings	Present	American Black
	Absent	
Major suture	Simple	American Caucasoid American Black
	Medium	
	Complex	Southwestern Mongoloid
Wormian bones	Present	Southwestern Mongoloid
	Absent	
Other ossicles	Present	Southwestern Mongoloid
	Absent	
Metopic trace	Present	American Caucasoid
	Absent	
Orbital shape	Rounded	Southwestern Mongoloid
	Rectangular	American Black
	Sloping	American Caucasoid
Nasal opening	Narrow	
	Medium	Southwestern Mongoloid
	Wide	American Black
Nasal depression	Deep	American Caucasoid
	Slight	Southwestern Mongoloid; American Black
	Straight	
Nasal form	Tower	American Caucasoid
	Tented	Southwestern Mongoloid
	Quonset	American Black
Nasal overgrowth	Present	Southwestern Mongoloid
	Absent	

Trait	**Scoring method**	**Associated group***
Nasal spine	Small	Southwestern Mongoloid; American Black
	Large	American Caucasoid
Nasal sill	Deep	American Caucasoid
	Shallow	
	Blurred	Southwestern Mongoloid
	Guttered	American Black
Zygomatic projection	Retreating	American Caucasoid
	Vertical	American Black
	Projecting	Southwestern Mongoloid
Malar tubercle	Present	Southwestern Mongoloid
	Absent	
Zygomatic posterior tubercle	Present	Southwestern Mongoloid
	Absent	
Canine fossa	Present	American Caucasoid
	Absent	
Prognathism	Moderate	American Black
	Slight	Southwestern Mongoloid
	None	American Caucasoid
Incisal shoveling	Double	
	Pronounced	Southwestern Mongoloid
	Medium	Southwestern Mongoloid
	Slight	Southwestern Mongoloid
	None	
Incisal rotation	Present	Southwestern Mongoloid
	Absent	
Enamel extensions	Present	Southwestern Mongoloid
	Absent	
Buccal pits	Present	Southwestern Mongoloid
	Absent	
Carabelli's cusps	Present	American Caucasoid
	Absent	
Molar crenulations	Present	American Black
	Absent	
Dental arcade shape	Parabolic	American Caucasoid
	Elliptic	Southwestern Mongoloid
	Hyperbolic	American Black
Shape of chin	Bilobate	American Caucasoid
	Blunt	Southwestern Mongoloid; American Black
	Pointed	
	Vertical	

Trait	Scoring method	Associated group*
Profile of chin	Vertical	Southwestern Mongoloid; American Black
	Prominent	American Caucasoid
Lower border of mandible	Straight	Southwestern Mongoloid; American Black
	Rocker	
	Undulating	American Caucasoid
Ascending ramus	Pinched	American Caucasoid; American Black
	Wide	Southwestern Mongoloid
Ascending ramus profile	Vertical	Southwestern Mongoloid
	Slanted	American Caucasoid; American Black
Gonial angle	Inverted	
	Straight	American Caucasoid; American Black
	Everted	Southwestern Mongoloid
External auditory meatus	Round	American Caucasoid; American Black
	Elliptic	Southwestern Mongoloid
Oval window visible	Present	American Caucasoid; American Black
	Absent	Southwestern Mongoloid
Inferior collar	Present	Southwestern Mongoloid
	Absent	
Palatine Suture	Straight	Southwestern Mongoloid
	Bulging	American Caucasoid; American Black
Zygomatico-maxillary Suture	Curved	American Caucasoid; American Black
	Angled	Southwestern Mongoloid

APPENDIX B: CHAID Decision Trees and Associated Probabilities for the Sexually Dimorphic Traits

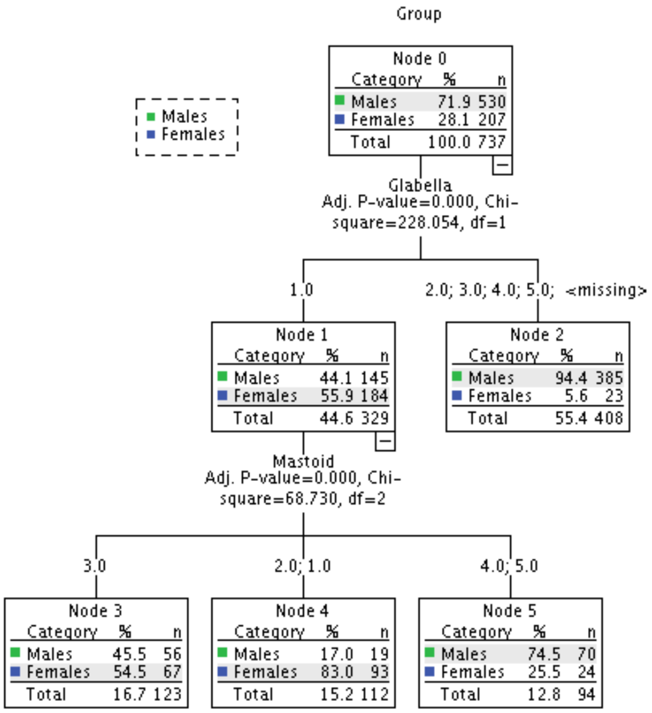

Figure A.1. CHAID cranial trait decision tree for the Japanese sample.

Table A.1. Associated CHAID cranial trait probabilities for the Japanese sample.

Node	Female probability	Male probability
2	0.06	0.94
3	0.54	0.46
4	0.83	0.17
5	0.26	0.74

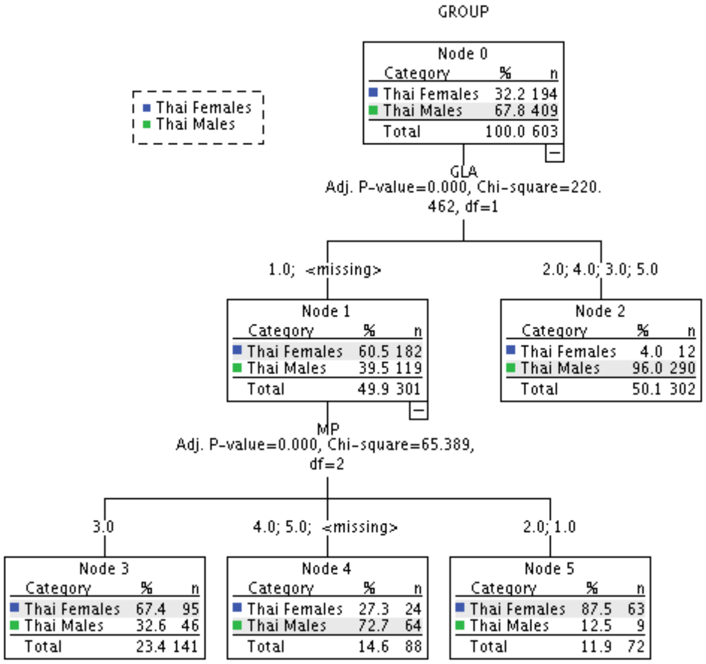

Figure A.2. CHAID cranial trait decision tree for the Thai sample.

Table A.2. Associated CHAID cranial trait probabilities for the Thai sample.

Node	Female probability	Male probability
2	0.67	0.33
3	0.67	0.33
4	0.27	0.73
5	0.88	0.13

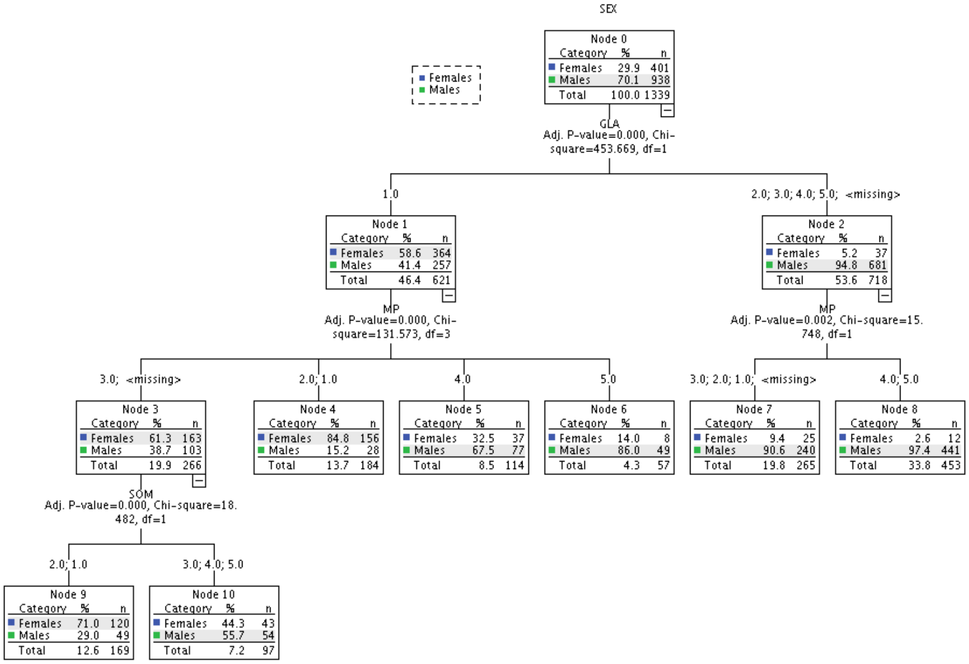

Figure A.3. CHAID cranial trait decision tree for the combined Japanese and Thai sample.

Table A.3. Associated CHAID cranial trait probabilities for the combined Japanese and Thai samples.

Node	Female probability	Male probability
4	0.85	0.15
5	0.32	0.68
6	0.14	0.86
7	0.09	0.91
8	0.03	0.97
9	0.71	0.29
10	0.44	0.56

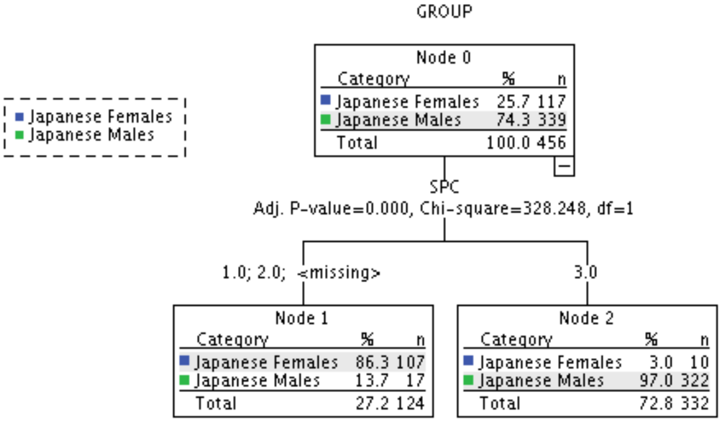

Figure A.4. CHAID pelvic trait decision tree for the Japanese sample.

Table A.4. Associated CHAID pelvic trait probabilities for the Japanese sample.

Node	Female probability	Male probability
1	0.86	0.14
2	0.03	0.97

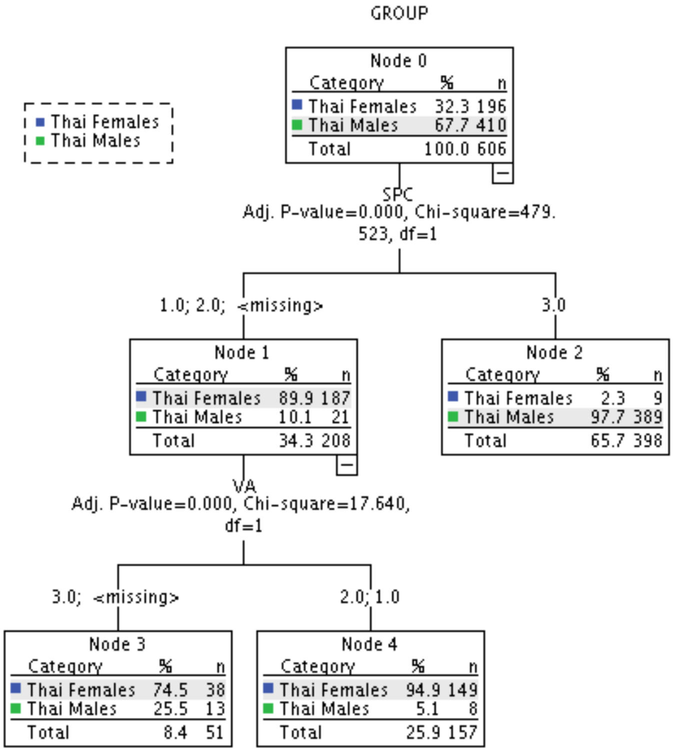

Figure A.5. CHAID pelvic decision tree for the Thai sample.

Table A.5. Associated CHAID pelvic trait probabilities for the Thai sample.

Node	Female probability	Male probability
2	0.02	0.98
3	0.75	0.25
4	0.95	0.05

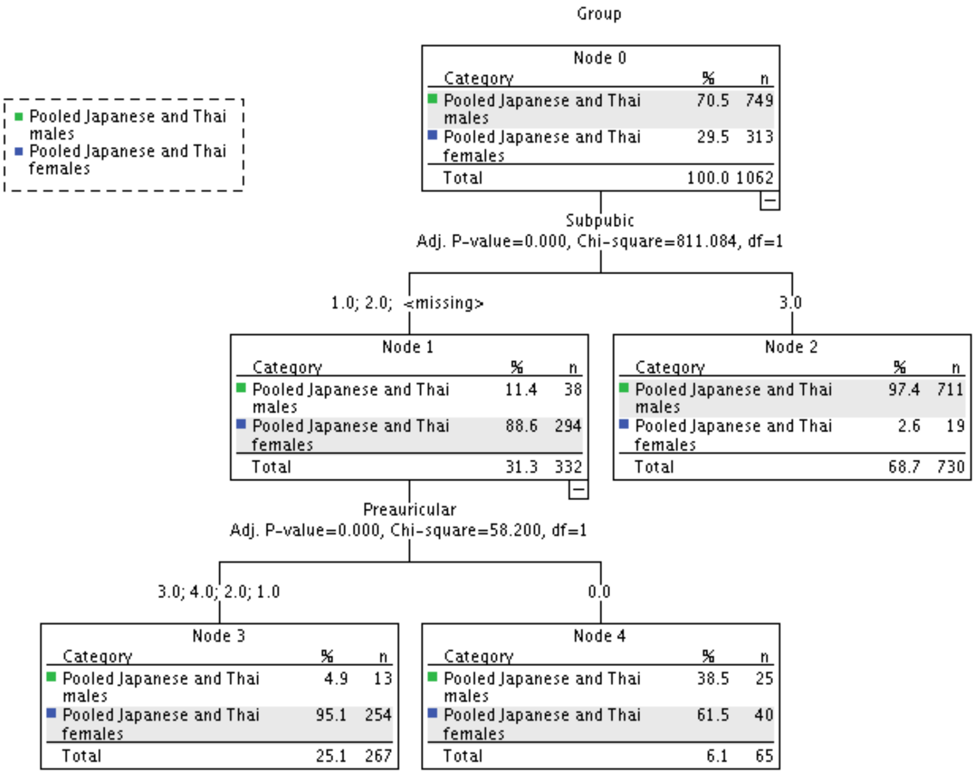

Figure A.6. CHAID pelvic decision tree for the combined Japanese and Thai samples.

Table A.6. Associated CHAID pelvic trait probabilities for the combined Japanese and Thai sample.

Node	Female probability	Male probability
2	0.03	0.97
3	0.95	0.05
4	0.62	0.38

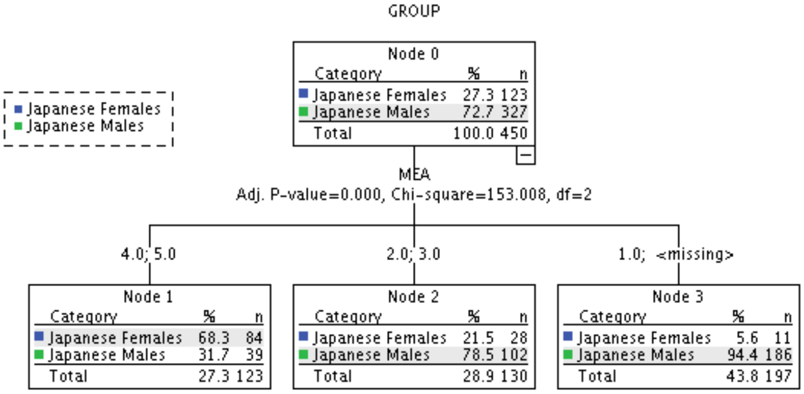

Figure A.7. CHAID distal humerus decision tree for the Japanese sample.

Table A.7. Associated CHAID distal humerus probabilities for the Japanese sample.

Node	Female probability	Male probability
1	0.22	0.78
2	0.68	0.32
3	0.06	0.94

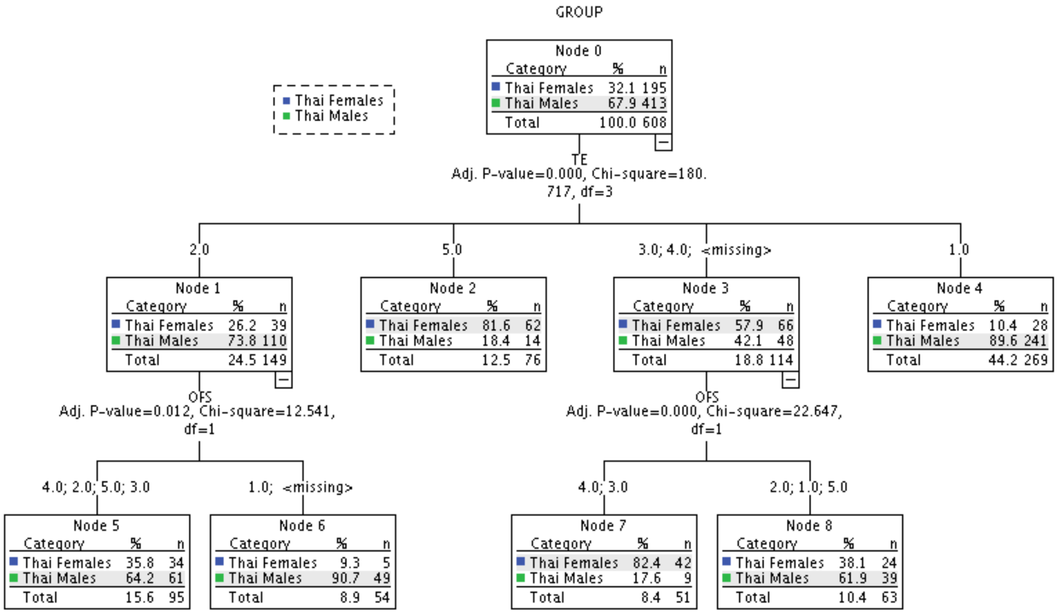

Figure A.8. CHAID distal humerus decision tree for the Thai sample.

Table A.8. Associated CHAID distal humerus probabilities for the Thai sample.

Node	Female probability	Male probability
2	0.82	0.18
4	0.10	0.90
5	0.36	0.64
6	0.09	0.91
7	0.82	0.18
8	0.38	0.62

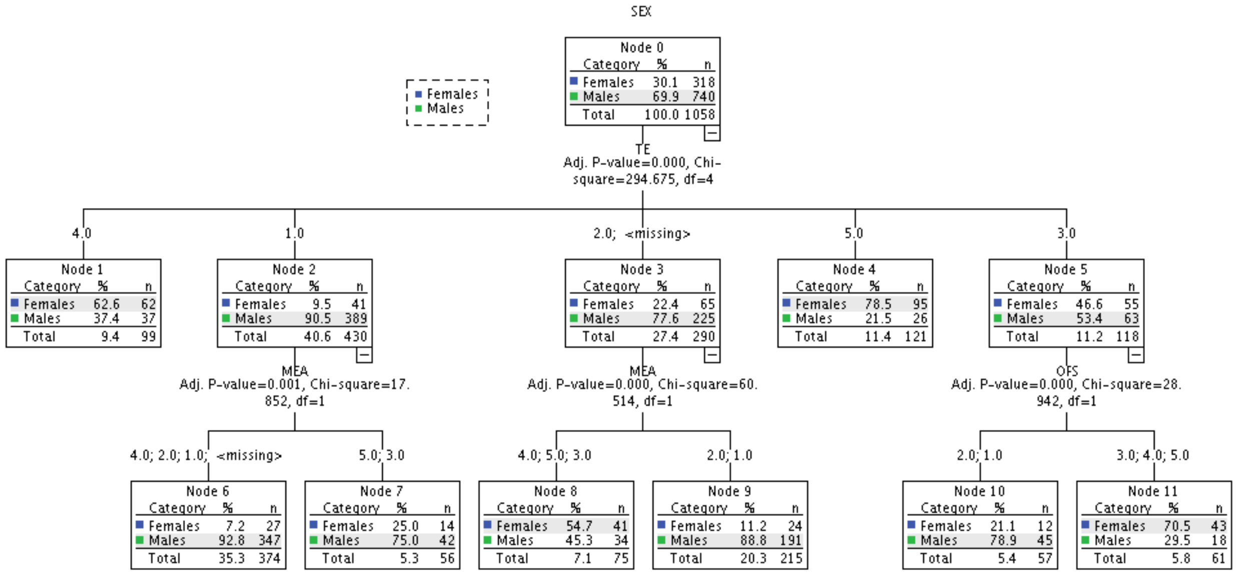

Figure A.9. CHAID distal humerus decision tree for the combined Japanese and Thai samples.

Table A.9. Associated CHAID distal humerus probabilities for the combined Japanese and Thai samples.

Node	Female probability	Male probability
3	0.79	0.21
5	0.63	0.37
6	0.07	0.93
7	0.25	0.75
8	0.11	0.89
9	0.55	0.45
10	0.70	0.30
11	0.21	0.79

APPENDIX C: Chi-Square Analyses of Secular Change for the Sexually Dimorphic Traits between the Historic (CU) and Modern (JU) Japanese Individuals

Trait	Group	N	Chi-square	Sig.*	Phi/Cramer's V	Difference
Nuchal crest	Females	204	9.850	**0.043**	0.213	JU: more gracile
	Males	517	26.582	**0.000**	0.227	JU: more gracile
Mastoid process	Females	205	2.698	0.609	0.115	--
	Males	514	33.549	**0.000**	0.255	JU: more gracile
Supraorbital margin	Females	205	3.536	0.474	0.131	--
	Males	516	16.470	**0.002**	0.255	JU: more gracile
Glabella	Females	205	4.418	0.110	0.120	--
	Males	515	12.476	**0.014**	0.179	JU: more gracile
Mental eminence	Females	194	3.441	0.329	0.108	--
	Males	506	20.707	**0.000**	0.202	JU: more gracile
Ventral arc	Females	101	0.318	0.853	0.056	--
	Males	333	9.380	**0.009**	0.168	JU: more scores of 3
Subpubic concavity	Females	115	0.572	0.751	0.070	--
	Males	338	1.171	0.557	0.059	--
Ischiopubic ramus ridge	Females	113	5.689	0.058	0.224	--
	Males	329	1.062	0.570	0.057	--
Sciatic notch	Females	117	5.801	0.215	0.221	--
	Males	339	14.908	**0.005**	0.203	JU: more constricted
Preauricular sulcus	Females	117	12.646	0.013	0.329	JU: more scores of 0 and 1
	Males	339	4.941	0.293	0.107	--
Right rhomboid fossa	Females	112	9.345	**0.003**	-0.289	JU: less fossae
	Males	304	10.091	**0.002**	-0.182	JU: less fossae
Left rhomboid fossa	Females	115	4.058	0.053	-0.188	--
	Males	304	1.309	0.257	-0.066	--
Medial epicondyle angle	Females	123	8.629	0.071	0.265	--
	Males	326	1.265	0.867	0.062	--
Olecranon fossa shape	Females	123	6.009	0.198	0.221	--
	Males	326	1.265	0.867	0.062	--
Trochlear extension	Females	123	10.337	**0.035**	0.290	JU: more extension
	Males	325	8.892	0.064	0.165	--
Trochlear constriction	Females	122	2.779	0.595	0.151	--
	Males	326	9.415	0.052	0.170	--

*statistically significant values in bold.

APPENDIX D: Comparative Cranial and Mandibular Trait Frequencies

Table A.10. ANS frequencies for Hefner's (2009) and Rhine's (1990) samples.

	Hefner (2009)				Rhine (1990)*			
ANS	African (N=218)	American Indian (N=262)	Asian (N=75)	European (N=146)	Anglo (N=49)	Hispanic (N=7)	Indian (N=3)	Black (N=3)
1	152 (69.7%)	178 (67.9%)	60 (80.0%)	53 (36.3%)	29 (59.2%)	7 (100.0%)	2 (66.7%)	2 (66.7%)
2	44 (20.2%)	56 (21.4%)	10 (13.3%)	38 (26.0%)	--	--	--	--
3	22 (10.1%)	28 (10.7%)	5 (6.7%)	55 (37.7%)	20 (40.8%)	0 (0.0%)	1 (33.3%)	1 (33.3%)

*1=small; 3=large

Table A.11. INA frequencies for Hefner's (2009) and Rhine's (1990) samples.

	Hefner (2009)				Rhine (1990)*			
INA	African (N=218)	American Indian (N=283)	Asian (N=75)	European (N=146)	Anglo (N=53)	Hispanic (N=7)	Indian (N=3)	Black (N=3)
1	64 (29.4%)	10 (3.8%)	9 (12.0%)	1 (0.7%)	7 (13.2%)	1 (12.5%)	0 (0.0%)	0 (0.0%)
2	63 (28.9%)	63 (24.0%)	13 (17.3%)	5 (3.4%)	34 (64.2%)	1 (12.5%)	0 (0.0%)	1 (33.3%)
3	47 (21.6%)	149 (56.9%)	48 (64.0%)	35 (24.0%)	11 (20.8%)	6 (75.0%)	3 (100.0%)	1 (33.3%)
4	29 (13.3%)	39 (14.9%)	3 (4.0%)	60 (41.1%)	1 (1.9%)	0 (0.0%)	0 (0.0%)	1 (33.3%)
5	15 (6.9%)	1 (0.4%)	2 (2.7%)	45 (30.8%)	--	--	--	--

*1=deep; 2=shallow; 3=blurred; 4=guttered

Table A.12. IOB frequencies for Hefner's (2005) sample.

IOB	African (N=218)	American Indian (N=262)	Asian (N=75)	European (N=146)
1	21 (9.6%)	155 (59.2%)	31 (41.3%)	45 (30.8%)
2	75 (34.4%)	96 (36.6%)	39 (62.0%)	92 (63.0%)
3	122 (56.0%)	11 (4.2%)	5 (6.7%)	9 (6.2%)

Table A.13. TUB frequencies for Hefner's (2009) and Rhine's (1990) samples.

	Hefner (2009)				Rhine (1990)*			
TUB	**African (N=218)**	**American Indian (N=262)**	**Asian (N=75)**	**European (N=146)**	**Anglo (N=53)**	**Hispanic (N=8)**	**Indian (N=3)**	**Black (N=3)**
0	110 (50.5%)	107 (40.8%)	32 (42.7%)	75 (51.4%)	30 (56.6%)	4 (50.0%	1 (33.3%)	0 (0.0%)
1	60 (27.5%)	98 (37.4%)	25 (33.3%)	47 (32.2%)	--	--	--	--
2	32 (14.7%)	40 (15.3%)	10 (13.3%)	18 (12.3%)	23 (43.3%)	4 (50.0%)	2 (66.7%)	3 (100.0%)
3	16 (7.3%)	17 (6.5%)	8 (10.7%)	6 (4.1%)	--	--	--	--

*0=absent; 2=present

Table A.14. NAW frequencies for Hefner's (2005) and Rhine's (1990) samples.

	Hefner (2009)				Rhine (1990)*			
NAW	**African (N=218)**	**American Indian (N=262)**	**Asian (N=75)**	**European (N=146)**	**Anglo (N=53)**	**Hispanic (N=8)**	**Indian (N=3)**	**Black (N=3)**
1	8 (3.7%)	22 (8.4%)	2 (2.7%)	79 (54.1%)	25 (47.2%)	1 (12.5%)	0 (0.0%)	0 (0.0%)
2	89 (40.8%)	204 (77.9%)	65 (86.7%)	48 (32.9%)	25 (47.2%)	6 (75.0%)	1 (33.3%)	1 (33.3%)
3	121 (55.5%)	36 (13.7%)	8 (10.7%)	19 (13.1%)	3 (5.7%)	1 (12.5%)	2 (66.7%)	2 (66.7%)

*1=narrow; 2=medium; 3=wide

Table A.15. NBC frequencies for Hefner's (2005) and Rhine's (1990) samples.

	Hefner (2009)				Rhine (1990)*			
NBC	**African (N=218)**	**American Indian (N=262)**	**Asian (N=75)**	**European (N=146)**	**Anglo (N=53)**	**Hispanic (N=8)**	**Indian (N=3)**	**Black (N=3)**
0	114 (52.3%)	30 (11.5%)	19 (25.3%)	11 (7.5%)	--	--	--	--
1	50 (22.9%)	67 (25.6%)	17 (22.7%)	23 (15.8%)	2 (4.0%)	1 (12.5%)	1 (33.3%)	1 (33.3%)
2	22 (10.1%)	65 (24.8%)	29 (38.7%)	27 (18.5%)	--	--	--	--
3	23 (10.6%)	90 (34.4%)	9 (12.0%)	37 (25.3%)	29 (58.0%)	2 (25.0%)	0 (0.0%)	0 (0.0%)
4	9 (4.1%)	10 (3.8%)	1 (1.3%)	48 (32.9%)	19 (38.0%)	5 (62.5%)	2 (66.7%)	2 (66.7%)

*1="Quonset"; 3=tower; 4=tented

Table A.16. NO frequencies for Hefner's (2009) and Rhine's (1990) samples.

	Hefner (2009)				Rhine (1990)*			
NO	**African (N=207)**	**American Indian (N=220)**	**Asian (N=75)**	**European (N=146)**	**Anglo (N=48)**	**Hispanic (N=8)**	**Indian (N=3)**	**Black (N=3)**
0	141 (68.1%)	97 (44.1%)	51 (68.0%)	77 (52.7%)	41 (85.4%)	5 (62.5%)	3 (100.0%	3 (100.0%)
1	66 (31.9%)	123 (55.9%)	24 (32.0%)	69 (49.2%)	7 (14.6%)	3 (37.5%)	0 (0.0%)	0 (0.0%)

*0=absent; 1=present

Table A.17. PBD frequencies for Hefner's (2009) and Rhine's (1990) samples.

	Hefner (2009)				Rhine (1990)			
PBD	**African (N=218)**	**American Indian (N=253)**	**Asian (N=75)**	**European (N=184)**	**Anglo (N=52)**	**Hispanic (N=8)**	**Indian (N=3)**	**Black (N=3)**
0	115 (52.8%)	235 (92.9%)	65 (90.3%)	121 (82.9%)	47 (90.4%)	7 (87.5%)	3 (100.0%)	2 (66.7%)
1	103 (47.2%)	18 (7.1%)	7 (9.7%)	25 (17.1%)	5 (9.6%)	1 (12.5%)	0 (0.0%)	1 (33.3%)

Table A.18. SNS frequencies for Hefner's (2009) sample.

SNS	African (N=215)	American Indian (N=262)	Asian (N=75)	European (N=146)
0	92 (42.8%)	90 (34.3%)	9 (12.0%)	57 (39.0%)
1	67 (32.2%)	82 (31.3%)	23 (30.7%)	57 (39.0%)
2	56 (26.0%)	90 (34.4%)	243 (57.3%)	32 (22.0%)

Table A.19. TPS frequencies for Hefner's (2009) and Rhine's (1990) samples.

	Hefner (2009)				Rhine (1990)*			
TPS	African (N=180)	American Indian (N=260)	Asian (N=75)	European (N=145)	Anglo (N=53)	Hispanic (N=12)	Indian (N=10)	Black (N=6)
1	33 (18.3%)	165 (63.5%)	34 (45.3%)	42 (29.0%)	2 (3.8%)	2 (16.6%)	5 (50.0%)	1 (16.6%)
2	85 (47.2%)	72 (27.7%)	25 (33.3%)	40 (27.6%)	51 (96.2%)	10 (83.3%)	5 (50.0%)	5 (83.3%)
3	45 (25.0%)	14 (5.4%)	11 (14.7%)	49 (33.8%)	--	--	--	--
4	17 (9.4%)	9 (3.5%)	5 (6.7%)	14 (9.7%)	--	--	--	--

*1=straight; 2=bulging

Table A.20. ZMS frequencies for Hefner's (2009) and Rhine's (1990) samples.

	Hefner (2009)				Rhine (1990)*			
ZMS	African (N=177)	American Indian (N=242)	Asian (N=75)	European (N=135)	Anglo (N=53)	Hispanic (N=11)	Indian (N=12)	Black (N=6)
0	9 (5.1%)	7 (2.9%)	4 (5.3%)	2 (1.5%)	10 (18.8%)	5 (45.4%)	4 (33.3%)	2 (22.3%)
1	56 (31.6%)	92 (38.0%)	21 (28.0%)	50 (37.0%)	43 (81.1%)	6 (54.5%)	8 (66.6%)	4 (66.6%)
2	88 (49.7%)	127 (52.5%)	38 (50.7%)	57 (42.2%)	--	--	--	--
3	24 (13.6%)	16 (6.6%)	12 (16.0%)	26 (19.3%)	--	--	--	--

*0=angled; 1=curved/S-shaped

Table A.21. KLN frequencies for Rhine's (1990) samples.

	Rhine (1990)*			
KLN	**Anglo (N=53)**	**Hispanic (N=11)**	**Indian (N=3)**	**Black (N=3)**
Absent	45 (84.9%)	11 (100.0%)	3 (100.0%)	2 (66.7%)
Present	8 (15.1%)	0 (0.0%)	0 (0.0%)	1 (33.3%)

Table A.22. SC frequencies for Rhine's (1990) sample.

SC	**Anglo (N=47)**	**Hispanic (N=6)**	**Indian (N=3)**	**Black (N=3)**
Simple	27 (57.4%)	4 (66.7%)	2 (66.7%)	2 (66.7%)
Medium	17 (36.2%)	2 (33.3%)	1 (33.3%)	1 (33.3%)
Complex	6.4%	3 (6.4%)	0 (0.0%)	0 (0.0%)

Table A.23. WB frequencies for Rhine's (1990) sample.

WB	**Anglo (N=52)**	**Hispanic (N=8)**	**Indian (N=3)**	**Black (N=3)**
Absent	36 (69.3%)	6 (75.0%)	2 (66.7%)	1 (33.3%)
Present	16 (30.8%)	2 (25.0%)	1 (33.3%)	2 (66.7%)

Table A.24. OS frequencies for Rhine's (1990) sample.

OS	**Anglo (N=61)**	**Hispanic (N=8)**	**Indian (N=3)**	**Black (N=3)**
Rounded	12 (22.6%)	3 (37.5%)	1 (33.3%)	1 (33.3%)
Rectangular	13 (24.5%)	2 (25.0%)	1 (33.3%)	1 (33.3%)
Sloping	36 (67.9%)	2 (37.5%)	1 (33.3%)	1 (33.3%)

Table A.25. ZMP frequencies for Rhine's (1990) sample.

ZMP	**Anglo (N=53)**	**Hispanic (N=8)**	**Indian (N=3)**	**Black (N=3)**
Retreating	16 (30.2%)	1 (12.5%)	2 (66.7%)	0 (0.0%)
Vertical	27 (50.9%)	3 (37.5%)	0 (0.0%)	0 (0.0%)
Projecting	10 (18.9%)	4 (50.0%)	1 (33.3%)	3 (100.0%)

Table A.26. ZPT frequencies for Rhine's (1990) sample.

ZPT	**Anglo (N=53)**	**Hispanic (N=8)**	**Indian (N=3)**	**Black (N=3)**
Absent	9 (17.0%)	1 (12.5%)	0 (0.00)	(0.0%)
Present	44 (83.0%)	7 (87.5%)	3 (100.0%)	3 (100.0%)

Table A.27. PRG frequencies for Rhine's (1990) sample.

	Rhine (1990)			
PRG	**Anglo (N=29)**	**Hispanic (N=4)**	**Indian (N=2)**	**Black (N=1)**
None	11 (37.9%)	1 (25.0%	0 (0.0%)	0 (0.0%)
Slight	15 (51.7%)	3 (75.0%)	0 (0.0%)	1 (100.0%)
Moderate	3 (10.3%)	0 (0.0%)	2 (100.0%)	0 (0.0%)

Table A.28. DAS frequencies for Rhine's (1990) sample.

DAS	**Anglo (N=45)**	**Hispanic (N=6)**	**Indian (N=3)**	**Black (N=2)**
Parabolic	19 (42.2%)	1 (16.7%)	0 (0.0%)	0 (0.0%)
Elliptic	25 (55.6%)	5 (83.3%)	3 (100.0%)	2 (100.0%)
Hyperbolic	1 (2.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)

Table A.29. PRI frequencies for Parr's (2005) African and European sample.

	African			European		
PRI	**Females**	**Males**	**Total**	**Females**	**Males**	**Total**
0	20.9%	31.4%	27.2%	59.2%	64.3%	61.6%
1	31.4%	36.4%	34.6%	27.2%	28.8%	28.0%
2	30.9%	23.9%	26.6%	12.6%	6.4%	9.5%
3	16.8%	8.3%	11.7%	1.0%	0.5%	0.9%

Table A.30. LRI frequencies for Parr's (2005) African and European sample.

	African			European		
LRI	**Females**	**Males**	**Total**	**Females**	**Males**	**Total**
1	47.9%	19.3%	30.9%	23.5%	17.8%	20.8%
2	37.2%	49.5%	44.6%	38.2%	28.9%	33.6%
3	14.9%	31.2%	24.5%	38.2%	53.3%	45.6%

Table A.31. PRI and GE frequencies for Rhine's (1990) sample.

Gonial angle	Anglo (N=45)	Hispanic (N=6)	Indian (N=3)	Black (N=2)
Inverted	3 (6.0%)	0 (0.0%)	0 (0.0)	0 (0.0%)
Straight	11 (22.0%)	6 (75.0%)	1 (33.3%)	1 (50.0%)
Everted	36 (72.0%)	2 (25%)	2 (66.7%)	1 (50.0%)

Table A.32. MBS frequencies in Parr's (2005) and Rhine's (1990) samples.

	Parr (2005)						Rhine (1990)			
	African			European			Anglo (N=51)	Hispanic (N=7)	Indian (N=3)	Black (N=3)
MBS	**Females**	**Males**	**Total**	**Females**	**Males**	**Total**				
1	51.3%	30.4%	38.9%	51.3%	38.4%	44.2%	15 (29.4%)	1 (14.3%)	2 (66.7%)	0 (0.0%)
2	46.4%	69.1%	59.9%	47.4%	61.1%	54.2%	34 (66.7%)	5 (71.4%)	1 (33.3%)	2 (67.7%)
3	2.3%	0.5%	1.2%	2.8%	0.5%	1.6%	2 (3.9%)	1 (14.3%)	0 (0.0%)	1 (33.3%)

Table A.33. MT frequencies for Parr's (2005) and Rhine's (1990) samples.

	Parr (2005)						Rhine (1990)*			
	African			European			Anglo (N=50)	Hispanic (N=8)	Indian (N=3)	Black (N=3)
MT	F	M	T	F	M	T				
0	89.3%	92.3%	91.0%	96.5%	91.2%	93.8%	45 (90.0%)	6 (75.0%)	2 (66.7%)	3 (100.0%)
1	8.7%	6.3%	7.4%	2.3%	1.2%	4.4%	5 (10.0%)	2 (25.0%)	1 (33.3%)	0 (0.0%
2	1.8%	1.0%	1.2%	1.2%	1.2%	1.4%	--	--	--	--
3	0.3%	0.3%	0.4%	0.0%	0.7%	0.5%	--	--	--	--

*0=absent; 1=present

Table A.34. GMA frequencies for Parr's (2005) African and European sample.

	African			European		
GMA	Females	Males	Total	Females	Males	Total
0	30.4%	12.6%	19.8%	37.7%	22.2%	29.9%
1	47.2%	35.8%	40.5%	44.7%	49.9%	47.2%
2	19.4%	40.8%	32.3%	16.9%	24.1%	20.6%
3	3.1%	10.7%	7.6%	0.7%	3.8%	2.3%

Table A.35. MHB frequencies for Parr's (2005) African and European sample.

	African			European		
MHB	Females	Males	Total	Females	Males	Total
0	88.0%	90.1%	89.2%	88.0	89.0%	88.5%
1	12.0%	9.9%	10.8%	12.0	11.0%	11.5%

Table A.36. AMF frequencies for Parr's (2005) African and European sample.

	African			European		
AMF	Females	Males	Total	Females	Males	Total
0	57.7%	54.4%	55.7%	64.8%	56.2%	60.5%
1	42.3%	45.6%	44.3%	35.2%	43.8%	39.5%

Table A.37. CP frequencies for Parr's (2005) and Rhine's (1990) samples.

	Parr (2005)						Rhine (1990)*			
	African			European			Anglo (N=52)	Hispanic (N=8)	Indian (N=3)	Black (N=3)
CP	F	M	T	F	M	T				
0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	--	--	--	--
1	35.7%	46.9%	42.4%	4.3%	5.1%	4.7%	16 (30.8%)	3 (37.5%)	3 (100.0%	3 (100.0%)
2	64.3%	53.1%	57.6%	95.7%	94.9%	95.3%	36 (69.2%	5 (62.5%)	0 (0.0%)	0 (0.0%)

*1=vertical; 2=prominent

Table A.38. CS frequencies for Parr's (2005) and Rhine's (1990) samples.

	Parr (2005)						Rhine (1990)*			
	African			European			Anglo (N=52)	Hispanic (N=8)	Indian (N=3)	Black (N=3)
CS	F	M	T	F	M	T				
1	60.2%	64.4%	62.7%	42.5%	36.3%	39.4%	16 (30.8%)	2 (25.0%)	3 (100.0%)	3 (100.0%)
2	33.2%	9.2%	18.9%	33.6%	12.1%	22.8%	11 (21.2%)	1 (12.5%)	0 (0.0%)	0 (0.0%)
3	6.6%	26.4%	18.4%	23.8%	51.6%	37.8%	25 (48.1%)	5 (62.5%)	0 (0.0%)	0 (0.0%)

*1=blunt; 2=pointed; 3=bilobate

Table A.39. NMF frequencies for Parr's (2005) African and European samples.

	African			European		
NMF	Females	Males	Total	Females	Males	Total
0	0.8%	0.3%	0.5%	1.5%	0.5%	1.0%
1	85.5%	80.9%	82.8%	93.5%	91.6%	92.5%
2	11.7%	14.9%	13.7%	4.3%	7.5%	5.9%
3	2.0%	3.6%	3.0%	0.7%	0.5%	0.6%
4	0.0%	0.2%	0.1%	0.0%	0.0%	0.0%

Table A.40. ARS frequencies for Rhine's (1990) sample.

ARS	Anglo (N=50)	Hispanic (N=8)	Indian (N=3)	Black (N=2)
Pinched	43 (86.0%)	7 (87.5%)	1 (33.3%)	3 (100.0%)
Wide	7 (14.0%)	1 (12.5%)	2 (66.7%)	0 (0.0%

Table A.41. ARP frequencies for Rhine's (1990) sample.

ARP	Anglo (N=45)	Hispanic (N=8)	Indian (N=3)	Black (N=2)
Vertical	13 (25.5%)	2 (25.0%)	2 (66.7%)	0 (0.0%)
Slanted	38 (74.5%)	6 (76.0%)	1 (33.3%)	3 (100.0%)

APPENDIX E: Correlation coefficients for the 37 cranial and mandibular nonmetric traits for the pooled Japanese and Thai samples

Table A.42. Correlation coefficients for ANS, INA, IOB, TUB, NFS, NAS, NBS, NAW, and NBC.

	ANS	INA	IOB	TUB	NFS	NAS	NBS	NAW	NBC
INA	0.183**	--							
IOB	-0.032	0.056*	--						
MT	0.033	-0.042	0.049	--					
NFS	-0.027	0.017	-0.024	-0.048	--				
NAS	-0.108**	-0.119**	0.065*	-0.041	0.036	--			
NBS	-0.048	0.000	-0.018	0.008	0.039	0.042	--		
NAW	-0.122**	-0.067*	0.133**	-0.029	0.021	0.404**	0.013	--	
NBC	0.047	-0.124**	-0.046	-0.009	0.036	-0.133**	0.069*	-0.137**	--
NO	0.017	0.057*	-0.006	-0.028	-0.042	0.064*	-0.002	-0.021	0.045
PBD	0.016	0.075**	0.013	-0.026	-0.034	-0.033	-0.027	-0.061*	0.013
SNS	0.080**	-0.027	0.013	0.086**	-0.052	-0.069*	-0.027	-0.009	0.083**
TPS	0.068*	-0.085**	-0.061*	-0.012	0.002	0.051	-0.045	-0.006	-0.064*
ZMS	0.076**	-0.021	-0.001	0.059*	0.007	0.067*	-0.030	0.054	-0.028
KLN	-0.049	0.003	0.013	-0.040	0.019	0.001	-0.013	0.023	0.034
SUT	0.057	-0.002	0.050	0.033	0.024	0.030	-0.014	0.007	-0.007
WB	0.047	-0.036	0.070*	0.024	-0.048	0.035	0.024	0.022	-0.093**
OS	-0.001	-0.048	-0.087**	0.006	-0.051	0.026	-0.09	0.017	-0.018
ZMP	-0.063*	-0.060*	-0.009	0.084**	0.015	0.022	0.013	0.026	0.045
ZPT	0.071*	-0.014	0.061*	0.082**	-0.020	-0.029	-0.012	-0.017	-0.003
PRG	-0.071*	0.019	-0.004	0.027	0.057*	-0.086**	0.042	-0.073**	0.132**
DAS	-0.020	-0.065*	-0.018	-0.067*	0.048	0.045	-0.020	0.046	-0.057*
OCC	-0.058	0.111*	-0.087	0.004	0.026	-0.154**	0.004	-0.083	-0.033
MIO	-0.060	0.132**	-0.027	0.011	0.092*	-0.084	0.028	-0.130**	0.045
MRI	-0.004	0.026	0.006	0.031	-0.042	0.027	-0.040	0.045	-0.042
LRI	0.088	-0.074	-0.156**	0.056	-0.053	-0.002	0.071	0.052	-0.089
GE	-0.023	0.003	0.048	-0.009	-0.050	-0.064*	0.020	-0.042	0.079**
MB	-0.075**	0.102**	0.016	-0.056	0.051	-0.067*	-0.004	-0.074*	0.081**
MTU	-0.054	-0.056	-0.029	0.027	-0.020	0.012	-0.023	-0.003	-0.004
GMA	0.102**	-0.140**	0.009	0.020	-0.112**	0.049	-0.035	0.084**	-0.065*
MHB	-0.021	-0.023	-0.019	-0.010	0.011	0.002	-0.035	0.005	0.025
AMF	0.002	-0.025	0.027	0.018	-0.015	0.018	-0.008	0.058*	0.016
CP	-0.045	0.008	0.015	0.013	0.009	-0.016	-0.002	0.015	-0.006
CS	0.023	-0.058*	-0.022	0.065*	0.028	0.024	0.029	-0.006	-0.023
NMF	-0.008	-0.007	0.026	-0.045	0.035	-0.028	-0.002	-0.029	-0.003
ARS	-0.043	0.038	0.015	-0.036	0.045	-0.077**	0.006	-0.085**	0.111**
ARP	-0.040	0.082**	0.021	-0.038	0.080**	-0.050	-0.007	-0.068*	-0.017

*statistically significantly at the 0.05 level (2-tailed); **statistically significantly at the 0.01 level (2-tailed).

Table A.43. Correlations coefficients for NO, PBD, SNS, TPS, ZMS, KLN, SUT, WB, and OS.

	NO	PBD	SNS	TPS	ZMS	KLN	SUT	WB	OS
PBD	0.003	--							
SNS	0.021	-0.001	--						
TPS	-0.053	-0.093**	-0.044	--					
ZMS	-0.008	-0.039	0.071*	0.026	--				
KLN	0.016	-0.009	0.087**	-0.075*	-0.020	--			
SUT	-0.011	0.060	0.019	0.062	0.014	-0.026	--		
WB	-0.045	-0.026	0.075*	0.097**	0.114**	-0.081*	0.267**	--	
OS	0.025	-0.012	0.111**	-0.015	-0.035	0.057*	0.009	-0.041	--
ZMP	-0.009	-0.051	0.018	-0.019	-0.029	0.047	0.002	0.013	0.020
ZPT	0.089**	-0.028	0.142**	-0.045	0.011	0.003	0.049	0.028	0.046
PRG	0.045	0.006	0.016	-0.163**	-0.112**	0.107**	-0.063*	-0.068*	-0.033
DAS	-0.005	-0.042	0.053	0.012	0.024	-0.033	-0.028	0.053	0.058*
OCC	0.072	0.002	-0.038	-0.081	-0.084	0.065	-0.023	0.036	-0.073
MIO	0.032	0.013	-0.073	-0.036	-0.117**	0.001	-0.048	-0.031	-0.028
MRI	-0.013	-0.023	-0.042	-0.035	-0.025	-0.069*	-0.105**	0.049	-0.030
LRI	-0.019	-0.056	0.011	-0.036	0.093	-0.017	-0.024	0.072	0.013
GE	0.022	0.057	0.073*	-0.018	-0.005	0.068*	0.039	-0.039	0.021
MB	0.067*	0.009	-0.006	-0.129**	0.034	0.071*	0.016	-0.033	-0.022
MTU	-0.045	-0.066*	-0.003	0.072*	0.010	-0.037	0.040	0.050	-0.026
GMA	-0.004	0.010	0.076**	0.078*	0.122**	-0.016	0.063	0.091**	0.081**
MHB	0.002	0.010	-0.017	0.043	-0.016	-0.037	0.025	0.030	0.014
AMF	0.007	-0.012	-0.018	-0.043	-0.009	-0.034	-0.054	0.013	0.038
CP	0.029	0.068*	0.009	-0.009	-0.005	0.010	-0.056	-0.032	0.012
CS	0.027	-0.022	0.020	0.005	0.042	0.030	-0.029	-0.015	0.046
NMF	0.037	-0.037	0.034	0.005	-0.014	-0.024	-0.032	0.010	-0.056
ARS	-0.032	0.043	-0.071*	-0.028	-0.054	-0.007	0.066*	-0.010	-0.036
ARP	-0.035	-0.010	-0.047	-0.029	0.011	0.016	-0.004	-0.009	0.007

*statistically significantly at the 0.05 level (2-tailed); **statistically significantly at the 0.01 level (2-tailed).

Table A.44. Correlation coefficients for ZPM, ZPT, PRG, DAS, OCC, MIO, MRI, LRI, and GE.

	ZPM	ZPT	PRG	DAS	OCC	MIO	MRI	LRI	GE
ZPT	0.027	--							
PRG	0.010	0.143**	--						
DAS	0.041	-0.023	-0.026	--					
OCC	0.098*	-0.004	0.205**	-0.080	--				
MIO	0.009	-0.056	0.273**	-0.055	0.438**	--			
MRI	-0.009	0.002	0.024	-0.057*	0.053	0.069	--		
LRI	0.017	0.092	0.044	-0.014	-0.037	-0.139	-0.022	--	
GE	0.052	0.032	0.056	-0.027	0.034	-0.076	-0.143**	0.134**	--
MB	-0.013	0.014	0.165**	0.007	0.129**	0.106*	0.024	0.012	0.072**
MT	-0.037	-0.018	-0.144**	0.057*	-0.119*	-0.075	-0.028	0.050	-0.071*
GMA	-0.001	0.035	-0.176**	0.037	-0.217**	-0.216**	-0.083**	0.112*	0.075*
MHB	-0.011	-0.041	-0.004	0.049	-0.022	-0.068	0.016	0.003	0.029
AMF	-0.005	0.011	-0.002	-0.020	0.078	-0.007	0.042	-0.005	0.012
CP	0.011	-0.001	0.070*	0.000	0.002	0.040	0.087**	-0.021	0.013
CS	-0.006	0.030	-0.070*	-0.016	-0.089	-0.109*	-0.026	0.022	-0.007
NMF	-0.015	0.006	0.030	-0.004	-0.018	0.020	-0.022	-0.034	-0.016
ARS	0.036	-0.032	0.028	-0.048	0.054	0.089	-0.009	-0.053	-0.017
ARP	-0.020	0.004	0.120**	-0.021	0.157**	0.112*	0.127**	0.020	-0.026

*statistically significantly at the 0.05 level (2-tailed); **statistically significantly at the 0.01 level (2-tailed).

Table A.45. Correlation coefficients for MB, MT, GMA, MHB, AMF, CP, CS, NMF, and ARS.

	MB	MT	GMA	MHB	AMF	CP	CS	NMF	ARS
MB	--								
MT	-0.106**	--							
GMA	-0.213**	0.110**	--						
MHB	-0.051	0.046	0.091**	--					
AMF	-0.002	0.030	-0.007	0.043	--				
CP	0.047	-0.083**	-0.066*	-0.050	-0.029	--			
CS	-0.037	0.014	0.129**	-0.033	0.045	0.210**	--		
NMF	0.032	-0.009	0.000	-0.003	0.003	-0.024	0.039	--	
ARS	0.064*	-0.015	-0.152**	-0.016	0.004	-0.002	-0.029	-0.002	--
ARP	0.158**	-0.130**	-0.348**	-0.040	-0.022	0.150**	-0.123**	-0.019	0.107**

*statistically significantly at the 0.05 level (2-tailed); **statistically significantly at the 0.01 level (2-tailed).

APPENDIX F: CHAID Decision Trees and Associated Probabilities for the Cranial and Mandibular Traits

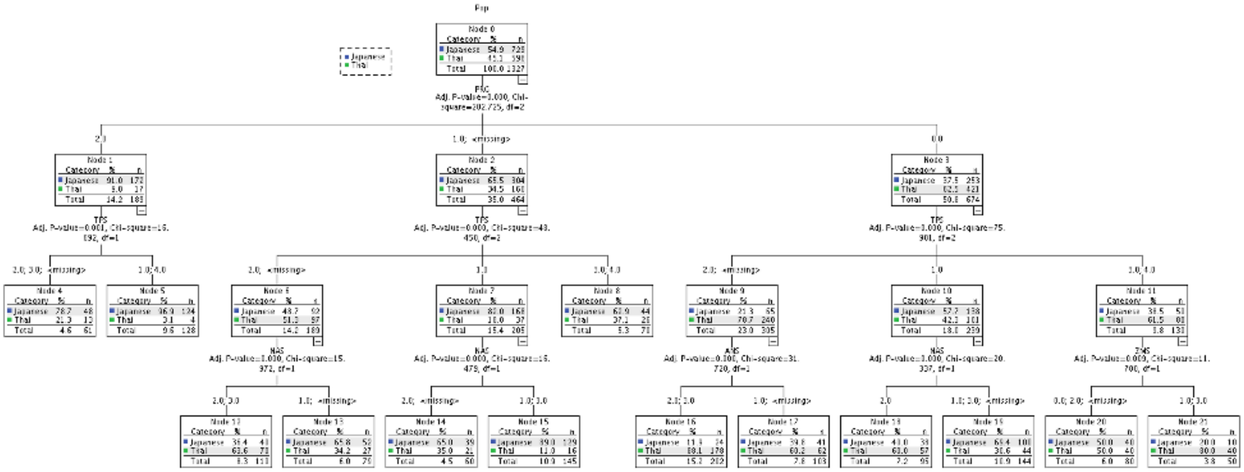

Figure A.10. CHAID cranial trait decision tree for the Japanese and Thai groups.

Table A.46. Associated CHAID cranial trait probabilities for the Japanese and Thai groups.

Node	Japanese probability	Thai probability
4	0.79	0.21
5	0.97	0.03
12	0.36	0.64
13	0.66	0.34
14	0.65	0.35
15	0.89	0.11
16	0.12	0.88
17	0.40	0.60
18	0.40	0.60
19	0.69	0.31
20	0.50	0.50
21	0.20	0.80

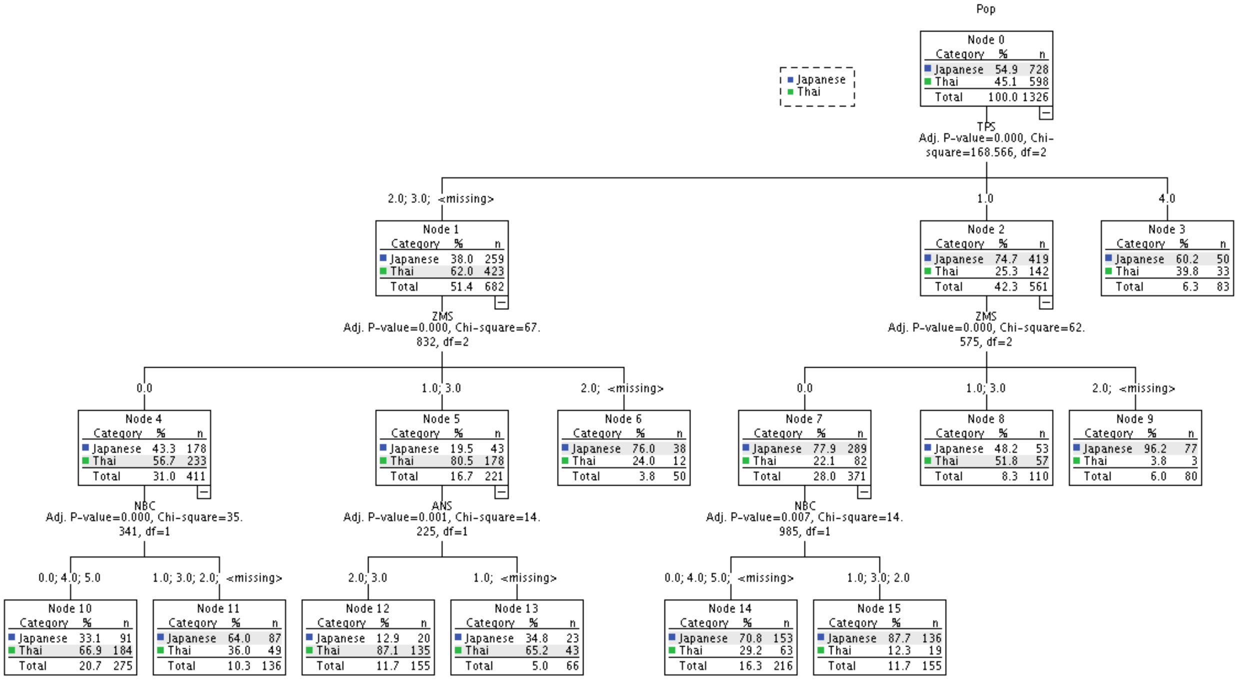

Figure A.11. CHAID decision tree for Hefner's (2009) traits.

Table A.47. Associated CHAID trait probabilities for Hefner's (2009) traits for the Japanese and Thai samples.

Node	Japanese probability	Thai probability
3	0.60	0.40
6	0.76	0.24
8	0.48	0.52
9	0.96	0.04
10	0.33	0.67
11	0.64	0.36
12	0.13	0.87
13	0.35	0.65
14	0.71	0.29
15	0.88	0.12

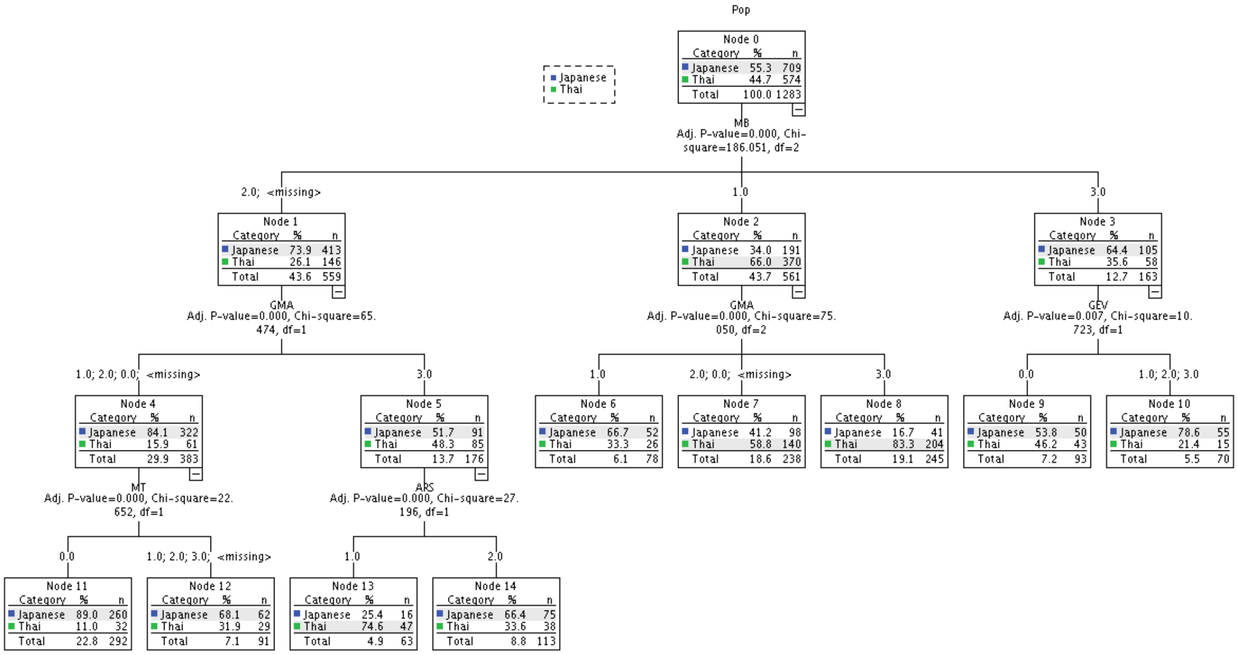

Figure A.12. CHAID mandibular trait decision tree for the Japanese and Thai groups.

Table A.48. Associated CHAID mandibular trait probabilities for the Japanese and Thai groups.

Node	Japanese probability	Thai probability
6	0.67	0.33
7	0.41	0.58
8	0.17	0.83
9	0.54	0.46
10	0.79	0.21
11	0.89	0.11
12	0.68	0.32
13	0.25	0.75
14	0.66	0.34

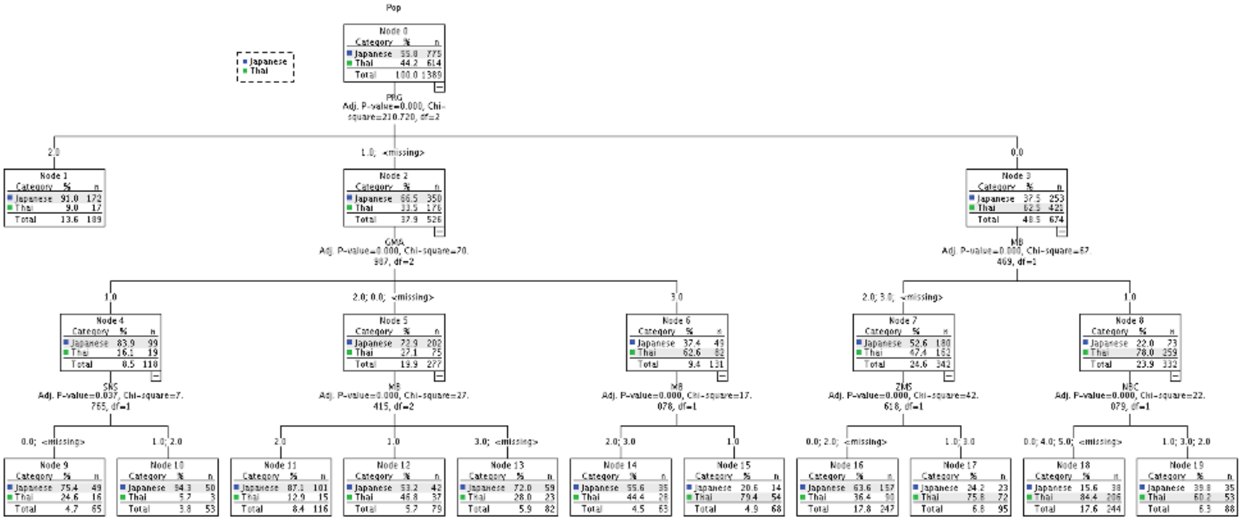

Figure A.13. CHAID decision tree analysis of the cranial and mandibular traits for the Japanese and Thai groups.

Table A.49. Associated CHAID cranial and mandibular trait probabilities for the Japanese and Thai groups.

Node	Japanese probability	Thai probability
1	0.91	0.08
9	0.75	0.25
10	0.94	0.06
11	0.87	0.13
12	0.53	0.47
13	0.72	0.28
14	0.56	0.44
15	0.21	0.79
16	0.64	0.36
17	0.24	0.76
18	0.16	0.84
19	0.40	0.60

APPENDIX G: Chi-Square Analyses of Secular Change for the Cranial and Mandibular Traits between the Historic (CU) and Modern (JU) Japanese Individuals

Trait	Group	N	Chi-square	Sig.*	Phi/Cramer's V	Difference
Anterior nasal spine	Females	200	5.017	0.081	0.158	--
	Males	512	2.641	0.267	0.072	--
Inferior nasal aperture	Females	205	3.543	0.471	0.131	--
	Males	514	9.587	**0.048**	0.137	JU: angular; CU: curved
Interorbital breadth	Females	201	14.639	**0.001**	0.270	JU: narrower
	Males	510	3.693	0.158	0.085	--
Malar tubercle	Females	204	11.756	**0.019**	0.240	JU: trace, pronounced; CU: medium, double
	Males	511	8.857	0.065	0.132	--
Nasofrontal suture	Females	204	7.070	0.070	0.186	--
	Males	511	8.400	**0.038**	0.128	JU: more squared
Nasal aperture shape	Females	205	7.141	**0.028**	0.187	JU: teardrop; CU: bowed
	Males	511	4.807	0.090	0.097	--
Nasal bone shape	Females	201	3.964	0.265	0.140	--
	Males	513	7.667	0.053	0.122	--
Nasal aperture width	Females	204	7.833	**0.020**	0.196	JU: narrower
	Males	512	0.910	0.635	0.042	--
Nasal bone contour	Females	202	5.542	0.302	0.164	--
	Males	512	5.189	0.393	0.101	--
Nasal overgrowth	Females	201	1.195	0.325	0.077	--
	Males	508	7.552	**0.008**	0.118	
Post-bregmatic depression	Females	192	4.267	**0.040**	0.149	JU: more depression
	Males	477	3.600	0.077	0.084	--
Supranasal suture	Females	204	8.247	**0.016**	0.201	JU: closed but visible; CH: obliterated
	Males	510	0.368	0.832	0.027	--
Transverse palatine suture	Females	201	9.445	**0.024**	0.217	JU: less straight
	Males	475	9.566	**0.023**	0.142	JU: less straight
Zygomatico-maxillary suture	Females	198	3.929	0.140	0.141	--
	Males	462	10.474	**0.015**	0.140	JU: one angle

Trait	Group	N	Chi-square	Sig.*	Phi/Cramer's V	Difference
Keeling	Females	192	3.046	0.118	0.126	--
	Males	477	0.982	0.612	0.045	--
Suture complexity	Females	165	13.798	**0.001**	0.289	JU: more complex
	Males	375	31.306	**0.000**	0.289	JU: more complex
Wormian bones	Females	161	1.477	0.278	0.096	--
	Males	369	0.220	0.714	0.024	--
Orbit shape	Females	205	8.680	**0.013**	0.206	JU: rectangular; CH: rounded
	Males	515	8.158	**0.017**	0.126	JU: rectangular; CH: rounded
Zygomatic/ maxillary projection	Females	203	1.070	0.586	0.073	--
	Males	509	7.948	**0.019**	0.125	JU: less projecting
Zygomatic posterior tubercle	Females	204	1.463	0.691	0.085	--
	Males	516	1.747	0.627	0.058	--
Prognathism	Females	205	26.328	**0.000**	0.358	JU: less prognathic
	Males	514	68.574	**0.000**	0.365	JU: less prognathic
Dental arcade shape	Females	202	1.133	0.539	0.075	--
	Males	507	13.593	**0.001**	0.164	CH: narrower
Occlusion	Females	88	1.017	0.753	0.107	--
	Males	224	12.904	**0.005**	0.240	JU: normal; CH: "overbite"
Maxillary incisor orientation	Females	89	0.926	0.629	0.102	--
	Males	232	0.989	0.610	0.065	--
Ramus inversion	Females	197	25.598	**0.000**	0.381	JU: less inverted
	Males	511	70.016	**0.000**	0.370	JU: less inverted
Location of inversion	Females	91	6.404	**0.036**	0.265	JU: low, medium; CH: high
	Males	169	10.580	**0.005**	0.250	JU: low, medium; CH: high
Gonial eversion	Females	198	2.738	0.454	0.118	--
	Males	511	15.380	**0.002**	0.173	JU: less everted
Mandibular border shape	Females	198	4.728	0.094	0.155	--
	Males	511	13.382	**0.001**	0.162	JU: straight; CU: undulating
Mandibular tori	Females	197	8.586	**0.005**	0.209	JU: more tori
	Males	511	6.672	0.083	0.109	--

Trait	Group	N	Chi-square	Sig.*	Phi/Cramer's V	Difference
Gonial muscle attachment ridging	Females	197	9.771	**0.021**	0.223	JU: more ridging
	Males	511	3.525	0.317	0.083	--
Mylohyoid bridging	Females	198	0.245	0.639	-0.035	--
	Males	511	0.001	1.000	0.001	--
Accessory mandibular foramen	Females	196	0.193	0.770	-0.031	--
	Males	510	28.391	**0.000**	-0.255	JU: less foramina
Chin prominence	Females	197	5.873	0.055	0.173	--
	Males	511	13.332	**0.004**	0.163	JU: blunt; CH: prominent
Chin shape	Females	198	3.616	0.164	0.135	--
	Males	511	12.826	**0.002**	0.158	JU: square; CH: pointed
Number of mental foramen	Females	199	0.260	1.000	0.036	--
	Males	511	3.883	0.274	0.087	--
Ascending ramus shape	Females	198	5.743	**0.031**	0.170	JU: wide; CH: pinched
	Males	511	0.256	0.674	0.022	--
Ascending ramus profile	Females	198	18.776	**0.000**	0.308	JU: straight; CH: slanted
	Males	511	15.319	**0.000**	0.173	JU: straight; CH: slanted

*statistically significant values in bold.

VITA

Sean D. Tallman earned his B.A. in anthropology from the University of Washington in 2000, followed by a M.A. in anthropology from the State University of New York at Binghamton in 2005. After receiving his M.A., Sean held positions of Osteologist, Archaeologist, Anthropology Instructor, and Consultant in various contexts in the Pacific Northwest. Sean was an Oak Ridge Institute for Science and Education Postgraduate Research Fellow from 2007 to 2009, and a Forensic Anthropologist from 2009 to 2013, at the Joint POW/MIA Accounting Command-Central Identification Laboratory (JPAC-CIL). In these capacities at the JPAC-CIL, Sean led archaeological recovery missions in Germany, Laos, Papua New Guinea, and Vietnam, and contributed to the identification of numerous U.S. service members killed during World War II, the Korean War, and the Vietnam conflict. In 2012, he joined the Department of Anthropology at the University of Tennessee, Knoxville, where he earned his Ph.D. in 2016. As a Ph.D. student, Sean was a Graduate Research Assistant for the Forensic Anthropology Center and a Graduate Teaching Assistant for the Department of Ecology and Evolutionary Biology where he taught human anatomy. Additionally, Sean received grant funding through the National Science Foundation and National Institute of Justice to conduct dissertation research in Japan and Thailand during the summer months of 2014 and 2014. Sean is presently an on-call Forensic Anthropologist for the Department of Health and Human Services' Disaster Mortuary Operational Response Team (DMORT IX), a Registered Professional Archaeologist (RPA), and a Fellow in the Anthropology Section of the American Academy of Forensic Sciences. His research interests include human skeletal biology, sex and ancestry estimation, and human skeletal variation in East and Southeast Asia.