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SEX AND ANCESTRY ESTIMATION METHODS IN MODERN FILIPINO CRANIA
*(MGA PARAANG PAGSUSURI NG KASARIAN AT LAHI MULA SA BUNGO NG MGA
KASALUKUYANG PILIPINO)*

BY

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DISSERTATION

Submitted in partial fulfillment of the requirements
for the degree of Doctor of Philosophy in Anthropology
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ABSTRACT

Diversity has been a central focus within anthropology since its disciplinary origins. In forensic anthropology this has come to include understanding the wide range of physical variation present in the human species across the spectra of geographies, generations, life stages, sexes, and different lived experiences for the purposes of estimating group membership and identification. Research has particularly flourished in the Americas, Europe, South Africa, and Australia largely owing to a history of prominent scholars, well-equipped university graduate programs and facilities, and large skeletal reference collections and databases that characterize these regions. Relative to these areas and the populations studied therein, East and Southeast Asia have received less scholarly attention. This is surprising given that the diversity found in these regions represents a substantial portion of both worldwide population and variation and that these regions are home to many forensically significant (i.e., vulnerable) groups. Filipinos, whom in particular have received little to no attention, are brought to focus here given the convergence of demographic, geographic, and historical factors that greatly contribute to the need for anthropological identification of human remains from this population. The current study ameliorates this problematic research gap by: (1) exploring methods of metric and nonmetric Asian sex and ancestry estimation that incorporate modern Filipino samples, specifically concentrating on the cranium, and (2) bolstering collaborative research capacities through the creation of a novel and internationally accessible Filipino reference collection from skeletons in the Philippines. The three methods explored include: (1) the optimized summed scored attributes (OSSA) method for sex estimation, (2) discriminant function analysis (DFA) via the Fordisc 3.1

(FD3) software for ancestry estimation, and (3) multivariate probit regression (MPR) for ancestry estimation.

First, the OSSA method originally intended for use in ancestry estimation was appropriated to test the applicability of the method for sex estimation using five cranial traits given the methodological similarities between classifying sex and ancestry. A large sample of documented crania from Japan and Thailand ($n = 744$ males, 320 females) are used to develop a heuristically selected OSSA sectioning point of ≤ 1 separating males and females. This sectioning point is validated using a holdout sample of Japanese, Thai, and Filipino ($n = 178$ males, 82 females) individuals. The results indicate a general correct classification rate of 82% using all five traits, and 81% when excluding the mental eminence.

Second, ancestry classification trends of the Filipino sample ($n = 110$) were analyzed when using craniometric measurements and DFA via FD3. Results show the greatest classification into Asian reference groups (72.7%), followed by Hispanic (12.7%), Indigenous American (7.3%), African (4.5%), and European (2.7%) groups included in FD3. This general pattern did not change between males and females. Moreover, replacing the raw craniometric values with their shape variables did not significantly alter the trends already observed.

Third, MPR models were used to classify the ancestral affiliation of Filipino crania using morphoscopic traits. The overall correct classification rates for three-group and four-group models were 72.1% and 68.6%, respectively. Filipinos classified as Asian 52.9% of the time using three ancestral parental groups and 48.6% using four groups. A large portion of Filipinos also classified as African. There were no significant differences in classification trends or accuracy rates between complete crania and crania with at least one missing variable.

Much as this work emphasizes methodological advancements in Filipino biological profile estimation, it also more broadly attempts to introduce forensic anthropology in and of the Philippines as a discourse worthy of more mainstream study. Both the generation and application of knowledge in forensic anthropology have only begun in the Philippines. The outcome of missing persons investigations is dependent on the scale, infrastructure, and political will of the context. This work hopes to inspire the improvement of all three and provide forensic anthropology in the Philippines its due attention.

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That said, may this be the last thesis I ever have to dedicate to any of you again!

*To the missing and unidentified Filipinos
of disaster and atrocity,
natural or anthropogenic,
may it never be too late
to find your way back home.*

*Sa mga nawawalang at hindi pa nakikilalang Pilipino
dulot ng sakuna at kalupitan,
natural man o sanhi ng tao,
maaaring hindi kailanman mahuli
para makauwi muli sa inyong tahanan.*

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CHAPTER 1

INTRODUCTION

1.1. Anthropology and Its Forensic Arm

Modern formations of science and empiricism were products of the Renaissance, and later paved the way for speculations on man's place in nature in the 18th century (Huxley 1863), making anthropology less than three centuries old. The Age of Exploration saw multiple encounters of European explorers with previously unknown cultures, and it was this diversity of peoples in combination with existing efforts to classify the natural world that led to the birth of anthropology. It was during this time that "race" became a lasting concept in European circles (Little and Sussman 2010).

The physical arm of anthropology sought to classify humans based on physical differences, whether through skin color, stature, or skull shape, among others, often with hierarchical and divisive agendas. Indeed, such a Eurocentric narrative is tightly bound to present-day colonial histories and scientific racism. Much of this early research force, even up to the early 20th century, focused on physical measurements of human skeletons. Craniology in particular played an instrumental role in the justification of human racial classification by the likes of proto-anthropologists such as Linnaeus, Blumenbach, Morton, and Broca (Shapiro 1959). Early scientific conclusions were warped to fit White supremacist ideologies such as degenerations of beauty from the Caucasian cranial type (Bhopal 2007), and greater intelligence linked to larger crania in men versus women and Caucasians versus other races (Broca 1861). Whether these early scientists subscribed to models of ranked superiority themselves as explanations of human diversity, their works would nevertheless later be appropriated to justify

some of the darkest episodes of human history. Some of the best studied examples are the Atlantic slave trade, the genocide in Nazi Germany, the Scramble for Africa, and eugenics movements across the Western world.

It was the gradual departure from the dominant theme of typology and fixed racial classification that allowed for a 'new' physical anthropology (Washburn 1951; Strum et al. 1999; Fuentes 2010). Later in the 19th century, Charles Darwin's (1859) theory of evolution would provide the link between mankind to fossil ancestors, contemporary apes, and human variation. Franz Boas pioneered growth studies, phenotypic plasticity, and popularized his four-field approach (Little 2010). Aleš Hrdlička (1919) professionalized physical anthropology in the United States and increased technical standards and the field's scope of study. Earnest Hooton had trained a whole generation of scholars with wide subspecialties of physical anthropology. His successful pedagogy still permeates our academic genealogies today (Kelley and Sussman 2007). In sum, 20th century physical anthropology was considering the broader biological implications of man while grappling with its erroneous antecedents.

Physical anthropology has expanded into a multi-disciplinary endeavor under the shared mantle of human evolution and variation. The application of this human variation to questions and issues of medico-legal significance would define a new branch of physical anthropology in the late 20th century (Ubelaker 2018). As early as 1849 with the murder of Harvard University professor Dr. George Parkman, Oliver Wendell Holmes I and Jeffries Wyman were using their knowledge of skeletal anatomy to reassemble Dr. Parkman's dismembered remains, produce age, race, and stature estimates, and arrive at an identification. This early case of identifying bones within a criminal justice context, alongside similar efforts by other anthropologists such as George Dorsey and Thomas Dwight, would become the formative period of American forensic

anthropology. Later, T. Wingate Todd would establish a skeletal reference collection in Cleveland, Ohio, and Robert Terry and Mildred Trotter would do the same in St. Louis, Missouri. These collections would serve as the material basis for the majority of the forensic anthropological techniques used today. In 1962, Wilton Marion Krogman (1962) would publish his seminal work *“The Human Skeleton in Forensic Medicine”*, the first book devoted to the study of human bones within forensic contexts that had originally emerged from a 1939 pamphlet he wrote for the Federal Bureau of Investigation. Forensic anthropology would formalize as a discipline with the creation of the Physical Anthropology Section (later simply the Anthropology Section to acknowledge contributions of the other subfields) within the American Academy of Forensic Sciences in 1972, and later with the creation of the American Board of Forensic Anthropology in 1977. This heavily abbreviated history of forensic anthropology highlights the youth and thus potential of this field in research and in practice.

It is with great hope that the following text will expand, even incrementally, current understanding of contemporary human skeletal variation, and that this knowledge will find its way into real-world cases of criminal investigation, disaster victim identification, repatriation, and situations yet to be anticipated.

1.2. Statement of the Problem

Deaths from accidents, homicides, mass disasters, armed conflicts or genocide can result in unidentified skeletonized remains that require identification before further investigation or prosecution. In such cases, a forensic anthropologist is often consulted to estimate the age, sex, ancestry, and stature of the remains (i.e., the biological profile) in order to narrow down potential identities. Current standard methods of estimation were first derived from skeletons of known

biological profiles (although ages-at-death were poorly documented; Hunt and Albanese 2005) housed in reference collections that were amassed in the late 19th to early 20th centuries. The majority of these skeletons are of European or African descent and largely reflect American demographics prior to the 1950s (Hunt and Albanese 2005; Komar and Buikstra 2008; Komar and Grivas 2008). Given the wide range of global human variation (Howells 1973, 1989; Algee-Hewitt 2016) and secular changes that have occurred since (Jantz and Meadows Jantz 2000; Wescott and Jantz 2005), these samples may not be reliably applied to all human groups. Considering this physical variation both spatially and temporally, coupled with the increasingly diverse biocultural demographics of modern American metropolises, expanding and refining population-specific methods is warranted. This is pertinent to forensic practices in the United States as the country's racial and ethnic makeup is one of the most heterogeneous in the world. Continued use of inappropriate reference samples may lead to incorrect identifications and stalled investigations.

Genuine effort in anthropological research needs to address the effects and limitations of method applicability on understudied groups. Asians remain a heavily understudied group despite making up 5.6% of the population in the 2010 US census (Hoeffel et al. 2012). The increasing importance of Asians in US demographics is easily demonstrated. Within a decade from 2000-2010 the Asian population in every state except Hawaii grew by at least 30%; 57% of Hawaii's population was comprised of Asians by 2010 (Hoeffel et al. 2012). Indeed, Asians represent the fastest growing racial group in the United States. Such numbers are important forensically because of the increasing likelihood of encountering human remains of Asian ancestry, and thus requiring appropriate methods of identification. The National Missing and Unidentified Persons System lists 264 out of 12,947 cases of unidentified Asians as of 23 August

2019, while the FBI National Crime Information Center reported 12,994 out of 612,846 entries of missing Asian individuals in 2018.

In addition to forensic case investigations, refined estimation methods are necessary in mass disaster contexts both nationally and abroad. For instance, tragedies such as the September 11 attacks, airline crashes, and natural disasters involve multiple casualties of various ages, sexes, and ancestries. International humanitarian aid in the form of disaster victim identification and management such as with the 2004 Indian Ocean tsunami involving 58 nationalities also requires knowledge and application of methods that can capture the diversity of skeletal variation (De Valck 2006). Indeed, underutilization of anthropological ancestry estimation during post-tsunami identification efforts produced significant delays and misidentifications (Black 2009). In addition, ongoing efforts by the Defense POW/MIA Accounting Agency to account for and return missing servicemen from previous US conflicts has involved sorting US from non-US remains in countries like Vietnam, North and South Korea, Cambodia, and Laos. In fact, an American Graves Registration Service laboratory for identification of fallen U.S. soldiers actually operated in Manila during the mid 20th century, headed by anthropologist Robert Fox and succeeded by Charles Warren (Warren 1981; Solheim 1984, 1987). There have been several iterations of the laboratory since then but it exists now as the Defense POW/MIA Accounting Agency in Hawaii, which still conducts disinterments and field recoveries in the Philippines. Other national teams such as from Australia and Japan are attempting similar wartime repatriation efforts. In both these contemporary and historic mass fatalities the ability to distinguish between sexes and ancestral affinities and then apply population-specific methods has the potential to assure and expedite accurate identifications.

Why then has there been such a delay in furthering this research? Asian reference skeletons are relatively rare or inaccessible. Only recently has the lack of Asian representation been explicitly addressed because of the fairly sudden availability of Asian skeletal samples to Western scholars in countries such as Japan and Thailand (e.g., Schmitt 2004; Gocha et al. 2013, 2015; Dudzik 2015; Tallman and Winburn 2015; Kim 2016; Tallman 2016). The term Asian is also incredibly broad; the US Census Bureau defines Asian as any person having ancestral origins in the Far East, Southeast Asia, and the Indian subcontinent. Tallman (2016) and Dudzik and Jantz (2016) have explored these population differences across national boundaries among modern Japanese, Chinese, Korean, Vietnamese and Thai skeletons. Indeed, there is a need for more representation across Asian groups in order to better incorporate the wide variation within this ancestral population.

Filipinos in particular have received little to no attention. This is surprising as Filipinos are the third largest Asian demographic in the United States. Over 3.4 million Americans report as having some degree of Filipino ancestry, with more than 2.5 million identifying as solely Filipino (United States Census Bureau 2010). The Philippines also represents the third and fifth largest source country for documented and undocumented immigrants, respectively (Baker and Rytina 2013; Lee and Baker 2017). In Canada, Filipinos rank first in number of permanent residents by source country (Citizenship and Immigration Canada 2015). The Republic of the Philippines has a census of more than 101 million people (Philippine Statistics Authority 2016), with the capital, Manila, being the most densely populated city in the world at 71,263 people per square kilometer. Nearly 2.5 million Overseas Filipino Workers fuel the country's foreign remittance (Philippine Overseas Employment Administration 2014), with other estimates at 7.29 million (Kanlungan Centre Foundation 2000), making the Philippines one of the largest labor

exporters in the world (Rodriguez 2010). Targeted violence against these Filipino migrant workers is prevalent, particularly towards women (Shah and Menon 1997; Alcid 2003; Hilsdon 2003; Piper 2003). Furthermore, more than a quarter of Filipinos in the Philippines live below the poverty line (Bersales 2016), which becomes pertinent when considering the frequency of natural disasters that affect the country (Brown 2013; Garschagen et al. 2016) or the history of turbulent militant and state-sanctioned violence (Hannibal 1987; Sales 2009; Thompson 2016). Rates of decomposition are rapid and often preclude reliable identification via facial recognition or fingerprinting in post-disaster settings. One study reported cases of full skeletonization only two weeks after a major typhoon had made landfall (Ballera et al. 2015). Other unique situations of importance to forensic identifications in the country are the prevalence of child and human trafficking cases (Guth 2010) and death fraud using black market cadavers (Greenwood 2016; Elliott 2017). The Philippines has also experienced unique peopling and Western colonization histories relative to other Asian countries (see Chapter III). These histories likely introduced gene flow and other microevolutionary processes not currently captured by present Asian skeletal samples (Bugawan et al. 1994; Tabbada et al. 2010; Delfin et al. 2011, 2014; Banda et al. 2015). Indeed, island Southeast Asia is absent from forensic anthropological discourse.

Despite factors such as population numbers, socioeconomic hardships, widespread diasporas, and natural disasters that could all play a role in Filipinos entering the forensic context, research on Filipinos has nonetheless been extremely marginal. This is likely due in large part to a lack of skeletal resources. The few specimens of Filipinos that are curated in the United States are archaeological, and so may not reflect subsequent secular changes (Jantz and Meadows Jantz 2000; Wescott and Jantz 2005). Further, archaeological remains do not have known biological profiles with which to establish method standards. Sparse osteological

collections can be found in teaching hospitals and universities around the Philippines, but these are most often used as anatomical training tools and rarely have antemortem data or elements still associated to a single individual. Only one previous study has used documented Filipino long bones to calculate stature (Oropilla et al. 1991), but this collection was destroyed shortly after the study. Others have relied on sampling living individuals to characterize sexual dimorphism in the Filipino dentition (Potter et al. 1981; Taturan 2012).

In its broadest sense, the goal of this research program is to advance and diversify forensic anthropological capacity, especially as applied to individuals of Asian descent. This not only means refining methods for estimating the Asian biological profile, but also enhancing the investigative and scientific power of law enforcement and researchers in the US and abroad. My dissertation will expand knowledge on Asian skeletal variation, specifically focusing on:

- (1) developing methods for estimating sex and ancestry in Filipino individuals from the crania, and
- (2) establishing an internationally accessible Filipino skeletal reference collection that sustains applied and practical research beyond this dissertation.

Ancestry is one of the first components estimated in order to calibrate later estimations of age, sex, and stature. Assessment of the sex of individual skeletons is also critical as it further calibrates age and stature estimates, and potentially reduces possible identifications by half. Results from this research will comply with the 1993 *Daubert* ruling for more rigorous scientific testing of methods, expand knowledge of human variation, aid in forensic and disaster victim identifications, and potentially ensure more accurate administration of criminal justice, especially for an understudied yet increasingly important group.

1.3. Hypotheses

This research questions (a) if the variation in Filipino crania is explained in part by sexual dimorphism, (b) if this dimorphism differs from that found in other populations, and (c) if there is additional Filipino cranial variation that significantly expands known variation among Asian individuals. Therefore, the objectives of this study are to:

1. Assess the degree of sexual dimorphism in modern Filipino crania, develop population-specific sex estimation methods, and compare the accuracy of sex estimation methods developed from other populations; and
2. Assess the phenotypic variation in modern Filipino crania versus other broad ancestral groups (e.g. European, African, Native American, and other Asian descended individuals), and use this variation to develop refined methods for estimating Asian ancestry from the cranium.

As discussed above, the need for Filipino-inclusive methods is not currently met by the availability of samples required to create and test them. Thus, a third objective of this research is to assemble an internationally accessible reference collection of modern and identified Filipino skeletons. Having a permanent collection will bolster regional and international forensic scientific capacity, meaning the advancement of knowledge continues beyond this dissertation.

To scientifically answer these questions and achieve these objectives, the following hypotheses are tested:

1. Sufficient sexual dimorphism exists within modern Filipino crania that sex can be accurately estimated given an unidentified Filipino cranium.
2. Sex in Filipino crania can be accurately estimated when using methods developed from other Asian populations.

3. Asian ancestral affinity can be accurately estimated from Filipino cranial morphology, and Filipino morphology is differentiable from that of other broad continental ancestral groups.
4. Lastly, Filipino cranial morphology contributes to knowledge of cranial variation not yet observed in the current samples representing Asian ancestry.

1.4. Organization of Chapters

Chapter II begins with a review of the literature on sex and ancestry estimation within forensic anthropology. It first briefly considers the rationale of considering these two components of the biological profile simultaneously. Sex estimation is then reviewed in terms of the metric and nonmetric methods employed within the field. Similarly, ancestry estimation is reviewed by metric and nonmetric approaches. The concept of race within ancestry estimation is also discussed.

Chapter III focuses on the geographical, historical, and forensic context of the Philippines. The chapter begins with a description of Philippine physical and human geography, followed by prevailing models and evidence for the initial and subsequent arrivals of the first anatomically modern humans into the archipelago. The colonial era is then discussed, and how this history has contributed to present day conceptions of race and ethnicity within the country and the United States. Finally, the state of forensic anthropology (and forensic sciences in general) within the Philippines is reviewed.

Chapter IV concerns the materials and methods used to test the previously mentioned hypotheses. These include descriptions of the generated and comparative datasets used, as well as a brief overview of the statistical methods employed in each of the succeeding chapters.

Chapter V reports the results of a study applying the Optimized Summed Scores Attributes methodology, or OSSA (Hefner and Ousley 2014), on sexually dimorphic ordinal traits of the cranium among various Asian populations, including Filipinos.

Chapter VI reports the results of a study evaluating the ancestry classification trends of Filipino crania using craniometric measurements run through linear discriminant function analyses provided by the Fordisc 3.1 software (Jantz and Ousley 2005).

Chapter VII reports the results of a study evaluating the ancestry classification trends of Filipino crania using ordinal morphoscopic traits run through ordinal multivariate probit regression models.

Chapter VIII concludes the dissertation with an overall summary, and brings forth future directions that can be pursued.

CHAPTER 2

SEX AND ANCESTRY ESTIMATION

2.1. The Biological Profile

One of the primary roles of the forensic anthropologist is to assign a biological profile to unidentified human skeletal remains, which can aid in narrowing down the list of potential identities. The major components of the biological profile are the decedent's probable biogeographic ancestry, biological (chromosomal) sex, chronological age in years at death, and stature. This information is estimated from phenotypic observations of their bones, particularly from their general appearance, size, shape, and measurements; in the case of sex and ancestry, these estimations of phenotype are used as imperfect measures of genotype. Furthermore, the different components are often interconnected in many ways – the degrees of difference between males and females may vary across different populations, the progression of skeletal age indicators may depend on the sex, or the calculation of stature may be altered by the population membership, sex, and age of the individual. This means that the order in which these components are estimated by the anthropologist matters. Because many methods can be population-specific, ancestry is often the first component of the biological profile to be estimated. After or in conjunction with ancestry is the estimation of sex, which can then inform assessments of age and stature.

Here, sex and ancestry are tackled together not only because they are the first two steps in completing a biological profile, but also because they share many methodological similarities in the ways they are observed, recorded, and analyzed (Konigsberg et al. 2009). The final determinations of sex and ancestry are categorical variables, either the individual is male or

female, and is Asian, African, European, or some other nominal assignment. Ancestry need not be a hard classification but may in some cases be estimated as a mixture between multiple groups (Algee-Hewitt 2016). This is in contrast to stature and age estimates, which are often reported as numerical ranges (e.g., 5 feet 7 inches to 5 feet 10 inches tall; 20 to 30 years old). Various methods of sex and ancestry estimation use both continuous metric (i.e., osteometric measurements) and dichotomous or ordinal nonmetric data (i.e., morphoscopic measurements), and thus employ similar statistical analyses. Both sex and ancestry estimation, specifically using morphoscopies, also suffer from biases introduced by a gestalt approach where the overall initial impression of the skull, for example, can often steer the observer's decisions based on their personal experience (Berg and Tersigni-Tarrant 2014). Lastly, lay interaction with these particular components of the biological profile are often confounded with their culturally constructed counterparts of gender and race. Identities and constructions of gender and race have generally appropriated biology to explain sex and population differences that have largely historic, social, and cultural origins (Cartmill 1998; Walker and Cook 1998).

This chapter provides an overview of sex and ancestry estimation within forensic anthropology, particularly on how historical, theoretical, and methodological advancements have contributed to current perspectives. Because this dissertation concerns methods of sex and ancestry estimation from the cranium, relevant literature from this region of the body is emphasized.

2.2. Sex Estimation

Sexual dimorphism, or the differences in phenotypic expression between sexes of a species, occurs in many sexually-reproducing organisms. Sexually dimorphic characteristics

include physical, physiological, and behavioral traits beyond mere gonadal, genital or chromosomal differences. In humans, most of the obvious observations of outward difference between the sexes such as height, muscularity, body hair, body size, breast formation, and voice pitch are secondary sex characteristics that become most prominent during puberty. Differences in the size, shape, and robusticity between the male and female skeleton are no exception, and anthropologists have sought to document these differences for virtually every bone in the body. Secondary sex characteristics are likely the result of sexually selective forces that maximize individual reproductive fitness (Puts 2010). Thus, pre-pubescent subadults generally do not display discernable differences and, understandably, finding such differences in subadult skeletal morphology is difficult, if not dubious.

Humans are sexually dimorphic in many ways, but they are the least sexually dimorphic among closely related primate species (Frayser and Wolpoff 1985). This means that despite trait differences, there will always be overlap across the two distributions for any trait of the two sexes. Nevertheless, the fact that humans are sexually dimorphic forms the basis for sex estimation in forensic anthropology. In general, males are larger than females, which may be proximately explained by greater muscle mass, greater bone mass accumulation, and longer growth periods in men (Bonjour et al. 1991; Janssen et al. 2000; Rogol et al. 2002; Wells 2007), and ultimately by intraspecific sexual selection and competition (Geary 1998; Pawlowski et al. 2000; Manning and Taylor 2001; Nettle 2002; Puts 2010). However, smaller males may be more consistent with female averages, and vice versa with larger females being more consistent with male averages.

The extent or degree of sexual dimorphism will always depend on the population being dealt with and the specific indicator(s) being observed. No universal sex estimation standard

exists that can be applied to all human groups save perhaps for the pelvis, and more specifically the pubic bone (Phenice 1969). Because secondary sex characteristics manifest later in development, variation in the onset and duration of pubertal changes are mediated by intrinsic genetic and extrinsic environmental interactions that follow distributions with different parameters depending on the population (Palmert and Boepple 2001; Palmert and Hirschhorn 2003; Parent et al. 2003). Puberty is initiated by the awakening of gonadotropin-releasing hormone from the hypothalamus and gonadotropins (primarily luteinizing hormone and follicle-stimulating hormone) from the pituitary gland and regulated by a host of genes including *GPR54* and *KiSS-1* (Seminara et al. 2003; Shahab et al. 2005; Topaloglu et al. 2009; Ojeda 2010). Modulating the output of these genes are signals linked to other genetic factors and the environment, which are numerous and intertwined (Parent et al. 2003). These factors can include family history, ethnicity, sex, geography (altitude, temperature, humidity, climate, and light availability), socioeconomic status (nutrition, medical care, sanitation, family size, and occupation), and stressors such as migration. Secular changes in age at menarche have also been shown for many populations around the world (e.g., Wyshak and Frisch 1982; Eveleth and Tanner 1990; Huen et al. 1997; Pasquet et al. 1999; Ong et al. 2006; Euling et al. 2008; Rigon et al. 2010).

While nearly every bone will display some degree of sexual dimorphism, the most relied upon indicator for sex is the human os coxa. The obvious cause for this difference between the sexes is due in large part to the obstetric requirements imposed on females during parturition (Correia et al. 2005; Moffett 2017). Following the pelvis, many texts suggest the skull as the second-best indicator for sex (e.g., Pickering and Bachman 1997; Bass 2005; Byers 2016), although Spradley and Jantz (2011) found many postcranial elements to be superior

discriminators. Indeed, Klepinger (2006: 28) had noted that “the skull is not the next best skeletal region for assessing sex—that standing probably belongs to the femur or humerus.” This may be due to secondary accommodations by other postcranial joints to wider hips in females such as a greater carrying angle at the elbow to avoid hitting the hips during arm swing (Bari et al. 2015) or a greater quadriceps femoris (Q-)angle at the knee for proper bipedal locomotion (Nguyen and Shultz 2007). Likewise, size differences in the femur or humerus between the sexes may be linked to sexual dimorphism in body mass. Common methods use metric size differences in the humeral and femoral heads (Stewart 1979), or shape differences as in the distal humerus (Rogers 1999). Furthermore, within-individual correlations between skeletal regions, such as between the os coxa and cranium, have also been found to be low such that an extremely masculine pelvis does not necessarily correspond with an equally masculine cranium as demonstrated by Best et al. (2018).

There are two general classes of data for analyzing sex: nonmetric and metric methods. Nonmetric, visual, or morphoscopic methods often employ qualitative scorings of bony features on dichotomous or ordinal scales. The most widely used method for sex estimation is Phenice’s (1969) scorings for the presence or absence of three pubic traits: the ventral arc, subpubic concavity, and ischiopubic ramus ridge. Buikstra and Ubelaker (1994) had applied a 3-point ordinal system to these traits (i.e., 1 = female, 2 = ambiguous, 3 = male), while Klales et al. (2012) had codified a 5-point system. Phenice (1969) had reported accuracy rates of 96% when using all three traits, which was retested by other studies that have produced similar (Kelley 1978; Sutherland and Suchey 1987; Klales et al. 2012) and slightly dissimilar results (Lovell 1989; McLaughlin and Bruce 1990; Ubelaker and Volk 2002). Other discriminating traits of the pelvis include the presence or absence of the preauricular sulcus and shapes of the greater sciatic

notch, pelvic inlet, obturator foramen, and acetabulum, among others (Buikstra and Ubelaker 1994; Rogers and Saunders 1994; Bruzek 2002; Walker 2005). Sex-specific nonmetric traits have also been studied in other postcranial elements such as presence or absence of a rhomboid fossa on the infero-medial aspect of the clavicle (Rogers et al. 2000) or morphology of the distal humerus (Rogers 1999, 2009; Falys et al. 2005; Vance et al. 2011) and sacrum (Rogers and Saunders 1994).

Morphoscopic sexual discrimination of the skull has focused on assessments of gracility versus robusticity, where features such as muscle attachment sites in females tend to be smaller, smoother, and less pronounced, while in males they tend to be larger, broader, and more rugose. While these “larger-smaller” traits are indeed reflective of sexual dimorphism, Weiss (1972) argues that there is a widespread tendency among observers to deem intermediate phenotypes as male. He attributes this bias to a greater allowable range of trait manifestations for males, such as moderately to strongly marked temporal lines, whereas the absence of a marked temporal would be categorized as female. Additionally, there is a historical emphasis of using male skulls as exemplars, for example in Hooton’s (1930) typological characteristics for race estimation. Reference collections also often contain a greater number of males due to an increased likelihood for men to both donate their bodies to science and to appear as unclaimed forensic cases (Komar and Grivas 2008; Asad et al. 2014), allowing for a greater familiarity with male variability over females. To the contrary, Meindl et al. (1985) found the opposite where both the skull and pelvis showed biases toward female assignments, while Rogers (2005) found no bias for the skull. However, as Weiss (1972) concludes, being aware of such biases may avoid them from occurring, which has been found to be true in the decades that have followed since his statements (Bone 1993).

Numerous traits have been recommended by various authors as useful for sex estimation from the skull (Krogman 1962; Rogers 2005; Williams and Rogers 2006; Byers 2017), the most common of which are the nuchal crest, mastoid process, supraorbital margin, glabella, and mental eminence first proposed by Broca (1875) and codified by Acsádi and Nemeskéri (1970) into a 5-point scale. Acsádi and Nemeskéri's (1970) diagrams, however, were problematic in that they specifically reflected European variation and were poorly drawn (Walker 2008). In response, Phillip Walker produced updated diagrams for Buikstra and Ubelaker's (1994) *Standards* volume that purportedly encompassed worldwide extremes, gave "geometrically even increases" between stages, and removed the assumption that "0" in a "-2" to "+2" scale was the default cut-off point between males and females (Walker 2008: 40) (Fig. 2.1).

The Walker traits maintain the 5-point scale, but from "1" to "5" with minimal and maximal expressions corresponding to more typically female and more typically male manifestations at each end of the spectrum. In general, females possess smooth and unpronounced nuchal crests, small mastoid processes, sharp supraorbital margins, somewhat flat and unpronounced glabellas, and little to no projection of the mental eminence above the surrounding bone. Inversely, males possess roughened and projecting nuchal crests, long and wide mastoid processes, thick and blunt supraorbital margins, rounded and projecting glabellas, and large mental eminences with easily palpable lateral borders. Of course, overlap in expression between the sexes occurs and will depend on both the individual trait and the population being examined.

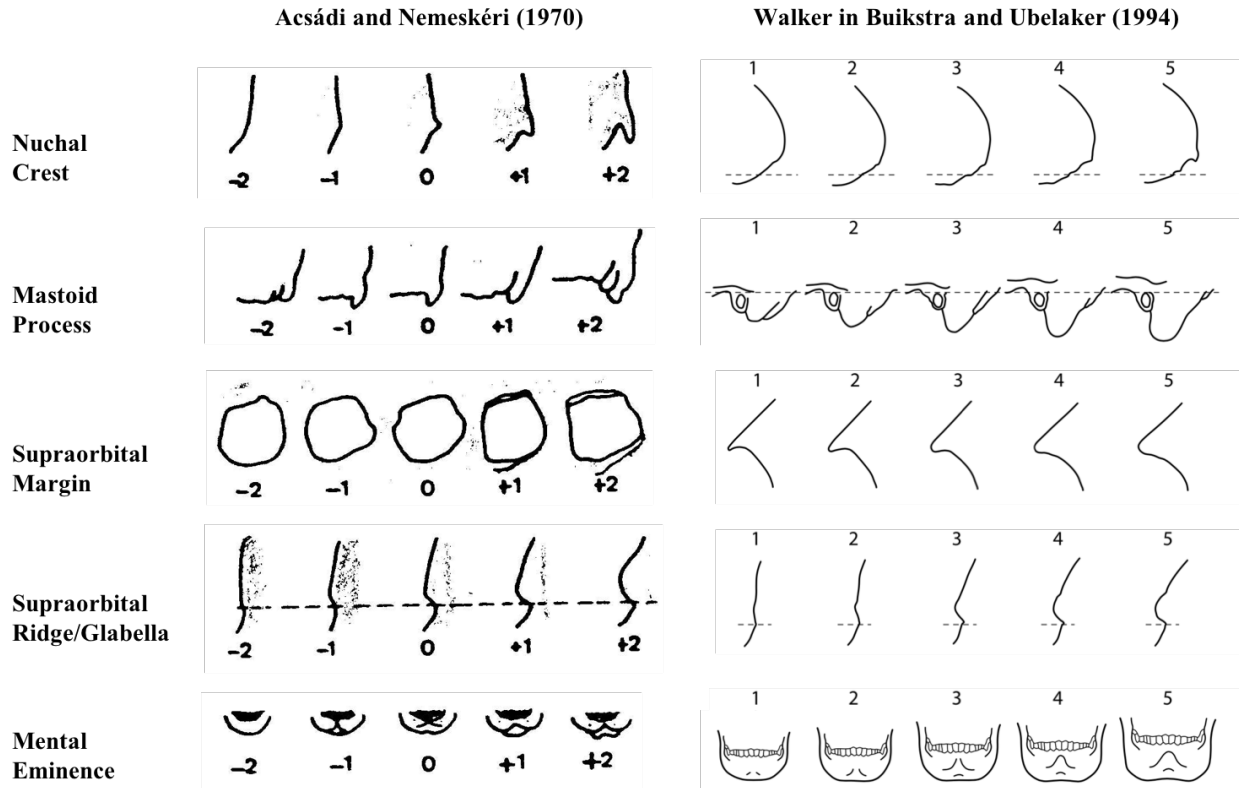


Figure 2.1. Phillip Walker's updates in Buikstra and Ubelaker (1994) to Acsádi and Nemeskéri's (1970) diagrams of five commonly used traits for nonmetric sex estimation from the skull.

Walker's (2008) definitions are becoming discipline standards for cranial nonmetric sex estimation, which allows for comparability and validation between scorers. MorphoPASSE (<https://www.morphopasse.com>) is a recently amassed and continually growing database of recorded Walker traits for many skeletal populations from around the world (Klaes and Cole 2018). The Walker traits have been evaluated across multiple populations and subjected to statistical validation using discriminant function analysis, logistic and probit regression, *k*-nearest neighbor clustering, cumulative probit modelling, and decision trees (e.g., Konigsberg and Hens 1998; Walker 2008; Garving et al. 2014; Krüger et al. 2015; Garvin and Klaes 2017; Klaes and Cole 2017). Furthermore, studies have shown that age and body size have weak effects on these

sexually dimorphic traits and do not need to be incorporated into sex estimation methods (Garvin et al. 2014; Lesciotto and Doershuk 2018).

Metric methods use continuous, quantitative variables such as linear, angular, arc, and volumetric measurements that seek to capture both size and shape. Metric measurement of the skull has a long history in anthropology, most notably beginning as the pseudoscientific pursuit known as phrenology to attach natural inequality in cognitive and social ability between human groups. While the emphasis of these earlier efforts was racially motivated, cranial measurements were also used to explain differences in ability between the sexes (Broca 1861; Staum 2003). Moving towards a more empirical understanding of human variation, later developments would advance modern craniometry via the standardization of measurement definitions, collection of large datasets, and subjection to statistical analyses.

Standardization of measurements and their definitions is essential to the reproducibility and validation of data across observers, datasets, cases, and publications. The measurement standards used today are borne from historical legacies of pioneering anthropologists and anatomists, most notably through the seminal volumes of Rudolf Martin (1914; Martin and Knussmann 1988), Aleš Hrdlička (1920), Ashley Montagu (1960), and W.W. Howells (1973), among others, who built upon each other's works. Understandably, the historical superimposition of definitions and standards has also created opportunities for confusion, such as Martin's versus Howell's prosthion location or the true maximum tibial length (Jantz et al. 1995). More or less universal and well-understood definitions now guide modern osteometry (Buikstra and Ubelaker 1994; Moore-Jansen et al. 1994; Langley et al. 2016).

Traditional craniometrics employ the use of standardized landmark points and the linear distance measurements between them. There are three types of landmarks with decreasing

consistency in location that may either be biologically or mathematically homologous: Type I (or anatomical) landmarks, Type II (or mathematical) landmarks, and Type III (or extremal) landmarks (Bookstein 1991). Type I landmarks are points of intersection or contact between cranial sutures and anatomical planes. Type II landmarks are points of curvature maxima. Type III landmarks are estimated opposite other landmarks or by virtue of information at other locations on the skull. Typically, the inter-landmark distances between any of these points only require either spreading or sliding calipers for measurement. More nonstandard, and therefore rarer, more obscure, or obsolete, measurements may require special instruments such as a coordinate caliper and are less frequently encountered in the literature. Some measurements of the mandible require a mandibulometer to accurately position the bone for data recording. Semilandmarks, which are more commonly encountered in geometric morphometric methods, are defined in terms of their positions along geometric features (Weber and Bookstein 2011).

Large global craniometric datasets comparable by way of these standardized measurements have been heavily mined for research. More easily accessible datasets include those from Howells (1996) (males = 54.2%; females = 45.8%) and Hanihara (1996) (males = 100%), which are spatially and temporally diverse, and more contemporary datasets representing forensically significant American demographics provided by the Forensic Anthropology Data Bank (Jantz and Moore-Jansen 1988) (males = 68.8; females = 31.2) and the Maxwell Museum Documented Skeletal Collection (Komar and Grivas 2008) (males = 61.8%; females = 38.2%).

Craniometrics, being quantitative in nature, benefit from an easier subjection to statistical manipulation, and therefore have a longer history of statistical rigor than nonmetric data. Despite Hrdlička's indefatigable aversion to statistics, claiming it to be the invention of the devil and the ruin of physical anthropology, Boas and Hooton persisted in championing for its value (Montagu

1944; Schultz 1944; Washburn 1984; Brues 1990; Little 2017). Modern computers have enabled the widespread use of multivariate statistics as opposed to earlier approaches limited to univariate descriptions and indices. In standard craniometric sex estimation, the most common technique used is discriminant function analysis, which usually employs either a linear (using equal variance-covariance matrices) or quadratic model (using separate variance-covariance matrices for each sex category) (e.g., Giles and Elliot 1963; Birkby 1966; Howells 1973; Calcagno 1981; Uytterschaut 1986; Konigsberg et al. 2009; Guyomarc'h and Bruzek 2011; Mahakkanukrauh et al. 2015; Ramamoorthy et al. 2016). Other discriminant analysis models have also been proposed (Bensmail and Celeux 1996). Logistic regression and support vector machines have also been used (Santos et al. 2014). However, while most practitioners prefer to use qualitative and quantitative methods in their assessments in tandem, when only one avenue is available qualitative methods are preferred over quantitative ones nearly twice as often in a survey of self-identified forensic anthropologists (Klales 2013).

2.3. Ancestry Estimation

Ancestry is arguably the most contentious component of the biological profile because of its close association with the concept of “race”. Both biological and cultural anthropologists have long expressed the maxim of race as a social construct without biological meaning (see Littlefield et al. 1982; Shanklin 1994; Cavalli-Sforza 1995; Harrison 1995; Lewontin 1995; American Association of Physical Anthropologists 1996; American Anthropological Association 1998; Cartmill 1998; Brace and Seguchi 2003; Foster and Sharp 2004; Graves 2004; Smedley and Smedley 2005; Edgar and Hunley 2009; Wagner et al. 2017). In other words, the lumping of a wide spectrum of human traits into discrete, finite groups or races is made on the basis of

cultural, societal, and historical legacies rather than any scientifically justifiable criteria. While all cultures create folk taxonomies under their own knowledge structures (Hirschfeld 1996; Prentice and Miller 2007), the Western race concept in particular conflates biology with society (Caspari 2010). For instance, racial categories used by the US census are constantly changing to adapt to historical developments in emancipation, imperialism, and immigration that often cater to the dominance in power of one group over others (Lee 1993; Rodríguez 2000). Governmental categorization for the same individual will change across different national systems, such as persons with African descent living in the United States, South Africa, or Brazil (Marx 1998; Fredrickson 2001). Indeed, constructions of race even at scales smaller than nations shift with class, ethnicity, religion, gender, politics, and other segregating lines of difference beyond physical appearance (e.g., Brah 1993; Austin-Broos 1994; Kibria 1999; Lindley 2002; Pérez-Torres 2006; Omi and Winant 2015). Currently, the US Census Bureau collects race data on the basis of self-identification into categories defined by the US Office of Management and Budget (Table 2.1) and acknowledges that these categories reflect social definitions specifically recognized within the American context rather than biological ones. It was not until the 2000 Census that respondents could self-identify with more than one race.

Biological race has often been defined on the basis of shared genotypes, and to a related extent shared phenotypes and geographic isolation (see Table 2.2), but studies have failed to support these definitions. Common arguments against the biological basis for race have been supported by genetic data. For one, all humans are closely related to each other (99.9% at the DNA level) owing to an evolutionarily recent emergence of the human lineage around 200,000 to 300,000 years ago (Collins and Mansoura 2001; The 1000 Genomes Project Consortium 2015). Second, genetic variation within populations is far greater (85-95%) than what is added to

the variation when comparing between populations (3-10%) (Lewontin 1972; Barbujani et al. 1997; Rosenberg et al. 2002; Witherspoon et al. 2007). Third, the highest levels of genetic diversity in the world are found within and between African populations (Campbell and Tishkoff 2010). Fourth, all populations are the result of serial founder effects originating in Africa (Ramachandran et al. 2005; Jakobsson et al. 2008). And fifth, phenotypes such as skin color or nose shape that are often used to define races are shared across multiple groups as a consequence of similar climatic adaptations and not solely on the basis of genes (Jablonski 2004; Zaidi et al. 2017). The cranial phenotypic data have also supported these statements (Roseman 2004, 2016; Harvati and Weaver 2006; Betti et al. 2009; Strauss and Hubber 2010; Von Cramon-Taubadel 2014).

Table 2.1. US 2010 Census categories for race.

<i>Race Category</i>	<i>Defined Region of Origin</i>	<i>Options Listed on Census Questionnaire</i>
White	Europe, Middle East, North Africa	- White
Black or African American	Africa	- Black, African Am., or Negro
American Indian or Alaska Native	North America, Central America, South America	- American Indian or Alaska Native – Print name of enrolled or principal tribe
Asian	Far East, Southeast Asia, Indian Subcontinent	- Asian Indian - Chinese - Filipino - Japanese - Korean - Vietnamese - Other Asian – Print race, for example, Hmong, Laotian, Thai, Pakistani, Cambodian, and so on.
Native Hawaiian or Other Pacific Islander	Hawaii, Guam, Samoa, Pacific Islands	- Native Hawaiian - Guamanian or Chamorro - Samoan - Other Pacific Islander – Print race, for example, Fijian, Tongan, and so on.
Some Other Race		- Some Other Race – Print race.

Yet, easily perceptible or “commonsense” physical differences such as skin color, eye color and shape, lip shape, nose shape, and hair color and texture, do exist across global populations. How do anthropologists reconcile the ostensible paradox of race as biological fiction while acknowledging that observable biological variation exists? Indeed, gene and trait variants may cluster or exist at higher frequencies in specific populations. Some researchers have equated these clusters to commonly used racial or ethnic labels (e.g., Risch et al. 2002; Burchard et al. 2003; Shiao et al. 2012; Guo et al. 2014). Sociologist Ann Morning (2014a, 2014b) rightly argues that the scientific practice to identify such clusters is itself laden with socially mediated decisions by the scientist, and that the sociopolitical origins of race lead to the search for biological pseudo-analogues. While pre-existing population categories may have certain frequencies of gene variants, “the ways in which individuals are grouped together determine the genetic frequencies that are attributed to such populations, not that genetic frequencies determine how to group individuals into populations” (Foster and Sharp 2004: 792). Furthermore, these clusters do not have finite or discontinuous borders, nor do gene or trait variants exist exclusively in certain groups as the race concept would require (Rhine 1990; Jorde and Wooding 2004; Serre and Pääbo 2004; Hefner 2009). And even when certain genes are geographically distinctive in their frequencies, they hardly typify the human genome overall for that region (Feldman et al. 2003). Additionally, because the race concept is given such social weight, it produces embodied biological consequences largely in the form of health disparities (Gravlee 2009; Meloni 2017), but also in assortative mating practices, among others (Ousley et al. 2009). In other words, race, despite being a social construct, influences and therefore intertwines biology.

Table 2.2. Some definitions of biological race.

<i>Reference</i>	<i>Definition</i>
Hooton 1926: 76	A race is a great division of mankind, the members of which, though individually varying, are characterized as a group by a certain combination of morphological and metrical features, principally non-adaptive, which have been derived from their common descent.
Dobzhansky 1944: 252	Races are defined as populations differing in the incidence of certain genes, but actually exchanging or potentially able to exchange genes across whatever boundaries (usually geographic) separate them.
Boyd 1950: 207	We may define a human race as a population which differs significantly from other human populations in regard to the frequency of one or more of the genes it possesses. It is an arbitrary matter which, and how many, gene loci we choose to consider as a significant “constellation”.
Garn 1960: 7	At present time there is a general agreement that a race is a breeding population, largely, if not entirely isolated reproductively from other breeding populations. The measure of race is thus reproductive isolation, arising commonly but not exclusively from geographical isolation.
Hulse 1963: 262	Races are populations which can be readily distinguished from one another on genetic grounds alone.
Mayr 1963: 348	A subspecies is an aggregate of local populations of a species, inhabiting a geographic subdivision of the range of species, and differing taxonomically from other populations of the species.
Baker 1967: 21	It is concluded that race may be defined as a rough measure of genetic distance in human populations and as such may function as an informational construct in the multidisciplinary area of research in human biology.
Brues 1977: 1–2	A race is a division of a species which differs from other divisions by the frequency with which certain hereditary traits appear among its members. Among these traits are features of external appearance that make it possible to recognize members of different populations by inspection with greater or less accuracy. Members of such a division of a species share ancestry with one another to a greater degree than they share it with individuals of other races. Finally, races are usually associated with particular geographic areas.

The histories of anthropology and race are inextricably linked. Indeed, anthropology was borne from the desire to document and understand the wide variation in human physicality, language, behavior, culture, worldview, and origins. Race was conceptualized as a biological explanation for these differences, aligning with three centuries worth of developments in

European exploration, capitalism, theology, and science (Baker 1998). The race concept was perpetuated even further in North America with the sudden juxtaposition of easily identifiable groups between indigenous peoples, European immigrants, and African slaves that were historically geographically disparate (Brace 1995). This juxtaposition, and the imposition of hierarchical superiority upon them, became a fundamental fabric of American society or what author Studs Terkel (1992) called the “American obsession”.

The early to middle 20th century saw a transitional phase in anthropological perspectives of race. Indeed, in its inaugural volume in 1918, articles in the *American Journal of Physical Anthropology* simultaneously reflected different views on race in the voices of Aleš Hrdlička, Earnest Hooton, and Franz Boas (Caspari 2009, 2018). Earlier studies based on cranial dimensions by notable figures such as Anders Retzius, Johann Blumenbach, Samuel Morton, Paul Broca, Aleš Hrdlička, and Carleton Coon advocated for fixed, and often ranked typologies of human races that possessed largely immutable traits (Ta’ala 2014). While Earnest Hooton believed in the typological races of Caucasoid, Negroid, and Mongoloid, he dispelled notions of “pure” races, racial hygiene, and using non-physical traits such as language and religion to characterize races (Hooton 1936; Watkins 2012). Franz Boas spoke strongly against the largely unchallenged racial typology of the time. Boas argued that biological differences between races were small, and discredited ethnocentric claims of cultural superiority. He also controversially demonstrated that head shape was not an immutable trait that could accurately determine races but was rather the effect of environmental influences (Gravlee et al. 2003). Boas influenced the work of others such as Harry Shapiro, who likewise demonstrated the role of environment on skeletal plasticity (Anderson 2012). Another important mid 20th century figure who challenged typological hierarchies was Ashley Montagu, who was a rapporteur for UNESCO (1952) in their

Statement on the Nature of Race and Race Differences. The statement was issued to combat scientific racism, noting that the race concept was empirically limited in value and that “because of the complexity of human history, there are... many populations which cannot easily be fitted into a racial classification” (UNESCO 1952: 11). Montagu’s (1942: 41) magnum opus called race “the witchcraft of our time... humankind’s most dangerous myth.”

It was during the 1960s that racial typology was seriously questioned. These criticisms were largely facilitated by the culmination of civil rights movements, the “new” physical anthropology, technological advances in genetic analysis, and increasing inclusion of ethnic minorities in science (Caspari 2003; Ta’ala 2014). Attempts to find genetic correspondence to racial categories failed (see above). Another famous maxim that arose as a product of these attempts comes from Frank Livingstone (1962: 279): “there are no races, there are only clines,” highlighting the clinal or gradient nature of human gene frequencies across space. Howells (1995: 103) later echoed this sentiment in his analysis of worldwide cranial variation: “there are no races, only populations.”

Despite today’s generally widespread acceptance of race as biological myth within the scientific community (Wagner et al. 2017), forensic anthropology maintains an awkward position within the paradox. Namely, if race does not exist, why do forensic anthropologists continue to excel at finding it (Sauer 1992)? But Sauer’s question must be framed within the context of a few widely dispersed points of origin for different populations. His comment is similar to Sewall Wright’s (1978: 439) statement that “it does not require a trained anthropologist to classify an array of Englishman, West Africans, and Chinese with 100% accuracy by features, skin color, and type of hair in spite of so much variability within each of these groups that every individual can easily be distinguished from every other.” Indeed, race

remains a fundamental component of the biological profile, and forensic anthropologists still use terms such as “Caucasoid/White/European”, “Mongoloid/Asian”, and “Negroid/Black/African” in their assessments. Some have criticized the validity of such methods, arguing that human variation is too limited and that the continued practice of race estimation leads to misidentifications and the perpetuation of an erroneous concept (Goodman and Armelagos 1996; Goodman 1997; Armelagos and Goodman 1998; Williams et al. 2005).

Richard Lewontin’s (1972) study of classic genetic markers is the most widely cited evidence that differences between human groups are too small to allow accurate classification, and that most variation is actually found within populations rather than between. While generally correct, Lewontin (1972) looked at each genetic marker independently and failed to account for correlations between variables. A more realistic view of human variation involves a multivariate perspective, which reduces the amount of overlap between groups (Edwards 2003) (Fig. 2.2). Both genetic (Pritchard et al. 2000; Rosenberg et al. 2002; Bamshad et al. 2003; Jorde and Wooding 2004; Allocco et al. 2007) and cranial morphological studies (Howells 1973, 1989, 1995; Roseman and Weaver 2004; Ousley et al. 2009; Relethford 2009) employing multiple variables have revealed geographic patterning in worldwide samples, which allows classification rates greater than those expected with random chance. However, overlaps will always exist, and accuracies will never reach 100%, therefore leading to the rejection of an extremist typological view of classification. A multivariate model also does not discount that individual groups are themselves diverse (Ousley et al. 2009). Furthermore, it is important to acknowledge that the naming and labeling of such groups are mediated by social processes with biological consequences.

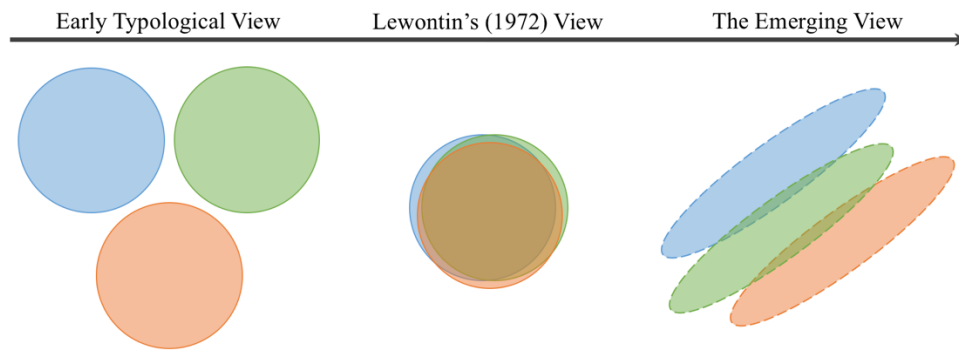


Figure 2.2. Scientific views on the nature of human variation have changed over time. The early “classical” view emphasized typology and different stocks of people. Lewontin (1972) later demonstrated that within group genetic variation is greater than between groups, indicating significantly large overlaps among all groups. The emerging view accounts for covariation of variables, recognizing Lewontin’s view of large within group variation and low between group variation while allowing for group separation. Dashed lines (*my own*) symbolize that these groups do not imply finite borders and are socially defined. Adapted from Fig. 1 in Ousley et al. (2009).

Therefore, estimation in forensic anthropology relies on a probabilistic translation of “biological traits to a culturally constructed labelling system” (Sauer 1992:109). This is not an attempt to reify the biological race concept, but to treat race as a social category that may have some inclusion criteria that are biological. Furthermore, such biological inclusion criteria vary across time and the social labels themselves. From a practical standpoint in order to achieve identifications, forensic anthropologists need to work within the cultural milieu that law enforcement, jurors, and the lay public operate within or is meaningful to them (Sauer 1992; Brace 1995; Konigsberg et al. 2009; Ousley et al. 2009).

In an effort to move away from the stigma that “race” carries and emphasize more heavily the biological bases for human group variation, many forensic anthropologists use “ancestry” instead, which correlates more strongly to human population history and geography. Race however still carries meaning in the broader social context of forensic casework and law enforcement, and is widely used for its utility in decedent identification. Here, the term “ancestry” is preferred over “race”, even though the two are often used interchangeably in the

literature in reference to biological profile estimation. The term “race” is used here when referencing its historical use in the literature.

As with sex estimation, ancestry methods primarily use nonmetric (i.e., morphoscopic) and metric measurement data. Skeletal assessments of ancestry are most focused on the cranium, although there have been attempts at using postcranial osteometrics and dental nonmetric traits (e.g., Holliday and Falsetti 1999; Wescott 2005; Edgar 2013; Spradley 2014; Liebenberg et al. 2015; Tallman and Winburn 2015; Scott et al. 2018; George and Pilloud 2019; Gross and Edgar 2019). Cranial morphological variation in the form of craniometrics and nonmetric traits have been shown to be heritable and serve as a reliable proxy for genetic markers, albeit at varying levels depending on the trait and population evaluated (Berry 1968; Lane 1977; Cheverud 1981, 1982; Cheverud and Buikstra 1981, 1982; Sjøvold 1984; Devor 1987; Relethford 1994, 2002, 2004; Roseman 2004; Carson 2006; Sherwood et al. 2008; Martínez-Abadías et al. 2009).

Perhaps the most eminent anthropologist of ancestry estimation was Hooton, who passed on to his plethora of students and grand-students his thorough search of and emphasis on non-adaptive morphological variants (i.e., nonmetric traits) in the skull. In his own words, Hooton remarked that “morphological features which can be observed and described but cannot be measured are probably of greater anthropological significance than diameters and indices” (Hooton 1930: 80). The majority of the traits he found useful in partitioning geographic races contributed to the “Harvard List” (or Harvard Blank) and marked an early and much needed attempt to standardize their recording. The list also provided the impetus for the proliferative use of nonmetric traits by his academic lineage (Brues 1990), eventually culminating in widely used “trait lists” believed to typify certain ancestries (Rhine 1990; Hughes et al. 2011). One pertinent caveat of Rhine’s (1990) trait lists apart from low sample sizes for certain groups is the untested

use of prehistoric Native American samples as proxies for a generalized “Mongoloid” or Asian form given Late Pleistocene population history.

Cranial nonmetric traits have historically been split between studies concerned with ancestry estimation in forensic anthropology and with biological distance analysis, population histories, group relatedness, and heritability in biological anthropology (Pink et al. 2016). Ousley and Hefner (2005) were the first to refer to the former as cranial macromorphoscopic or morphoscopic traits, while the latter have been called cranial quasi-continuous (Grüneberg 1952), epigenetic (Berry and Berry 1967; Hauser and De Stefano 1989), discontinuous (Ossenberg 1969), discrete (Rightmire 1972), or, simply, nonmetric traits. Cumulatively, the possibly greater than a hundred nonmetric traits described in the literature can generally be scored based on their presence or absence, qualitative shape or appearance, or degree of expression. Nonmetric traits typically include extrasutural bones, proliferative ossifications, ossification failure, suture variation, or foramina variation. On the other hand, morphoscopic traits are those that may correlate with perceptible facial soft-tissue differences during life, and characterize cranial form via bone or suture shape, feature morphology, and feature prominence or lack thereof (Hefner et al. 2012). A distinction made based on bony features affecting facial soft-tissue appearance is somewhat problematic as certain morphoscopic traits such as suture shape do not affect outward appearance in life. Perhaps the more important distinction is that morphoscopic traits were historically ascertained by forensic anthropologists as useful in the “racial” identification of a single individual, as opposed to measuring the relatedness between groups. Pink (2016) recently attempted to sort individuals using nonmetric traits but concluded that the nature of the data was ill-suited for ancestry estimation. Thoma (1981) and Wijnsman and Neves (1986) arrived at similar conclusions. However, Ossenberg (1976) and Corruccini (1974)

were able to find significant variation between Africans versus Amerindians and Africans versus Europeans, respectively.

Despite their long-standing use in anthropology, morphoscopic traits were only recently thoroughly updated with standardized definitions and line drawings, and only for 16 traits (Hefner 2007, 2009, 2012). Moreover, a large global dataset of morphoscopic traits now exists as the Macromorphoscopic Databank, mimicking the intentions of the Forensic Anthropology Data Bank for craniometrics (Hefner 2018). These two developments have revitalized efforts to subject morphoscopic data to more rigorous multivariate statistical testing, including discriminant function analysis, logistic regression, *k*-nearest neighbor clustering, canonical analysis of principal coordinates, and a suite of machine learning techniques such as artificial neural networks, decision trees and random forest modelling, and support vector machines, among others (Hefner and Ousley 2014; Hefner et al. 2014, 2015; Hefner 2016; Monsalve and Hefner 2016).

Apart from visual methods for ancestry estimation such as the use of morphoscopic traits, traditional inter-landmark distances or craniometrics have widely been used to classify individuals into groups. One of the earliest and most common multivariate statistical treatments of craniometrics has been discriminant function analysis, which has been used to estimate ancestry since the 1960s (Giles and Elliot 1962; Birkby 1966; Giles 1966). Discriminant function analysis also underlies the popular software Fordisc, where craniometric scores from an unknown individual can be plugged into the software, and a classification into one of its built-in reference groups is generated along with posterior and typicality probabilities that speak to the statistical strength of the classification.

One of the greatest limitations of discriminant analysis is its forced classification into one of the initial reference groups. This is not problematic for sex estimation, where there is generally no allowance for crossover of membership between males and females. However, admixed individuals or those that share membership with more than one ancestral group may either fall at the overlap or be atypical of each parent population and therefore potentially misclassify. Misclassification trends using Fordisc have been documented for individuals that are understandably not well represented in the existing reference samples (Ubelaker et al. 2002; Williams et al. 2005; Manthey et al. 2018) or have shared or divergent population histories or periods of admixture between multiple ancestral groups (L'Abbé et al. 2013; Dudzik and Jantz 2016; Hughes et al. 2018). The posterior probabilities allocated to each reference group, which must sum to one, can be interpreted as estimates of admixture proportions rather than applying a hard classification to the reference group with the highest posterior (Konigsberg and Frankenberg 2018). This inference has led some investigators to use unsupervised model-based clustering methods such as finite mixture analysis to allow overlapping clusters, whereby an individual is assigned some fraction of membership given by posterior probabilities across all clusters, and interpreted as admixture proportions (Algee-Hewitt 2016, 2017a, 2017b). Another important caveat is that the labeling of such groups, which may stem from inconsistent *a priori* inclusion criteria such as race (e.g., African American), ethnolinguists (e.g., Hispanic), or nationality (e.g., Japanese), ignores potential population substructure and is largely based on the convenience of available skeletal samples to draw from.

In the next chapter the Philippines will be discussed to provide context for these theoretical underpinnings to the practical endeavors of ancestry and sex estimation, namely how population variation and history may affect method validity.

CHAPTER 3

THE PHILIPPINE CONTEXT

3.1. Geography

The present-day Republic of the Philippines is a sovereign archipelagic nation in Southeast Asia sharing maritime borders with Taiwan to the north, Vietnam to the west, Malaysia and Indonesia to the South, and the Pacific Ocean to the east (Fig. 3.1). It is comprised of 7,641 islands, around 2,000 of which are inhabited. These islands are clustered geographically into three major island groups: Luzon to the north, Visayas in the center, and Mindanao to the south. Many of these islands are volcanic in origin and mountainous with narrow coastal planes due to the Pacific Ring of Fire.

The country's tropical climate and equatorial position generally mean the year can be divided into two seasons of rain and drought. Being west of the warm Pacific Ocean also makes it the target of northwestward moving typhoons. It is the most typhoon-hit country in the world (Brown 2013) and is ranked third for most disaster-prone country according to the World Risk Index (Garschagen et al. 2016). With increasing climate change these cyclones and other environmental dangers are expected to intensify (Walsh et al. 2016). Rising sea-levels in the Philippines are already five times greater than the global average, and it has the highest risk for coastal destruction (Rietbroek 2016). Volcanic and seismic in addition to cyclone activity are extremely high.

Administratively, the country is divided into a hierarchy of 17 regions further subdivided into 81 provinces and 38 independent cities (Table 3.1). Each province is further divided into component cities and municipalities, which are further broken up into barangays (i.e., village,

district, or neighborhood), the smallest local government unit. Each region usually has a designated city for branches of major government offices and are accordingly designated as regional centers. Special regions include the National Capital Region (or Metro Manila), which contains no provinces but instead 16 independent cities and one independent municipality administratively equivalent to a province, and the Autonomous Region of Muslim Mindanao, which is the only region to have a local government unit at the regional level. The capital city of Manila is part of the National Capital Region and is located on the western edge of Luzon island, east of Manila Bay.



Figure 3.1. Map of the Philippines and its island groups (green) relative to other member states of the Association Southeast Asia Nations (dark gray).

Table 3.1. Regions and regional centers of the Philippines.

<i>Island Group</i>	<i>Region</i>	<i>Regional Center</i>
Luzon	National Capital Region (NCR; Metro Manila)	Manila
	Cordillera Administrative Region (CAR)	Baguio
	Ilocos Region (Region I)	San Fernando
	Cagayan Valley (Region II)	Tuguegarao
	Central Luzon (Region III)	San Fernando
	CALABARZON (Region IV-A)	Calamba
	MIMAROPA	Calapan
	Bicol Region (Region V)	Legazpi
Visayas	Western Visayas (Region VI)	Iloilo
	Central Visayas (Region VII)	Cebu
	Eastern Visayas (Region VIII)	Tacloban
Mindanao	Zamboanga Peninsula (Region IX)	Pagadian
	Northern Mindanao (Region X)	Cagayan de Oro
	Davao Region (Region XI)	Davao City
	SOCCSKSARGEN (Region XII)	Koronadal
	Caraga Region (Region XIII)	Butuan
	Autonomous Region of Muslim Mindanao (ARMM)	Cotabato City

The Philippines is the 12th most populous country in the world, 8th in Asia, and 2nd in Southeast Asia, with the latest national census at 101 million people (Philippine Statistics Authority 2016). Half of all highly urbanized cities belong to the National Capital Region, with the actual city proper of Manila boasting 71,263 people per square-kilometer, the highest population density in the world. An additional 10 million Filipinos live overseas, comprising one of the world's largest diasporas and exporters of labor (Rodriguez 2010). These numbers do not include Filipinos that have sought citizenship or permanent residence elsewhere. The Philippines is the third and first largest source country for immigrants to the United States and Canada, respectively (Baker and Rytina 2014; Citizenship and Immigration Canada 2015). The country remains largely agricultural but has seen rapid growth in manufacturing and service industries, and is Asia's fastest growing economy (Alegado and Yap 2016). Nevertheless, the poor continue

to lag behind as the gap between social classes widens (Kakwani and Krongkaew 2000). Abject poverty remains a critical social problem, with more than 26% of Filipinos living below the poverty line in 2015 (Bersales 2016).

3.2. Early Peopling of Southeast Asia and the Philippines

The uniqueness of the Philippines in terms of natural, cultural, and geographic diversity plays an integral role in studying human population history and origins in the Asia-Pacific region more broadly. Many scholars have long speculated on the possible initial and subsequent arrivals of anatomically modern humans (AMHs) into the Philippines, having proposed a record number of models of migration routes and epicenters (Gaillard and Mallari 2004). These hypotheses have often been based largely on linguistic classification, searching for a “proto-Austronesian” homeland (the language family that dominates present-day Southeast Asian dialects). Internal indigenous development within Southeast Asia has been proposed (Meacham 1988, 1995; Bronson 1992), as well as exogenous migrations from neighboring areas. Of these migrations, Polynesia and Melanesia (Dyen 1962, 1965; Coates 1974), the area surrounding the Celebes Sea (Solheim 1988, 2002), mainland South China through Indochina moving either southward (Heine-Geldern 1932) or westward (Manuel 1966, 1991, 1994), and Taiwan (Bellwood 1988, 1991, 2004) have all been suggested as possible homelands. H. Otley Beyer (1948; Beyer and de Veyra 1947) has even suggested major contributions from multiple sources. Some of these can be considered “fringe” hypotheses such as a Melanesian origin. The most widely accepted model is that of an initial southwestern point of arrival during the Pleistocene, and whether present-day Filipinos represent the descendants of these initial Pleistocene inhabitants (as with the Regional

Continuity Model) or of a later displacing Holocene migration (as with the Waves of Migration Model) summarizes current debates.

The environment of Pleistocene Southeast Asia some 50,000 years ago was drastically different from what we observe today. Namely, lower sea levels from glaciation exposed terrestrial areas connecting the Indonesian islands of Sumatra, Java, and Borneo and the Philippine island chain of Palawan to the Asian mainland via the Malay-Indochina peninsula (i.e., the Sunda Shelf). Likewise, continental Australia was connected to the island of Guinea (i.e., the Sahul Shelf), leaving the archipelago of Wallacea in between these two shelves (Voris 2000). These paleogeographic reconstructions have largely been inferred from what was thought to be a distinct dividing line between types of fauna on either shelf; originally, Alfred Wallace had grouped the whole modern political territory of the Philippines northwest of this line, but Thomas Huxley later moved this line to divide Palawan from the other Philippine islands (Esselstyn et al. 2010). Of particular interest to the present discussion are the land bridges via the archipelagos of Palawan and Sulu that would have granted access from mainland Asia to the rest of the Philippine islands (Scott 1984; Jocano 1998). Two major fossil sites, Tabon Cave in Palawan west of Huxley's line and Callao Cave in Luzon east of Huxley's line, have yielded Pleistocene human remains dated to 30,000 (Détroit et al. 2004) and 67,000 years BP (Mijares et al. 2010), respectively. Such time ranges suggest the Philippines was occupied rapidly during the initial peopling of the region around 60,000 to 70,000 years ago (O'Connell and Allen 2004; Barker et al. 2007; Oppenheimer 2009; Demeter et al. 2012; Curnoe et al. 2016; Westaway et al. 2017).

The Negritos of the Andaman Islands, Southeast Asia, New Guinea, Australia, and Melanesia are so grouped because of their shared phenotypes, particularly dark skin (linked to

the racist etymology of the term), short stature, and woolly hair. These peoples have been compared to the pygmies of Central Africa, which sparked the initial considerations of rapid coastal migrations of early AMHs from Africa through Saudi Arabia and South Asia to Southeast Asia, Sahul, and beyond via these Pleistocene land bridges and narrowed sea corridors (Oppenheimer 2012). However, more recent genetic work comparing different Negrito groups and African pygmies suggests such physical similarities are the result of convergent evolution (Jinam et al. 2017). Under the hypothesis of rapid coastal migration, Negritos represent the earliest AMH occupants of Southeast Asia (grouped as “Australoid” or “Australo-Melanesian” populations), maintaining a largely hunter-gatherer lifestyle. Extant Negrito ethnic groups in Southeast Asia are found in Thailand and Malaysia, with greatest geographic diversity in the Philippines, among them the Agta, Aeta, Ati, Batak, and Mamanwa (Padilla 2013).

Mitochondrial, non-recombining Y-chromosome, autosomal, and human polyomavirus 2 genetic studies have isolated ancient, unique founding haplogroup lineages among Negritos in conjunction with more recent lines, lending support for an initial colonizing wave (Macaulay et al. 2005; Stoneking and Delfin 2010; Delfin et al. 2011, 2014; Gunnarsdóttir et al. 2011; Jinam et al. 2012). Overall, however, Negritos are most genetically similar to neighboring non-Negrito groups, which scholars have interpreted as evidence of “a history that unites the Negrito and non-Negrito populations of Southeast and East Asia via a single primary wave of entry of humans into the continent” (HUGO Pan-Asian SNP Consortium 2009: 1545; Scholes et al. 2011).

Stoneking and Delfin (2010: R190) counter that “early isolation followed by recent admixture” would reconcile their results supporting the Waves of Migration Model with the HUGO (2009) study’s interpretation for regional continuity. A more recent comprehensive analysis reveals

common ancestry between Taiwan and island Southeast Asia prior to the Neolithic, but with signals from two Late Holocene southward migrations (Soares et al. 2016).

The physical anthropological literature has also been divided between these two models. Perhaps most strongly pervasive amongst advocates of the Regional Continuity Model are the landmark studies conducted by Christy Turner (1979, 1987, 1990, 1992). In his evaluation of nonmetric dental traits, Turner identified two main dental complexes: Sundadonty among southern East Asians, Southeast Asians, Polynesians, and Micronesians, and Sinodonty among northern East Asians (except the Ainu of Japan) and the northeast Asian-derived populations of the Americas. According to Turner, Sundadonty represents the predecessor of more derived Sinodont patterning, indicating south to north gene flow. Moreover, he asserts that consistent Sundadonty across Southeast Asian populations is evidence for a single continuum (Turner 1987, 1992). Other researchers have followed suite, expanding the argument for independent regional continuity using cranial and postcranial observations as well (Bulbeck 1982; Hanihara 1992, 1993b; Pietrusewsky 2006, 2010; Stock 2013). In contrast, Matsumara and colleagues (Matsumara and Hudson 2005; Matsumara and Oxenham 2014) have shown that genes flowed in the opposite direction from north to south using a spatially and temporally expanded set of nonmetric dental traits and populations. Matsumara demonstrates that most modern Southeast Asian groups exhibit intermediate dental phenotypes between East Asians and early Southeast Asians and Australo-Melanesians. A mathematical model combining genetic single nucleotide polymorphism, phenotypic cranial 3D morphometric, geographical distance, and chronological and hypothetical F_{ST} data agreed with early Australo-Melanesian arrival and isolation, followed by subsequent migration events from other Asian populations (Reyes-Centeno et al. 2014). The

dental debate demonstrates that, while tooth form correlates strongly as a proxy for neutral genomic markers (Rathmann et al. 2017), interpretation of the data can be varied.

Under the Waves of Migration Model (also known as the “Two-Layer” model (Jacob 1967) or “Out-of-Taiwan” model), a second major demic diffusion into Southeast Asia displaced or more likely intermixed with already established Negritos (Gunnarsdóttir et al. 2011; Jinam et al. 2012, 2017). Driven by agriculturally-mediated population expansions in the Neolithic of China, the second wave was composed of Austronesian-speaking peoples (Fig. 3.2). Taiwan is thought to be the source of Austronesian expansion as the island has the highest diversity of Austronesian languages among its indigenous groups (Blust 1977, 1978, 1999). Presumably, the southward spread of Austronesian languages into the Philippines replaced original Australo-Melanesian dialects spoken by Negrito groups. Reid (1987, 1989, 1994, 2013) demonstrates that present-day Philippine Negrito languages, while classified as Austronesian, have underlying non-Austronesian substrata and subsequently creolized a pidgin trade language to facilitate interaction with immigrating Austronesians. Diamond (1988) extends these dispersal routes eastward from Indonesia into the Pacific, hypothesizing an “express train to Polynesia.”

Archaeological evidence of transmitted agricultural technologies and species, pottery styles, and other material culture from East (China and Taiwan) to Southeast Asia and beyond further supports this model (Hung 2005, 2008; Bellwood et al. 2011; Hung et al. 2011). The Batanes Islands immediately south of Taiwan (north of Luzon) have not yielded any pre-Neolithic deposits (Bellwood and Dizon 2005, 2008), but northern Luzon cave sites show interaction between Neolithic arrivals and Paleolithic hunter-gatherers (Mijares 2005).

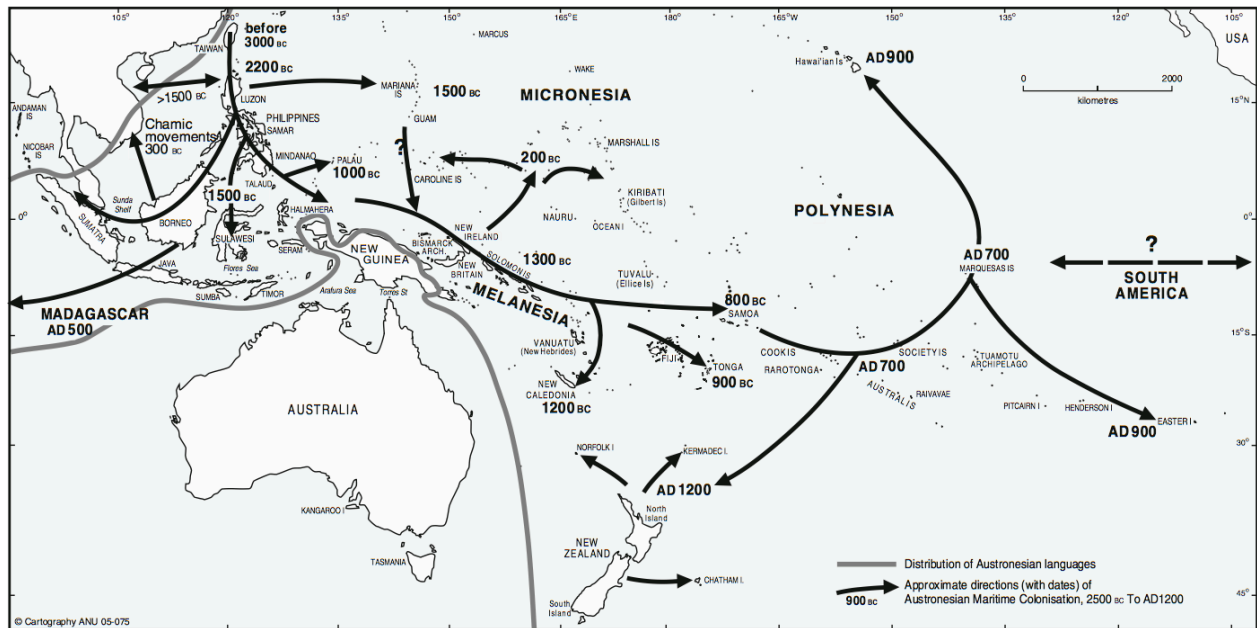


Figure 3.2. Dispersal of Austronesians into Southeast Asia and the Pacific based on linguistic directionality and archaeological chronology, in support of the Waves of Migration Model. Taken from Bellwood et al. (2011).

Genetic studies of the Philippines have positioned the archipelago as a population viaduct between Taiwan to Indonesia and the rest of Polynesia (Trejaut 2005; Tabbada et al. 2010). Others have added an “early train” out of South China, dating to the transition from the Pleistocene to the Holocene (Jinam et al. 2012). Indeed, a significant ancestry cline across mainland Asia, island Southeast Asia, and the Pacific likely “reflects mixing of two long-separated ancestral source populations—one descended from the initial Melanesian-like inhabitants of the region, and the other related to Asian groups that immigrated during the Paleolithic and/or with the spread of agriculture” (Cox et al. 2010: 1589).

To summarize, there are two competing models for the origin of ancestral Filipinos. Initial peopling of the Philippines by modern humans occurred in the Paleolithic/Late Pleistocene epoch before submergence of the Sunda shelf. In one model, Filipinos evolved *in situ* from these initial peoples with negligible gene flow events from outside populations. In the other model, a significant influx of migrants from the north during the Neolithic/Early to Middle Holocene

admixed with local communities. Taking the archaeological, linguistic, physical anthropological, and genetic evidence holistically, it is inconceivable to frame the Philippines as a relatively isolated yet geographically interconnected bubble for thousands of years prior to Western colonization, as suggested by the Regional Continuity Model. Events described by the Waves of Migration Model are more likely to have occurred, with the most significant wave linked to Austronesian expansion and the invention of agriculture. Undoubtedly, several minor gene flow routes must have been continuously maintained between neighboring islands and the Asian mainland up to Spanish contact in 1521 and to the present day.

3.3. The Prehispanic Philippines

It is important to point out that there was no such term as a collective ‘Filipino’ identity before Spain’s arrival in the 16th century. Instead, the peoples inhabiting the islands of what would later be grouped together as the Philippines were organized into independent but highly interconnected chiefdoms, tribes, and bands. The simplest dichotomy between these prehispanic peoples has been between Negritos and non-Negritos, a dichotomy crafted and perpetuated by the Spanish themselves.

Making the distinction between prehispanic Filipino Negrito and non-Negrito groups may come easy given obvious differences in phenotype, subsistence practices, and territory. Negritos were, and largely still are, mobile small-band hunter-gatherers dwelling in the interior tropical rainforests of most of the major Philippine islands. Negritos can be contrasted with the sedentary agriculturalists and maritime chiefdoms that inhabited the lowland river valleys and coasts of the archipelago. If we are to believe the Waves of Migration Model, Negritos and non-Negritos correspond to the initial Australo-Melanesians and subsequent Austronesians, respectively. Early

ethnographic accounts fallaciously described Negritos as ‘pristine’ and isolated. On the contrary, more updated ethnographic, archaeological, and linguistic evidence shows a considerable time depth for socioeconomic interactions between these lowland and interior prehispanic peoples including exchange of trade goods, kin, labor, and ceremonies (Junker 1996). As mentioned above, more recent genetic evidence has supported these claims (HUGO Pan-Asian SNP Consortium 2009).

The larger prehispanic communities were comprised of Austronesian agriculturalists and maritime cultures living in lowland coasts and valleys, and eventually organized into chiefdoms that steadily assimilated neighboring barangays. The word barangay actually derives from *balangay*, the oldest known watercrafts found in the Philippines, echoing the importance of the sea in daily life. Thalassocracies emerged early on based on extensive international trade networks involving food, raw materials, and prestige goods. Such networks extended throughout maritime and mainland Southeast Asia, reaching the civilizations of China and India. Song Dynasty porcelains from as early as the 10th century have been excavated in the Philippines (Beyer 1948, 1964; Scott 1968; Ronquillo 1987), as well as several artefacts and an alphabet of Hindu and Buddhist influence (Beyer 1947; Francisco 1963; Rye 1993; Bennett 2009). These globalized sea routes brought multiple cultures to the archipelago, including Islam in the 13th century, which retains a strong foothold and several sultanates in Sulu and Mindanao to this day (Abubakar 2005).

As a monopolized intermediary between Chinese goods to the rest of the islands, the Kingdom of Tondo north of the Pasig River delta in Luzon acquired considerable prestige in the region (Dery 2001; Abinales and Amoroso 2017). By the 13th century, the Hindu-Indonesian Majapahit Empire had settled in fortified lands south of Tondo and the river delta (Hassell 1953;

Fox 1957; Zaide 1957). However, Rausa-Gomez (1967) argues that historical evidence for this direct Indonesian-Philippine interaction is dubious. Two centuries later, the Sultanate of Brunei invaded this area, instilling powers to local leaders and establishing the Kingdom of Maynila as a satellite state. It was through this Bruneian incorporation that Islam had reached Luzon (Abubakar 2005). The Kingdoms of Tondo and Maynila would eventually merge their cultural, political, and economic clout as one city until the mid-16th century prior to Spanish arrival (Santiago 1990; Scott 1994).

3.4. Western Colonialism

American journalist Stanley Karnow (1989: 9) summarized Philippine history as “three centuries in a Catholic convent and fifty years in Hollywood.”

The 1493 Papal bull *Inter caetera* and the 1494 Treaty of Tordesillas had split the world along a meridian into a Western half conquerable by Spain and an Eastern half open only to Portugal. This restriction created considerable pressure for the Spanish crown to find an alternative Western route to lucrative commercial opportunities with the Asiatic kingdoms. In 1517, Portuguese explorer Ferdinand Magellan sailed across both the Atlantic and Pacific Oceans under the auspices of Spain in search of such a route. Four years later, Magellan reached the island of Homonhon on the eastern side of the Philippines with a surviving crew of 150, marking the first arrival of Europeans to the archipelago. His presence there was short lived, as his quest to Christianize the indigenous peoples resulted in his eventual death in a conflict against Datu Lapu-Lapu on the island of Mactan that same year. Three more unsuccessful expeditions were launched, strongly motivated by the potential profits of entering the spice trade. A fifth expedition from 1541-1543 led by Ruy López de Villalobos was commissioned by the

first Viceroy of New Spain. The expedition mapped portions of the central and southern islands but was also somewhat unsuccessful in its attempts to establish settlements. Villalobos is, however, credited with naming the islands *Las Islas Filipinas* in honor of then Prince of Spain, Philip II. In 1564 under orders from now King Philip II and commissioned by then Viceroy of New Spain Luis de Velasco, Miguel López de Legazpi led a sixth expedition to the Philippines and established the first Hispanic settlement in the East Indies on the island of Cebu in 1565. Legazpi would eventually become Governor-General of the Philippines and establish his capital in Manila in 1571.

Violent opposition from indigenous inhabitants was quelled by divide and rule tactics. The Philippines became Spain's outpost in the Orient and Manila the seat of power in the Spanish East Indies. The newly founded capital was decisively cosmopolitan, an international entrepôt of goods, cultures, and immigrants (Iaccarino 2008). The flourishing economy owed its success to a new-found trade route between Asia, the Americas, and Europe. The Manila-Acapulco Galleon Trade lasted 250 years from 1565 to 1815, bringing products from East, Southeast, and South Asia across the Pacific to Acapulco, Mexico and then to the rest of New Spain and Peru (and vice versa) and across the Atlantic to Spain. Countless slaves were also transported in this way as the Spanish Philippines was an early participant in the Trans-Pacific slave trade (Seijas 2014). The Galleon Trade ceased in 1815 with the mounting Mexican War of Independence. Since its founding, the colonial Philippines was administered through the Viceroyalty of New Spain until 1821 when Mexico gained independence, and henceforth was directly ruled by the Spanish crown in Madrid.

Spanish subjugation over the Philippines used a double-edged sword of imperialism and proselytism as they had done in the Americas (Rafael 1988; Phelan 2011). The *encomienda*

system carved out territories and awarded them to conquistadors for a virtual monopoly on the labor and tributes within the *encomienda*. While the majority of bureaucrats were centralized in Manila and other major posts, encomenderos and Catholic friars were spread throughout the provinces. The most active Christian orders were the Augustinians (1565), the Discalced Franciscans (1578), the Jesuits (1581), the Dominicans (1587), and the Augustinian Recollects (1606). It was the mass indoctrination of native peoples to Christianity that was most successful in hispanicizing Philippine culture (Phelan 2011). Far flung from the capital, and even further from the governing eyes of Mexico City or Madrid, secular and parish elites would abuse their powers over native peoples for centuries. It is also worth noting that the Muslim inhabitants of Mindanao and pagan tribes of the mountainous regions of Luzon were largely successful in resisting Spanish conquest.

The Philippines was later ceded to the United States in 1898 along with Puerto Rico and Guam following Spain's defeat in the Spanish-American War and ratification of the 1899 Treaty of Paris. Prior to this, 19th century liberal ideas of freedom and equality had been brewing among the oppressed, especially among the *ilustrados* (enlightened ones), a group of European-educated Filipino middle classmen (Thomas 2012). Filipino revolutionaries had already declared independence from Spain in June of 1898, and they did not recognize the legitimacy of the Treaty of Paris and subsequently continued to revolt against the United States. The Philippine-American War officially ended in 1902, although some skirmishes continued for several years afterward.

The United States ruled the Philippines under a policy of what then US President William McKinley (1899) proclaimed as "benevolent assimilation", marketing themselves not as yet another iteration of imperialist overlords, but rather as "friends, to protect the natives in their

homes, in their employment, and in their personal and religious rights". It was important for the US government to highlight this benevolence, as territorial expansion was contradictory to their own anticolonialist origins (Miller 1984). Still, protracted congressional debates ensued as to whether the Philippines would be incorporated into American nationhood or be allowed to develop its own sovereignty. Both sides of the argument were however motivated by similarly racist defenses (Go 2004; Baldoz 2011). On one side, the expansionists claimed that the United States was morally obligated to bestow the gift of democratic civilization and economic development to this backwards territory incapable of self-governance. On the other hand, opponents worried that annexation would lead to mass migrations to the imperial center and unfit lower races would compete for resources and miscegenate with true-blooded White Americans. Regardless of the latter's xenophobically charged support, the former prevailed in their duty-bound quest to remake the Philippines in America's image, yet unincorporated into the American polity. As economic gain was undoubtedly the deciding factor, then Indiana Senator Albert Beveridge's sentiment is worth quoting in full:

American factories are making more than the American people can use; American soil is producing more than they can consume. Fate has written our policy for us; we must get an ever increasing portion of foreign trade. We shall establish trading-posts throughout the world as distributing points for American products. We shall cover the oceans with our merchant marine. We shall build a navy to the measure of our greatness. Great colonies, flying our flag and trading with us will grow about our posts of trade. Our institutions will follow our flag on the wings of commerce. And American law, American order, American civilization, and the American flag will plant themselves on shores, hitherto bloody and benighted, but, by those

agencies of God henceforth to be made beautiful and bright. ...The Philippines are logically our first target (Beveridge 1908: 43–45).

Philippine nationalists continued to push for independence within legislative bodies. US Congress passed the Jones Law or the Philippine Autonomy Act in 1916, paving the way for eventual independence as soon as a stable government could be achieved. Several missions to the US Congress by Filipino nationalists failed at ratifying independence until the Tydings-McDuffie Act of 1934 was passed by both US Congress and the Philippine Senate, promising for the first time a firm date for independence by 1946. The decade prior to 1946 was intended to be a peaceful transition period towards independence, but in 1941 the Japanese attacked several US military bases in the Philippines just a few hours after the attack on Pearl Harbor marking entry of both the United States and the Philippines into World War II. The Japanese occupied the Philippines from 1942 to 1945 until Japan's official surrender. In 1946, the Treaty of Manila was signed between the United States and the Philippines, relinquishing American sovereignty over the finally independent archipelago. The US continued some of its military and economic interests in the country even after granting independence in 1946, making the US-Philippine relationship one of the oldest in the region.

Filipinos were the first historic Asian group to arrive in the Americas, at first by escaping servitude aboard Spanish ships in 16th century California (Cordova 1983), and then later establishing the first Asian settlement in 18th century Louisiana (Espina 1988). American rule had only accelerated the migration of Filipinos to the US (Espiritu 2003). Later in the early 1900s, *sakadas* or Filipino farmers were exported to Hawai'i to work in sugar plantations and later to California for similar agricultural needs. Government-sponsored *pensionados* were also sent to the US during this time to be indoctrinated in US history and government. The American

occupation and onset of numerous 20th century global conflicts also saw many Filipino men conscripted into American military service. Filipinos emigrating to the US during this period also faced strict anti-miscegenation laws (Baldoz 2004). Later capitalist booms such as oil in the Gulf States in the 1970s, Asian Tiger economies in the 1980s, and health care and information technology industries in the 1990s increased demand for cheap domestic and manual labor. Filipinos were encouraged by their government to pursue this demand abroad and provide a form of foreign remittance for the country. The tradition of deploying Overseas Filipino Workers en masse remains strong today (Rodriguez 2010).

3.5. Filipino Racial Formation

Filipino identity is a complex issue that is at one end rooted in heterogeneous prehispanic cultures and at another end further complicated by a nation's colonial past. Social stratification has long been imbedded in Philippine society. Spanish accounts of prehispanic Tagalogs by Father Juan de Plasencia (1589) used divisions such as *principales* (*datu*, chiefs), *hidalgos* (*maharlika*, gentry), *pecheros* (property-owning, tribute-paying serf class), and *esclavos* (*alipin*, slaves), though these simplified and often misunderstood translations do not capture the complexities of this perceived system (Scott 1992).

European conquest subsequently introduced racialized castes (see Comisión Central de Manila 1887 for a contemporary account of Spanish colonial racial classification). Blood, birthplace, and book (or notions of *mestizaje*, territorial nativity, and religious civilization (Kramer 2006: 39)) quickly dictated racial hierarchy in the colony. There were, in decreasing order of prestige, the *Peninsulares* (or the Spanish born in Spain), *Américanos* (or the Spanish born in Spanish America), *Insulares* (or the Spanish born in the Philippines; *creoles*), *Mestizos*

de Tornatrás (or mixed Spanish, Chinese, and indigenous Filipino), *de Español* (or mixed Spanish and native Filipino), *de Sangley* (or mixed Chinese and indigenous Filipino), *Indios* (or the native Christianized Filipinos), *Sangleyes* (or the Chinese), and *Negritos* (or the indigenous, dark-skinned “infidels”). On the expansionist frontiers were the *Moros* (or Muslims) in the south and the *infieles* animists (referred to as Igorots) in the Luzon highlands whom resisted evangelization. The tendentious naming of native inhabitants as *indios* placed them in the same pot as their namesakes in the New World.

Spaniards and Spanish mestizos were exempted from paying tribute, while the *indios* were forced to pay taxes in addition to providing mandatory labor for a set period each year. Chinese mestizos were taxed double that of the *indios*, and Chinese were taxed even higher. The Spanish ensured proxy authority by bestowing *datus* political power and prestige over their respective communities as *gobernadorcillos* (“little” governors) and *cabezas de barangay* (heads of villages), creating a hereditary *principalía* class. The *principalía* benefitted greatly from commercial prosperity, and wealth trickled down to make an emergent middle class of Spaniards, mestizos, and enterprising natives alike, especially in Manila (Majul 1977). Educational reforms and opening of respected professions to natives in the 1860s produced a new subclass of *ilustrados* (the educated middle class; intellectuals) among the *principalía*. *Ilustrados* who would soon seek reform and equitable arrangements of power (Thomas 2012), led to an influx of *peninsulares*, *insulares*, and Spanish mestizo immigrants attempting to maintain hold over government and military offices (Majul 1977).

Although the relationship between China and the Philippines extended from prehistoric times (Beyer 1964; Scott 1968), the Chinese dually suffered massacres and expulsions while at the same time enjoying economic growth and trade within the Spanish colony (Liao 1964). The

Chinese were viewed by the Spanish as untrustworthy, but economically essential. Chinese individuals were mandated to live in *parianes* (or ghettos) dotted across Manila and were regularly attacked. This targeted discrimination and common struggle facilitated social cohesion among the Chinese, facilitating an ethnically Chinese merchant elite that would come into fruition in the 20th century (Wilson 2004).

Rising antipathy in colonial Manila fueled by racial and class distinctions prompted Spanish authorities to consider policies for amalgamation of the races. The secret report by diplomat Sinibaldo de Mas (1843) to the Spanish crown moved for open admittance to medical education for all races, to abolish unequal annual tributes, and to promote monetary incentives for miscegenation, the latter of which awarded specific values depending on particular racial pairings. This was a strategy employed before by the Catholic Church with hopes to accelerate native conversion, and by the garrisons to satisfy soldiers' temperaments (Barter 2016). Colonial racial and class constructions have fermented in the archipelago for centuries and is at the root of Filipino society and stratification today.

The Philippines experienced over four centuries of consecutive colonial rule under Spain (1521 to 1898) and then the US (1898 to 1946), 250 years of which saw regular trade routes between Latin America via the Manila-Acapulco Galleon Trade (1565 to 1815). Historical documents suggest intermarriages between Filipino "*indios*", Latin Americans, Spanish and Chinese were encouraged during Spanish colonization (De Mas 1843), although these pairings were likely most prolific in the capital and other major posts (Phelan 2011). During American rule, intermarriages between Filipinos and American Whites in the Philippines "occurred with a frequency that was troubling to many colonial officials" (Winkelman 2017: 41). The flow of European genes into the archipelago was undoubtedly male biased owing to gendered colonial

activities of subjugation via religious conversion, state exertion, and military expansion, or what historian Nicholas Molnar (2017) terms “bachelor colonization”.

Enumeration by the ruling hegemony can provide insight not only into racial statistics, but also into how race was defined, constructed, and imposed by the colonists over the subjugated. The first available census of the Philippines came in the form of a 1591 report by Governor Gomez Perez Dasmariñas to King Philip II called the *Relación de las Encomiendas Existentes en Filipinas*. In it 166,903 *tributos* or taxpayers were registered, which was multiplied by four assuming that this was the average family size, for a total of 667,612. This highly inaccurate enumeration was limited to the colonized lowland areas of Luzon and Visayas during that time. Only two official censuses were commissioned by the Spanish government in 1877 and 1887 during the colonial period, but very few more detailed data are available from these aside from the total population counts of 5,567,685 and 5,984,727, respectively. One early influential account had claimed that some 1,200 Spanish households were residing in the Manila area alone, along with around 400 Spanish soldiers in the garrisons (Morga 1609).

During American occupation, three pre-World War II censuses were commissioned, which began collecting data on race (Table 3.2). As Baldoz (2011: 23) argues, “the publication of the [1903] territorial census was important because it registered as social fact the intention of colonial administrators to use race as an organizing principle of the new Philippine social structure.” The color-based categories used by American censuses of the Philippines were largely influenced by Johann Blumenbach’s 18th century classifications: Filipino natives apart from Negritos were of the Brown or Malay race, East Asians of the Yellow or Mongolian race, Europeans of the White or Caucasian race, Negritos and Africans of the Black or Ethiopian race, and mestizos as mixed. The imposition of American conceptions of race on Filipino peoples is

made even more evident with American anthropologist David Barrows' entry on the history of the population in the 1903 census:

However, one impression that has gained foothold in regard to the tribes of the Philippines I believe to be erroneous, and that is as to the number of distinct types or races and the multiplicity of tribes. Owing to the fact that nowhere in the Philippines do we encounter large political bodies or units, we have a superlative number of designations for what are practically identical peoples. The tribe itself as a body politic is unknown in this archipelago. The Malayan has never by his own effort achieved so important a political organization. Such great and effective confederacies as we find among the North American Indians are far beyond the capacity of the Filipino of any grade. For example, among the powerful and numerous Igorot of northern Luzon the sole political body is in the independent community... This fact of deficient social cohesion has resulted in the application of an indefinite number of designations for these mountain Igorot, who, throughout the Cordillera for a distance of 150 miles, are all members of one common stock (Barrows 1905: 453–454).

This excerpt reveals the multiple meanings that race took on, which at one time referred to blood and biology, and at other times arranges a historical hierarchy of stages of civilization (Go 2004). Barrows' (1905) description reveals how race was more than just physical appearance, but also translated into measures of social, cultural, and political capabilities.

While all three national censuses conducted under American rule collected racial statistics, the 1948 census was the first and last time the newly liberated state would collect data on race. Succeeding enumerations would happen more or less at the beginning of every

Table 3.2. Census data on race in the Philippines during and shortly after (1948) American colonization.^a

<i>Race^b</i>	<i>Census Year 1903</i>	<i>Census Year 1918</i>	<i>Census Year 1939</i>	<i>Census Year 1948</i>
Brown	6,914,880	9,386,826	15,758,637	19,052,801
Males	3,435,848	4,692,426	7,905,222	9,535,665
Females	3,479,032	4,694,400	7,853,415	9,517,136
Yellow	42,097	50,826	141,811	103,565
Males	41,071	47,296	107,093	74,002
Females	1,026	3,530	34,718	29,563
White	14,271	12,390	19,300	9,449
Males	11,450	8,592	11,112	5,805
Females	2,821	3,798	8,188	3,644
Black	1,019	7,623	29,157	11,791
Males	767	4,029	15,511	6,093
Females	252	3,594	13,646	5,698
Mixed	15,419	34,663	50,519	55,815
Males	7,516	17,974	25,868	29,337
Females	7,903	16,689	24,651	26,478
Unreported			879	761
Total	6,987,686	9,492,328	16,000,303	19,234,182
Males	3,496,652	4,770,317	8,065,281	9,651,195
Females	3,491,034	4,722,011	7,935,022	9,582,987

^aData from the United States Bureau of the Census (1905), Census Office of the Philippine Islands (1920), Commonwealth of the Philippine Commission of the Census (1941), and Bureau of the Census and Statistics (1954).

^bRacial terminology reflects those used in the original census, where Brown refers to “Malay” Filipinos, Yellow refers to East Asians such as Chinese and Japanese, White refers to European descent, and Black includes both Negritos and African descent.

decade or half-decade. We see a shift away from divisions by color to one by language. Mother tongue was used “as a sensitive index of ethnic origin” (National Statistics Office 1990: 99). Enumerator’s manuals recorded ethnicity as the first language or dialect learned at home at earliest childhood (e.g., Tagalog, Cebuano, Ilocano), while defining it as a primary sense of belonging and consanguinity to an ethnic group. In earlier versions of the definition, ethnicity was inherited and thus not a choice, but later enumeration guides relied on respondent self-

ascription and allowed ethnicity to differ from that of the first language learned if such was the case. In cases where the respondent was a child that had not learned to speak yet, the mother's ethnicity was used. Additionally, ethnicity/mother tongue data was limited only to those with Filipino citizenship.

Apart from anecdotal claims (Potter et al. 1981: 34, Howells 1989: 110; Delfin et al. 2014: 236, Delfin 2015: 450), no study has explicitly evaluated the degree of European genetic admixture in post-colonial Philippine populations. One study found only 3.57% (1/28) of their small Filipino sample possessed a European Y-chromosome haplotype (Capelli et al. 2001). Using ancestry informative markers and the STRUCTURE clustering algorithm, another study by Yang et al. (2005) found overwhelming correspondence between predicted ancestry and self-identification within their entire Asian subgroup of 80 Koreans, Japanese, Chinese, and Filipinos with the exception of two out of 26 Filipinos with large contributions from the European American cluster. A larger study (total n = 103,006, Filipino n = 1,708) found similar results, noting that “for self-reported Filipinos, a substantial proportion [of the ~10% exhibiting Asian-European admixture that self-reported as Asian] have modest levels of European genetic ancestry reflecting older admixture” (Banda et al. 2015: 1293). It is worth noting that the latter two studies sampled Filipinos living in California, while Capelli et al. (2001) do not provide more details on their sample apart from that they are “from the Philippines”. Still, census counts demonstrate that the level of Spanish immigration to the colonial Philippines did not reach such heights as those with colonial Mexico (Barrows 1905: 478; Phelan 2011), even into the American period (Table 3.2). However, the US actually increased its military interests in the country even after granting independence in 1946. When US military bases in the Philippines permanently closed in 1992 and their troops withdrew, an estimated 50,000-plus infants,

children, and adolescents sired by American soldiers were left orphaned and impoverished (Kutschera et al. 2012). The estimate of these biracial military Filipino “Amerasians” grows to 250,000 when including adults and second-generation progeny (Kutschera and Caputi 2012). These post-installation cities have continued informally sanctioned military prostitution systems today in the form of sex tourism hotspots catered to white men (Kutschera et al. 2015; Chapman 2017). Certainly, the degree of admixture across Philippine populations is likely highly varied across regional, temporal, and social lines of difference.

The actual term ‘Filipino’ has a fluid racial etymology (Andaya 2014: 275). Initially, Filipinos were synonymous with *insulares* or those with Spanish parentage born in the Philippines, similar to *Américanos* or those Spaniards born in Spanish America. This was a contentious hierarchy for the *insulares* whose only “inferiority” to the *peninsulares* was birthplace. ‘Filipino’ later expanded to include mestizos of varying pedigree. Nineteenth century movements against colonial oppression, principally championed by the *ilustrados*, consequently highlighted a common struggle. Nationalists such as Jose Rizal used ‘Filipino’ to refer to all those born in the Philippines – *insulares*, mestizos, and *indios* alike. This situation at the close of the 19th century was described by Benedict Anderson (1998) as islands essentially constituting a territorially demarcated country but whose people were only beginning to form a self-conscious collective identity. Given the diversity of identities to the present day – from ethnolinguistics, to religions, to civil conflict for autonomy or territory or political rule, to diaspora – historian Vicente Rafael (2000: 7) rightfully points out that “attempts at establishing a clear and undisputed fit between the Philippines and Filipinos is far from complete, and in fact, may never be realized.” Today, everyday discourse on race in the Philippines still popularizes the 20th century American notion of Filipinos as collectively ‘Malay’ but as a category within the broader

‘Asian’ classification, while acknowledging distinct regionally specific ethnolinguistic memberships.

3.6. Philippine Forensic Anthropology

Anthropology, or its precursory practice prior to its formulation as a discipline (Abaya et al. 1999; Rubiés 2003), was an extension of colonial enterprise naturally aligned to the Spanish imperial agenda. Subjugation of native peoples necessitated the study by conquerors of indigenous cultures, languages, and bodies. This included the activities of friars sent to convert pagan religions, expeditions to discover unknown lands, and the collection of artifacts, skeletons, and at many times living people themselves for exposition. Certainly, the anthropological enterprise of documentation and collection continued, and indeed formalized, with the handover from Spanish to American hegemony, as evinced by the introductory sentence of U.S. anthropologist Daniel Brinton’s (1899: 122) dedication to Ferdinand Blumentritt’s ethnographic surveys of the Philippines: “Now that the Philippine islands are definitely ours, for a time at least, it behooves us to give them that scientific investigation which alone can afford a true guide to their proper management.”

Anthropology in the Philippines was formalized as an academic pursuit with its first offering as an undergraduate 101 course in 1914 at the University of the Philippines, the flagship educational institution of American rule. Three years later in 1917, anthropology became a standalone department within the university, the first in Asia. Henry Otley Beyer was the sole instructor of anthropology in incipient years and founding chair until his retirement in 1947 (some sources claim it was in 1954); he is regarded by many as the father of Philippine anthropology. The department became decidedly four-field, with particular strengths in

archaeology and physical anthropology due to colonially derived interests in prehistory, race, and ethnicity (Tatel 2010, 2014). Otley Beyer was succeeded as department chair by his student Marcelo Tanco, whom was the first Filipino to pursue graduate studies in anthropology in the United States at Harvard and Berkley, specializing in physical anthropology.

Jerome Bailen (1967) provides, to my knowledge, the only published review of Philippine physical anthropology, which covers the late 19th to middle 20th century. Bailen's (1967: 549) conclusion remarks that "while it is a sad fact that there still is not a single professionally-trained physical anthropologist in the country today... it is hoped that a greater number of trained and no less dedicated individuals backed by a continuously generous support from enlightened government and private sector, will come up in the immediate future with more significant findings and thereby delineate for the Filipinos a sharper image of their identity." Unfortunately, while a few professionally-trained physical anthropologists have cropped up since, educational and research strengths in physical anthropology have waned in recent decades with the decrease of specialized faculty.

More forensically-oriented anthropological research is sparse. The earliest publication regarding forensic osteology appeared only towards the end of the 20th century. Quintin Oropilla, a doctor of rehabilitation medicine at the University of the Philippines College of Medicine (UPCM) later in his career developed an interest in anthropology. At the recommendation of Eusebio Dizon, an archaeologist at the National Museum, Oropilla was urged to develop Filipino-specific regression formulae for stature estimation from long bones (Oropilla et al. 1991). His study was based on a sample of 16 male and 12 female anatomical teaching cadavers at UPCM and used all six limb long bones to develop a number of equations. While the authors stated their intentions to "accumulate hopefully in a number of years a total

sample of 100 male and 100 female cadavers with the goal of formulating valid regression equations to predict stature, age and sex of Filipino skeletal remains” (Oropilla et al. 1991: 22), this collection was short lived as the bones were either buried or cremated soon after the study (Eusebio Dizon, personal communication, 2016). Interestingly, Oropilla’s daughter Angelie took after her father’s interests and is currently head of the Department of Legal Medicine at the University of Santo Tomas Faculty of Medicine and Surgery and medico-legal officer of the National Bureau of Investigation. She is also pursuing graduate studies in anthropology at the University of the Philippines Diliman. Apart from Oropilla’s initial 1991 publication on stature, no other publications have come out from him or his daughter.

Other researchers have had to rely on advancing the science by studying living subjects, a considerable limitation for a discipline that primarily focuses on the dead. Two decades earlier, Leonor Cruz (1971) had conducted a purely descriptive odontometric study on mesiodistal crown diameters among Filipinos for the purposes of education and dental materials manufacturing standards in the Philippines. Potter et al. (1981) had followed up on Cruz’s (1971) study, but considerably expanded sample size and specificity, variable number, and analytical approach. They also explicitly tested for differences between sexes and cursorily among worldwide populations, concluding that there were no substantial differences in odontometric dimensions between Filipino males and females. Taduran (2012) was the first however to explicitly explore sexual dimorphism of Filipino canine dimensions for forensic identification purposes, yielding relatively low accuracy rates through decision tree modeling at 56.41% and 74.36% using the maxillary and mandibular dentition, respectively. All materials from these three odontometric studies had relied on living subjects that had gone to university dental clinics for services. Additionally, Taduran et al. (2017a) evaluated the accuracy of self-reported versus kin-reported

stature among Filipinos. They concluded that the stature recalled by friends or family of a missing person was a reliable proxy for the missing person's own perceptions of their stature. While their study does not deal with skeletal material per se nor does it produce any methods for actual stature estimation, it provides a justification for the use of stature estimation in Filipino identification. Other work by Taduran et al. (2016, 2017b) gathered fingerprints obtained from applicants seeking police clearance, and used ridge count and density variation for sex estimation.

Now that the Philippine context is juxtaposed with the previous chapter on sex and ancestry estimation, the next chapter will discuss the materials and methods with which to evaluate the specific effects Filipinos may have when they are incorporated into these methods.

CHAPTER 4

MATERIALS AND METHODS

4.1. Creating a Filipino Skeletal Reference Collection

Prior to the current dissertation, no appropriate skeletal materials (i.e., skeletons from contemporary Filipinos of known provenience and demographics) were readily available for investigation. Previous studies have relied on museum collections of ancient and historic crania, the majority of which were collected during the colonial era, from various regions and ethnolinguistic groups of the Philippines. Notable sample locations that appear in the literature are at the Rijks Ethnographisch Museum in Leiden, the Natural History Museum in London, the Duckworth Laboratory at the University of Cambridge, the Musée de l'Homme in Paris, the Museum für Naturkunde in Berlin, the Museum für Völkerkunde in Dresden, the University Museum at the University of Tokyo, and the National Museum of the Philippines in Manila (Koeze 1904; Von Bonin 1931; Pietrusewsky 1981, 1984; Uytterschaut 1984; Hanihara et al. 2003; Auerbach and Ruff 2004, 2006; Matsumara and Hudson 2005; Green and Curnoe 2009; Matsumara and Oxenham 2014). Additionally, there are Filipino samples that are not reported in the literature. Museum collections pose a number of problems, including small sample sizes, biased sex ratios commonly in favor of males, and ambiguity in provenance, sex, and biological and geological age, to name a few. Howells (1989: 110) also measured crania from male convicts who died in prison in Manila prior to World War II, but notes “the series must be accepted as a very general one for the islands.” However, it is unclear what has become of this collection, as it no longer seems to be in its reported location at the University of the Philippines College of Medicine. Likewise, the same medical school had intended to create a skeletal

reference collection from dissection cadavers, but the few bones that were initially defleshed were subsequently buried or destroyed (Oropilla et al. 1991; Eusebio Dizon, personal communication, 2016). There exist a few local university osteological collections, but these are most often used as anatomical training tools and rarely have antemortem information or elements still associated to a single individual.

Given the paucity of available materials, it was therefore necessary to create a novel skeletal reference collection of modern Filipinos with associated antemortem information. To create the collection, remains already disinterred from low-cost niche tombs in arrears were accessioned from Manila North Cemetery, a 54-hectare (133 acre) public cemetery administrated by the Manila Health Department (Fig. 4.1). The cemetery is one of the largest, densest, oldest, and most actively used in the country, housing well over a million graves. Several other collections around the world have served as precedent for cemetery-sourced protocols (Fig. 4.2; Table 4.1).



Figure 4.1. Satellite image of Manila North Cemetery outlined in blue, courtesy of Google Earth (left), and a corresponding map drawing with the location of stacked niche tombs highlighted in yellow (right).



Figure 4.2. Contemporary (black dot) or historic (green dot) cemetery-sourced skeletal collections around the world. Orange dot is the present Philippine collection. See Table 4.1 for description and references of these collections.

Table 4.1. Published cemetery-sourced skeletal reference collections around the world.

<i>Name/Location of Collection</i>	<i>City, Country</i>	<i>Reference</i>
Luis Lopes Collection (Bocage Museum)	Lisbon, Portugal	Cardoso 2006
Coimbra Identified Skeletons Collection	Coimbra, Portugal	Ferreira et al. 2014
Universidad Complutense de Madrid	Madrid, Spain	Trancho et al. 1997
Universitat Autònoma de Barcelona	Barcelona, Spain	Rissech and Steadman 2011
Granada Osteological Collection	Granada, Spain	Aleman et al. 2012
University of Geneva	Geneva, Switzerland	Gemmerich 1999
Schoten Collection	Brussels, Belgium	Orban et al. 2011
Sassari Collection	Bologna, Italy	Facchini et al. 2006
Certosa Cemetery Collection	Bologna, Italy	Belcastro et al. 2017
CAL Milano Cemetery Collection	Milan, Italy	Cattaneo et al. 2018
Hallstatt Skull Collection	Hallstatt, Austria	Martínez-Abadías et al. 2009
University of Athens	Athens, Greece	Eliopoulos et al. 2007
Cretan Collection	Heraklion, Greece	Kranioti et al. 2008
Yishui Medical School	Yishui, China	İşcan and Ding 1995
University of Hong Kong	Hong Kong, China	King 1997
University of the Philippines Diliman	Quezon City, Philippines	Go et al. 2017
Universidad Autónoma de Yucatán	Merida, Mexico	Chi-Keb et al. 2013
Chacarita Collection	Buenos Aires, Argentina	Bosio et al. 2012
Prof. Dr. Rómulo Lambre Collection	La Plata, Argentina	Salceda et al. 2012

Roman Catholicism, an import of Spanish colonialism, and Protestantism, an import of American colonialism, constitute the religious faiths of more than 90% of the population in the Philippines (Philippine Statistics Authority 2013). The ecclesiastically persuaded reverence for death and whole-body burial remain strong in Philippine culture despite harsh socioeconomic obstacles (Cannell 1999). In public cemeteries, the cheapest burial option is a stacked niche tomb just large enough to house a coffin (Fig. 4.3). Niche tombs cannot be held in perpetuity but are typically rented for a minimum of five years at ₱1,000.00 (around US\$20.00) per year, which also covers the cost of a permit from city hall and a tombstone. A limited number of niches are made available for free by the city but fill up quickly and are also used for unidentified bodies. On completion of the five-year lease, next-of-kin must renew the lease or claim the body for reburial elsewhere. Otherwise, remains are exhumed and placed into rice sacks, becoming wards of the administration (Fig. 4.3). Unclaimed remains await reinternment in mass graves, ossuaries, or transfer to other cemeteries. Some have accused administrators of deliberately neglecting to inform families for an excuse to make space available for incoming occupants (Cruz 2012). Manila North Cemetery has made it customary to allow one year between exhumation and reburial as final accommodations for families to claim remains, although this unofficial grace period is often extended indefinitely due to a lack of personnel or resources. Unclaimed remains often fall into disarray and are prone to commingling (Fig. 4.4).

The increasing demand for physical space in a suffocating metropolis evinces the (re)creation of the cemetery deathscape along segregating lines of class, power, and state (Kong 2012). Tremlett (2007: 32) notes that Philippine cemeteries seemingly constitute an “anatomy of hierarchy” following a radiating pattern of decreasing opulence, with lavish mausoleums at the



Figure 4.3. Crowded above-ground concrete tombs typify the style of interment at Manila North Cemetery, with stacked niche tombs in the background (left). Exhumed human remains from recycled graves are kept in rice sacks waiting to be claimed by next of kin or otherwise buried en masse (right).



Figure 4.4. Informal settlers at Manila North Cemetery collect and burn a pile of commingled human remains in an attempt to dispose of the overwhelming number of unclaimed individuals.

center, followed by standalone tombs, then stacked niches along the perimeter. These patterns also radiate decreasing permanence, as niche tombs become first and easy targets for grave recycling. As governments adopt a utilitarian view of space as a resource, “efficient management... seems to prevail over the demand for sensory connections between the dead and the living” (Klaufus 2016: 2453). Social inequality subverts the position of next-of-kin from cemetery patron to bystander. Moreover, a third party in the Philippine public cemetery is its informal settlers, who have been pushed by the outside city into living amongst the graves or have lived their whole lives in the cemetery. In this cemetery microcity, residents find their means as hawkers, small business owners, scavengers, flower vendors, and epitaph inscribers. Some are employed as caretakers by families to keep graves clean and skeletons watched over but are also employed by the administration as labor to clear out overstays and dispose the forgotten. Indeed, the living cemetery resident occupies a liminal space between familial caretaker and administrative undertaker. Manila North Cemetery is a prime dialectic stage not only more obviously between the living and the dead, but also the rich and the poor (or the ability to purchase permanence and identity) (e.g., Barretto-Tesoro and Reyes 2013), space and time (and their proportional decrease), and idealism and pragmatism (or the affective versus economic value of sepulture).

Graves at Manila North Cemetery are stratified across both ends of the socioeconomic spectrum, from past presidents and celebrities to nameless victims of homicide. Arguably, the demographics of the cemetery largely reflect the postcolonial configurations of the city to which it belongs. Thus, the most impermanent interments from niche tombs, and the source of the current collection, represent the lowest classes of Manila. Not age nor sex distinguish them, but rather race, class, and power or lack thereof. These individuals enter skeletal collections because

they are vulnerable to commodification by the educational and scientific communities that consume them, this dissertation included. Indeed, there is a black-market trade for bones and teeth in Manila, often sourced from overflowing cemeteries (Garceau 2002).

A permit for the recovery of these remains was issued by the Manila Health Department that stated the remains are to be stored and available for non-destructive research at the Archaeological Studies Program of the University of the Philippines on an indefinite basis (in accordance with Marcos 1976: Section 97, 100.e). Two major considerations that were brought up by city health officials were (1) ordinances requiring the mass reburial of exhumed remains for sanitary concerns, and (2) actions to be taken if some family members did come forward looking to retrieve their relative's skeleton. In consultation with legal officials at the University of the Philippines, proper sanitation and storage of the remains during the study satisfied the mass burial ordinance (Danilo Concepcion and Rose Beatrix Cruz-Angeles, personal communications, 2016; see Noriega-Reodica 1996). The cemetery administrative office also has a running list of individuals accessioned, and remains will be immediately returned to requesting family members. A notarized Memorandum of Agreement outlining the partnership between the University of the Philippines and the Manila Health Department was then signed.

While the information gained from these remains have vast academic and applied import to the fields of forensics, medicine, evolution, and human biology, the ethical and social implications of such practices remain underemphasized. We strive to conduct the research as legitimately as possible, but fieldwork is fraught with problems. Legally, consent by proxy is granted by local government units, but as is the case for the Manila North Cemetery, the government's motivations for clearing remains should be questioned. For the state, reduction in the amount of exhumed remains reflects well on them in the public eye. The cemetery becomes

uncluttered and seemingly better managed. Informal settlers express similar feelings of relief. Residents share that on the one hand there are purely sanitary concerns for their living conditions, the other hand holds comfort in knowing more care is being given to the remains versus current conditions. Additionally, many residents attribute superstitious fear towards the remains as haphazard disposal does not constitute “resting in peace.” However, there is also the air of economic opportunity that some residents feel when they assist in recovering remains.

Missing from the conversation are next-of-kin whom are unaware that their loved ones have left cemetery grounds. While one could argue that inclusion in the collection serves as a much more respectful form of interment, the dead themselves have ultimately not consented to the research. At best, such an argument constitutes mere rationalization in the hopes for ethical absolution. Because the majority of these skeletons come from destitute contexts, it is nearly impossible to contact living next-of-kin and inform them that research efforts are taking place. To this effect, cemetery personnel have agreed to inform the families of future exhumations of the possibility to have the remains included in the collection. Likewise, the cemetery has a running list of all the individuals that have been accessioned. We also work closely with resident caretakers to identify the individuals that have not been visited for some time. Lastly, we emphasize the implications of our work to the common good. Forensic anthropology has always sought to be at the service of the community, working on scales from the individual case to mass disasters and humanitarian crises. The Philippine context is particularly relevant. Here, research from the Philippine skeletal collection has the opportunity to create direct links between the community it is sourced from and the same vulnerable community who stands to benefit the greatest from refined forensic identification techniques.

Remains were collected between June and August of 2016 and June of 2017. Entire rice sacks, each supposedly containing a single disinterred individual, were brought from Manila North Cemetery to the Archaeological Studies Program at the University of the Philippines. The name of the deceased and birth and death dates were recorded at the cemetery when the tombstone was available. Upon arrival at the university, the rice sacks were completely emptied onto mats, and cursory checks were done to ensure the maximum number of individuals was one as well as to verify that gendered names matched gendered clothing and pelvic morphology (Phenice 1969). Each individual was then assigned a unique identification number.

The majority of the individuals were fully skeletonized at recovery but adhered with associated soft tissue decomposition resembling soil as well as harboring swarms of carrion arthropods such as cockroaches, ants, centipedes, and spiders. Excess debris was brushed off the bones using the hands and placed in plastic crates with openings no larger than 1cm in diameter. Smaller bones of the hands and feet were placed in mesh bags and then placed in the crates; often, foot bones were still inside socks, which allowed for reliable siding of the phalanges. Individuals were then stacked two crates high and submerged in large tubs of soapy water to loosen adhering dirt. After one day of soaking, each bone was brushed clean using a soft-bristled tooth brush and resubmerged in soapy water for three to five days, and then in an aqueous solution of 3% hydrogen peroxide for five to seven days to assist with removing grease. Finally, bones were then submerged in plain water for one day to extract any remaining peroxide, rinsed, and then air-dried under the sun until completely dry. While it has been demonstrated that hydrogen peroxide is not the most ideal means of skeletal processing (Steadman et al. 2006), the method was the most logistically feasible and shortcomings were minimized by using a low concentration over a short amount of time. Once fully dried, bones were labeled with their

identification numbers using a black ultra-fine point marker and individually stored in labeled plastic bins with desiccant silica gel packs for long-term curation (Fig. 4.5). In the event sided feet were present, these were individually packed in sealed labeled plastic bags and placed in the bin. Commingled remains were also treated in the same way and sorted by element, primarily for teaching purposes.



Figure 4.5. The Filipino skeletal reference collection curated at the University of the Philippines.

Within the two summer seasons of collection, a total of 128 individuals were accessioned along with an undetermined number of commingled remains, which were sorted by element.

Eighty-one of the 128 individuals are identified through the availability of tombstone epitaphs. The sex ratio is approximately double (1.95:1) the number of males to females. There are also two unidentified subadults, and one unidentified adult of indeterminate sex. Additionally, crania from 27 individuals (F = 10; M = 17) with documented ages and sexes were measured on site for craniometrics only, but not accessioned into the collection.

Documented age in decimal years was calculated from subtracting the decimal date of birth from the decimal date of death (Toops 1922; Pearl and Miner 1932; McVarish 1962). For example, an individual born on December 23, 1993 who died on December 25, 2015 would have an age of 22 years and two days, or 22.005 years. For identified individuals, the earliest year of birth is 1911 (1921 for the accessioned sample) and the most recent year of death is 2011 (Fig. 4.6). Pooled mean age is 53.3 years old (54.0 years for the accessioned sample). The mean age for males is 52.5 years (53.0 years for the accessioned sample) with the earliest year of birth in 1911 (1929 for the accessioned sample). The mean age for females is 54.7 years (55.7 years for the accessioned sample) with the earliest year of birth in 1921. Descriptive statistics for the ages are presented in Table 4.2, and the age distribution of the sample is presented in Figure 4.7.

Table 4.2. Descriptive statistics of known ages of the study sample and collection.

<i>Entire Study Sample with Known Ages</i>						
	n	Mean	SD	Median	Minimum	Maximum
Males	68	52.5	18.5	55.7	8.5	98.5
Females	40	54.7	19.3	57.3	18.4	88.2
Total	108	53.3	18.7	56.5	8.5	98.5
<i>Accessioned (Collection) Individuals Only</i>						
	n	Mean	SD	Median	Minimum	Maximum
Males	51	53.0	17.5	56.4	15.0	81.8
Females	30	55.7	20.9	58.2	18.4	88.2
Total	81	54.0	18.7	57.1	15.0	88.2

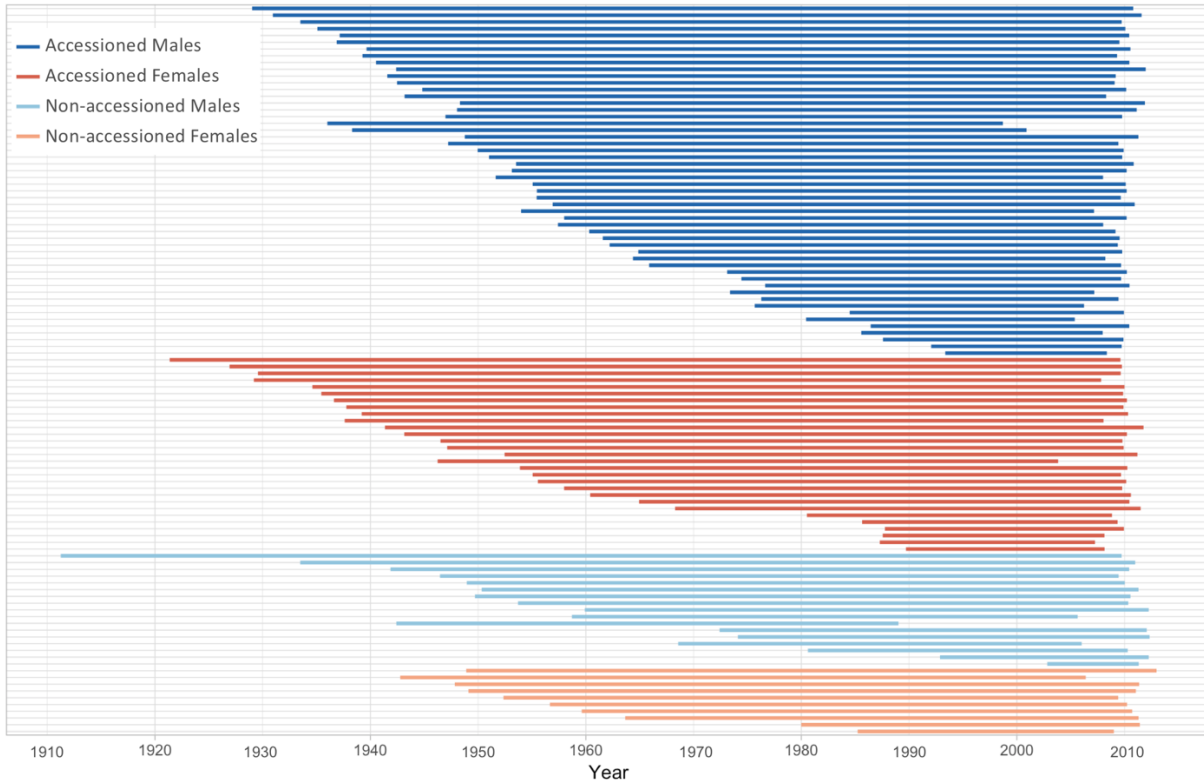


Figure 4.6. Individual lifespans of males and females accessioned into the collection, and individuals whose data were recorded but were not accessioned. Only individuals with documented ages are shown.

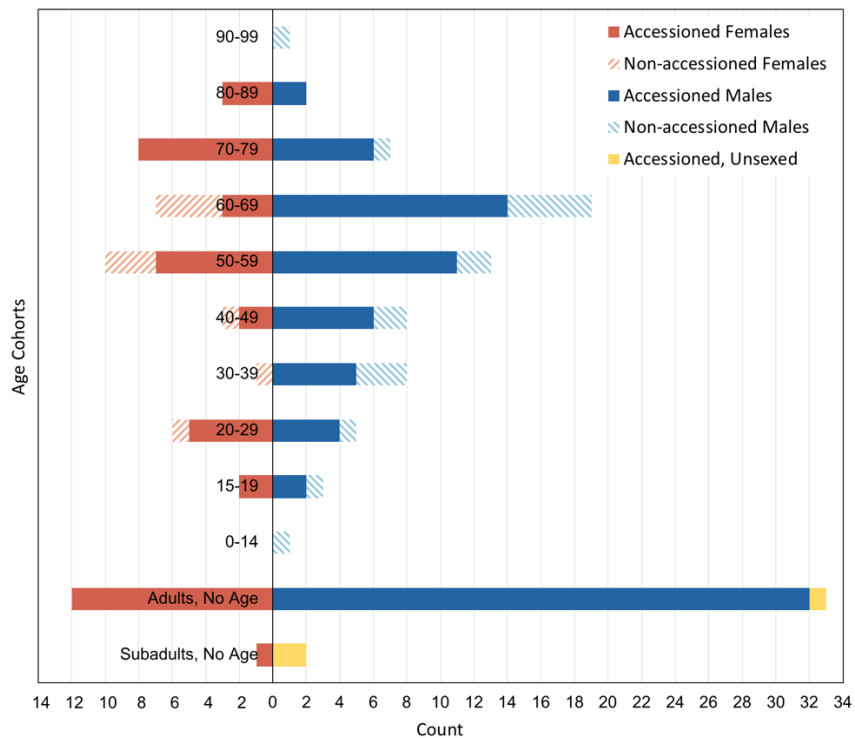


Figure 4.7. Sample demographics.

As this is a mutually beneficial arrangement between cemetery administration and the collection, unidentified individuals were accepted into the collection. Certain analyses and future research projects may still benefit from inclusion of remains without documented age and sex. Additionally, while not the focus of this research, several pathologies, surgical procedures, and sharp, blunt, and ballistic traumas are represented in the collection.

4.2. Data Collection Procedures

A total of 48 metric and morphoscopic variables were recorded for each cranium. Twenty-eight standardized inter-landmark distances (craniometric measurements) were recorded with either manual spreading or sliding calipers according to the latest definitions proposed by Langley et al. (2016), which is an update to Moore-Jansen et al.'s (1994) widely used data collection procedures (Table 4.3). These measurement definitions were themselves largely derived from the volumes of Howells (1973) and Martin and Knussmann (1988). Morphoscopic traits were visually or tactilely assessed with the aid of standardized definitions, line drawings, and a contour gauge for nasal bone contour (Table 4.4). These include four traits used in sex estimation (Buikstra and Ubelaker 1994; Walker 2008), and 16 traits used in ancestry estimation (Hefner 2007, 2009, 2012). These measurements encompass neuro-, splanchno-, and basicranial regions, and are those used for individuals included in the Forensic Anthropology Data Bank (craniometrics) (Jantz and Moore-Jansen 1988), Macromorphoscopic Databank (ancestry morphoscopies) (Hefner 2018), and MorphoPASSE database (sex morphoscopies) (Klales and Cole 2018), and used in traditional casework (Figs. 4.8 and 4.9).

All measurements were taken blind, meaning age and sex of the skeleton were not known during data collection. Both left and right sides of bilateral measurements were recorded, with

random side selection employed for statistical analyses. Paired t-tests assuming unequal variances showed no significant differences between left and right sides for every bilateral variable included in the study.

Table 4.3. Standardized inter-landmark distances and their landmark and three/four-letter abbreviations.

<i>Measurement</i>	<i>Abbreviations</i>	<i>Measurement</i>	<i>Abbreviations</i>
Maximum cranial length	g-op GOL	Nasal breadth	al-al NLB
Nasio-occipital length	n-op NOL	Orbital breadth	d-ec OBB
Maximum cranial breadth	eu-eu XCB	Orbital height	OBH
Bizygomatic breadth	zy-zy ZYB	Biorbital breadth	ec-ec EKB
Basion-bregma height	ba-b BBH	Interorbital breadth	d-d DKB
Cranial base length	ba-n BNL	Frontal chord	n-b FRC
Basion-prosthion length	ba-pr BPL	Parietal chord	b-l PAC
Maxillo-alveolar breadth	ecm-ecm MAB	Occipital chord	l-o OCC
Maxillo-alveolar length	pr-alv MAL	Foramen magnum length	o-ba FOL
Biauricular breadth	ra-ra AUB	Foramen magnum breadth	FOB
Nasion-prosthion height	n-pr NPH/UFHT	Mastoid height	po-ms MDH
Minimum frontal breadth	ft-ft WFB	Biasterionic breadth	ast-ast ASB
Upper facial breadth	fnt-fnt UFBR	Bimaxillary breadth	zma-zma ZMB
Nasal height	n-ns NLH	Zygoorbitale breadth	zo-zo ZOB

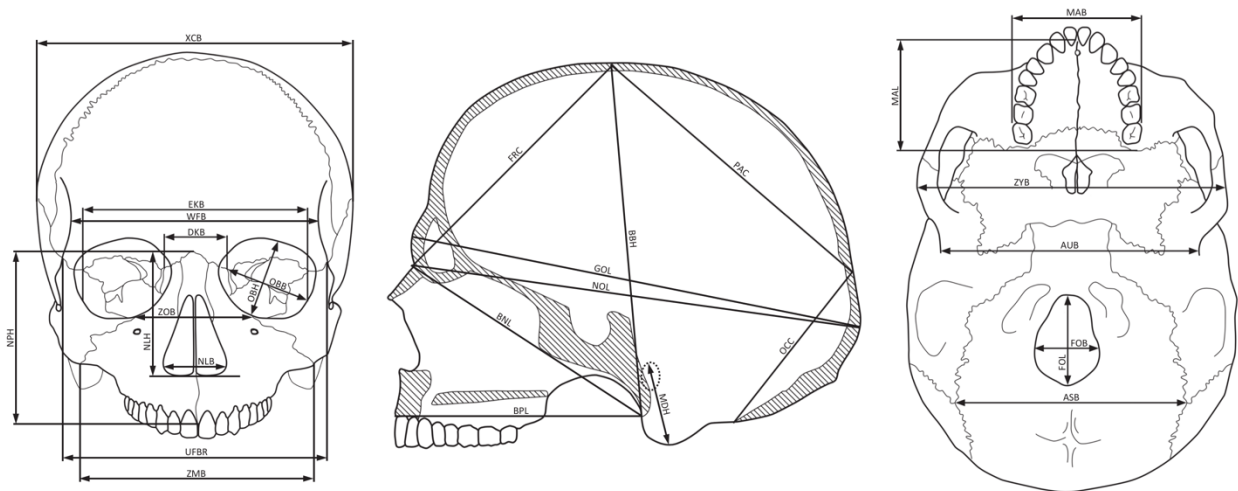


Figure 4.8. Standardized inter-landmark distances.

Table 4.4. Standardized morphoscopic traits for sex and ancestry, their scoring states, and abbreviations.

<i>Measurement</i>	<i>States and Abbreviation</i>		<i>Measurement</i>	<i>States and Abbreviation</i>	
Glabella	1-5	GLB	Mastoid process	1-5	MP
Supraorbital margin	1-5	SOM	Nuchal crest	1-5	NC
Anterior nasal spine	1-3	ANS	Nasofrontal suture	1-4	NS
Inferior nasal aperture	1-5	INA	Nasal overgrowth	0-1	NO
Interorbital breadth	1-3	IOB	Supranasal suture	0-2	SPS
Malar tubercle	0-3	MT	Orbital shape	1-3	OBS
Nasal aperture shape	1-3	NAS	Postbregmatic depression	0-1	PBD
Nasal aperture width	1-3	NAW	Posterior zygomatic tubercle	0-3	ZT
Nasal bone contour	0-4	NBC	Zygomaticomaxillary suture	0-3	ZS
Nasal bone shape	1-4	NBS	Transverse palatine suture	1-4	TPS

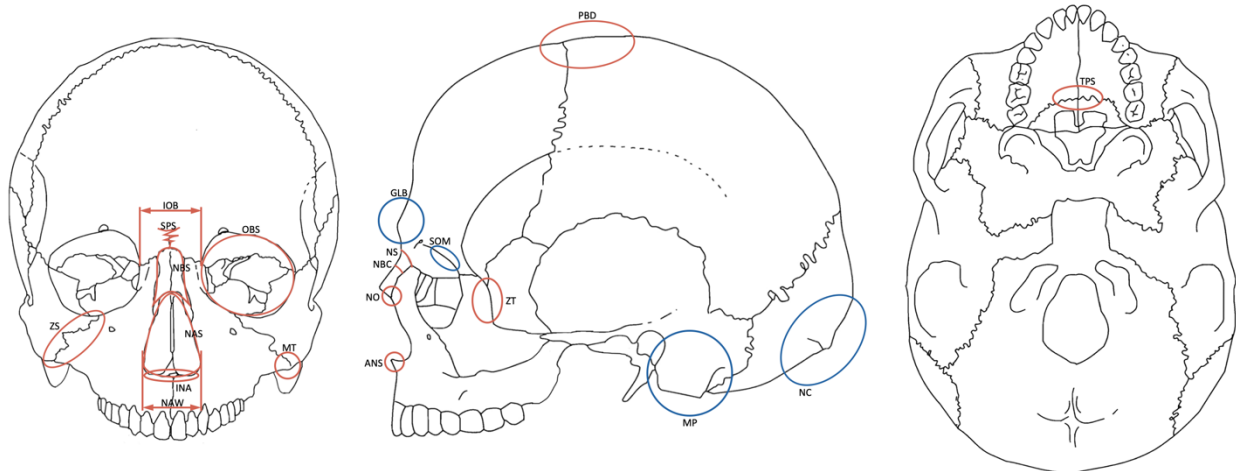


Figure 4.9. Standardized morphoscopic traits used in sex (blue) and ancestry (red) estimation.

4.3. Global Comparative Datasets

Comparative data from other populations of the world were sourced from databases employing the same standardized data collection procedures. As previously mentioned, these databases include the Forensic Anthropology Data Bank for craniometrics (FDB) (Jantz and Moore-Jansen 1988) and the Macromorphoscopic Databank (MaMD) for ancestry morphoscopic

traits (Hefner 2018), as well as Japanese and Thai data for sex morphoscopic traits (Tallman 2016).

4.4. Statistical Analyses

The succeeding three chapters are organized as independent research articles, which all share a focus on Filipinos as the population of study. More detailed descriptions of the statistical methodology used in each chapter are therein contained. In summary, Chapter V evaluates sex morphoscopic trait variation, whereas Chapters VI and VII evaluate ancestry estimation methods that use craniometric and morphoscopic traits, respectively.

Sexually dimorphic cranial morphoscopic traits are subjected to a frequency distribution splitting technique termed the optimized summed scored attributes (OSSA) method originally developed for ancestry estimation (Hefner and Ousley 2014). In OSSA, the distributions of ordinal trait scores between two groups are dichotomized to maximally separate the groups. Sectioning points are then selected based on the cumulative frequency distributions for each trait, and an overall sectioning point between the summed dichotomized scores (the OSSA score) is ascertained.

For evaluations of ancestry, craniometric measurements are subjected to linear discriminant function analyses (LDA) through the Fordisc 3.1 software. The LDA method is a multivariate statistical technique that finds a linear combination of variables with the goal of maximally separating groups with *a priori* category labels. The resulting function can then be used as a linear classifier that can assign unknown or “unlabeled” individuals into one of the reference groups based on closest similarity.

Lastly, ordinal morphoscopic traits useful in ancestry estimation are subjected to multivariate probit regression (MPR). Probit analysis is a parametric regression technique where the output or result is categorical given a set of recorded variables, which can be continuous, dichotomous, or categorical. Under a MPR model, ancestry, which is a categorical result, can be estimated given a set of ordinal predictor variables such as cranial morphoscopic traits.

CHAPTER 5

APPLICATION OF THE OPTIMIZED SUMMED SCORED ATTRIBUTES METHOD TO SEX ESTIMATION IN ASIAN CRANIA¹

5.1. Introduction

Sex is one of the most important components of the biological profile. In addition to potentially narrowing down the list of possible identifications by half, knowing the sex of a decedent also further calibrates later estimates of age and stature. Sexual dimorphism in the skeleton is detected by either metric or non-metric means. Nonmetric traits are used widely in both forensic casework and research (Phenice 1969; Rogers and Saunders 1994; Williams and Rogers 2006; Walker 2008; Klales 2013; Garvin et al. 2014; Lewis and Garvin 2016; Tallman 2016; Klales and Cole 2017). Nonmetric methods involve visually scoring morphological traits on an ordinal scale or as present/absent (e.g., Phenice (1969) traits of the pubis). For the skull, the most common traits used are the nuchal crest (NC), mastoid process (MP), supra-orbital margin (SM), supra-orbital ridge or glabella (SR), and mental eminence (ME) (Buikstra and Ubelaker 1994; Walker 2008). Each of these traits is scored ordinally on a scale from 1 to 5, with 1 being the most gracile and 5 being the most robust.

The magnitude of sexual dimorphism is known to vary among populations (Van Vark et al. 1989; Rogers and Saunders 1994; Walker 2008; Green and Curnoe 2009; Spradley and Jantz 2011; Garvin et al. 2014; Klales 2017), even when confined to a regional and temporal level

¹Portions of this chapter have been published as: Tallman SD, Go MC. 2018. Application of the optimized summed scored attributes method to sex estimation in Asian crania. *Journal of Forensic Sciences* 63: 809–814.

(Cunha and Van Vark 1991; İşcan et al. 1998; Kemkes and Göbel 2006). This is likely a combined result of environmental pressures, genetic factors, secular change, and to a lesser degree assortative mating practices (Alexander et al. 1975; Eveleth 1975; Wolfe and Gray 1982; Freyer and Wolpoff 1985). East and Southeast Asian skeletal variation in particular has received little attention relative to populations from more accessible skeletal reference collections (i.e., African and European American collections). A large sample of contemporary and documented Japanese and Thai crania was analyzed not only to test a novel computational method for sex estimation, but also to explore sexual dimorphism more generally for this region of the world. Additionally, the method was validated using a regionally diverse holdout sample of Japanese, Thai, and Filipino individuals to assess its generalizability across Asian groups.

While metric methods are more readily subjected to statistical treatment and validation, ordinal nonmetric traits have lagged behind in their compliance with Daubert evidentiary standards (Williams and Rogers 2006; Grivas and Komar 2008; Walker 2008; Christensen and Crowder 2009; Hefner 2009). However, motivated by Daubert, Hefner and Ousley (2014) proposed a novel technique for ancestry estimation termed optimized summed scored attributes (OSSA). OSSA proceeds by dichotomizing ordinal morphoscopic traits used in ancestry, and in Hefner and Ousley's (2014) case between American Black and White individuals, to maximally separate two groups. Heuristically selected sectioning points are based on cumulative frequency distributions for each trait, and an overall sectioning point between the summed dichotomized scores (the OSSA score) is ascertained. The effectiveness of OSSA in ancestry estimation has been validated by Kenyhercz et al. (2017), but the methodology is limited to comparison between only two groups. In the context of OSSA, many similarities exist between the nature of data used in sex and ancestry estimations (Konigsberg et al. 2009), namely that both use

ordinally scored categorical variables and both have only two outcomes (i.e., American Black vs. American White; female vs. male). Both sex and ancestry estimation also suffer from biases introduced by a gestalt approach where the overall initial impression of a skull based on personal experience often steers an observer's decision (Berg and Tersigni-Tarrant 2014). Motivation to avoid these biases push for more systematic and objective collection and treatment of the data. Thus, the aim of the current study is to appropriate the OSSA methodology and test its applicability as a sex estimation technique using cranial traits.

5.2. Materials and Methods

The dataset is comprised of 1,324 Japanese, Thai, and Filipino crania, with all but 12 Filipino crania of known sex (Table 5.1). Sex for the undocumented Filipino crania was verified through pelvic morphology and agreement between at least four observers, as well as associated gendered clothing when available. The Japanese data were collected from Chiba University's Department of Bioenvironmental Medicine (late 19th to early 20th century) and Jikei University's School of Medicine (1960s to 1990s). The Japanese sample is comprised of individuals from the greater Tokyo region who were dissection room cadavers. The Thai data were collected from Khon Kaen University's Faculty of Medicine (20th to 21st century) and Chiang Mai University's Department of Forensic Osteology (20th to 21st century). The Thai sample is comprised of individuals from northern Thailand who willed their bodies through ongoing body donation programs (Mann 2013; Tallman 2016; Techataweewan et al. 2017). Lastly, the Filipino data were collected from the University of the Philippines' Archaeological Studies Program (late 20th to 21st century) and were accessioned from abandoned graves at a local public cemetery in Manila (Go et al. 2017). All observations for the Japanese and Thai

skulls were collected by SDT, while all observations for the Filipino skulls were done by MCG. Only intact and non-pathological crania were used who were adults, 17 years of age or older at the time of death. The entire sample was divided into two sets: (i) a larger dataset of Japanese and Thai individuals that would serve as the basis for OSSA calculations, and (ii) a holdout validation sample that comprised 15% of the total subsample size for Japanese and Thai individuals by sex as well as all the Filipino individuals.

Table 5.1. Sample demographics by population, sex, and institution. Holdout sample sizes are in parentheses.

Populations ^a	Males	Females	Total
Japanese (CU)	107 (13)	41 (7)	592 (105)
Japanese (JU)	317 (62)	127 (23)	
Thai (KKU)	253 (41)	114 (22)	472 (83)
Thai (CMU)	67 (15)	38 (5)	
Filipino (UPD)	(47)	(25)	(72)
Total	744 (178)	320 (82)	1064 (260)

^aCU, Chiba University; JU, Jikei University; KKU, Khon Kaen University; CMU, Chiang Mai University; UPD, University of the Philippines, Diliman

Five sexually dimorphic cranial traits (nuchal crest [NC], mastoid process [MP], supra-orbital margin [SM], glabella [SR], and mental eminence [ME]) were each scored 1 (gracile) through 5 (robust) for each individual in accordance with descriptions and line drawing guides provided by Walker (2008). The scores were then dichotomized based on their frequency distributions following the OSSA procedure described by Hefner and Ousley (2014). For each trait, the frequencies per character state among males and females were tabulated. Using the cumulative frequency, scores more common in females were reduced to “0,” and those more common in males were reduced to “1.” Once all five cranial traits were dichotomized, the sum of all traits is calculated to produce OSSA scores per individual ranging from 0 to 5.

Classification accuracies were evaluated in two ways. First, the classification rates for the larger Japanese and Thai samples that produced the OSSA sectioning points were evaluated. This is the method by which Hefner and Ousley (2014) and Kenyhercz et al. (2017) achieved their classification rates. Subsequently, a holdout validation sample consisting of randomly excluded individuals from the larger Japanese and Thai samples and Filipino individuals that did not contribute to the selection of OSSA sectioning points was also evaluated. In the case of the Filipino sample, the mental eminence was excluded from analysis due to frequent resorption of the alveolar process from antemortem tooth loss. Lewis and Garvin (2016) also recommend avoiding the mental eminence as it exhibits the highest intra- and inter-observer error among the five traits and Walker's (2008) diagrams for the mental eminence do not capture the range of variation. When only four of the five traits were analyzed, OSSA sectioning points were recalculated accordingly. All Filipinos were used as validation cases because of the relatively smaller sample size of this population compared to the larger Japanese and Thai datasets. We also wanted to evaluate the efficacy of using sectioning points developed in one population to another population, and if the OSSA sex estimation method could be generalized across Asian groups. Additionally, error rates ($100.0 - \text{correct classification rate}$), sensitivities ($\text{correctly assigned females} / [\text{correctly assigned females} + \text{females assigned as males}]$), specificities ($\text{correctly assigned males} / [\text{correctly assigned males} + \text{males assigned as females}]$), positive predictive values ($\text{PPV} = \text{correctly assigned females} / [\text{correctly assigned females} + \text{males assigned as females}]$), and negative predictive values ($\text{NPV} = \text{correctly assigned males} / [\text{correctly assigned males} + \text{females assigned as males}]$) were calculated for the holdout sample.

5.3. Results

Trait Frequency

The mean scores for each trait in each population are presented in Table 5.2. The trait frequencies and OSSA transformations for the Japanese and Thai samples are presented in Tables 5.3 and 5.4, respectively. For both samples, each trait had the same dichotomized sectioning points based on the cumulative frequencies by sex. These sectioning points may also be calculated by taking the median of each sex per trait. The separations between dichotomized 0 and 1 were between the original ordinal scores 2 and 3 for NC, SM and ME; 3 and 4 for MP; and 1 and 2 for SR. Using frequencies from a pooled sample did not alter these sectioning points.

Table 5.2. Population-specific female and male mean trait values (and standard errors). Difference in means reflects the degree of sexual dimorphism in each trait.

	<i>Japanese</i>			<i>Thai</i>			<i>Filipino</i>		
	F	M	Diff.	F	M	Diff.	F	M	Diff.
NC	2.56 (0.06)	3.38 (0.05)	0.82	2.16 (0.06)	2.81 (0.05)	0.65	1.76 (0.21)	2.53 (0.20)	0.77
MP	2.64 (0.07)	3.80 (0.04)	1.16	2.82 (0.06)	3.92 (0.04)	1.10	1.56 (0.13)	3.06 (0.15)	1.50
SM	2.25 (0.06)	3.21 (0.04)	0.96	2.13 (0.06)	2.83 (0.05)	0.70	2.24 (0.22)	2.94 (0.16)	0.70
SR	1.12 (0.03)	2.07 (0.04)	0.95	1.11 (0.04)	2.18 (0.05)	1.07	1.20 (0.10)	3.15 (0.17)	1.95
ME	2.08 (0.05)	2.64 (0.04)	0.56	2.40 (0.05)	2.90 (0.04)	0.50	-	-	-

Optimized summed scored attributes score distributions for the larger Japanese, Thai and pooled samples suggest a heuristically defined sectioning point of ≤ 1 for optimal separation between females and males (Fig. 5.1 and Table 5.5). The median OSSA score for females is 1, while for males is 4 regardless of sample. When ME is omitted from the analysis (i.e., OSSA scores now range from 0 to 4), the sectioning point of ≤ 1 for both groups and median OSSA score for the Japanese sample is maintained, but the median score for Thai females shifts to 0 and for Thai males shifts to 3.

Table 5.3. Frequency distributions for ordinal scores and OSSA scores for each cranial trait in the Japanese sample.

	Original	<i>n</i>		<i>%</i>		<i>Cum. %</i>		OSSA
		F	M	F	M	F	M	
NC	1	18	17	0.11	0.04	0.11	1.00	0
	2	70	65	0.42	0.15	0.52	0.96	0
	3	54	148	0.32	0.35	0.85	0.81	1
	4	24	127	0.14	0.30	0.99	0.46	1
	5	2	67	0.01	0.16	1.00	0.16	1
MP	1	19	4	0.11	0.01	0.11	1.00	0
	2	61	32	0.36	0.08	0.48	0.99	0
	3	59	129	0.35	0.30	0.83	0.91	0
	4	23	132	0.14	0.31	0.96	0.61	1
	5	6	126	0.04	0.30	1.00	0.30	1
SM	1	29	12	0.17	0.03	0.17	1.00	0
	2	77	93	0.46	0.22	0.63	0.97	0
	3	52	150	0.31	0.35	0.94	0.75	1
	4	9	122	0.05	0.29	0.99	0.40	1
	5	1	47	0.01	0.11	1.00	0.11	1
SR	1	150	120	0.89	0.28	0.89	1.00	0
	2	13	186	0.08	0.44	0.97	0.72	1
	3	5	80	0.03	0.19	1.00	0.28	1
	4	0	35	0.00	0.08	1.00	0.09	1
	5	0	3	0.00	0.01	1.00	0.01	1
ME	1	32	25	0.19	0.06	0.19	1.00	0
	2	88	155	0.52	0.37	0.71	0.94	0
	3	43	193	0.26	0.46	0.97	0.58	1
	4	5	47	0.03	0.11	1.00	0.12	1
	5	0	4	0.00	0.01	1.00	0.01	1

Table 5.4. Frequency distributions for ordinal scores and OSSA scores for each cranial trait in the Thai sample.

	Original	<i>n</i>		<i>%</i>		<i>Cum. %</i>		OSSA
		F	M	F	M	F	M	
NC	1	24	20	0.16	0.06	0.16	1.00	0
	2	83	102	0.55	0.32	0.70	0.94	0
	3	39	131	0.26	0.41	0.96	0.62	1
	4	6	53	0.04	0.17	1.00	0.21	1
	5	0	14	0.00	0.04	1.00	0.04	1
MP	1	5	0	0.03	0.00	0.03	1.00	0
	2	49	13	0.32	0.04	0.36	1.00	0
	3	78	91	0.51	0.28	0.87	0.96	0
	4	14	120	0.09	0.38	0.96	0.68	1
	5	6	96	0.04	0.30	1.00	0.30	1
SM	1	29	15	0.19	0.05	0.19	1.00	0
	2	84	110	0.55	0.34	0.74	0.95	0
	3	34	125	0.22	0.39	0.97	0.61	1
	4	4	58	0.03	0.18	0.99	0.22	1
	5	1	12	0.01	0.04	1.00	0.04	1
SR	1	142	86	0.93	0.27	0.93	1.00	0
	2	6	140	0.04	0.44	0.97	0.73	1
	3	2	51	0.01	0.16	0.99	0.29	1
	4	2	33	0.01	0.10	1.00	0.13	1
	5	0	10	0.00	0.03	1.00	0.03	1
ME	1	14	6	0.09	0.02	0.09	1.00	0
	2	75	83	0.49	0.26	0.59	0.98	0
	3	56	177	0.37	0.55	0.95	0.72	1
	4	7	45	0.05	0.14	1.00	0.17	1
	5	0	9	0.00	0.03	1.00	0.03	1

Table 5.5. OSSA score frequency distribution by sex and population (%).

OSSA Score	<i>Japanese</i>		<i>Thai</i>		<i>Pooled</i>	
	F	M	F	M	F	M
0	22.6	3.1	27.6	2.2	25.0	2.7
1	37.5	3.8	39.5	6.3	38.4	4.8
2	22.0	16.3	24.3	16.6	23.1	16.4
3	13.7	21.9	7.2	23.4	10.6	22.6
4	2.4	30.7	0.0	31.9	1.3	31.2
5	1.8	24.3	1.3	19.7	1.6	22.3

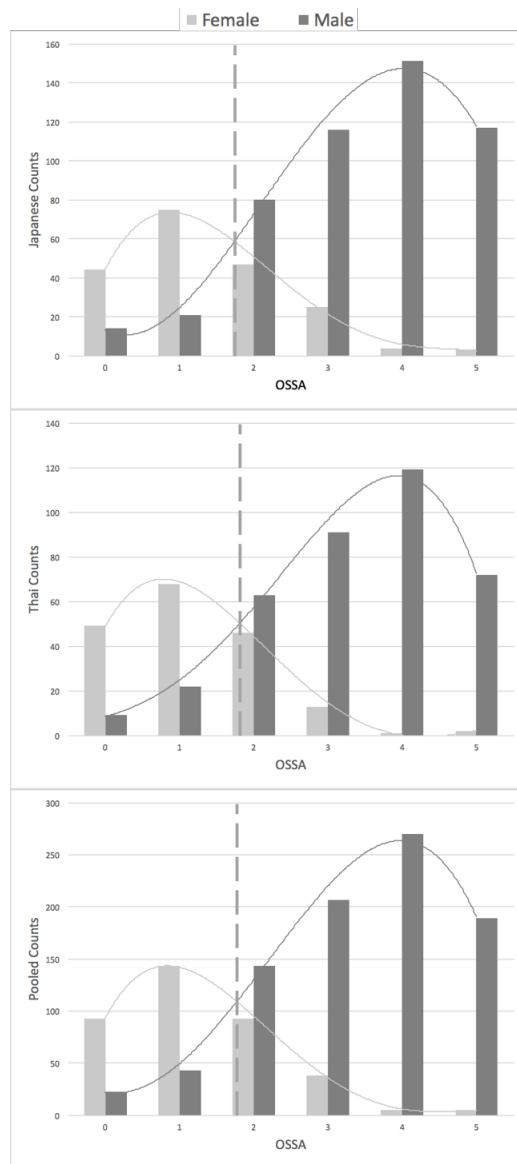


Figure 5.1. OSSA score distributions for the samples. Sectioning points are shown by dashed lines.

Classification

The overall correct classification rate for the larger Japanese sample is 83.8% (F = 60.1%, M = 93.2%). The larger Thai sample achieves a similar correct classification rate of 83.7% (F = 67.1%, M = 91.6%). With the larger samples pooled together, the correct classification rate is 83.7% (F = 63.4%, M = 92.5%).

Classification rates and associated statistics including error rates, sensitivities, specificities, PPVs, and NPVs for the holdout sample represent a less biased picture of success because observations from these individuals did not contribute to the frequency data used to determine sectioning points (Tables 5.6 and 5.7). Using all five traits, the overall correct classification rate for Japanese is 82.9% (F = 60.0%, M = 92.0%) and for Thai is 80.7% (F = 55.6%, M = 92.9%). Similarly, the correct classification rate is 81.9% (F = 57.9%, M = 92.4%) when the two samples are pooled together. When ME is omitted from the holdout samples, the overall classification rate for Japanese is 81.0% (F = 66.7%, M = 86.7%), for Thai is 81.9% (F = 77.8%, M = 83.9%), and for Filipinos is 80.6% (F = 84.0%, M = 78.7%). Pooling all three populations, the correct classification rate becomes 81.2% (F = 75.6%, M = 83.7%). We note that in examining the frequency distributions of ordinal scores for the Filipino sample independently, the overall OSSA sectioning point is maintained at ≤ 1 , but the dichotomized division between NC is at ordinal scores 1 and 2 (between 2 and 3 for Japanese and Thai), and for MP is at 2 and 3 (between 3 and 4 for Japanese and Thai). The sectioning points for SM and SR are the same as in the Japanese and Thai samples. Recalculating OSSA scores for the Filipino sample using these sectioning points (i.e., NC 1/2, MP 2/3, SM 2/3, SR 1/2) only slightly increases correct classification to 81.9% from 80.6%, but widens the sex bias (F = 68.0%, M = 89.4%).

Table 5.6. Classification accuracies using the holdout sample.

<i>Five Traits</i>				<i>Four Traits</i>			
	Female	Male	% Correct	Japanese	Female	Male	% Correct
Japanese				Female	66.7	33.3	81.0
Female	60.0	40.0	82.9	Male	13.3	86.7	
Male	8.0	92.0		Thai			
Thai				Female	77.8	22.2	81.9
Female	55.6	44.4	80.7	Male	16.1	83.9	
Male	7.1	92.9		Filipino			
Pooled				Female	84.0	16.0	80.6
Female	57.9	42.1	81.9	Male	27.0	78.7	
Male	7.6	92.4		Pooled			
				Female	75.6	24.4	81.2
				Male	16.3	83.7	

Table 5.7. Classification statistics for the holdout sample (% four traits / five traits).

	<i>Japanese</i>	<i>Thai</i>	<i>Filipino^a</i>
Error	19.0 / 17.1	18.1 / 19.3	19.4
Sensitivity	66.7 / 60.0	77.8 / 55.6	84.0
Specificity	86.7 / 92.0	83.9 / 92.9	78.7
PPV	66.7 / 75.0	70.0 / 78.9	67.7
NPV	86.7 / 85.2	88.7 / 81.2	90.2

^aFour traits only (ME excluded).

There is considerable bias between sexes using five traits, with females having a much lower correct classification rate than males (Table 5.6). This bias is reduced but still evident when only four traits are used. This is because an OSSA score of 2 represents roughly 23% of females of the total sample, but would misclassify as male due to the ≤ 1 sectioning point (Table 5.5). Shifting the sectioning point to ≤ 2 would inversely switch the bias against males, but roughly 16% of males would then misclassify as female and the overall correct classification rate would decrease. An alternative option is to designate OSSA score 2 as indeterminate, thus using two sectioning points at ≤ 1 for females and ≥ 3 for males. Without considering individuals with

Table 5.8. Classification accuracies using the holdout sample omitting OSSA = 2 individuals.

<i>Five Traits</i>				<i>Four Traits</i>			
	Female	Male	% Correct	Japanese	Female	Male	% Correct
Japanese				Female	100.0	0.0	86.8
Female	94.7	5.3	91.6	Male	17.9	82.1	
Male	9.4	90.6		Thai			
Thai				Female	95.5	4.5	84.4
Female	83.3	16.7	89.1	Male	21.4	78.6	
Male	8.7	91.3		Filipino			
Pooled				Female	95.5	4.5	80.0
Female	89.2	10.8	90.5	Male	30.3	69.7	
Male	9.1	90.9		Pooled			
				Female	96.9	3.1	84.1
				Male	22.1	77.9	

Table 5.9. Classification statistics for the holdout sample omitting OSSA = 2 individuals (% four traits / five traits).

	<i>Japanese</i>	<i>Thai</i>	<i>Filipino^a</i>
Error	13.2 / 8.4	15.6 / 10.9	20.0
Sensitivity	100.0 / 94.7	95.5 / 83.3	95.5
Specificity	82.1 / 90.6	78.6 / 91.3	69.7
PPV	66.7 / 75.0	70.0 / 78.9	67.7
NPV	100.0 / 98.3	97.1 / 93.3	95.8

^aFour traits only (ME excluded).

an OSSA score of 2 for the holdout sample, the sex bias between correct classification rates drastically narrows except for Thais and Filipinos using only four traits (Table 5.8). Female classification success increases by over 30% using five traits and over 20% using four traits, which are accompanied by a related increase in the sensitivities (Table 5.9). Conversely, male classification success decreases by just 1.5% using five traits and 5.8% using four traits. This more conservative classification scheme of designating OSSA score 2 as indeterminate results in an increase of 8.6% overall correct classification using five traits, but only an increase of 2.9%

correct classification using four traits. However, nearly 22% of individuals using five traits and 25% of individuals using four traits would remain unclassified or indeterminate.

5.4. Discussion

While the OSSA method has been successfully applied to ancestry assessment for African and European Americans (Hefner and Ousley 2014; Kenyhercz et al. 2017), it has yet to be used in other components of the biological profile. However, because the OSSA method dichotomizes and maximizes differences between two groups based on frequency distributions, the assessment of sex represents a novel and appropriate area of application that works well within the commonly used 1–5 cranial ordinal scoring scheme (Buikstra and Ubelaker 1994; Walker 2008). Subsequent to ordinally scoring the cranial traits, the analyst converts the five or four (without ME) ordinal trait scores to OSSA scores (Tables 5.3 and 5.4), then sums the OSSA scores. Based on a robust dataset ($n = 1,064$) of modern Japanese and Thai individuals presented here (Table 5.1), final OSSA scores of 0–1 indicate female and scores of 2–5 indicate male, which resulted in correct classification rates of 55.6–92.9% (Table 5.6). In this scoring system, males were more often correctly classified than females ($M = 78.7$ –92.9%, $F = 55.6$ –84.0%), which may be related to the disparity in the holdout sample sizes ($M = 178$, $F = 82$). Alternately, the analyst can use a more conservative approach, wherein final OSSA scores of 0–1 indicate female, 2 is indeterminate, and scores of 3–5 indicate male, which resulted in correct classification rates of 69.7–100.0% (Table 5.8). Further, this scoring system significantly reduced the sex biases ($M = 69.7$ –91.3%, $F = 83.3$ –100.0%).

The correct classification rates documented with the OSSA method (Tables 5.6 and 5.8) are consistent with the accuracies presented in other studies that utilize multiple cranial

nonmetric traits. In particular, Walker's (2008) study of 304 African American, European American, and English-born individuals found that univariate statistics correctly classified individuals 69–83% of the time, while population-specific logistic regression equations for pooled African and European Americans and ancient Native Americans resulted in 84–88% correct classification rates. Similarly, in Garvin et al.'s (2014) study of 499 Arikara Native American, medieval Nubian, U.S. Black, and U.S. White individuals, they found that univariate statistics correctly classified 63–79%, while logistic regression equations increased correct classification rates to 74–99%. These studies, along with the new OSSA sex assessment method presented here, demonstrate that multiple cranial traits together perform better than individual traits. Moreover, the results of this study, along with those of Walker (2008) and Garvin et al. (2014), show that the correct classification rates achieved using multiple cranial nonmetric traits are on par with, or perform better than, cranial metric analyses, which rarely produce correct classification rates in excess of 90% (Giles and Elliot 1963; Cunha and Van Vark 1991; Steyn and İşcan 1998; Franklin et al. 2005; Spradley and Jantz 2011). The classification statistics associated with the OSSA sex assessment method (Tables 5.6–5.9) help to satisfy the Daubert ruling, which requires methods used by expert witnesses to be peer reviewed, empirically tested, maintained by operational standards, be accepted by the scientific community, and have known error rates (United States Supreme Court 1993; Christensen and Crowder 2009). The relatively high correct classification rates (80.0–91.6%), sensitivities (83.3–100.0%), specificities (69.7–91.3%), PPVs (66.7–78.9%), and NPVs (93.3–100.0%) accompanied by relatively low error rates (8.4–20.0%) for the holdout sample indicate that the OSSA sex assessment method is fairly accurate and valid when scores of 2 are considered indeterminate. While nonmetric analyses are arguably more subjective, and therefore more error prone than metric analyses, their success and

widespread usage 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.

A critique of the OSSA sex assessment method is that it weighs all five cranial traits equally. Studies that use the ordinal cranial trait scores in binary logistic regression equations (Williams and Rogers 2006; Walker 2008; Garvin et al. 2014; Tallman 2016) have demonstrated that some traits perform better than others and that trait utility is population dependent. In particular, Garvin et al. (2014) found that the mastoid process and glabella performed the best, while the nuchal crest performed the worst, in differentiating females and males in Arikara, Nubian, U.S. Black, and U.S. White groups. This was similarly found with the Japanese and Thai individuals included in the present study (Tallman 2016).

A further and related critique of the OSSA sex assessment method is that it ignores correlations and covariance between traits. Garvin et al. (2014) found that the supra-orbital margin and glabella were the most correlated, while the mental eminence was least correlated in Arikara, Nubian, U.S. Black, and U.S. White groups. Likewise, Tallman (2016) found that the cranial traits are minimally to moderately correlated, with the glabella and mastoid process being most correlated and the mental eminence being least correlated in the Japanese and Thai individuals. Correlations between cranial traits are expected, as the cranium is one of the most highly integrated structures within the human body (Cheverud 1982; Lieberman et al. 2000; Hallgrímsson et al. 2007).

Previous research has demonstrated that the ME exhibits high intra- and inter-observer error rates due to the difficulty in assessing (observing and palpating) variation in the amount of projection (Williams and Rogers 2006; Garvin et al. 2014; Lewis and Garvin 2016; Tallman

2016); however, the inclusion of ME scores somewhat improved the correct classification rates for the Japanese and Thai holdout sample (Table 5.8). In particular, the inclusion of the ME increases the correct classification rates for males (without ME = 69.7–86.7% vs. with ME = 90.6–92.9%) and decreases the correct classification rates for females (without ME = 66.7–100.0% vs. with ME = 55.6–94.7%; Tables 5.6 and 5.8). Therefore, due to the difficulty in scoring the ME and its variable expression, the decision to include the ME when analyzing Asian remains is at the discretion of the analyst. Further, given that edentulism, alveolar resorption, or missing mandibles may prohibit the inclusion of the mandible in analyses, the OSSA method presented here allows for sex assessment for crania lacking ME scores.

Research has demonstrated that differences exist in the non-metric expression of sexual dimorphism between Asian and non-Asian groups such that the application of methods developed on African, European, and Native American individuals will not accurately classify Japanese or Thai individuals (Tallman 2016). In general, Japanese and Thai individuals exhibit reduced sexual dimorphism compared to non-Asian groups, thereby necessitating the development of Asian-specific sex assessment methods. In particular, Japanese and Thai SR are very gracile, whereby an ordinal score of 1 is more common in females, and scores of 2 (or higher) are associated with males (Tables 5.3 and 5.4). Further, significant overlap exists in OSSA scores of 2 for Japanese and Thai females and males. When an OSSA score of 2 is considered male, 81.9% of the Japanese and Thai holdout sample were correctly classified using the five traits, while 81.2% of the Filipino, Japanese, and Thai holdout sample were correctly classified using four traits (excluding ME). Alternately, when an OSSA score of 2 is considered indeterminate, the correct classification rate increases to 90.5% for the Japanese and Thai holdout sample, and 84.1% of the Filipino, Japanese, and Thai holdout sample. Perhaps more

importantly, the use of an OSSA score of 2 as an indeterminate category significantly reduces the sex biases. If OSSA scores of 2 are considered male, then the pooled sex bias for the Japanese and Thai holdout sample is 35.0%, which is reduced to 1.7% if scores of 2 are considered indeterminate. Similarly, the sensitivities (i.e., female classification performance) increase between 11.5 and 34.7% when scores of 2 are considered indeterminate (Tables 5.7 and 5.9). Therefore, while at the discretion of the analyst, it is recommended to consider final OSSA scores of 0–1 as female, 2 as indeterminate, and scores of 3–5 as male when applied to Asian populations.

A more nuanced measure of sexual dimorphism across the populations studied here is presented through individual trait score means in Table 5.2, which are unobscured by the collapsing of scores based on trait frequencies required by OSSA. On average, the NC and MP are more gracile in Filipinos than in both the Japanese and Thai, the SR is more robust in Filipinos than in both the Japanese and Thai, and the SM is more gracile in Filipinos than in the Japanese but more robust than in the Thai. The least amount of sexual dimorphism is seen in the ME for both Japanese and Thai samples. Generally across the three populations, the degree of sexual dimorphism is smallest in the NC and SM, particularly for Thais and Filipinos. The greatest degree of sexual dimorphism is found in Filipino SR scores, showing nearly two scores difference between female and male means. However, using measures provided by Garvin et al. (2014), all three Asian male groups possess more gracile NC and SR scores compared to White males and all three Asian female groups possess more gracile SR scores compared to White females. Beyond these, there is considerable variation in mean score among both sexes of each of the three Asian groups, Whites, and Blacks.

While the Japanese and Thai collections do not represent the entirety of morphological skeletal variation within Asia, they exemplify two geographically disparate populations from East and Southeast Asia who are broadly and distantly related, yet morphologically and genetically distinct, each having their own unique population histories. Based on the frequency distributions presented in Tables 5.3 and 5.4 and Figure 5.1, the Japanese and Thai are similarly sexually dimorphic. However, the relatively low correct classification rate for the Filipino males in the holdout sample (69.7%, Table 5.8), as well as the values provided in Table 5.2, indicate that population differences exist between the Japanese/Thai and Filipino individuals. Filipino males appear to be more gracile than Japanese or Thai males, as the OSSA method exhibits somewhat reduced discriminatory power in the Filipino individuals. Despite population variation between Asian groups, the OSSA sex assessment method presented here can be cautiously applied to other Asian populations and amended as additional collections become available for research.

5.5. Conclusions

The adapted OSSA sex assessment method was developed on a robust set of 1,064 Japanese and Thai individuals and applied to 260 Filipino, Japanese, and Thai individuals held out from the original analysis. Using the five commonly employed sexually dimorphic cranial traits following Buikstra and Ubelaker (1994) and Walker (2008), correct classification rates ranged from 55.6% to 100.0%. Due to significant overlap in the expression of sexual dimorphism between Japanese and Thai females and males, it is recommended that final OSSA scores of 2 represent an indeterminate category, while scores of 0–1 indicate female and scores

of 3–5 indicate male. As such, the OSSA method can be cautiously employed when estimating the sex of individuals from Asian populations.

CHAPTER 6

CLASSIFICATION TRENDS AMONG CONTEMPORARY FILIPINO CRANIA USING FORDISC 3.1¹

6.1. Introduction

The estimation of ancestral affiliation of unidentified forensic skeletal cases is an integral part of the identification process. Not only does ancestry offer an avenue for narrowing down putative identifications, but knowing ancestry also further calibrates other biological profile components such as age, sex, and stature. Ancestry can also be one of the most challenging of these inferred parameters. From a statistical standpoint, the classifications are conditional on the assumption that reference datasets capture the range of pertinent human variation for any given case. In actual practice, many groups remain underrepresented or absent in these datasets, and, because reference materials are opportunistically acquired, even large samples are often limited in coverage, so that classification analyses must operate under the unrealistic expectation of broad regional homogeneity. The increasing ethnic diversity of the United States and the growth of transnational metropolises around the world necessitate a more inclusive approach to forensic anthropological case methods.

Best practice recommendations for forensic anthropologists caution practitioners against the use of reference samples that are not representative of the unidentified skeletal remains in

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2019. Classification trends among contemporary Filipino crania using Fordisc 3.1. *Forensic Anthropology* 2(4): 293–303.

question, whether in terms of sex cohort, biogeographic population, or time period (Scientific Working Group for Forensic Anthropology 2012). However, in the applied context of medico-legal casework, rarely is the case subject to forensic anthropological evaluation drawn from a closed population where “ancestry” is *a priori* known. When case ancestry is truly unknown, reference samples that may or may not be representative of the unknown’s population of origin must be used to provide an estimate of ancestry for the individual case. While it is unrealistic for any ancestry method to include every possible population, we contend that it is also *unnecessary* when appropriate statistical tools and adequate reference populations are available for ancestry inference, as in the case of Fordisc (Jantz and Ousley 1993, 2005, 2012; Ousley and Jantz 1996, 2012).

The software, Fordisc 3.1 (FD3), makes it possible for a broad audience of forensic anthropologists to apply discriminant function analysis to craniometric data from unidentified skeletal cases for the allocation of population membership using an unparalleled collection of forensically relevant and globally sourced reference samples (Jantz and Ousley 1993, 2005, 2012; Ousley and Jantz 1996, 2012). Beyond providing hard classifications for forensic cases into one of the available reference populations, FD3 also captures broad continental ancestry (Asian, African, European, Native American) variation – yielding results comparable to hard classifications generated from unsupervised approaches to population inference (Algee-Hewitt 2016). This information, while not immediately diagnostic, can be highly useful for understanding the general ancestry composition of the individual case in question, as already demonstrated by Hughes et al. (2018) for Latin American samples. Therefore, the methods implemented via FD3 can be applicable in unidentified death case scenarios for estimating continental ancestry, even when the true population of origin is not represented by the current

aggregate of reference samples. We argue that the nature of the variation reflected by the FD3 reference samples can be used to reveal continental ancestry patterns that can be informative of population membership and, in turn, be of value to forensic anthropological casework investigations.

Here, we provide an example of the utility of FD3 for assessing general continental ancestry of Filipino individuals. While the Howells series from the Philippines is available in FD3, we consider only those reference data that are forensically-relevant, including temporally appropriate given concerns for secular change in the cranium (Jantz 2001; Wescott and Jantz 2005; Weisensee and Jantz 2011), and are believed to be similar in their ancestral makeup. To this latter point, Algee-Hewitt et al. (2018b) have observed differences in the mean quantities of trihybrid ancestry between the Howells and Hanihara samples and the contemporary individuals from the Manila North Cemetery (Go et al. 2017) studied here. Accordingly, we choose only from the individuals sourced from the Forensic Anthropology Data Bank (FDB) (Jantz and Moore-Jansen 1988). The contemporary subset of Asians included in FD3 contains only peoples of Chinese, Japanese, and Vietnamese origins or descent. By establishing the classification trends for our Filipino cases into the continental categories comprised of the FDB groups in FD3, we can evaluate accuracy (defined here as the assignment of an individual case to one of the reference populations that would make up a larger continental-level Asian reference sample) and rates of error (defined here as the classification to any one of the populations that would not fall into this macrogeographic Asian reference sample) for inferred ancestry. We employ these contextual definitions of accuracy and rates of error to reflect how the FD3 outcomes would potentially lead investigators to make inferences of inclusion and exclusion based on continental ancestry. For example, if the FD3 group classification “accurately” associated with Asian

continental ancestry, then the Philippines (along with other Asian populations) would be included as a potential source population for the unknown case. In contrast, if FD3 classified a case into a non-Asian group, the practitioner would likely exclude the Philippines (along with other Asian populations) as a potential source population for the unknown case. This study does not aim to provide general recommendations for the use of FD3 in ancestry estimation.

Because of the complex population history of the Philippines, and, thus, the potential for highly heterogeneous cranial morphologies among present day Filipinos, it is helpful to determine if FD3 classifications of Filipino crania are both consistent and sufficiently intuitive, such that they signify to the investigator possible Asian ancestry and imply that the Philippines should not be excluded as a possible source population. For this study, we posit that (1) the majority of the Filipino crania will be assigned into FD3 groups with East and Southeast Asian ancestry, and (2) given Philippine colonial history specific to the Manila-based study sample, some proportion of these individuals will be alternatively allocated into groups with a limited proportion of European ancestry (e.g., classified as Hispanic). Misclassification of Hispanics using FD3 has previously been demonstrated, and is likely associated with both first peopling, and later Western colonial histories of Latin America (Dudzik and Jantz 2016; Hughes et al. 2018). The results of this study will provide a better understanding of classification and general ancestry estimation trends of FD3 for crania representing populations not explicitly captured by the available reference samples.

Asians (defined as persons with ancestral origins in the Far East, Southeast Asia, or the Indian Subcontinent) remain an understudied group despite making up 5.6% of the population recorded in the 2010 US census (Hoeffel et al. 2012) and 60% of the global population. The increasing importance of Asians in US demographics is easily demonstrated by the rapid shift in

their share of the US population-at-large. Within a decade from 2000-2010 the Asian population in every state except Hawaii grew by at least 30%; 57% of Hawaii's population was comprised of Asians by 2010 (Hoeffel et al. 2012). Although Asians represent the fastest growing racial group in the US, Filipinos in particular have received little to no attention in forensic anthropological literature (see Go 2018). This is further surprising given that Filipinos are the third largest Asian demographic group in the United States. Over 3.4 million Americans report as having some degree of Filipino ancestry (24.4% of Asians in the US), with more than 2.5 million identifying as solely Filipino (United States Census Bureau 2010). Filipinos comprise the most populous Asian group in most of the Western half of the country including Alaska and Hawaii. The Philippines also represents the third and fifth largest source country for documented and undocumented immigrants, respectively (Baker and Rytina 2013, 2014), with 52% of Filipinos in the US being foreign-born (United States Census Bureau 2010). Thinking more broadly, these trends are consistent as, in Canada, Filipinos rank first in number of permanent residents by source country (Citizenship and Immigration Canada 2015).

The Philippines has experienced a unique Western colonization history relative to other Asian countries. The Philippines experienced over four centuries of consecutive colonial rule under Spain (1521 to 1898) and then the US (1898 to 1946), 250 years of which saw regular trade routes between Latin America via the Manila-Acapulco Galleon Trade (1565 to 1815). Historical documents suggest intermarriages between Filipino "*indios*", Latin Americans, Spanish and Chinese were encouraged during Spanish colonization (De Mas 1843), although these pairings were likely most common in the capital and other major posts (Phelan 2011). During American rule, intermarriages between Filipinos and American Whites in the Philippines continued (Winkelmann 2017). The flow of European genes into the archipelago was

undoubtedly male biased owing to gendered colonial activities of subjugation via religious conversion, state exertion, and military expansion, or what has been called “bachelor colonization” (Molnar 2017).

This history most certainly encouraged gene flow, among other microevolutionary processes that may not be immediately tractable from the morphological study of presently available Asian skeletal samples. Research exploring nuclear, mitochondrial, and Y-chromosome diversity have shown Filipinos to possess unique genetic histories relative to the surrounding region, not only reflecting initial colonization of the Asia-Pacific region, but also several waves of migration thereafter, including the post-colonial period (e.g., Bugawan et al. 1994; Tabbada et al. 2010; Delfin et al. 2011, 2014; Banda et al. 2015). Apart from anecdotal claims (Potter et al. 1981: 34; Howells 1989: 110; Delfin et al. 2014: 236; Delfin 2015: 450), no study has explicitly evaluated the degree of European genetic introgression in post-colonial Philippine populations. One study found only 3.57% (1/28) of their small Filipino sample possessed a European Y-chromosome haplotype (Capelli et al. 2001). Using STRUCTURE to analyze a set of ancestry informative markers, another study by Yang et al. (2005) found overwhelming correspondence between predicted ancestry and self-identification within their entire Asian subgroup of 80 Koreans, Japanese, Chinese, and Filipinos. Only two out of 26 Filipinos showed large European contributions. Similar results were found by a larger study (total $n = 103,006$, Filipino $n = 1,708$), as they remark that “for self-reported Filipinos, a substantial proportion [of the ~10% exhibiting Asian-European admixture that self-reported as Asian] have modest levels of European genetic ancestry reflecting older admixture” (Banda et al. 2015: 1293). It is worth noting that the latter two studies sampled Filipinos living in California, while Capelli et al. (2001) do not provide more details on their sample apart from that they are “from the

Philippines.” Conversely, a genetic admixture study by Rodriguez-Rodriguez et al. (2018) reported nearly one-third of people sampled from Guerrero, Mexico, particularly from the city of Acapulco, had greater than 5%, and up to 10% Asian ancestry, which they found was most closely related to populations from the Philippines and Indonesia. Most recently, Algee-Hewitt et al. (2018b) report, using craniometrically-derived continental ancestry proportions, that present-day Filipinos are notably admixed, as they carry about 20% less Asian ancestry than the mean quantity (90%) estimated for the other Asian groups, representing specifically peoples from Vietnam, Thailand, China (Hong Kong), Japan, and Korea, included in their study. Certainly, the degree of admixture across Philippine populations is likely highly varied across regional, temporal, and social lines of difference.

Census counts demonstrate that the level of Spanish immigration to the colonial Philippines did not reach such heights as those with colonial Mexico (Barrows 1905: 478; Phelan 2011), even into the American period (Table 6.1). However, the US actually increased its military interests in the country even after granting independence in 1946. When US military bases in the Philippines permanently closed in 1992 and their troops withdrew, an estimated 50,000-plus infants, children, and adolescents sired by American soldiers were left orphaned and impoverished (Kutschera et al. 2012). The estimate of these “biracial” Filipino “Amerasians” grows to 250,000 when adults and second-generation progeny are included (Kutschera and Caputi 2012). These post-installation cities have continued informally sanctioned military prostitution systems today in the form of sex tourism hotspots catered to white men (Kutschera et al. 2015; Chapman 2017).

Table 6.1. Census data on race in the Philippines during American colonization.^a

<i>Race</i> ^b	1903	1918	1939
Brown	6,914,880	9,386,826	15,758,637
Males	3,435,848	4,692,426	7,905,222
Females	3,479,032	4,694,400	7,853,415
Yellow	42,097	50,826	141,811
Males	41,071	47,296	107,093
Females	1,026	3,530	34,718
White	14,271	12,390	19,300
Males	11,450	8,592	11,112
Females	2,821	3,798	8,188
Black	1,019	7,623	29,157
Males	767	4,029	15,511
Females	252	3,594	13,646
Mixed	15,419	34,663	50,519
Males	7,516	17,974	25,868
Females	7,903	16,689	24,651
Unreported			879
Total	6,987,686	9,492,328	16,000,303
Males	3,496,652	4,770,317	8,065,281
Females	3,491,034	4,722,011	7,935,022

^aData from the United States Bureau of the Census (1905), Census Office of the Philippine Islands (1920), and Commonwealth of the Philippine Commission of the Census (1941).

^bRacial terminology reflects those used in the original census, where brown refers to “Malay” Filipinos, yellow refers to East Asians such as Chinese and Japanese, white refers to Europeans, and black includes both Negritos and Africans.

Filipinos were the first historic Asian group to immigrate in the Americas, at first by escaping servitude aboard Spanish ships in 16th century California (Cordova 1983), and then later by establishing the first Asian settlement in 18th century Louisiana (Espina 1988). American rule had only accelerated the transport of Filipinos to the US (Espiritu 2003). In the early 1900s, *sakadas* or Filipino farmers were exported to Hawaii to work in sugar plantations and later to California for similar agricultural needs. Government-sponsored *pensionados* were

also sent to the US during this time to be schooled in US history and government. The American occupation and onset of numerous 20th century global conflicts also saw many Filipino men conscripted into American military service. Filipinos emigrating to the US during this period also faced strict anti-miscegenation laws (Baldoz 2004). Later capitalist booms such as oil in the Gulf States in the 1970s, Asian Tiger economies in the 1980s, and health care and information technology industries in the 1990s increased demand for cheap domestic and manual labor. Filipinos were encouraged by the government to pursue this demand abroad and provide a form of foreign remittance for the country. The tradition of deploying such Overseas Filipino Workers en masse remains strong today (Rodriguez 2010).

The consequences of a unique colonial history and the strong Filipino presence within the US and around the world at the present time necessitate a better grasp of Filipino skeletal variation for forensic anthropological investigations. To begin to understand such variation, we use, for the first time, the FD3 software as a tool to evaluate ancestry estimates relative to Filipino skeletal remains. Appreciation of these results will further the call for practicing forensic anthropologists to more fully comprehend the biological and statistical motivations for cranial [mis]classification trends in order to give the appropriate weight to or interpretation of the software's output when assigning ancestry to unidentified remains.

6.2. Materials and Methods

The current test sample consists of mostly identified adult Filipino crania curated by the Archaeological Studies Program, University of the Philippines Diliman (Go et al. 2017). These individuals were accessioned from a large public cemetery in Manila, having been exhumed from low-cost niche tombs with unpaid burial maintenance fees. They represent cases that

remain unclaimed by next-of-kin. The earliest individual birth year is 1911; the majority of individuals in this sample died in 2010 and 2011. Ages-at-death ranged from 20 to 88 years old, with an average age of 52 years.

All craniometric data were recorded by MCG. Measurements are among those employed by FD3 and their collection followed the most recent definitions used by the FDB (Langley et al. 2016). In cases of bilateral variables, the left side measurement was used, substituting with the right side if the left side was absent. Two-sample t-tests assuming unequal variances showed no significant differences between left and right sides for every bilateral variable included in the study. A small number of fragmented crania were reassembled, in which case only reliable interlandmark distances were recorded. When a landmark was absent, associated measurements were not recorded.

We explore FD3 classification trends within the context and traditional methodology of actual casework, whereby users are cognizant of its recommended guidelines that guard against model overfitting, especially with an unknown case. In order to avoid such overfitting – arising from the inclusion of too many measurements with respect to the minimum group sample size – a maximum of nine standard cranial measurements were chosen via forward stepwise variable selection using Wilk’s lambda (Table 6.2). For the purposes of this paper, we employ a common practice of limiting the number of variables used to $3m \leq n$, where m is the number of variables and n is the smallest group sample size (Huberty 1994). The most recent updates to the Fordisc Help File relax this requirement to $n - 1$ variables (Ousley 2012: 83). Given our current evaluation of a population not represented within the FDB groups, we follow the more conservative $3m \leq n$ rule. Individual test cases with two or greater missing variables out of the nine were omitted from analysis. Multivariate outliers flagged by FD3 and those individuals with

two or greater univariate outliers (less than or greater than three times the standard deviation) were also omitted. When an individual only had one outlying variable, it was run through FD3 with the outlying variable omitted. This resulted in a final Filipino crania sample size of 41 females (PHF) and 69 males (PHM); their univariate descriptive statistics are shown in Table 6.2.

Table 6.2. Standard cranial measurements used, their abbreviations, and univariate statistics for the Filipino study sample.

Measurement	Abbreviation	Males (n = 69)		Females (n = 41)	
		Mean	SD	Mean	SD
Maximum cranial length	GOL	175.07	6.95	167.46	7.19
Maximum cranial breadth	XCB	141.10	5.74	136.34	5.08
Bizygomatic breadth	ZYB	131.34	4.51	124.55	5.24
Basion-bregma height	BBH	136.94	5.24	131.33	4.80
Biauricular breadth	AUB	123.03	4.18	118.12	4.35
Upper facial height	UFHT	66.54	4.55	63.80	4.79
Bimaxillary breadth	ZMB	95.49	5.38	93.40	4.45
Nasal breadth	NLB	26.66	1.89	25.95	1.63
Orbital breadth	OBB	38.01	2.00	36.68	2.13

Each individual was run through FD3 (Version 3.1.314), and, of the software generated output, both the assigned membership to one among the available reference groups and the associated probabilities were recorded. The 13 FD3 reference groups originate from the FDB, and include individuals with biogeographic ancestral ties to Europe, Africa, the Americas, and Asia (Table 6.3). More information about the provenience of each of these reference samples can be found in the Fordisc help file (Ousley 2012). Sexes of the Filipino test crania were treated as unknown, and therefore all FD3 reference groups were used for each case regardless of sex. We opted not to focus sex-specific categories for each Filipino test case to reflect the most conservative casework scenario where sex may be indeterminate. Therefore, the results of this

study may differ if sex-specific analyses were performed in FD3. However, because so few female Asian reference samples are available, it may prove beneficial to include both male and female reference samples in the FD3 analyses of female Filipino test cases. Aside from regular interlandmark distances, shape-transformed values, for which the effect of size was reduced (Darroch and Mosimann 1985; Rosas and Bastir 2002), were also run through FD3 for each individual to account for scaling differences related to sex.

Table 6.3. Fordisc reference groups used in this study and their abbreviations, grouped into broad continental ancestry categories.

<i>Reference Group</i>	<i>Abbreviation</i>	<i>N</i>
African		
American Black Females	BF	34
American Black Males	BM	60
European		
American White Females	WF	165
American White Males	WM	340
Asian		
Japanese Females	JF	123
Japanese Males	JM	194
Chinese Males	CHM	74
Vietnamese Males	VM	48
Indigenous American		
American Indian Females	AF	26
American Indian Males	AM	49
Guatemalan Males	GTM	70
Hispanic		
Hispanic Females	HF	35
Hispanic Males	HM	165

Because FD3 assigns group membership to one of the reference groups included in the analysis, two probability measures are provided for evaluation. These values should be assessed simultaneously with the classification choice in order to gauge the strength of the classification

(Ousley and Jantz 2012). Posterior probabilities are measures of membership in each of the reference populations, and, as proportions, they must sum to one. As they are relative to the groups included in the function, they assume that the unknown belongs to one of these groups. Typicality probabilities “represent how likely an unknown belongs to a particular group, based on the average variability of all the groups in the analysis. Absolute distances are evaluated, rather than relative distances as in calculating [posterior probabilities]” (Ousley 2012: 23). FD3 produces three measures of typicalities based on the F distribution, chi-square distribution, or ranked distances. This study uses the F distribution, which takes into account both the Mahalanobis distances and group sample sizes for each case. Recently, Konigsberg and Frankenberg (2018) have evaluated FD3’s calculation of typicalities from the F distribution, providing an alternative and what they state is the more appropriate equation. We use FD3-generated typicalities here, as this paper focuses on the software’s outputs specifically.

Lastly, the FDB craniometric dataset was downloaded via the “Save Analyzed Data” option and combined with the Philippine sample in order to run a canonical variate analysis (CVA) using shape-transformed measurements in the software JMP® 10.0.0. Multivariate and univariate outliers as determined above were excluded. CVA was used in order to visualize group relationships and centroid trends in 2-dimensional space.

6.3. Results

For the overall model, the maximum total leave-one-out cross-validation rate acquired using nine variables was 50.6% for untransformed measurements and 40.2% for shape-transformed measurements. Generally, decreasing the number of variables used or removing the

effects of size decreased the total cross-validation rate of the discriminant function, as expected (Ousley 2012).

Of the results generated by FD3, this study focuses on the first and second population classification choice identified by the program (Tables 6.4 and 6.5), as well as the associated posterior and typicality (F distribution) probabilities for each case (Table 6.6 and Fig. 6.1). Regardless of sex, the majority of individuals classified into an Asian group (PHM = 72.5%, PHF = 73.2%), then the second-most common group being Hispanic (PHM = 10.1%, PHF = 17.1%), third-most into an Indigenous American group (PHM = 7.2%, PHF = 7.3%), fourth-most as African (PHM = 5.8%, PHF = 2.4%), and least into a European group (PHM = 4.3%, PHF = 0.0%). Furthermore, over half of the 29 individuals (51.9%) who did not first classify as Asian had an Asian group as their second classification choice. Hispanics (HF and HM) and Indigenous Americans (GTM, AF, and AM) were also generally the next most common first or second choices after Asians. Excluding the effects of size, shape-transformed measurements did not significantly alter the classification trends for either sex. Looking only within those individuals that classified as Asian and using untransformed values, Filipino males most commonly classified into the three Asian male reference groups (36.0% into VM, 26.0% into CHM, and 24.0% into JM) and least into JF (14.0%), while Filipino females most commonly classified into the sole Asian female reference group (73.3% into JF) and then into VM (23.3%) and CHM (3.3%). When using shape-transformed values, males and females now follow a shared trend, mostly classifying as VM (PHM = 40.0%, PHF = 51.6%), then JF (PHM = 24.0%, PHF = 29.0%), and equally into JM (PHM = 18.0%, PHF = 9.7%) and CHM (PHM = 18.0%, PHF = 9.7%).

Table 6.4. FD3 classification counts by first then second choice.

	<i>Filipino Males (n = 69)</i>								<i>Filipino Females (n = 41)</i>								
	<i>Untransformed</i>				<i>Shape-Transformed</i>				<i>Untransformed</i>				<i>Shape-Transformed</i>				
	<i>1st Choice</i>	<i>2nd Choice</i>	<i>1st Choice</i>	<i>2nd Choice</i>	<i>1st Choice</i>	<i>2nd Choice</i>	<i>1st Choice</i>	<i>2nd Choice</i>	<i>1st Choice</i>	<i>2nd Choice</i>	<i>1st Choice</i>	<i>2nd Choice</i>	<i>1st Choice</i>	<i>2nd Choice</i>			
Asian	VM	18	JF	6	VM	20	JF	8	JF	22	HF	8	VM	16	JF	7	
			CHM	5			CHM	7			VM	6			CHM	5	
			GTM	4			GTM	4			GTM	3			HF	2	
			JM	1			AM	1			BF	3			AF	1	
			HM	1	JF	12	JM	3			JM	1			GTM	1	
			AM	1			VM	3			CHM	1	JF	9	JM	3	
	CHM	13	JM	6			CHM	3	VM	7	JF	4			VM	2	
			VM	5			HF	1			CHM	1			CHM	2	
			JF	1			GTM	1			GTM	1			HF	1	
			GTM	1			BF	1			AF	1			BF	1	
	JM	12	CHM	7	JM	9	CHM	6	CHM	1	JM	1	JM	3	CHM	2	
			VM	2			JF	2							JF	1	
			JF	2			WM	1					CHM	3	JM	3	
			WM	1	CHM	9	JM	3									
	JF	7	HF	3			JF	2									
			JM	2			VM	2									
			VM	1			GTM	1									
			GTM	1			WM	1									
	Hispanic	HM	4	VM	2	HF	5	JF	2	HF	7	JF	5	HF	5	JF	4
				JM	1			HM	1			VM	1			VM	1
			WF	1			AF	1			AF	1					
HF		3	HM	1			GTM	1									
			AF	1	HM	3	GTM	1									
			GTM	1			BM	1									
Indigenous American	GTM	4	HM	2	GTM	4	CHM	3	GTM	3	JF	1	GTM	2	HM	2	
			JF	1			BM	1			HM	1	AM	1	AF	1	
			CHM	1	AM	3	VM	2			BF	1					
	AF	1	GTM	1			AF	1									
African	BF	2	JF	1	BM	2	JF	1	BF	1	HF	1	BM	1	AM	1	
			BM	1			WM	1									
	BM	2	CHM	1	BF	1	BM	1									
European			HM	1													
	WM	3	CHM	1	WM	1	BM	1					WF	1	HF	1	
			HM	1													
		BM	1														

Table 6.5. FD3 classification percentages (and counts) based on the first choice.

	<i>Males (n = 69)</i>		<i>Females (n = 41)</i>		<i>Sexes Pooled (n = 110)</i>	
	<i>Untransformed</i>	<i>Transformed</i>	<i>Untransformed</i>	<i>Transformed</i>	<i>Untransformed</i>	<i>Transformed</i>
Asian	72.5% (50)	72.5% (50)	73.2% (30)	75.6% (31)	72.7% (80)	73.6% (81)
Hispanic	10.1% (7)	11.6% (8)	17.1% (7)	12.2% (5)	12.7% (14)	11.8% (13)
Indigenous American	7.2% (5)	10.1% (7)	7.3% (3)	7.3% (3)	7.3% (8)	9.1% (10)
African	5.8% (4)	4.3% (4)	2.4% (1)	2.4% (1)	4.5% (5)	4.5% (5)
European	4.3% (3)	1.4% (1)	0.0% (0)	2.4% (1)	2.7% (3)	1.8% (2)

Using untransformed values, the median posterior probability was 0.42 (PHM = 0.38; PHF = 0.45) and median typicality probability was 0.50 (PHM = 0.51, PHF = 0.48). Only seven (6.4%) of the test cases had posterior probabilities greater than 0.70, four classifying as JF and one each into VM, GTM, and WM, all of which had typicalities greater than 0.05. However, there is no required threshold for posterior probabilities because they are relative to each included reference group (Ousley and Jantz 2012). Greater than 90% (100/110) of the Filipino test cases had typicality probabilities that exceeded the value of 0.05 (or 5%) – the threshold adopted here to signify questionable membership or measurement error (see Ousley 2012; Ousley and Jantz 2012). Using shape-transformed values, the median posterior probability was 0.36 (PHM = 0.36, PHF = 0.36) and median typicality probability was 0.61 (PHM = 0.59, PHF = 0.64). Nine cases (8.2%) had posteriors greater than 0.70, eight classifying as VM, three of which with typicalities less than 0.05, and one as BM. As with regular measurements, greater than 90% (101/110) had typicalities exceeding 0.05.

The Mahalanobis distance matrix and plot generated from the CVA are found in Table 6.7 and Figure 6.2, respectively. The first two canonical variables explain a cumulative total of 68.8% of the variation (43.8% and 25.0%, respectively).

Table 6.6. Median posterior probabilities (PP), typicality probabilities (TP), and leave-one-out cross-validation rates (CV) per first-choice classification group.

	<i>Males</i>						<i>Females</i>					
	<i>Untransformed</i>			<i>Shape-Transformed</i>			<i>Untransformed</i>			<i>Shape-Transformed</i>		
	<i>PP</i>	<i>TP</i>	<i>CV</i>	<i>PP</i>	<i>TP</i>	<i>CV</i>	<i>PP</i>	<i>TP</i>	<i>CV</i>	<i>PP</i>	<i>TP</i>	<i>CV</i>
VM	0.468	0.564	0.347	0.454	0.488	0.541	0.383	0.384	0.612	0.521	0.506	0.490
CHM	0.427	0.510	0.581	0.352	0.923	0.149	0.332	0.565	0.500	0.372	0.975	0.027
JM	0.385	0.565	0.441	0.371	0.780	0.256				0.231	0.705	0.410
JF	0.355	0.724	0.423	0.325	0.644	0.459	0.501	0.436	0.676	0.329	0.455	0.691
HM	0.175	0.532	0.451	0.244	0.658	0.444						
HF	0.411	0.714	0.375	0.257	0.846	0.167	0.602	0.854	0.167	0.298	0.837	0.139
GTM	0.308	0.336	0.648	0.410	0.378	0.620	0.304	0.450	0.535	0.345	0.622	0.401
AF	0.437	0.458	0.667									
AM				0.307	0.192	0.700				0.246	0.410	0.451
BF	0.420	0.055	0.943	0.331	0.002	0.971	0.328	0.629	0.514			
BM	0.306	0.469	0.549	0.510	0.604	0.562				0.229	0.507	0.689
WF										0.271	0.458	0.687
WM	0.261	0.124	0.848	0.579	0.825	0.152						

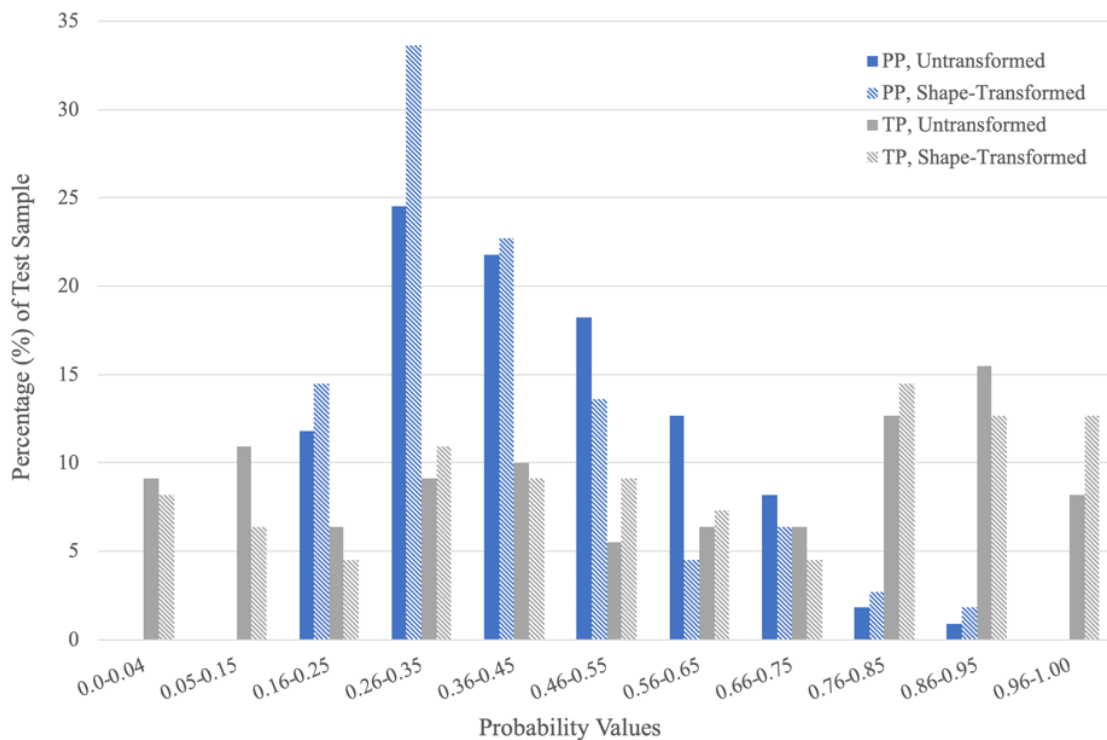


Figure 6.1. Distribution of posterior probability (PP) and typicality probability (TP) values for the Filipino test sample.

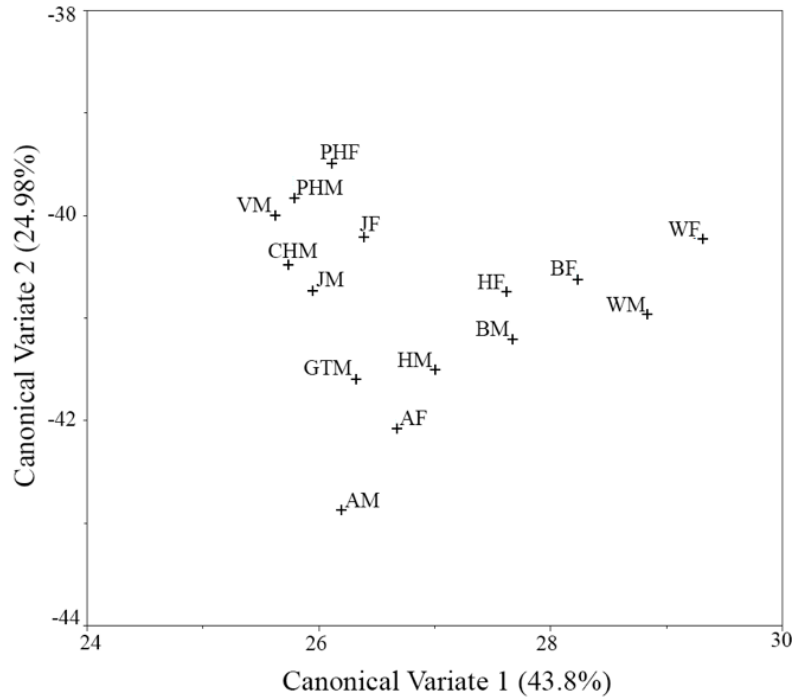


Figure 6.2. Plot of group centroids based on the first two canonical variables and using shape-transformed craniometric values.

Table 6.7. Mahalanobis distance matrix of Philippine and FD3 reference groups based on canonical variate analysis and shape-transformed values.

	AF	AM	BF	BM	CHM	GTM	HF	HM	JF	JM	PHF	PHM	VM	WF	WM
AF	0														
AM	3.09	0													
BF	7.06	13.53	0												
BM	7.68	11.07	1.52	0											
CHM	7.88	10.09	7.95	6.67	0										
GTM	3.37	4.21	6.39	5.04	2.48	0									
HF	3.30	9.28	2.73	5.56	7.08	4.10	0								
HM	3.71	6.74	3.93	3.54	3.37	0.90	2.94	0							
JF	5.57	9.81	4.12	4.65	1.12	2.62	3.35	2.60	0						
JM	6.43	8.30	7.07	5.48	0.49	2.25	6.43	2.89	1.17	0					
PHF	9.90	12.29	9.36	10.99	4.99	6.37	6.47	8.67	3.56	6.20	0				
PHM	10.52	10.39	10.82	10.62	3.83	5.30	8.60	8.22	3.89	4.56	1.04	0			
VM	7.80	10.86	9.32	9.98	1.54	3.51	5.61	4.84	1.49	2.64	2.71	3.36	0		
WF	11.78	18.32	3.68	7.89	14.93	11.75	4.23	8.25	9.48	13.62	12.98	14.99	14.27	0	
WM	9.47	13.27	2.31	3.46	10.61	7.42	4.61	4.58	7.26	9.05	12.66	12.54	12.58	1.76	0

6.4. Discussion

Apart from visual methods for ancestry estimation, such as the use of macromorphoscopic traits (Rhine 1990; Hefner 2009), traditional craniometrics, as interlandmark distances, have been widely used to classify individuals into groups. Discriminant

function analysis, which underlies the Fordisc software, has played prominently in the multivariate treatment of craniometric variables since the 1960s (Giles and Elliot 1962; Birkby1966; Giles 1966). Owing to the nature of the statistical framework for this now standard approach to ancestry estimation, classification success is tied to the assumption that the true population of origin for the unknown case is represented by the reference samples presently available in the FD3 software. In the forensic anthropology context, complete population representation is unrealistic on a worldwide scale. Therefore, it is useful instead to gain insight into the classification trends when populations not included in the reference samples are classified with discriminant function analysis. Do they adhere to likely classifications given their known population history? This study explores trends for Filipinos using FD3, noting that no Filipino population is currently represented among the program's reference groups from the FDB.

The majority of Filipino crania tested here classified into Asian groups regardless of sex. Among these Asian groups, Vietnamese Male was the most common classification when only incorporating shape differences, which is also concordant with the expectation of classification based on geographic proximity to the Philippines. When using shape and size, Filipino males classified most as Vietnamese Male and females as Japanese Female, indicating that sexual dimorphism is an important factor when considering population affinity. A negligible sex-bias was observed. Both male and female Filipino crania were assigned Asian ancestry more than 70% of the time. After Asians, most individuals classified as Hispanic, and then Indigenous Americans to a lesser degree – a pattern likely owing to the shared Native American ancestry of those peoples who comprise the social category of “Hispanic” and the weighted representation of Latinos of Mexican origin among the FDB Hispanics (Algee-Hewitt 2017a). Classification into

the White Male or White Female group was the least likely result regardless of sex or measurement transformation, perhaps indicating that the majority of the potential Asian-European admixture present in this sample is captured through the Hispanic classification, as hypothesized.

The high percentage of ‘typical’ Filipinos suggests the FD3 reference samples collectively capture the cranial variation present within the test sample. Low to moderate posterior probabilities for any given case also indicate that these posteriors are distributed across multiple reference samples, and no one reference group adequately represents Filipino variation. Typicalities greater than 0.05 and low posteriors could reflect the admixture represented in the cranial variation in that these individuals are falling into the region of overlap between multiple FD3 reference samples, similar to what is commonly seen with Hispanic individuals submitted to FD3 (Dudzik and Jantz 2016; Hughes et al. 2018; Spradley et al. 2008) and what unsupervised clustering has revealed for similarly admixed groups (Algee-Hewitt 2016, 2017a, 2017b; Algee-Hewitt et al. 2018a). Examining the CVA plot, an oblique gradient from the top left to bottom right shows all Asian groups, then Indigenous Americans, then Hispanics, then African Americans, and finally European Americans. The second canonical variate (accounting for 15.7% of the variation) assists in discriminating among the six Asian samples (VM, CHM, JM, JF, PHM, PHF). On this axis, we see a gradient that corresponds with latitudinal proximity of the Asian samples, with Japanese and Chinese samples more closely associated midplot, while the Filipinos are plotted in the upper quadrant and closest to the Vietnamese sample.

Several limitations were imposed on this study’s design. One, only the program’s first, and to a lesser extent second, classification choice was considered here, but the distribution of posterior probabilities across the top three to four groups may also be informative of potential

admixture. Two, in a conservative approach, sexes and possible ancestries of the test cases were treated as unknown, and therefore every available group within the FDB was used for each case. Selection of only the relevant sex-specific reference groups per test case may produce different classification trends, but due to the results, particularly for females, it is unlikely that excluding male reference samples (and the majority of Asian reference groups with them), would improve outcomes. Three, between eight to nine variables were input into the program depending on the completeness of each cranium. Classification trends may shift with the inclusion of more craniometric variables, most likely resulting in an increase in what are already robust correct classification rates for the Filipino sample. Four, reference groups were limited to those made available in the program sourced from the FDB. However, FD3 has the option of including 20th century samples from the Howells database, which includes Filipino males that died before World War II. We did not include the Howells data, as it does not represent contemporaneous (i.e., forensically significant) groups in keeping with published statements on best practice for ancestry estimation (Scientific Working Group for Forensic Anthropology 2012). Finally, other more nuanced analytical approaches to exploring ancestry, admixture, postcolonialism, and Filipino craniometrics are needed. Work done by Algee-Hewitt et al. (2018b) using mixture analysis has revealed, in a model-bound but unsupervised way, that Filipinos are considerably more admixed compared to other Asian populations, with observable differences in admixture proportions between Philippine samples with differing provenience, including the Howells Philippine dataset.

6.5. Conclusions

In our sample of 110 individuals, nearly three-fourths of the cases would have led to a conclusion of Asian ancestry using FD3 when their assignment is based on the first classification choice alone. The estimation of ancestry for the remaining cases would have yielded potentially misleading identifications as, most notably, Hispanic, but also Indigenous American. Although there are reasonable population history explanations for these misclassifications, in a truly unknown casework context, the incorporation of such prior expectations into the interpretive process may not be possible. Moreover, the generally low to moderate posterior probabilities even in cases of Asian classifications should cause the forensic anthropologist to question the reliability and, so, the utility of the results, and, at the very least, revisit the input data and the decisions made when running the analysis. In a real laboratory setting the analyst would likely opt to remove the most dissimilar group and rerun the analysis in a stepwise fashion in hopes of achieving a more satisfactory classification (Ousley and Jantz 2012). Recall that Filipinos are not currently represented as one of the reference groups. Furthermore, an actual “real case” laboratory assessment of ancestry would likely draw from multiple indicators in conjunction with craniometrics such as macromorphoscopic traits. This study does not aim to provide general recommendations for the use of FD3 in ancestry estimation. FD3 is used here specifically to provide information on the heterogeneity represented in modern Filipino cranial variation and the effect this diversity in morphology may have on correctly associating Philippine cases with continental Asian ancestry. Overall, Filipinos would likely and rightly classify as Asian, but with a small percentage classifying as Hispanic. These results warn against assumptions of group homogeneity for broad regional categories such as Asian, which itself represents multiple nations and ethnicities that have each undergone unique histories. Indeed, the variation in the Philippines

is so complex that Algee-Hewitt et al. (2018b) have even found differences in admixture proportions by sample source, indicating that there is within-population structure which may be related to geography, ethnicity, and time. The classification trends presented here may help us better understand the evolutionary, population historical, and statistical reasons for FD3 results. They also demonstrate how further research that gives due consideration to the effects of colonialism and admixture on ancestry estimation is warranted in forensic anthropology.

CHAPTER 7

MORPHOSCOPIC ANCESTRY ESTIMATES IN FILIPINO CRANIA USING MULTIVARIATE PROBIT REGRESSION MODELS¹

7.1. Introduction

The advent of several federal court rulings on the admissibility of evidence and expert testimony (i.e., the Daubert Trilogy) played a major role in the push for more statistically empirical approaches to biological profile estimation (Christensen 2004; Christensen and Crowder 2009; Grivas and Komar 2008; Holobinko 2012; Saks and Koehler 2005). Estimation methods using ordinal categorical data abound in forensic anthropology yet have lagged behind in statistical rigor versus more computationally manageable osteometric data. In this regard, cranial morphoscopic traits useful in ancestry estimation have generally seen the least progress in statistical validation versus other components of the biological profile that also use categorical variables. Only recently have Hefner and Ousley (2014) addressed this issue by subjecting cranial macromorphoscopic traits to statistical frameworks. Their methods include discriminant function analyses, logistic regression, machine learning techniques, nonparametric classification methods, and a novel method termed Optimized Summed Scores Attributes, or OSSA (Hefner and Ousley 2014). Others have followed suit while also expanding population samples (Hefner 2016; Hefner et al. 2014, 2015; Kenyhercz et al. 2017; Klales and Kenyhercz 2015; Maier et al. 2015; Monsalve and Hefner 2016; Pilloud et al. 2018; Plemons and Hefner 2016).

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As yet, the probit regression model has not been applied to ancestry estimation in forensic anthropology. Probit analysis is a parametric technique similar to the more common logistic regression (or logit) as the output or result is categorical (e.g., male or female, White or Black) given a set of recorded variables, which can be continuous, dichotomous, or categorical. Unlike logit, which produces probabilities using the logistic function (the cumulative logistic distribution), probit uses the normal distribution and assumes a standard normal distribution of errors. Under a multivariate ordinal probit, ancestry can be estimated given a set of ordinal variables such as cranial morphoscopic traits.

Multivariate probit analysis has been applied to other components of the biological profile that use multiple ordinal categorical traits. Konigsberg and Hens (1998) evaluated five commonly used cranial traits for sex estimation each ordered from “1” to “5”, while others have focused on ordered trait stages used in age estimation such as ectocranial suture closure, dental development, and pubic symphyseal morphology (Fanning 1961; Konigsberg 2015; Konigsberg and Herrmann 2002; Konigsberg and Holman 1999; Konigsberg et al. 2008; Moorrees et al. 1963a,b). Konigsberg and Frankenberg (2019) also demonstrate the advantages of probit analysis over logistic regression in sex estimation using ordinalized Phenice traits (see also Klales et al. 2019). They argue that despite probit analysis being more computationally demanding than logistic regression, the method offers considerable advantages over logit when classifying using ordinal traits. While probit and logit methods produce similar results when the degree of trait difference between groups is large and prior probabilities are equal across groups, probit outperforms logit when these factors do not hold true. Furthermore, multivariate ordinal probit models can accommodate individual classifications with any combination of missing data by imposing limits of negative infinity and infinity for missing variables; logit must produce

multiple equations to cover all possible missing data patterns. Probit analysis is also the more logically correct method of the two as it reflects the actual causal relationship between the dependent variables (e.g., morphoscopic traits) regressed onto the independent variable (e.g., ancestry), keeping with the philosophy of transition analysis wherein skeletal traits are dependent on an independent demographic criterion and not vice versa (Boldsen et al. 2002; Milner and Boldsen 2012).

In this respect, the Philippines and Filipino population are an interesting region and demographic group for the study of ancestry. The Philippines has a unique population history in Asia, contributed by its early peopling, long Western colonial period, and continued global interconnectedness in the modern world (Go 2018). The archipelago was rapidly occupied during the initial peopling of the region around 60,000 to 70,000 years ago via Pleistocene land bridges and narrowed sea corridors (O'Connell and Allen 2004; Barker et al. 2007; Oppenheimer 2009; Demeter et al. 2012; Curnoe et al. 2016; Westaway et al. 2017). Waves of migration to the islands from mainland Asia continued into the Holocene, driven by the advent of large-scale agriculture (Mijares 2005; Trejaut 2005; Tabbada et al. 2010; Gunnarsdóttir et al. 2011; Jinam et al. 2012, 2017). European expansionism quickly turned the Philippines into a cosmopolitan entrepôt between the Far East, the Americas, and Spain as far back as the 16th century (Iaccarino 2008; Phelan 2011). By 1565, Miguel López de Legazpi had established the first Hispanic settlement in Asia, and in 1571, became the Governor-General of the new Spanish colony, declaring Manila as its capital. The Manila-Acapulco Galleon Trade lasted 250 years, bringing products and people from East, Southeast, and South Asia across the Pacific to Acapulco, Mexico and then to the rest of New Spain and Peru (and vice versa) and then across the Atlantic to Europe (Seijas 2014). The Philippines was later ceded to the United States in 1898 following

Spain's defeat in the Spanish-American War, and only gained official independence in 1946. Hence, the Philippines was a Western colony of either Spain or the United States for nearly 400 years. In that time, a unique context of gene flow between the continents of Asia, Europe, and the Americas was present. The United States maintained a strong military presence in the country until 1992, and its legacy systems of prostitution and sex tourism in postmilitary installation areas continue today (Kutschera et al. 2012, 2015). Likewise, the reverse direction of Filipinos migrating to other countries, particularly to North America, also remains strong. Capitalist booms such as oil in the Gulf States in the 1970s, rapid economic growth in several Asian economies in the 1980s, and health care and information technology industries in the 1990s increased demand for cheap domestic and manual labor. Filipinos were encouraged by the government to pursue this demand abroad as a form of foreign remittance for the country. The tradition of deploying Overseas Filipino Workers en masse remains strong today (Rodriguez 2010).

Despite the collective racial grouping of Filipinos as Asian by the U.S. Office of Management and Budget, which defines the racial categories adopted by the U.S. Census Bureau, the population history of the Philippines provides a context by which the skeletal manifestations of ancestral admixture may be more fully appreciated. We hypothesize that while Filipinos are likely most similar morphologically to other East and Southeast Asian populations, they will also exhibit intermediate phenotypes aligned with the other continental ancestries of Africa and Europe. This admixture will be captured through classification into groups other than Asian using hard classification methods (Go et al. 2019), and through mixed proportions of posterior probabilities of group membership (Algee-Hewitt et al. 2019). Therefore, the goals of this study are twofold: first, to evaluate the performance of probit analysis as a classification tool

for ancestry estimation methods that use ordinal categorical data, and second, expand our current understanding of human cranial morphoscopic variation for an underrepresented and understudied population.

7.2. Materials and Methods

For this study, we evaluated the morphoscopic traits of a large, mixed-sex, worldwide cranial assemblage (Table 1). Reference populations were obtained from the Macromorphoscopic Databank (MaMD), a repository for cranial morphoscopic trait data from primarily modern and documented skeletons (Hefner 2018). These reference populations were pooled into broad African (American Black, East Africa, and West Africa), Asian (Thailand, Japan, and China), and European (American White) ancestral groups representing a three-group continental ancestry model. A fourth group, Hispanic (Colombia and Mexico; see Monsalve and Hefner [2016] for a discussion of the relationship between the Colombian sample and Hispanic populations documented in the United States), was also included as a reference population in a four-group model given previous research demonstrating a classification relationship between Filipinos and Hispanics using craniometrics (Go et al. 2019). Two Filipino skeletal samples with differing provenience were used in this study: (1) a small historic sample from the collections at the Smithsonian National Museum of Natural History and at the University of Pennsylvania Museum of Archaeology and Anthropology, included in the MaMD ($n = 28$) (Ratliff 2014), and (2) a modestly sized modern collection sourced from a cemetery in Manila ($n = 112$) (Go et al. 2017).

The definitions and scoring procedures for cranial morphoscopic traits followed Hefner (2007, 2009, 2012). Nine morphoscopic traits were selected based on possessing scoring

Table 7.1. Sample sizes of skeletal populations used in study.
Individuals with missing data possessed from five to eight of the nine traits.

<i>Population</i>	<i>Complete Data</i>	<i>Missing Data</i>	<i>Total</i>
Africa	218	130	348
American Black	180	92	272
East Africa	13	11	24
West Africa	25	27	52
Asia	504	75	579
China	33	18	51
Japan	6	2	8
Thailand	465	55	520
Europe	422	296	718
American White	422	296	718
Hispanic	174	33	207
Colombia	165	22	187
Mexico	9	11	20
Filipino	93	47	140
Historic	11	17	28
Modern	82	30	112
Total	1414	578	1992

definitions most closely aligned with the definition of a truly ordinal trait (i.e., possible values or scoring states for a given trait have an inherent order and progression as the value increases, and permutation of the order of states would disrupt this progression). Following this reasoning, eye orbit shape, for example, was excluded because it is scored more nominally than ordinally, whereby rectangular (Score 1) becomes circular (Score 2) and then progresses to angular (Score 3), yet the scoring system would still work if the order of scoring states was permuted. Additionally, while any dichotomous present-absent trait is nominal, this can be analyzed simultaneously with ordinal traits because there is only one threshold between the two scoring states and was therefore included in this study. The nine traits selected were: anterior nasal spine

(ANS), inferior nasal aperture (INA), posterior zygomatic tubercle (PZT), postbregmatic depression (PBD), nasal overgrowth (NO), nasal aperture width (NAW), malar tubercle (MT), interorbital breadth (IOB), and zygomaticomaxillary suture (ZS). Score 3 of ZS, defined as the complete obliteration of the suture, was treated as non-observable due to the scoring definition relating to age. Only three modern Filipino individuals out of our total sample of 1,992 individuals had a ZS score of 3. Nasal bone shape was considered truly ordinal, defined by the degree of superior “pinched-ness”, but was excluded based on limited sample sizes. Traits with standardized scoring beginning at 0 were recoded to begin at 1 for ease of computation (i.e., PZT, PBD, NO, MT, and ZS). Lastly, because the multivariate probit model can accommodate individuals with missing data, any individual with at least five of the nine traits observable were retained in the analyses (Table 1). Statistical significance in trait expressions was tested between the modern Filipino sample and other groups using the chi-squared goodness of fit test at the $p < 0.01$ level. The historic Filipino sample was excluded from significance tests due to small sample size.

Using only cases with complete observations from the African, Asian, and European reference pools for the three-group model and the African, Asian, European, and Hispanic reference pools for the four-group model, the multivariate probit was first fit in “R” (R Core Team 2016) using the “mvord” function from the package “mvord” (Hirk et al. 2019), which uses composite likelihood estimation (Varin et al. 2011). The generated probit models were reapplied to the entire sample of 1,992 crania including the Filipino samples and those with missing data to test classification accuracy. Because roughly 57% and 66% of the test samples included individuals in the training samples for the three and four-group models, respectively, it

should be expected that the correct classification rates would be biased upward for the African, Asian, and European groups, and for the Hispanic group in the four-group model.

Using numerical multivariate integration from the R package “mvtnorm” (Genz et al. 2019) such as in Figure 6 in Konigsberg (2015), the posterior probability of being one ancestry designation over another was found after assuming a prior probability of 0.33 for each group in the three-group model and 0.25 for each group in the four-group model. Each individual was assigned three posterior probabilities into each group for the three-group model and four posteriors into each group for the four-group model, which respectively sum to one. The highest posterior probability among the parental ancestral groups for an individual was selected as the hard classification choice. For hard classification of Filipinos, a classification into the Asian group was considered a correct classification. Finally, posterior probabilities were also interpreted as admixture proportions of an individual with allowance for multiple memberships across the ancestral reference groups. The modal posterior probabilities, used as a measure of central tendency, were estimated using the “venter” function from the package “modeest” (Poncet 2019).

7.3. Results

The univariate frequencies of the nine selected traits are presented in Tables 2–10. On pairwise (by ancestral groups) tests, statistically significant differences were observed between modern Filipinos and (1) Africans for six of the nine traits (ANS, PZT, and NAW did not differ significantly), (2) Asians for six of the nine traits (PZT, PBD, and ZS did not differ significantly), (3) Europeans for all nine traits, and (4) Hispanics for seven of the nine traits (INA and PZT did not differ significantly) (Table 11).

Table 7.2. Anterior nasal spine (ANS) frequencies in four ancestral groups and historic (H) and modern (M)

Filipino samples.

ANS	Africa		Asia		Europe		Hispanic		Filipino (H)		Filipino (M)	
	(N = 326)		(N = 567)		(N = 658)		(N = 201)		(N = 20)		(N = 88)	
	n	%	n	%	n	%	n	%	n	%	n	%
1	191	58.6	212	37.4	156	23.7	14	7.0	16	80.0	66	75.0
2	111	34.0	310	54.7	337	51.2	88	43.8	4	20.0	17	19.3
3	24	7.4	45	7.9	165	25.1	99	49.3	0	0.0	5	5.7

Table 7.3. Inferior nasal aperture (INA) frequencies in four ancestral groups and historic (H) and modern (M)

Filipino samples.

INA	Africa		Asia		Europe		Hispanic		Filipino (H)		Filipino (M)	
	(N = 348)		(N = 573)		(N = 714)		(N = 203)		(N = 27)		(N = 104)	
	n	%	n	%	n	%	n	%	n	%	n	%
1	125	35.9	58	10.1	6	0.8	10	4.9	1	3.7	12	11.5
2	88	25.3	225	39.3	34	4.8	25	12.3	9	33.3	9	8.7
3	92	26.4	224	39.1	353	49.4	70	34.5	11	40.7	31	29.8
4	37	10.6	56	9.8	235	32.9	46	22.7	4	14.8	36	34.6
5	6	1.7	10	1.7	86	12.0	52	25.6	2	7.4	16	15.4

Table 7.4. Posterior zygomatic tubercle (PZT) frequencies in four ancestral groups and historic (H) and modern

(M) Filipino samples.

PZT	Africa		Asia		Europe		Hispanic		Filipino (H)		Filipino (M)	
	(N = 315)		(N = 571)		(N = 591)		(N = 199)		(N = 27)		(N = 112)	
	n	%	n	%	n	%	n	%	n	%	n	%
0	11	3.5	18	3.2	35	5.9	1	0.5	0	0.0	3	2.7
1	150	47.6	261	45.7	422	71.4	93	46.7	9	33.3	55	49.1
2	105	33.3	204	35.7	119	20.1	81	40.7	14	51.9	40	35.7
3	49	15.6	88	15.4	15	2.5	24	12.1	4	14.8	14	12.5

Table 7.5. Postbregmatic depression (PBD) frequencies in four ancestral groups and historic (H) and modern (M) Filipino samples.

PBD	Africa (N = 318)		Asia (N = 571)		Europe (N = 575)		Hispanic (N = 198)		Filipino (H) (N = 28)		Filipino (M) (N = 112)	
	n	%	n	%	n	%	n	%	n	%	n	%
	0	158	49.7	461	80.7	432	75.1	120	60.6	21	75.0	98
1	160	50.3	110	19.3	143	24.9	78	39.4	7	25.0	14	12.5

Table 7.6. Nasal overgrowth (NO) frequencies in four ancestral groups and historic (H) and modern (M) Filipino samples.

NO	Africa (N = 274)		Asia (N = 552)		Europe (N = 627)		Hispanic (N = 190)		Filipino (H) (N = 16)		Filipino (M) (N = 109)	
	n	%	n	%	n	%	n	%	n	%	n	%
	0	193	70.4	449	81.3	363	57.9	28	14.7	15	93.8	104
1	81	29.6	103	18.7	264	42.1	162	85.3	1	6.3	5	4.6

Table 7.7. Nasal aperture width (NAW) frequencies in four ancestral groups and historic (H) and modern (M) Filipino samples.

NAW	Africa (N = 343)		Asia (N = 577)		Europe (N = 714)		Hispanic (N = 204)		Filipino (H) (N = 27)		Filipino (M) (N = 107)	
	n	%	n	%	n	%	n	%	n	%	n	%
	1	11	3.2	25	4.3	401	56.2	59	28.9	1	3.7	2
2	156	45.5	482	83.5	291	40.8	91	44.6	12	44.4	41	38.3
3	176	51.3	70	12.1	22	3.1	54	26.5	14	51.9	64	59.8

Table 7.8. Malar tubercle (MT) frequencies in four ancestral groups and historic (H) and modern (M) Filipino samples.

MT	Africa (N = 342)		Asia (N = 579)		Europe (N = 717)		Hispanic (N = 207)		Filipino (H) (N = 27)		Filipino (M) (N = 112)	
	n	%	n	%	n	%	n	%	n	%	n	%
0	22	6.4	36	6.2	184	25.7	8	3.9	2	7.4	18	16.1
1	152	44.4	270	46.6	391	54.5	66	31.9	13	48.1	54	48.2
2	105	30.7	208	35.9	117	16.3	94	45.4	12	44.4	26	23.2
3	63	18.4	65	11.2	25	3.5	39	18.8	0	0.0	14	12.5

Table 7.9. Interorbital breadth (IOB) frequencies in four ancestral groups and historic (H) and modern (M) Filipino samples.

IOB	Africa (N = 346)		Asia (N = 578)		Europe (N = 715)		Hispanic (N = 207)		Filipino (H) (N = 28)		Filipino (M) (N = 112)	
	n	%	n	%	n	%	n	%	n	%	n	%
1	41	11.8	100	17.3	273	38.2	57	27.5	5	17.9	1	0.9
2	122	35.3	399	69.0	417	58.3	88	42.5	16	57.1	60	53.6
3	183	52.9	79	13.7	25	3.5	62	30.0	7	25.0	51	45.5

Table 7.10. Zygomaticomaxillary suture (ZS) frequencies in four ancestral groups and historic (H) and modern (M) Filipino samples.

ZS	Africa (N = 307)		Asia (N = 554)		Europe (N = 561)		Hispanic (N = 198)		Filipino (H) (N = 25)		Filipino (M) (N = 106)	
	n	%	n	%	n	%	n	%	n	%	n	%
0	79	25.7	206	37.2	221	39.4	34	17.2	18	72.0	48	45.3
1	130	42.3	188	33.9	279	49.7	130	65.7	2	8.0	31	29.2
2	98	31.9	160	28.9	61	10.9	34	17.2	5	20.0	27	25.5

Table 7.11. Differences in trait expressions between groups that were not found to be statistically significant at the $p < 0.01$ level using the chi-squared goodness of fit test. Traits not listed were found to be significantly different between groups. The historic Filipino sample was excluded from the significance test due to small sample size.

	African	Asian	European	Hispanic	Filipino
African	-				
Asian	PZT, MT	-			
European		PBD	-		
Hispanic	PZT, PBD	PZT		-	
Filipino (M)	ANS, PZT, NAW	PZT, PBD, ZS		INA, PZT	-

The parameters of the multivariate ordinal probit models are presented in Tables 12–14 using 1,144 complete training crania for the three-group model and 1,318 complete training crania for the four-group model. These parameters are the threshold values between each scoring state for each trait, the group means per trait for each ancestral reference group, and the correlation matrices, respectively.

Table 7.12. Threshold parameters between scoring states from the multivariate probit.

	Three-Group Ancestry Model				Four-Group Ancestry Model			
	1 2	2 3	3 4	4 5	1 2	2 3	3 4	4 5
ANS	0.0946	1.5788			0.0918	1.5873		
INA	-0.5566	0.4627	1.8065	2.9267	-0.5206	0.4632	1.7297	2.7005
PZT	-2.0613	-0.0360	0.9902		-2.0922	-0.0416	1.0097	
PBD	0.0806				0.0806			
NO	0.5565				0.5565			
NAW	-2.3073	-0.0012			-2.0666	-0.0338		
MT	-1.5207	-0.0004	1.0364		-1.5170	-0.0096	1.0504	
IOB	-1.8211	0.1588			-1.698	0.1213		
ZS	-0.7621	0.3680			-0.8167	0.4095		

Table 7.13. Group means per trait from the multivariate probit.¹

	Three-Group Ancestry Model		Four-Group Ancestry Model		
	Asia	Europe	Asia	Europe	Hispanic
ANS	0.3177	0.9192	0.3185	0.9224	1.6392
INA	0.5888	1.8556	0.5724	1.7541	1.6981
PZT	-0.0529	-0.7317	-0.0537	-0.7430	-0.0130
PBD	-0.7885	-0.5752	-0.7885	-0.5753	-0.1077
NO	-0.3197	0.4314	-0.3195	0.4314	1.6471
NAW	-0.9710	-2.3893	-0.8927	-2.1779	-1.1318
MT	-0.0786	-0.9076	-0.0791	-0.9078	0.3009
IOB	-0.9043	-1.4378	-0.8562	-1.3530	-0.6697
ZS	-0.3095	-0.6190	-0.3197	-0.6409	-0.1616

¹African means were fixed at 0.0 for all traits.

Table 7.14. Residual polychoric correlation matrix from the multivariate probit. The lower triangle represents the three-group ancestry model, while the upper triangle represents the four-group ancestry model.

	ANS	INA	PZT	PBD	NO	NAW	MT	IOB	ZS
ANS	1	0.3000	0.0678	0.0726	0.0842	-0.1990	-0.0188	-0.1484	0.0923
INA	0.3051	1	-0.0781	0.0709	0.0238	-0.1075	-0.0980	-0.0577	-0.0922
PZT	0.0815	-0.0753	1	-0.0388	0.0197	0.0255	0.0843	-0.0150	0.0980
PBD	0.0943	0.0665	-0.0372	1	-0.0300	0.0044	-0.0386	-0.0103	0.0068
NO	0.0562	-0.0062	0.0171	-0.0184	1	-0.0181	0.0105	-0.0284	0.0358
NAW	-0.1768	-0.0598	0.0392	-0.0162	-0.0002	1	-0.0686	0.3376	-0.0180
MT	-0.0058	-0.1509	0.1092	-0.0546	0.0217	-0.0841	1	0.0421	0.0985
IOB	-0.1403	-0.0468	-0.0465	-0.0203	0.0061	0.3196	0.0454	1	0.0732
ZS	-0.0844	-0.1045	0.1229	0.0278	0.0363	0.0148	0.1059	-0.0917	1

Classification results for the three-group and four-group models are presented in Table 15. The overall correct classification rate for the three-group model when considering Asian as the correct hard classification choice for Filipinos and when excluding results for Hispanics was 72.1%. For the four-group model including Hispanics as a reference group, the overall correct classification rate was 68.6%. The combined correct classification rates for historic and modern

Filipinos were 52.9% with three groups as choices and 48.6% with four groups. Filipinos in the historic and modern samples followed similar classification trends, most commonly classifying as Asian as expected, followed by a large portion as African, a smaller number as European and the least number as Hispanic for both models. Classification rates of the reference groups show Asians were more likely to misclassify as African over European or Hispanic as was the trend with Filipinos, and conversely, Africans were more likely to misclassify as Asian over European or Hispanic. When comparing the classification trends between Asians and modern Filipinos, differences in classification counts were nearly significant for the three-group model ($\chi^2 = 8.7937$, $df = 2$, $p = 0.0123$) or significant for the four-group model ($\chi^2 = 13.748$, $df = 3$, $p = 0.0033$) at the level of $p < 0.01$. Hence, Filipino patterns of misclassification differ from those of the Asian reference sample.

Table 7.15. Classification percentages (and counts) into one of three or four ancestral groups.

		Predicted							
		Three-Group Ancestry Model				Four-Group Ancestry Model			
		Africa	Asia	Europe		Africa	Asia	Europe	Hispanic
Actual	Africa	68.7 (239)	22.1 (77)	9.2 (32)	63.8 (222)	17.8 (62)	7.8 (27)	10.6 (37)	
	Asia	20.6 (119)	66.1 (383)	13.3 (77)	18.3 (106)	63.0 (365)	10.5 (61)	8.1 (47)	
	Europe	2.6 (19)	15.0 (108)	82.3 (591)	2.4 (17)	12.8 (92)	73.3 (526)	11.6 (83)	
	Hispanic	29.0 (60)	18.4 (38)	52.7 (109)	11.6 (24)	6.8 (14)	15.9 (33)	65.7 (136)	
	Filipino (H)	42.9 (12)	50.0 (14)	7.1 (2)	39.3 (11)	53.6 (15)	3.6 (1)	3.6 (1)	
	Filipino (M)	33.0 (37)	53.6 (60)	13.4 (15)	31.3 (35)	47.3 (53)	15.2 (17)	6.3 (7)	

Table 16 presents classification results specifically for the two Filipino samples broken down by the number of missing observations. Chi-squared goodness of fit tests did not show any significant differences between the classification distributions into ancestry groups for both historical (Three-Group: $\chi^2 = 3.7932$, $df = 2$, $p = 0.1501$; Four-Group: $\chi^2 = 2.5908$, $df = 3$, $p = 0.4591$) and modern (Three-Group: $\chi^2 = 0.4266$, $df = 2$, $p = 0.8079$; Four-Group: $\chi^2 = 0.7687$, $df = 3$, $p = 0.8591$)

= 3, $p = 0.8569$) complete crania and crania with at least one missing observation, although comparative sample sizes were small. With three classification choices, classification success for complete crania was 50.5% (modern = 52.4%; historic = 36.4%). The success rate for incomplete crania was 57.4% (modern = 56.7%; historic = 58.8%). With four choices, complete crania correctly classified in 46.2% of cases (modern = 46.3%; historic = 45.5%), while incomplete crania correctly classified in 53.2% of cases (modern = 50.0%; historic = 58.8%). The overall descending trend in classification preference into Asian, African, European, and then Hispanic groups was preserved between complete crania and crania with at least one missing observation, except for complete historic Filipino crania, which classified more often into African over Asian groups and may be due to the very small subsample size ($n = 11$). Modal posterior probabilities of membership in each group did not drastically differ between complete and incomplete crania when pooling historic and modern samples (Table 17).

Table 7.16. Classification percentages (and counts) for the two Filipino samples into one of three or four ancestral groups by number of missing trait observations (NAs).

		Predicted													
		Three-Group Ancestry Model						Four-Group Ancestry Model							
		NAs	Africa	Asia	Europe	Africa	Asia	Europe	Hispanic						
Historic	0	63.6	(7)	36.4	(4)	0.0	(0)	54.5	(6)	45.5	(5)	0.0	(0)	0.0	(0)
	1	27.3	(3)	63.6	(7)	9.1	(1)	27.3	(3)	63.6	(7)	9.1	(1)	0.0	(0)
	2	25.0	(1)	50.0	(2)	25.0	(1)	25.0	(1)	50.0	(2)	0.0	(0)	25.0	(1)
	4	50.0	(1)	50.0	(1)	0.0	(0)	50.0	(1)	50.0	(1)	0.0	(0)	0.0	(0)
	≥1	29.4	(5)	58.8	(10)	11.8	(2)	29.4	(5)	58.8	(10)	5.9	(1)	5.9	(1)
Modern	0	32.9	(27)	52.4	(43)	14.6	(12)	30.5	(25)	46.3	(38)	15.9	(13)	7.3	(6)
	1	33.3	(7)	52.4	(11)	14.3	(3)	33.3	(7)	42.9	(9)	19.0	(4)	4.8	(1)
	2	0.0	(0)	100.0	(3)	0.0	(0)	0.0	(0)	100.0	(3)	0.0	(0)	0.0	(0)
	3	40.0	(2)	60.0	(3)	0.0	(0)	40.0	(2)	60.0	(3)	0.0	(0)	0.0	(0)
	4	100.0	(1)	0.0	(0)	0.0	(0)	100.0	(1)	0.0	(0)	0.0	(0)	0.0	(0)
	≥1	33.3	(10)	56.7	(17)	10.0	(3)	33.3	(10)	50.0	(15)	13.3	(4)	3.3	(1)

Table 7.17. Modal posterior probabilities between complete (NAs = 0) and incomplete (NAs ≥ 1) crania for the two Filipino samples.

Modal Posterior Probabilities								
		Three-Group Ancestry Model			Four-Group Ancestry Model			
	NAs	Africa	Asia	Europe	Africa	Asia	Europe	Hispanic
Historic	0	0.5915	0.4984	0.0207	0.3993	0.3080	0.0223	0.0043
	≥1	0.1240	0.5981	0.0409	0.1177	0.4123	0.0345	0.0199
Modern	0	0.3289	0.4843	0.0402	0.2631	0.5349	0.0451	0.0390
	≥1	0.3128	0.6161	0.0219	0.2610	0.2856	0.0259	0.0308
Total	0	0.3535	0.4809	0.0368	0.2653	0.4191	0.0325	0.0184
	≥1	0.2710	0.5594	0.0296	0.2468	0.5086	0.0309	0.0295

While the highest posterior probability for a specific individual determined the hard classification choice, posterior probabilities were also interpreted as admixture proportions of an individual across ancestral reference groups. Figures 1 and 2 show the structure plots for historic and modern Filipinos, illustrating each individual's percentage of membership across the African, Asian, European, and Hispanic components. The modal posterior probabilities in the three-group model for the pooled Filipino sample were 0.5732 for Asia (modern = 0.4811; historic = 0.5966), 0.3194 for Africa (modern = 0.3185; historic = 0.5536), and 0.0323 for Europe (modern = 0.0345; historic = 0.0217). The four-group model had modal posteriors of 0.4390 for Asia (modern = 0.4186; historic = 0.3351), 0.2518 for Africa (modern = 0.2438; historic = 0.4735), 0.0322 for Europe (modern = 0.0306; historic = 0.0344), and 0.0215 for Hispanic (modern = 0.0195; historic = 0.0283). Table 18 presents these values with the modal posteriors for the other samples included in this study. Figures 3 and 4 show the distribution of posterior probability values for each sample into each ancestry group.

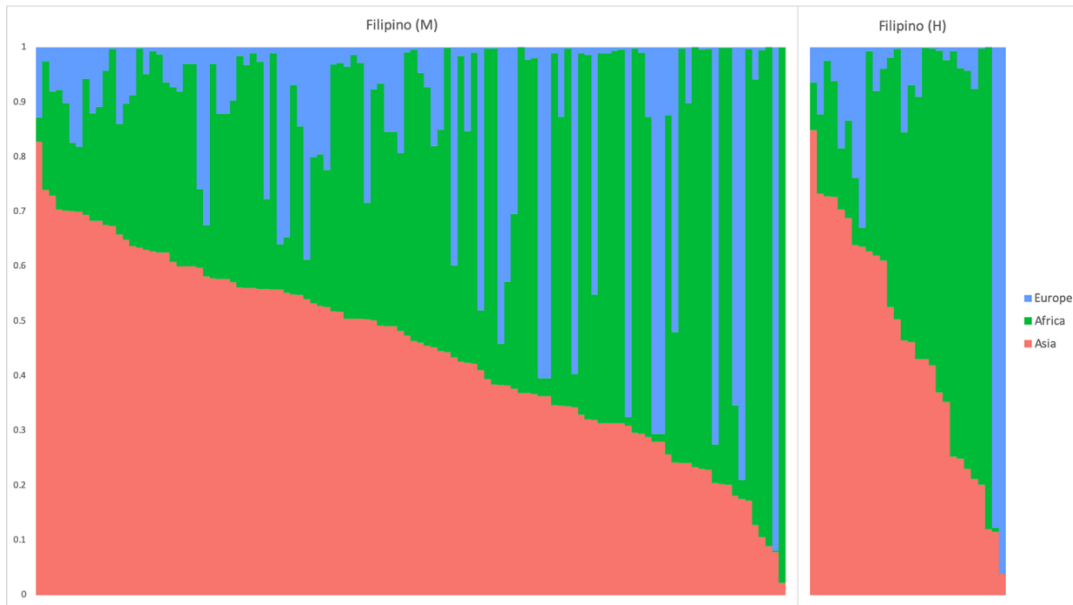


Figure 7.1. Structure plot displaying relative proportions of ancestry for the modern (M) and historic (H) Filipino samples when plotted using posterior probabilities of group membership across African, Asian, and European reference pools. Each individual is represented by a single vertical line that is partitioned into three differently colored segments corresponding to the ancestry components. The length of the colored segment is the value of the posterior probability. The individuals are sorted in descending order of their quantity of Asian ancestry.

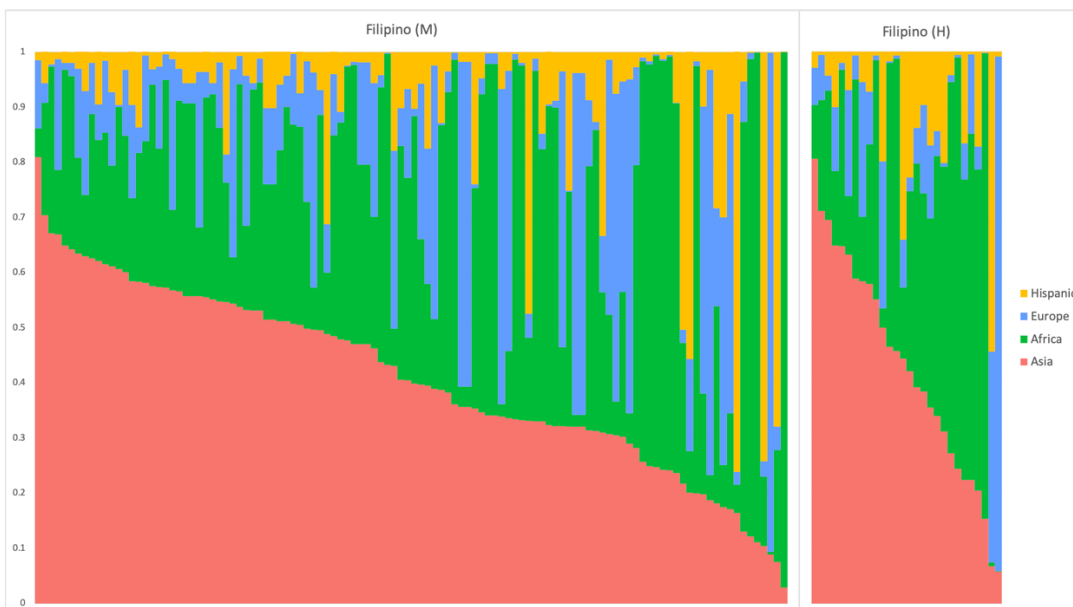


Figure 7.2. Structure plot displaying relative proportions of ancestry for the modern (M) and historic (H) Filipino samples when plotted using posterior probabilities of group membership across African, Asian, European, and Hispanic reference pools. Each individual is represented by a single vertical line that is partitioned into four differently colored segments corresponding to the ancestry components. The length of the colored segment is the value of the posterior probability. The individuals are sorted in descending order of their quantity of Asian ancestry.

Three-Group Ancestry Model

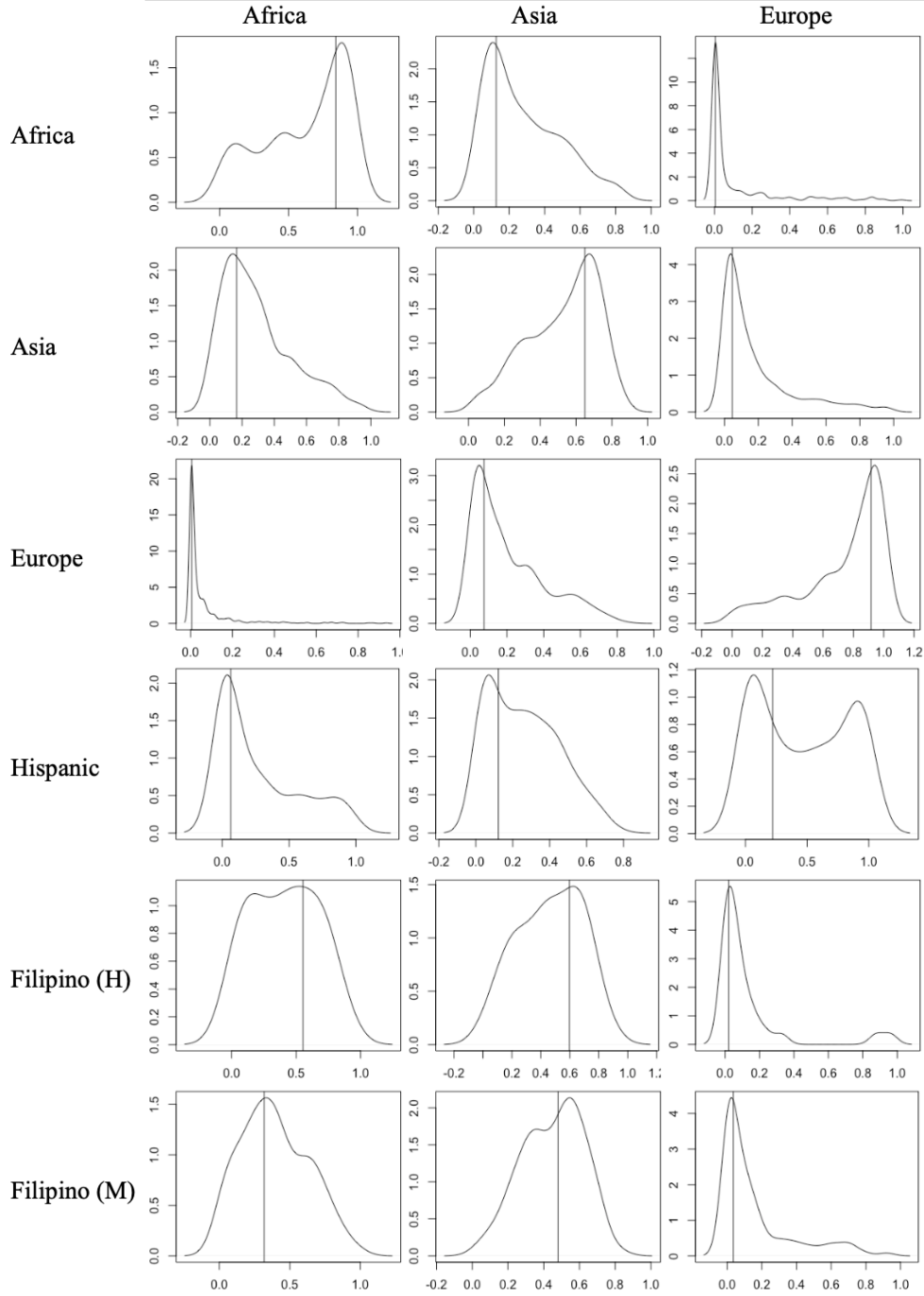


Figure 7.3. Distributions of posterior probabilities for each population into one of three ancestry categories. The kernel density is plotted on the y-axis and the posterior probability values are plotted on the x-axis. The vertical black line indicates the estimated mode of the distribution.

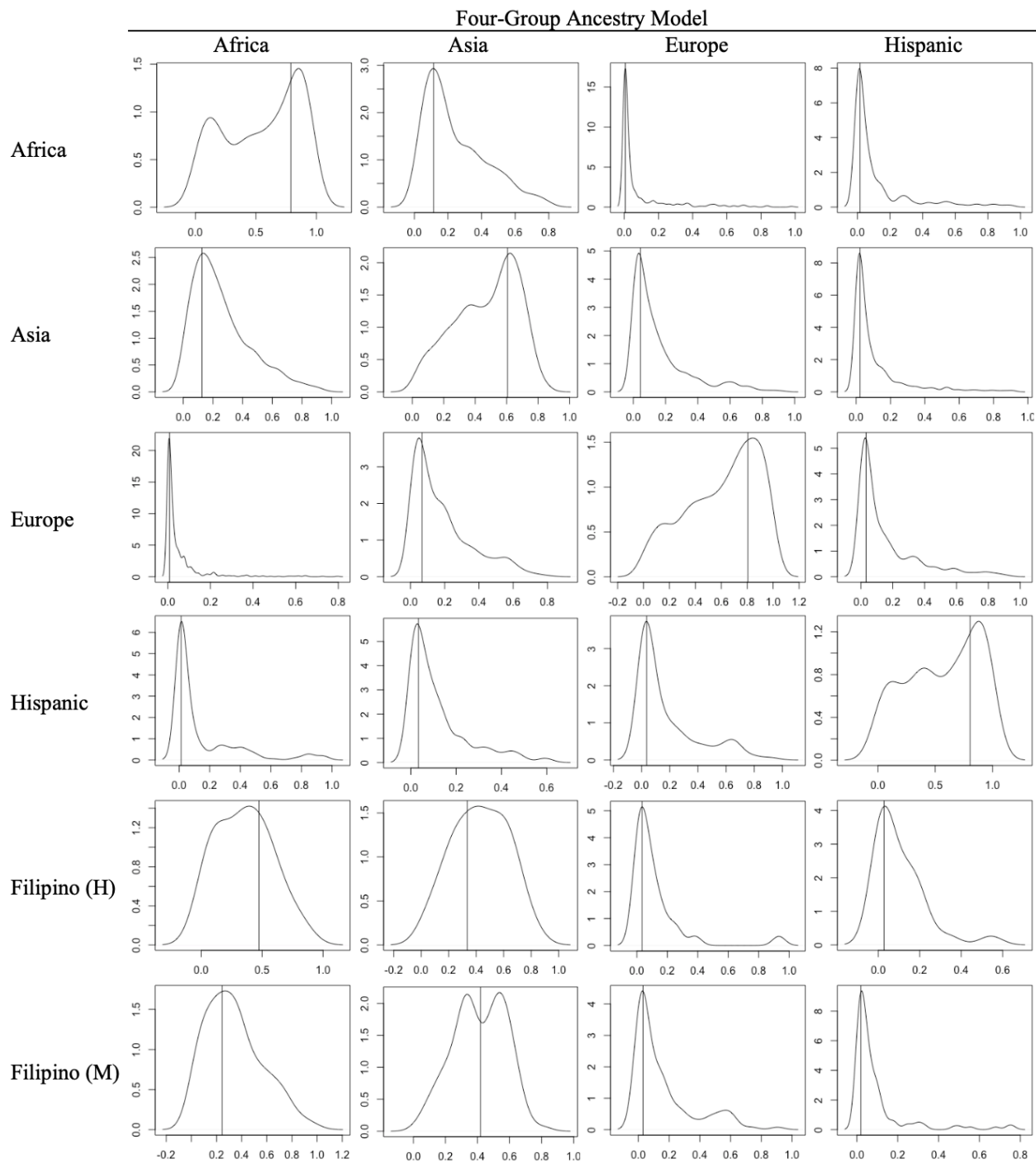


Figure 7.4. Distributions of posterior probabilities for each population into one of four ancestry categories. The kernel density is plotted on the y-axis and the posterior probability values are plotted on the x-axis. The vertical black line indicates the estimated mode of the distribution.

Table 7.18. Modal posterior probabilities for each sample into the three or four classification choices.

	Modal Posterior Probabilities						
	Three-Group Ancestry Model			Four-Group Ancestry Model			
	Africa	Asia	Europe	Africa	Asia	Europe	Hispanic
Africa	0.8429	0.1271	0.0045	0.7895	0.1151	0.0062	0.0167
Asia	0.1660	0.6492	0.0460	0.1255	0.6060	0.0436	0.0228
Europe	0.0056	0.0751	0.9163	0.0079	0.0676	0.8049	0.0325
Hispanic	0.0631	0.1223	0.2215	0.0131	0.0339	0.0361	0.8041
Filipino (H)	0.5536	0.5966	0.0217	0.4735	0.3351	0.0344	0.0283
Filipino (M)	0.3185	0.4811	0.0345	0.2438	0.4186	0.0306	0.0195

7.4. Discussion

Through advancements in computational statistics, standardized scoring methodology, and large reference databases, ancestry estimation using morphoscopic traits need not be limited to traditional trait lists and archotyping. We applied parametric multivariate probit regression models to classify the ancestral affiliation of Filipino crania using ordinal morphoscopic traits. We chose the probit method not only because of its advantages over logit, but also because it has not been previously applied to questions of ancestry. In a similar vein, we chose Filipinos not only because they have not been the subject of extensive forensic anthropological studies, but also because they provide an opportunity to evaluate admixture and variability among Asian populations.

For the total study sample including reference populations, the overall classification rates of the multivariate probit models performed relatively well at 72.1% with three reference groups, and 68.6% with four reference groups. Although not entirely comparable due to differences in the samples, traits, and validation methods used, the probit performed slightly better than the overall accuracy reported by Hefner and Ousley (2014) using logistic regression with three

groups (Blacks, Whites, and Hispanics) (66.4%), but underperformed compared to Klales and Kenyhercz (2015) using two groups (Blacks and Whites) (88.6%). Furthermore, the current probit classification rates included populations, namely Filipinos, that were not included in the model training sets. Hefner and Ousley (2014) and Klales and Kenyhercz (2015) used leave-one-out cross-validation to assess their accuracy estimates, and this validation method would therefore be biased more optimistically than when including an entire test group that was absent from the training sample. As with other classification methods such as logistic regression or discriminant function, probit works best when training samples include representatives that are also present in test samples. When considering only those groups present in both training and testing of the model, the accuracy of the three-group model was at 73.7% and the four-group model was at 67.4%.

One considerable advantage of probit over logit is the accommodation of missing data. The probit models performed similarly when classifying between complete and incomplete crania for both the historic and modern Filipino samples. Correct classification rates were slightly higher with incomplete crania than with crania possessing all nine traits, ranging in difference from 3.7% to 22.4%. These differences may be attributed to sample size, as significance testing showed no difference in the classification distributions between complete and incomplete crania. Moreover, most of the individuals with missing data were only missing one of the nine variables. Overall classification trends were also preserved between complete and incomplete crania, both sets showing a descending order of assignment to Asian, African, European, and then Hispanic. The addition of a fourth Hispanic category did not significantly alter classification choices. Furthermore, modal posterior probabilities did not change dramatically for the pooled Filipino sample.

In both the three and four-group models, the majority of Filipinos classified as Asian (52.9% and 48.6%, respectively), but with a large portion classifying as African (35.0% and 32.9%, respectively), and only a small portion classifying as either European (12.1% and 12.9%, respectively) or Hispanic (5.7%). The modal posterior probabilities of Filipinos for African and Asian membership were also higher and lower, respectively, than those posteriors of the Asian reference sample. The close affiliation of Filipinos to African classifications has been supported by Algee-Hewitt et al.'s (2018) study using craniometrics, which showed most Asian samples having significantly lower mean African contributions than Philippine samples. Contributions to an African phenotype may stem from ancient and sustained genetic admixture with Philippine Negrito groups that stretch from as far back as the initial rapid peopling of the archipelago (HUGO Pan-Asian SNP Consortium 2009; Stoneking and Delfin 2010; Lipson et al. 2014). Negritos have long been compared to the pygmies of Africa based on similarities in dark skin pigmentation, short stature, facial morphology, and woolly hair. They, along with other ethnic groups such as Australians, Papuans, Melanesians, and Dravidian-speaking South Asians, have been hypothesized to represent relic descendants of a first dispersal out of Africa into Asia via a southern coastal route (Howells 1973; Mirazón Lahr 1996). Although several studies using both genetic and osteological evidence support a closer relationship between Negritos to neighboring non-Negritos rather than to African pygmies or other regional Negrito groups (Hanihara 1993a; HUGO Pan-Asian SNP Consortium 2009; Bulbeck 2013; Migliano et al. 2013; Stock 2013), signals of ancient Pleistocene founding lineages are still present and are thought to have been subsequently heavily obscured by admixture with members of a secondary Holocene wave of Austronesian migrations (Stoneking and Delfin 2010; Rasmussen et al. 2011; Jinam et al. 2012; Pugach et al. 2013; Reyes-Centeno et al. 2014). Nevertheless, morphological similarities

between Negritos and African pygmies are likely to be largely due to convergent evolution via natural selection, but genetic drift cannot be completely ruled out (Migliano et al. 2013; Jinam et al. 2017). Coupled with extensive admixture with non-Negrito Filipinos, which are represented by the current sample under study, these morphological similarities may provide one explanation for the high African classification rates in the probit models.

Another important explanation for high African classification is that the majority of the parental African sample used here is comprised of African Americans, who have been shown to be considerably admixed themselves with European contributions moreso than White Americans exhibiting African ancestry (Parra et al. 1998; Kayser et al. 2003; Lind et al. 2007; Bryc et al. 2010; Baharian et al. 2016). Beyond the African sample relating to African variation linked to the Negrito lineage, it may also be capturing the admixture potentially present in the Filipino sample.

In contrast, linear discriminant analysis using the Fordisc software classified Filipino crania as American Black only 4.5% of the time, while Hispanic was the most frequent choice after Asian at 12.7% (Go et al. 2019). Here, Filipinos were classified the least often as Hispanic despite a long colonial history of biological and cultural admixture with Latin America, Spain, and the United States relative to other Asian countries. Likewise, the low modal posteriors for European and Hispanic membership, especially when compared to the corresponding posterior values obtained for the Asian sample, is discordant with expectations. One possible explanation is that the scoring methodology for ordinal morphoscopic traits does not capture the resolution of variation seen with continuous data such as craniometrics. Apart from resolution, morphoscopic traits may be capturing sources of craniofacial variation alternative to the variation in integrated size and shape changes of the cranium as a whole when using craniometrics.

Assuming Asian would be the correct classification for a Filipino cranium in a modern forensic case work context and that approximately half of the present cases would have thus been misidentified, probit analysis did not perform ideally for this population (48.6–52.9% compared to 72.7–73.6% using Fordisc). An argument could be made that the low classification rate for Filipinos can be attributed to their absence in the training sample that constructed the probit models. Indeed, better classification rates were obtained for the African, Asian, and European samples, which did contribute to the models. Furthermore, Hispanics showed moderate classification rates into all of the three categories in the three-group model but showed a good classification rate as Hispanic when they themselves were added into the training set in the four-group model. In a forensic case work setting it is unrealistic for an ancestry estimation method to include samples from every possible population. It may, however, be unnecessary to include every population when inclusive reference samples are able to capture the heterogeneity present in the broad continental categories used by forensic anthropologists. Here, the large sample of Thai reference data with much smaller contributions from China and Japan was not sufficient to successfully predict Asian ancestry for Filipinos with minimal error rates. The results of this study demonstrate that Filipinos are more phenotypically similar to Africans than the other Asian samples used here, but still affiliate most closely to Asia, as evidenced by the probit classification trends and the spread of posterior probabilities across the categories. Ancestry methods would thus benefit from including Filipinos as a reference sample given the additional phenotypic variation they provide to the continental category of Asian. More broadly, this work also demonstrates the importance of understanding the evolutionary and population historical context that underlie the different reference samples used in forensic anthropology, and how this context may affect the outcomes of ancestry classification methods.

CHAPTER 8

CONCLUSION

The populations of East and Southeast Asia have traditionally been collectively lumped together under a cranial archetype historically and obsolescently referred to as the Mongoloid form (Takezawa 2012). Moreover, Native American crania have also been included in this lumping given a proximal yet temporally distant biogeographic link between Northeast Asia and the Americas. Until more recently, archaeological and proto-historic Native American samples and small, interspersed Asian samples have largely formed the basis for the biological profile estimation of Asian individuals. While the term Asian may have largely replaced Mongoloid in contemporary use, little has been done to address the actual diversity masked by the broad continental category of Asian. Thankfully, as forensic anthropology matures within the context of a globally connected 21st century and more resources open up to a wider audience of researchers, the core purpose of anthropology – human variation and diversity – may more fully be explored. The purposes of this study were to assess the degree of sexual dimorphism and relative phenotypic variation among Filipino crania as these relate to issues of sex and ancestry estimation in forensic anthropology, respectively. Related to these goals, a third objective of this research was to assemble an internationally accessible reference collection of Filipino skeletons that would provide the means to advance the science in the region beyond the limits of this dissertation.

Filipinos as a population of study are emphasized here given their mismatched representation in the forensic anthropological literature compared to their forensic significance on the global stage. As previously mentioned, this significance is attributable to the interplay

between geography and population history that, on the one hand, increases the likelihood of Filipinos entering the forensic context, and on the other hand, produces human variation not adequately captured by existing biological profile estimation methods. The studies that form this dissertation explore such methods, specifically for sex and ancestry, and emphasize the inclusion of Filipinos in their development. These methods were: (1) the optimized summed scored attributes method applied to sex estimation using ordinal morphoscopic traits, (2) the linear discriminant analysis method via the software Fordisc applied to ancestry estimation using craniometric measurements, and (3) the probit regression method applied to ancestry estimation using ordinal morphoscopic traits.

Based on OSSA sectioning parameters developed from a pooled Japanese and Thai sample, Filipinos correctly classified as male 78.7% of the time and as female 84.0% of the time. When a more conservative assignment criterion was applied by designating an OSSA score of 2 as indeterminate, the correct classification rate for males decreased to 69.7% and for females increased to 95.5%. The discrepancy between the sexes can be explained by disproportionately larger male sample sizes compared to females, as well as more males falling into the OSSA = 2 bin. Despite being geographically distant, the populations from Japan and Thailand were similarly sexually dimorphic based on dichotomized cutoffs. Filipinos, on the other hand, did not correctly classify as well as the Japanese and Thai holdout cases, which may indicate slight population differences. Filipinos appear to be more gracile than the Japanese or Thai individuals in the nuchal crest and mastoid process, intermediary between the two populations in the supraorbital margin, and more robust in the supraorbital ridge. Regardless, applying Japanese and Thai based OSSA standards to Filipinos produced slightly lower accuracy scores such that the standards developed here for OSSA sex estimation may cautiously be applied to other Asian

populations when no other means are available, but population-specific equations are still warranted.

Discriminant function analysis provided a robust classification tool for the assignment of Filipinos into an Asian ancestry category using either untransformed or shape-transformed craniometric measurements. Filipino males classified as Asian 72.5% of the time, while females classified between 73.2% (untransformed) to 75.6% (shape-transformed) of the time. This, however, still leaves one in every four Filipinos to potentially misclassify or at least to remain indeterminate. Hispanic was the second-most common classification choice and may be linked to historical colonial ties between Mexico and the Philippines given the preponderance of Mexican Hispanics within the Hispanic reference group. Indigenous American was the third-most common choice, which may be related to the temporally distant Asian origin of the first humans into the Americas. However, the low to moderate posterior probabilities for Filipino individuals across multiple reference groups speaks to the inadequacy of any one particular reference group in capturing Filipino variation. In other words, Filipinos tend to fall within the overlap of multiple reference groups, but most closely affiliate as Asian.

Lastly, multivariate probit models using ordinal morphoscopic traits of the cranium only moderately succeeded in correctly classifying Filipinos, with only 52.9% classifying as Asian given three ancestral categories and 48.6% given four categories. Surprisingly, greater than 30% of the sample consistently classified as African, which may be attributed to long-term admixture with ethnic groups that are phenotypically similar to Africans as a result of convergent evolution. Additionally, these results may stem from the already admixed nature of African Americans that stand in as the African parental pool. The juxtaposed classification results between craniometrics and cranial morphoscopies may indicate that these two classes of data are capturing different

sources of variation. The posterior probability values and classification trends obtained for Filipinos using probit suggests that, while Filipinos have a closer affinity to other Asian populations, there are significant levels of morphological heterogeneity that also make them distinct within the broader continental category of Asian.

With respect to these results, the four hypotheses enumerated at the introduction of this work, and reiterated here, are supported:

1. Sufficient sexual dimorphism exists within modern Filipino crania that sex can be accurately estimated given an unidentified cranium.
2. Sex in Filipino crania can be accurately estimated (i.e., correctly classified at rates greater than random allocation) when using methods developed from other Asian populations.
3. Asian ancestral affinity can be accurately estimated (i.e., correctly classified at rates greater than random allocation) from Filipino cranial morphology, and Filipino morphology is differentiable from that of other broad continental ancestral groups.
4. Lastly, Filipino cranial morphology contributes to knowledge of cranial variation not yet observed in the current samples representing Asian ancestry.

The conclusions drawn here were made within the limits of the samples and statistical methods used, which subsequently opens further avenues of future research. For one, the Filipino samples used here do not even moderately encompass the diversity of peoples living in the archipelago, of which there are greater than a hundred ethnolinguistic groups by some counts. Just as the different nations of Asia have undergone distinct population and colonial histories from one another, so too have different Filipino groups in different regions of the country and the world. For instance, the southern Moros and highland tribes of Luzon largely resisted foreign

conquest, whereas the lowland peoples were swiftly brought under Spanish imperial rule. While diversity can be explored spatially, it can also manifest temporally. Secular changes brought about by globalization, increased quality in nutrition and health care, and microevolutionary forces such as drift, among others, may all potentially affect differences in morphology between archaeological, proto-historic, historic, and contemporary populations. Whereas this work seeks to frame Filipinos against other Asian populations and the broader continental groups of Europe, Africa, and the Americas, future work may find fruitful discoveries comparing the plethora of different Filipino populations amongst each other. Furthermore, this work utilized only three statistical methods out of many other available tools. Indeed, each technique has its own merits and disadvantages depending on the questions at hand. In the realm of ancestry and admixture estimation, more sophisticated computational approaches such as unsupervised machine learning or clustering techniques may show promise in elucidating these complex relationships.

Much as this dissertation emphasizes methodological advancements in Filipino biological profile estimation, it also more broadly attempts to introduce forensic anthropology in and of the Philippines as a discourse worthy of more mainstream study. Both the generation and application of knowledge in forensic anthropology have only begun in the Philippines. As Blau (2016) points out, the outcome of missing persons investigations is dependent on the scale, infrastructure, and political will of the context. This work hopes to inspire the improvement of all three and provide forensic anthropology in the Philippines its due attention.

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