12-2020

# Master's Portfolio

Alexis Joy Rizzolo

MASTER'S PORTFOLIO

By

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Bachelor of Science, University of Arkansas, Fayetteville, Arkansas, 2018
Bachelor of Arts, University of Arkansas, Fayetteville, Arkansas, 2018

Professional Paper

presented in partial fulfillment of the requirements
for the degree of

Master of Arts
in Anthropology

The University of Montana
Missoula, MT

Official Graduation Date December 2020

Approved by:

Scott Whittenburg, Dean of The Graduate School
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Department of Anthropology

# MASTER OF ARTS PORTFOLIO

Alexis Joy Rizzolo

University of Montana

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# THEME

Entering the Master of Arts program in Anthropology at the University of Montana provided an opportunity to continue my education, hone my skills in molecular and forensic anthropology, all while refining my career goals. Expanding upon knowledge acquired during my Bachelor of Science program, pivotal courses selected provided diverse biological anthropological theories of thought. These courses afforded hands-on experience utilizing the application of theories as well as acquired statistical, skeletal, and data analysis skills to solve the same problem from varying viewpoints. Examples of the comprehensive education acquired at the University of Montana are provided within this portfolio submission, which tie together and build upon the following courses taken.

*Contemporary Anthropological Thought* provided an all-encompassing look at the multitude of methods used throughout the subfields of cultural, biological, and archaeological anthropology, and provided a foundation for linking research to the wide-ranging field of anthropology. *Theory and Methodology in Biological Anthropology* introduced different statistical software programs and their application to datasets. These programs are utilized to support research projects which address real-world problems. *Advanced Forensic Anthropology* offered practice in the completion of forensic case reports which when applied resulted in the creation and completion of a research project required as part of the curriculum for *Seminar in Bioarchaeology and Skeletal Biology*. Finally, *Seminar in Human Variation and Evolution*, along with the course *Evolution and Genetic Variation in Human Populations*, provided a foundation and application for the understanding of the different molecular anthropological theories as well as hands-on experience completing lab work.

## THEME, CONTINUED

Applying knowledge acquired throughout this program resulted in the following opportunities:

- presentation (a poster) at the Western Bioarchaeology Group Conference (2019 WeBiG) in Denver, Colorado.
    - afforded networking opportunities with other bioarcheologists and faculty from western North America universities,
    - enabled discussion of issues in bioarchaeological theory and current methods being utilized,
    - resulted in new found knowledge and concepts utilized by others in the field of bioarchaeology.
- completion and submission of forensic report FSD 94-0988.
- enhanced educational and research techniques as a:
    - teacher's assistant for *Anthropology and the Human Experience*
        - acquired skills to manage large lecture classes
        - aided struggling students with class concepts.
    - preceptor for *Osteology*
        - mentored and answered questions during regular lab times
        - provided experience exam set-up with hands-on component
        - sharpened communication skills
        - resulted in the ability to discuss anthropological topics in a multitude of ways to a variety of people with varying knowledge levels and to be understood by all.

## THEME, CONTINUED

Reflecting on the knowledge gained throughout my time here at the University of Montana, I believe my achievements make me a successful candidate for the completion of my Master of Arts Degree. As I continue with my educational goals, I will be attending Florida International University to complete a forensic science certificate program with an emphasis in Forensic Biomolecular Biology. This program is endorsed by the Forensic Science Education Programs Accreditation Commission (FEPAC). Please see the following chart (on the next page) which highlight completed educational goals and outcomes as well as the attachments for an in-depth look at my accomplishments throughout this program.

## EDUCATIONAL COURSE WORK COMPLETED AND OUTCOMES

| COURSE TITLE | PORTFOLIO REFERENCE |
|---|---|
| ANTY 512: Advanced Forensic Anthropology | Attachments 1, 2, 3, 4, 5, and 6 |
| ANTY 510: Seminar in Human Variation and Evolution | Attachment 7 |
| ANTY 418: Evolution and Genetic Variation in Human Populations | In Class Presentation Completed |
| ANTY 513: Seminar in Bioarchaeology and Skeletal Biology | Attachment 8 |
| ANTY 515: Theory and Methods in Biological Anthropology | Attachment 9, 10, and 11 |
| CJUS 488: Forensic Science Beyond the Crime Lab | Attachment 12 |
| ANTY 500: Contemporary Anthropological Thought | In Class Presentations Completed |

# ANTY 512: ADVANCED FORENSIC ANTHROPOLOGY

Teamwork was utilized (both a leader and member) to analyze cases from the University of Montana's Forensic Collection. Team roles included estimation of sex, estimation of age, trauma analysis, etc. to gain experience in all areas. The skillset produced from this course included how to obtain appropriate outside sources to complete a forensic analysis, completion of case findings and addendums for presentation. Collaborative findings were assembled weekly and presented to the class. Discussions regarding theory and practice ensued. Final written reports are represented on the following pages.

## ATTACHMENT 1 – OUTSIDE SOURCES

The following are outside sources utilized to complete various forensic analyses:


Albanese, J., Tuck, A., Gomes, J., & Cardoso, H. F. V. (2016). An alternative approach for estimating stature from long bones that is not population- or group-specific. *Forensic Science International, 259*, 59-68. doi:10.1016/j.forsciint.2015.12.011

Passalacqua, N. V. (2009). Forensic Age-at-Death Estimation from the Human Sacrum*. *54*(2), 255-262. doi:doi:10.1111/j.1556-4029.2008.00977.x

Pokines, J. T., Symes, S. A., & ebrary, I. (2014). Manual of forensic taphonomy. In. Boca Raton [Fla.]: Boca Raton Fla. : Taylor & Francis.

Ríos, L., & Cardoso, H. F. V. (2009). Age estimation from stages of union of the vertebral epiphyses of the ribs. *American Journal of Physical Anthropology, 140*(2), 265-274. doi:10.1002/ajpa.21065

# ATTACHMENT 2 - CASE FINDING - UMFC 62

**UMFC 62**
To: Dr. Skelton
From: Alexis Rizzolo, Anna Hampton, Felicia Sparozic
February 6th, 2019

**Chain Custody**

On January 30th, 2019, a box containing a human cranium to be analyzed was received by Alexis Rizzolo, Anna Hampton, Felicia Sparozic. Upon completion of the analysis, the box containing the cranium was returned to the University of Montana Forensic Collection. No alterations to the remains were made upon completion of the analysis. Remains were returned on January 30th, 2019.

**Summary of Findings**

The individual was found to have a female skull with male postcranial remains, of Peoples of India ancestry, and 30+ years of age at the time of death. The individual is estimated to have the stature of 61.7”-72.1” (5’2’’-6’0’’).

**Inventory and Condition**

The majority of the skeleton was present for analysis. The cortical surface of the bone is not sun-bleached, and the integrity of the bone is not compromised by salt formations. Some portions of the bones exhibited postmortem fracturing due to handling and care of the remains, in addition to having painting on the bones in accordance with muscle attachment. The remains were anatomically articulated and missing the lacrimals.

**Age**

Individual 62 is a middle adult between the ages of 35-50 years old based on the cranial suture closure scores (Meindl and Lovejoy 1985). Sutures 1-7 created a composite score of 5 and was assigned to category S2 (Meindl and Lovejoy 1985). The mean age of this group is 41.1 with a standard deviation of 10.0 years. However, the Anterior sagittal and bregma sutures were unable to be analyzed due to the faceting of hardware into these sutures. This in turn resulted in a lower composite score. Sutures 6-10 created a composite score of 13 and resulted in the assignment of category S7 (Meindl and Lovejoy 1985). The mean age of this group is 56.2 years with a standard deviation of 8.5 years. Mild dental wear is consistent with an age of a middle adult, 35-50 years old, (Scott 1979).

**Sex**

The probable female estimation for the cranium is based on the morphology of the cranial remains. Walkers (2008) regression is indicative that the cranium is female. The features suggesting the individual is a probable female rather than a probable male include the gracile nuchal crest, glabella, left mastoid process and mental eminence (Buikstra and Ubelaker 1994; Bass 2005) (Addendum X-1). Sex estimation utilizing the pelvis indicates the postcranial remains to be male (Klales et al. 2012) (Addendum X-2). This determination was made by utilizing the Sub-pubic concavity as well as the ventral arch in addition to the angle of the sacrum and os-coxae.

# ATTACHMENT 2 - CASE FINDING - UMFC 62, CONTINUED

**Ancestry**

Ancestry estimation was determined to be of African Ancestry for the school utilizing FDB of Foridsc (Jantz and Ously 2005) (Addendum X-4). However, when looking at the Graph representation of this it shows that our cranium is outside of the of the probable area for all female craniums utilized within FORDISC. Howells indicates the cranium to have the ancestry of North Japanese (Jantz and Ously 2005) (Addendum X-5). However, the probability of this is only round 35%. OSSA indicated the cranial remains to be of Caucasian ancestry (Addendum X-3). Ancestry of the postcranial remains to be of African Ancestry (Jantz and Ously 2005) (Addendum X-6). Due to the remains being identified as an anatomical specimen, ancestry is known to be "peoples of India".

**Stature**

Utilizing the African estimation with 20th century statistics for the postcranial remains calculated by FORDISC stature was estimated (Jantz and Ously 2005) (Addendum X-7). Male Statistics estimates the individual's stature to be 61.7"-72.1" (5'2''-6'0'').

**Skeletal Lesions, Trauma and Anomalies**

There is recent taphonomic trauma of the remains which resulted in fracturing of the teeth postmortem. The cranium has been sawed apart proximal of the eye orbits, due to the medical examiner creating this for an anatomical specimen. The upper eye orbits experienced thinning and postmortem fracturing most likely due to the manner in which it was handled. Hardware was facetted to the skull to reattach the skull cap, in addition to the mandible having springs attached for the anatomical placement of the cranium. There was paint located on the bones, that indicated the locations for muscle attachments, which further implies that this is ana anatomical specimen. The ribs were experiencing postmortem fractures due to the materials applied to keep them in anatomical positioning.

**Dental Inventory, Lesions, Wear, Anomalies**

The dental remains of Individual 62 consists of 31 erupted mandibular and maxillary permanent teeth. No teeth were lost antemortem and there are no abscesses. The mandibular left central incisor was lost postmortem. There was post-mortem fracturing of the mandibular left lateral incisor canine and third molar. In addition, there was postmortem fracturing to the right mandibular lateral incisor and canine. There was fracturing of the maxillary left central incisor and canine as well as the right maxillary central and lateral incisors. A post-mortem sealant was applied to keep the integrity of the teeth. There was one carious lesion located on the distobuccal cusp of the right third molar. The general wear of teeth is mild with wear scores ranging from one to three per tooth/cusp.

Thank you for the opportunity to examine this case.

## ATTACHMENT 2 - CASE FINDING - UMFC 62, CONTINUED

**Signatures**

*Alexis Rizzolo*
Alexis Rizzolo, BS/BA
Graduate Student, Forensic Anthropology

*Anna Hampton*
Anna Hampton, BA
Graduate Student, Forensic Anthropology

*Felicia Sparozic*
Felicia Sparozic , BA
Graduate Student, Forensic Anthropology

**References**

Bass W. Human Osteology: A Laboratory and Field Manual. 5th ed. Missouri Archaeological Society. 2005.

Buikstra JE, Ubelaker DH, editors. 1994. Standards: for Data Collection from Human Skeletal Remains. Arkansas Archeological Survey.

Jantz, R. L., & Ousley, S. D. 2005. FORDISC 2.0: personal computer forensic discriminant functions. Knoxville, TN: University of Tennessee.

Klales AR, Ousley SD, Vollner JM. 2012. A New Method of Sexing the Human Innominate Using Phenice's Nonmetric Traits and Statistical Methods. *American Journal of Physical Anthropology* 149:104-114.

Lovejoy, C.O., R.S. Meindl, R.P. Mensforth, and T.J. Barton, 1985. Multifactorial determination of skeletal age at death: A method and blind tests of its accuracy. Am. J. Phys, Anthrop. 68: 1-14.

Rhine, S. 1990. Non-metric skull racing. In: Gill, G., and Rhine, S. (eds) Skeletal Attribution of Race: Methods for Forensic Anthropology. Pp. 9-20. Albuquerque, New Mexico: Maxwell Museum of Anthropology, Anthropological Papers Number 4.

Scott, E.C. 1979. Dental Wear Scoring Technique. American Journal of Anthropology. 51:213-218.

Walker PL. Sexing skulls using discriminant function analysis of visually assessed traits. American Journal of Physical Anthropology 2008;136(1):39–50.

White, T., Folkens P., 2005. The Human Bone Manual. Elsevier Academic Press, Burlington.

# ATTACHMENT 2 - CASE FINDING - UMFC 62 - ADDENDUM

## ADDENDUM X-1

**Sex estimation from Walker (2008)** Version 1.02

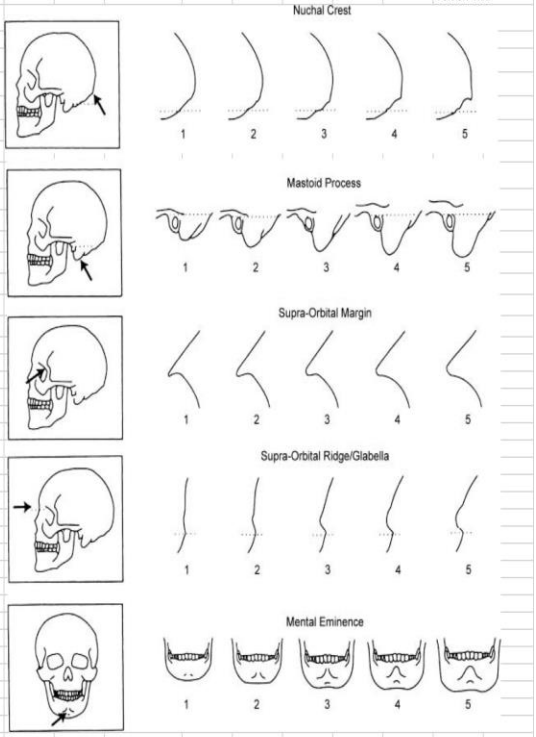
Table 9. Logistic Regression Equations

**Scores:**

| nuchal | mastoid | orbit | glabella | mental |
|---|---|---|---|---|
| 1 | 3 | 1 | 1 | 3 |

**Sex estimations:**

| score | sex | prob Male | prob F | accuracy | vars |
|---|---|---|---|---|---|
| 0.748 | **FEMALE** | 0.32 | 0.68 | 88 / 86 | gl-ma-me |
| 1.489 | **FEMALE** | 0.18 | 0.82 | 85 / 83 | gl-ma |
| 1.392 | **FEMALE** | 0.20 | 0.80 | 87 / 82 | gl-me |
| -1.75 | **MALE** | 0.85 | 0.15 | 70 / 84 | me-ma |
| -0.539 | **MALE** | 0.63 | 0.37 | 78 /78 | or-me |
| -0.048 | **MALE** | 0.51 | 0.49 | 77 / 83 | nu-ma |




## ADDENDUM X-2

**Sex estimation from Klales et al. (2012):** Spreadsheet version 1.3 9/13/13

Klales AR, Ousley SD, Vollner JM. 2012. A New Method of Sexing the Human Innominate Using Phenice's Nonmetric Traits and Statistical Methods. *American Journal of Physical Anthropology* 149:104-114.

**Scores:**

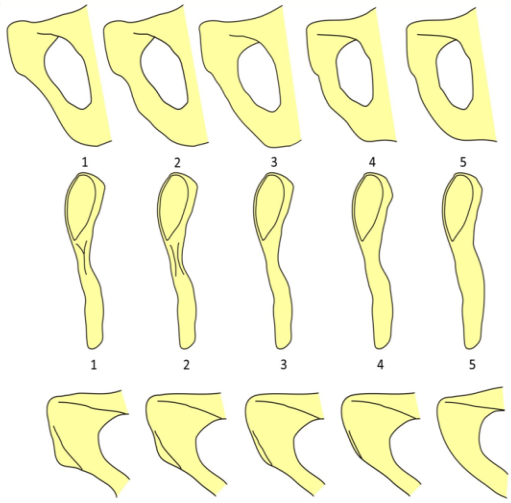
| Sub-Pub Conc | Med Isch Pub Ram | Vent Arc |
|---|---|---|
| 4 | | 5 |

**Linear Discriminant Functions (unpublished)**

| score | sex | prob M | prob F | accuracy | vars |
|---|---|---|---|---|---|
| - | - | - | - | 92 / 97 | MV |
| - | - | - | - | 89 / 98 | SMV |
| -9.521 | **MALE** | 1.00 | 0.00 | 88 / 98 | SV |
| - | - | - | - | 87 / 96 | SM |

**Logistic regression equation**

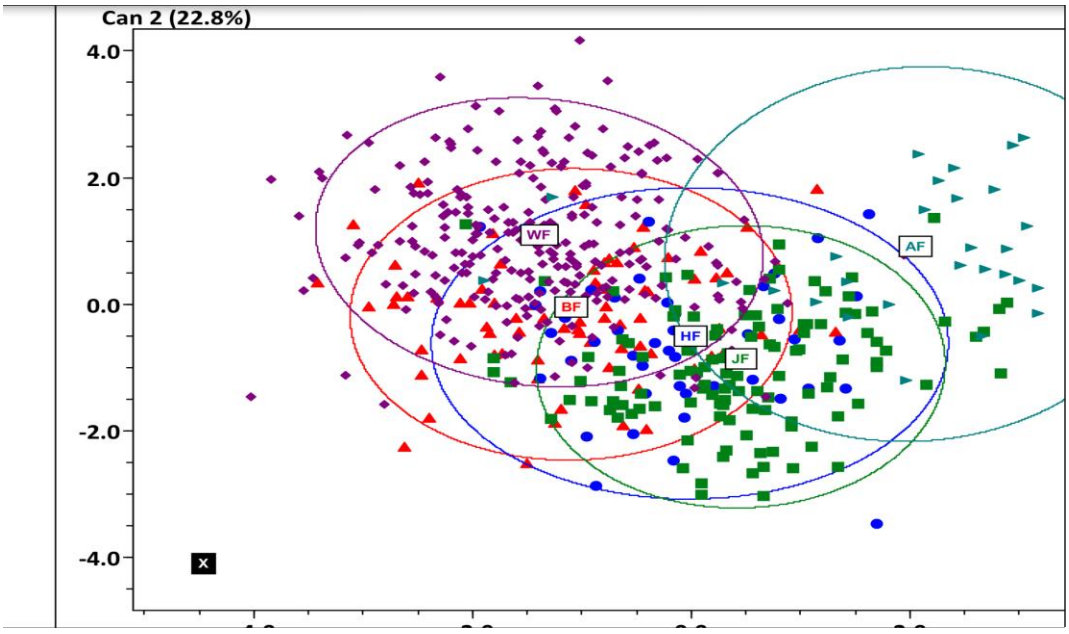
| | | | | | |
|---|---|---|---|---|---|
| - | - | - | - | 98 / 74 | SMV |



# ATTACHMENT 2 - CASE FINDING - UMFC 62 – ADDENDUM, CONT.

## ADDENDUM X-3


## ADDENDUM X-4



# ATTACHMENT 2 - CASE FINDING - UMFC 62 – ADDENDUM, CONT.

## ADDENDUM X-5

**FORDISC 3.1 Analysis of Current Case** **2/1/2019 4:14:24 PM** **Page 1**

FORDISC 3.1.315 Analysis of Current Case
Using cranial data file version 1.23

DFA results using 9 measurements:
DKB EKB GOL MDH NLB NLH OBB OBH ZYB

Measurement Checks and Group Means

| Current Case | | Chk | Group Means BF20 | DOGF | NJAF | PERF | ZULF |
|---|---|---|---|---|---|---|---|
| **DKB** | **14** | **---** | 22.2 | 22.2 | 20.3 | 19.4 | 22.3 |
| EKB | 92 | | 95.1 | 95.2 | 94.5 | 90.8 | 97.7 |
| GOL | 170 | | 177.8 | 169.8 | 171.1 | 169.0 | 179.0 |
| MDH | 32 | ++ | 28.2 | 25.2 | 26.6 | 26.3 | 25.6 |
| NLB | 27 | | 25.0 | 27.7 | 25.7 | 24.0 | 28.0 |
| NLH | 44 | - | 48.4 | 46.2 | 50.3 | 47.7 | 47.3 |
| OBB | 36 | - | 38.6 | 38.1 | 38.2 | 36.8 | 39.2 |
| **OBH** | **39** | **+++** | 34.5 | 32.8 | 34.4 | 34.1 | 32.9 |
| ZYB | 114 | -- | 121.7 | 121.0 | 124.6 | 125.6 | 122.8 |

+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- deviates at least 3 STDEVs

Natural Log of VCVM Determinant = 15.1548

Classification Table

| From Group | Total Number | Into Group (counts) BF20 | DOGF | NJAF | PERF | ZULF | Correct |
|---|---|---|---|---|---|---|---|
| BF20 | 79 | 57 | 3 | 8 | 4 | 7 | 72.2 % |
| DOGF | 52 | 1 | 36 | 5 | 0 | 10 | 69.2 % |
| NJAF | 32 | 4 | 4 | 16 | 5 | 3 | 50.0 % |
| PERF | 55 | 1 | 4 | 3 | 47 | 0 | 85.5 % |
| ZULF | 46 | 1 | 6 | 3 | 0 | 36 | 78.3 % |

Total Correct: 192 out of 264 (72.7 %) *** CROSS-VALIDATED ***

Multigroup Classification of Current Case

| Group | Classified into | Distance from | Probabilities Posterior | Typ F | Typ Chi | Typ R |
|---|---|---|---|---|---|---|
| NJAF | | 70.6 | 0.350 | 0.000 | 0.000 | **0.030 (32/33)** |
| DOGF | | 71.0 | 0.276 | 0.000 | 0.000 | **0.019 (52/53)** |
| ZULF | | 71.8 | 0.192 | 0.000 | 0.000 | **0.021 (46/47)** |
| BF20 | | 71.9 | 0.176 | 0.000 | 0.000 | **0.013 (79/80)** |
| PERF | | 78.4 | 0.007 | 0.000 | 0.000 | **0.018 (55/56)** |

Current Case is too dissimilar to all groups; all TPs < 0.01

# ATTACHMENT 2 - CASE FINDING - UMFC 62 – ADDENDUM, CONT.

## ADDENDUM X-6

**FORDISC 3.1 Analysis of Current Case** **2/1/2019 4:07:28 PM** **Page 1**

FORDISC 3.1.315 Analysis of Current Case
Using postcranial data file version 1.18

DFA results using 18 measurements:
CLAAPD CLAVRD FEMEBR FEMMAP FEMMTV FEMSAP FEMSTV FIBMDM
HUMMWD HUMMXD ILIABR RADAPD RADTVD SCAPHT TIBNFT TIBNFX
ULNDVD ULNTVD

Measurement Checks, Group Means, and Discriminant Function Coefficients

| Current Case | | Chk | BM 80 | WM 422 | DF Weights | Relative Weights |
|---|---|---|---|---|---|---|
| CLAAPD | 16 | ++ | 13.9 | 13.2 | 0.181 | 3.9 % |
| CLAVRD | 10 | - | 10.8 | 10.9 | -0.071 | 0.3 % |
| **FEMEBR** | **31** | **----** | 83.7 | 85.8 | -0.133 | 8.6 % |
| FEMMAP | 29 | - | 31.8 | 31.1 | 0.285 | 5.5 % |
| FEMMTV | 25 | -- | 28.0 | 28.4 | 0.080 | 1.0 % |
| FEMSAP | 28 | - | 28.4 | 28.6 | -0.243 | 1.0 % |
| FEMSTV | 29 | -- | 32.1 | 32.6 | -0.071 | 1.0 % |
| FIBMDM | 16 | | 15.7 | 16.1 | -0.291 | 3.9 % |
| HUMMWD | 18 | - | 19.6 | 18.9 | 0.314 | 6.7 % |
| HUMMXD | 22 | - | 23.7 | 23.5 | 0.055 | 0.4 % |
| ILIABR | 141 | -- | 154.8 | 162.4 | -0.125 | 29.2 % |
| RADAPD | 12 | - | 13.1 | 13.0 | -0.069 | 0.2 % |
| RADTVD | 15 | - | 16.1 | 16.5 | -0.452 | 4.5 % |
| SCAPHT | 150 | -- | 161.4 | 163.9 | -0.012 | 0.9 % |
| **TIBNFT** | **33** | **+++** | 26.8 | 25.1 | 0.481 | 24.2 % |
| **TIBNFX** | **27** | **----** | 37.5 | 36.8 | 0.152 | 3.5 % |
| ULNDVD | 15 | | 15.2 | 14.5 | 0.215 | 5.1 % |
| ULNTVD | 15 | - | 17.0 | 17.5 | -0.006 | 0.1 % |
| Constant | | | | | 13.735 | |
| Scores | | | 1.606 (Group means) | -1.606 | 11.491 (Case) | |

Mahalanobis Distance = 3.211

+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- at least 3 STDEVs

Natural Log of VCVM Determinant = 24.0745

Classification Matrix

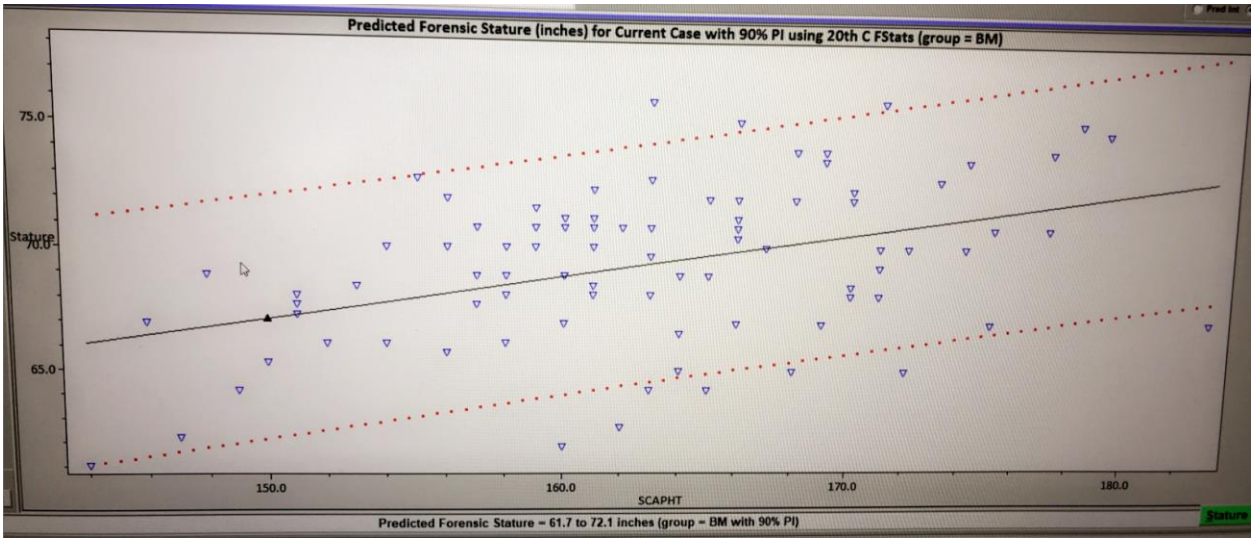
| From Group | Group Counts | Into Group (counts) BM | WM | Percent Correct |
|---|---|---|---|---|
| BM | 80 | 65 | 15 | 81.3 % |
| WM | 422 | 82 | 340 | 80.6 % |
| Total Correct: | 405 / 502 ( 80.7 %) *** CROSS-VALIDATED *** | | | |

Two Group Discriminant Function Results

| Group | Classified into | Distance from | Probabilities Posterior | Typ F | Typ Chi | Typ R |
|---|---|---|---|---|---|---|
| BM | | 321.2 | 1.000 | 0.000 | 0.000 | **0.012 (81/81)** |
| WM | | 344.2 | 0.000 | 0.000 | 0.000 | 0.002 (423/423) |

# ATTACHMENT 2 - CASE FINDING - UMFC 62 – ADDENDUM, CONT.

## ADDENDUM X-7



# ATTACHMENT 3 - CASE FINDING - UMFC 63

**UMFC 63**
To: Dr. Skelton
From: Alexis Rizzolo, Anna Hampton, Felicia Sparozic
February 6th, 2019

**Chain Custody**

On January 30, 2019, a complete skeleton was received by Alexis Rizzolo, Anna Hampton, and Felicia Sparozic. Upon completion of the analysis, the skeleton was returned to the University of Montana Forensic Collection. No alterations to the remains were made upon completion of the analysis. Remains were returned on January 30th, 2019.

**Summary of Findings**

The individual was male for the cranium, and female for the postcranial remains. The ancestry is deemed to be "peoples of India" ancestry, and 26-42 years of age at the time of death. The individual is estimated to have the stature of 51.4"-62.6" (4'3''-5'2'').

**Inventory and Condition**

The only element present was the complete cranium. No post-cranial bones were present. The cortical surface of the bone is not sun-bleached. The only bone found to missing is the left lacrimal.

**Age**

Individual 63 is a young adult between the ages of 26-42 years old based on the cranial suture closure scores (Meindl and Lovejoy 1985). Sutures 1-7 created a composite score of 0 and as a result could not be assigned to any category due to the sutures being open (Meindl and Lovejoy 1985). This could be due to the hardware attached to the cranium to allow it to hang for anatomical purposes. Sutures 6-10 created a composite score of 3 and resulted in the assignment of category S3 (Meindl and Lovejoy 1985). The mean age of this group is 34.7 years with a standard deviation of 7.8 years. Mild dental wear is consistent with an age of a young adult, 18+ (Scott 1979).

**Sex**

The male estimation of the cranium is based on the morphology of the cranial remains. Walkers (2008) regression indicates the cranial remains are male. The features suggesting the individual is a male include the robust nuchal crest, glabella, and left mastoid process, and the mental eminence (Buikstra and Ubelaker 1994; Bass 2005) (Addendum X-1). Sex estimation utilizing the pelvis indicates the postcranial remains to be female (Klales et al. 2012) (Addendum X-2). This determination was made by utilizing the Sub-pubic concavity as well as the ventral arch in addition to the angle of the sacrum and os-coxae.

**Ancestry**

Ancestry estimation was determined to be of Indian ancestry. The cranium exhibits complex sutures with wormian bones. The cranium is low and sloping, which is present in both Asian and African ancestry. The features present suggesting Asian ancestry include wormian bones, zygomatic tubercles, flaring zygomatics, complex sutures, and medium nasal aperture (Gill,

# ATTACHMENT 3 - CASE FINDING - UMFC 63, CONTINUED

1995; Rhine, 1990). FORDISC 3.1 suggests the individual is of Caucasian ancestry (Jantz and Ously 2005) (Addendum X-4), while Howell's data set suggest the individual is of Norse Ancestry (Addendum X-5). OSSA scores the individual to be white as well (Addendum X-3). Postcranial remains were classified as having Caucasian ancestry within FORDISC 3.1(Jantz and Ously 2005). Due to the remains being identified as an anatomical specimen, ancestry is known to be "peoples of India".

**Stature**

Stature estimation utilizing FORDISC and a classification of white females using 20th Century Female Statistics estimates the stature of the individual to be 51.4"-62.6" (4'3''-5'2'') (Jantz and Ously 2005) (Addendum X-6).

**Skeletal Lesions, Trauma and Anomalies**

There is recent taphonomic trauma of the remains which resulted in fracturing bones postmortem due to the addition of facets and hardware to hand the individual in anatomical position. Hardware was facteted to the skull to reattach the skull cap, in addition to the mandible having springs attached for the anatomical placement of the cranium. In addition to wiring being attached to all the bones to align them in anatomical positioning. A hook was placed in the top of the cranium to all the specimen to be hung up. The cranium has been sawed apart proximal of the eye orbits, due to the medical examiner creating this for an anatomical specimen. Due to this cut there is a portion of the frontal bone missing. The right and left scapula experienced thinning. There are fractures in the right ilium, right humerus trochlea, and left humerus trochlea. This is most likely due to the drilling and wiring of hardware for anatomical positioning. The bone has been patched in two areas on the right scapula, once on the left scapula, once on the left ilium, and once on the right ilium due to fracturing of these bones' postmortem. There is linear enamel hypoplasia present on the teeth.

**Dental Inventory, Lesions, Wear, Anomalies**

The dental remains consist of 30 erupted mandibular and maxillary permanent teeth. No teeth were lost antemortem and there are no abscesses. There was post-mortem fracturing of the teeth; a sealant was applied to maintain the integrity of the teeth. There are carious lesions present on the mandibular right first and second molars. In addition, there is linear enamel hypoplasia present. The general wear of teeth is mild with wear scores ranging from one to three per tooth/cusp.

Thank you for the opportunity to examine this case.

## ATTACHMENT 3 - CASE FINDING - UMFC 63, CONTINUED

**Signatures**

*Alexis Rizzolo*
Alexis Rizzolo, BS/BA
Graduate Student, Forensic Anthropology

*Anna Hampton*
Anna Hampton, BA
Graduate Student, Forensic Anthropology

*Felicia Sparozic*
Felicia Sparozic, BA
Graduate Student, Forensic Anthropology

**References**

Bass W. Human Osteology: A Laboratory and Field Manual. 5th ed. Missouri Archaeological Society. 2005.

Buikstra JE, Ubelaker DH, editors. 1994. Standards: for Data Collection from Human Skeletal Remains. Arkansas Archeological Survey.

Jantz, R. L., & Ousley, S. D. 2005. FORDISC 2.0: personal computer forensic discriminant functions. Knoxville, TN: University of Tennessee.

Klales AR, Ousley SD, Vollner JM. 2012. A New Method of Sexing the Human Innominate Using Phenice's Nonmetric Traits and Statistical Methods. *American Journal of Physical Anthropology* 149:104-114.

Lovejoy, C.O., R.S. Meindl, R.P. Mensforth, and T.J. Barton, 1985. Multifactorial determination of skeletal age at death: A method and blind tests of its accuracy. Am. J. Phys, Anthrop. 68: 1-14.

Rhine, S. 1990. Non-metric skull racing. In: Gill, G., and Rhine, S. (eds) Skeletal Attribution of Race: Methods for Forensic Anthropology. Pp. 9-20. Albuquerque, New Mexico: Maxwell Museum of Anthropology, Anthropological Papers Number 4.

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Walker PL. Sexing skulls using discriminant function analysis of visually assessed traits. American Journal of Physical Anthropology 2008;136(1):39–50.

White, T., Folkens P., 2005. The Human Bone Manual. Elsevier Academic Press, Burlington.

# ATTACHMENT 3 - CASE FINDING - UMFC 63 - ADDENDUM

## ADDENDUM X-1

**Sex estimation from Walker (2008)** Version 1.02

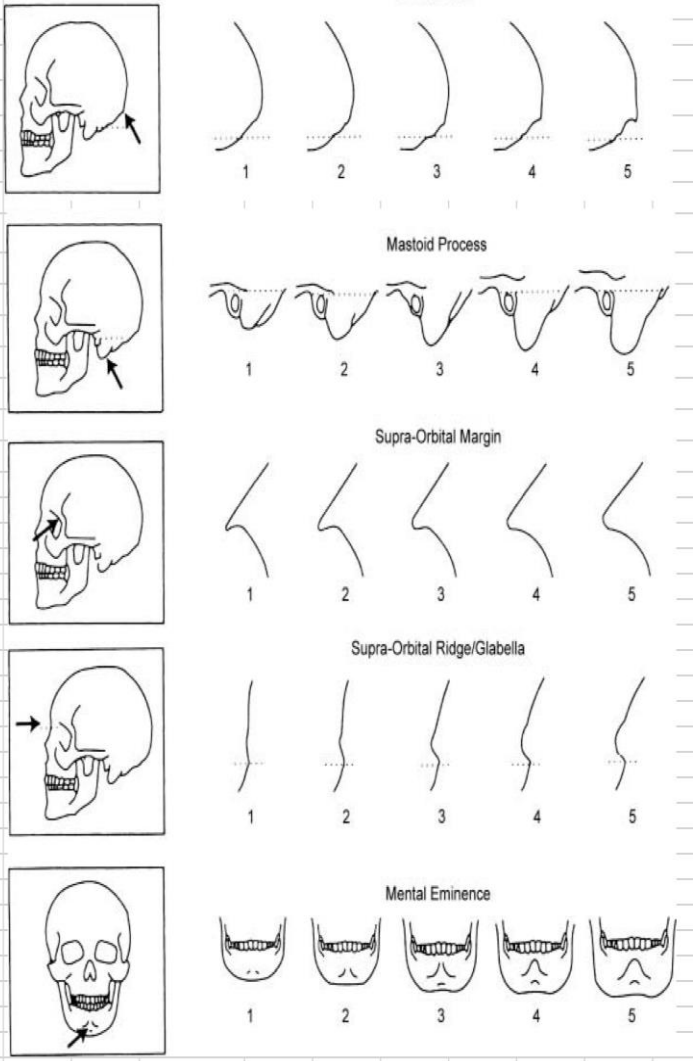
Table 9. Logistic Regression Equations

**Scores:**

| nuchal | mastoid | orbit | glabella | mental |
|---|---|---|---|---|
| 3 | 2 | 3 | 3 | 3 |

**Sex estimations:**

| score | sex | prob Male | prob F | accuracy | vars |
|---|---|---|---|---|---|
| -0.817 | **MALE** | 0.69 | 0.31 | 88 / 86 | gl-ma-me |
| -0.188 | **MALE** | 0.55 | 0.45 | 85 / 83 | gl-ma |
| -1.658 | **MALE** | 0.84 | 0.16 | 87 / 82 | gl-me |
| -0.335 | **MALE** | 0.58 | 0.42 | 70 / 84 | me-ma |
| -2.553 | **MALE** | 0.93 | 0.07 | 78 /78 | or-me |
| 0.111 | **FEMALE** | 0.47 | 0.53 | 77 / 83 | nu-ma |



# ATTACHMENT 3 - CASE FINDING - UMFC 63 – ADDENDUM, CONT.

## ADDENDUM X-2

**Sex estimation from Klales et al. (2012):**

**Spreadsheet version 1.3 9/13/13**

Klales AR, Ousley SD, Vollner JM. 2012. A New Method of Sexing the Human Innominate Using Phenice's Nonmetric Traits and Statistical Methods. *American Journal of Physical Anthropology* 149:104-114.

**Scores:**

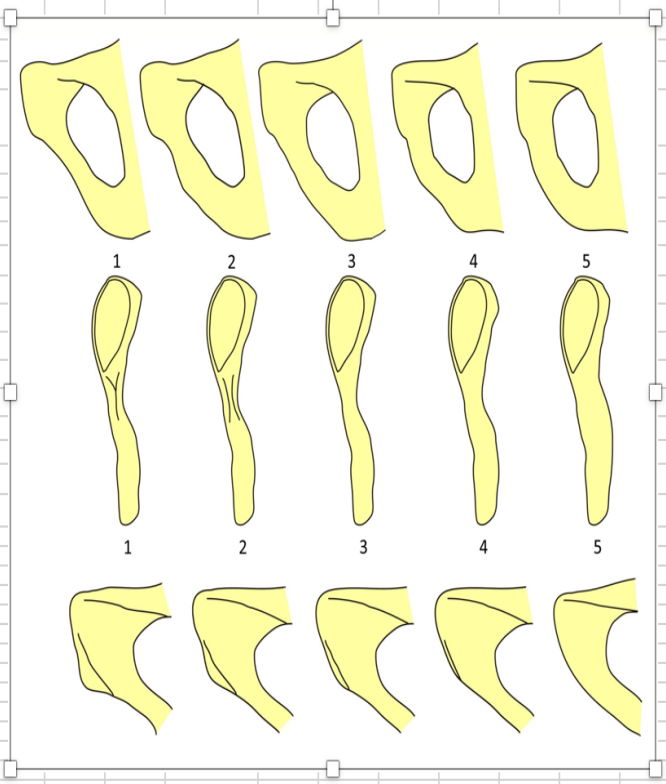
| Sub-Pub Conc | Med Isch Pub Ram | Vent Arc |
|---|---|---|
| 1 | | 2 |

**Linear Discriminant Functions (unpublished)**

| score | sex | prob M | prob F | accuracy | vars |
|---|---|---|---|---|---|
| - | - | - | - | 92 / 97 | MV |
| - | - | - | - | 89 / 98 | SMV |
| 7.594 | FEMALE | 0.00 | 1.00 | 88 / 98 | SV |
| - | - | - | - | 87 / 96 | SM |

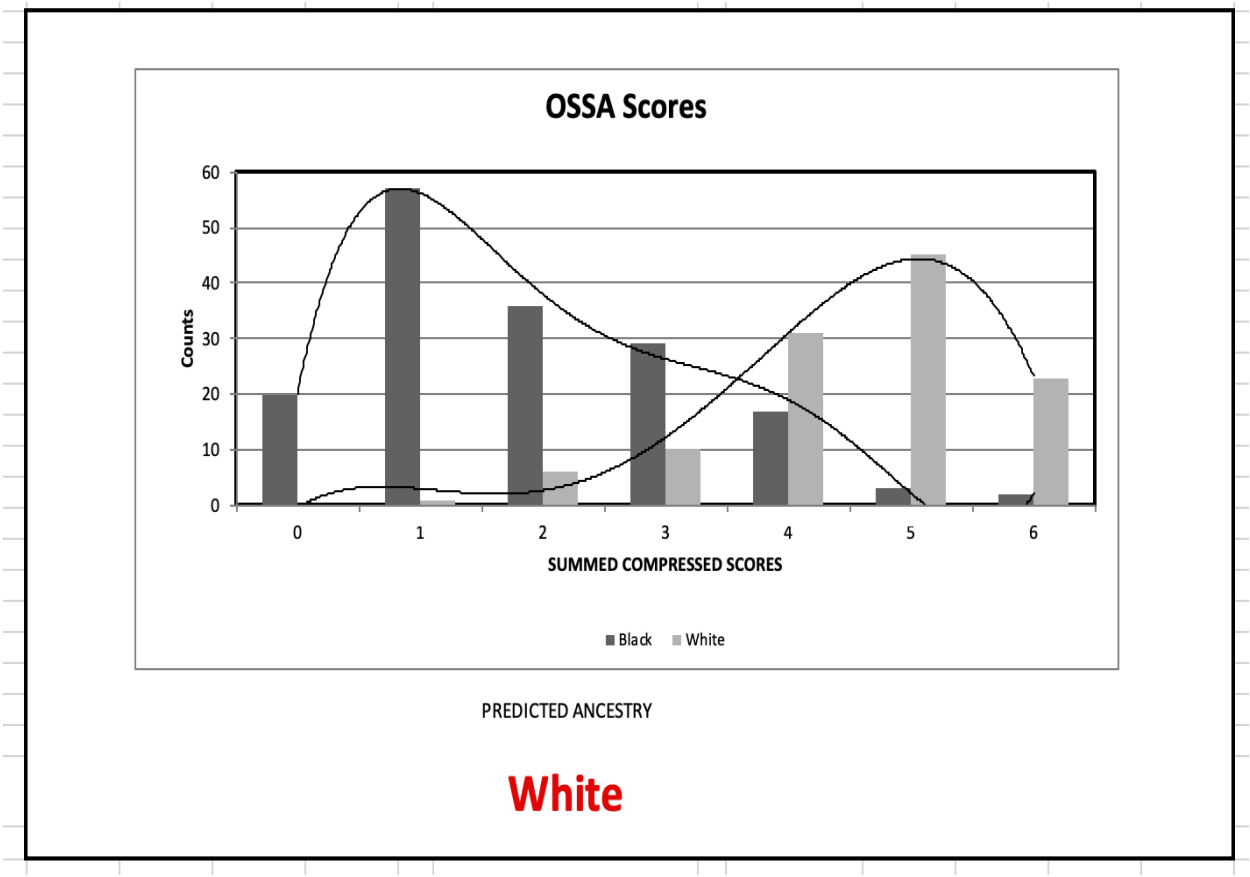
**Logistic regression equation**

| | | | | | |
|---|---|---|---|---|---|
| - | - | - | - | 98 / 74 | SMV |



# ATTACHMENT 3 - CASE FINDING - UMFC 63 – ADDENDUM, CONT.

## ADDENDUM X-3



# ATTACHMENT 3 - CASE FINDING - UMFC 63 – ADDENDUM, CONT.

## ADDENDUM X-4

Measurement Checks and Group Means

| | | | Group Means | | | | |
|---|---|---|---|---|---|---|---|
| | | | AF | BF | HF | JF | WF |
| Current Case | | Chk | 29 | 78 | 45 | 121 | 261 |
| DKB | 24 | + | 22.3 | 22.2 | 19.9 | 20.5 | 20.1 |
| EKB | 97 | | 98.0 | 95.1 | 93.5 | 93.5 | 93.5 |
| GOL | 183 | + | 177.4 | 178.0 | 170.0 | 171.9 | 177.4 |
| MDH | 24 | - | 25.0 | 28.2 | 25.6 | 26.2 | 27.7 |
| NLB | 25 | | 25.3 | 25.0 | 24.1 | 25.0 | 22.6 |
| NLH | 52 | + | 51.6 | 48.4 | 49.0 | 48.9 | 48.9 |
| OBB | 39 | | 40.8 | 38.6 | 38.9 | 37.7 | 39.2 |
| OBH | 33 | - | 35.0 | 34.5 | 35.5 | 33.9 | 33.4 |
| UFHT | 70 | | 70.6 | 66.9 | 67.3 | 68.5 | 66.6 |
| WFB | 99 | ++ | 91.8 | 93.3 | 91.0 | 90.1 | 93.7 |
| ZYB | 122 | | 131.9 | 121.7 | 123.4 | 124.9 | 120.8 |

+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- deviates at least 3 STDEVs

Natural Log of VCVM Determinant = 21.4552

Classification Table

| From Group | Total Number | Into Group (counts) AF | BF | HF | JF | WF | Correct |
|---|---|---|---|---|---|---|---|
| AF | 29 | 22 | 0 | 0 | 5 | 2 | 75.9 % |
| BF | 78 | 3 | 49 | 11 | 3 | 12 | 62.8 % |
| HF | 45 | 5 | 7 | 22 | 6 | 5 | 48.9 % |
| JF | 121 | 12 | 10 | 23 | 74 | 2 | 61.2 % |
| WF | 261 | 3 | 31 | 21 | 13 | 193 | 73.9 % |

Total Correct: 360 out of 534 (67.4 %) *** CROSS-VALIDATED ***

Multigroup Classification of Current Case

| Group | Classified into | Distance from | Probabilities Posterior | Typ F | Typ Chi | Typ R |
|---|---|---|---|---|---|---|
| WF | **WF** | 7.8 | 0.592 | 0.748 | 0.733 | 0.710 (76/262) |
| BF | | 8.8 | 0.359 | 0.668 | 0.642 | 0.722 (22/79) |
| HF | | 14.1 | 0.025 | 0.262 | 0.226 | 0.370 (29/46) |
| JF | | 14.6 | 0.020 | 0.228 | 0.204 | 0.148 (104/122) |
| AF | | 18.0 | 0.004 | 0.110 | 0.081 | 0.100 (27/30) |

Current Case is closest to WFs

# ATTACHMENT 3 - CASE FINDING - UMFC 63 – ADDENDUM, CONT.

## ADDENDUM X-5

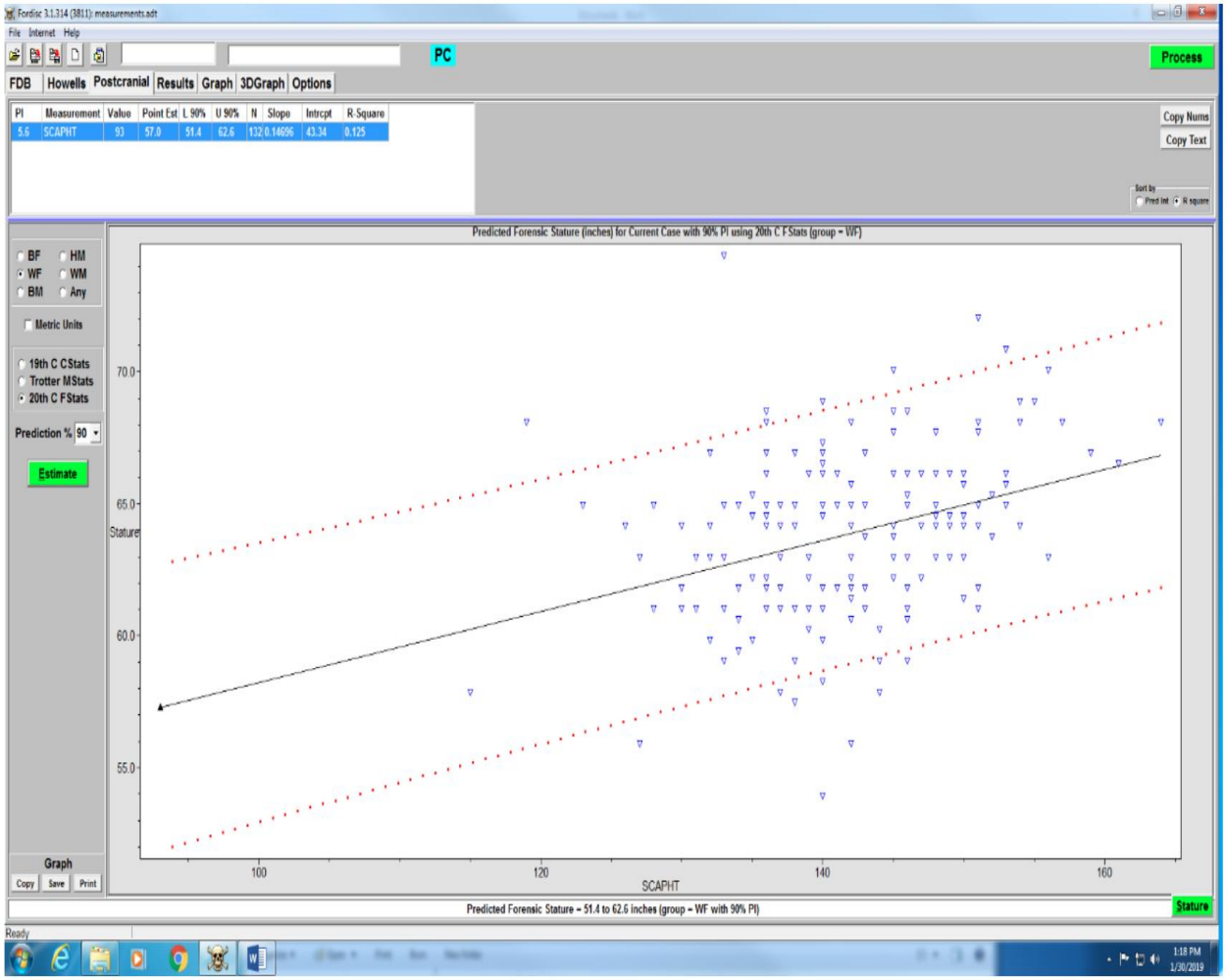
Multigroup Classification of Current Case

| Group | Classified into | Distance from | Probabilities Posterior | Typ F | Typ Chi | Typ R |
|---|---|---|---|---|---|---|
| NORF | **NORF** | 6.7 | 0.257 | 0.682 | 0.665 | 0.589 (23/56) |
| EGYF | | 6.9 | 0.236 | 0.665 | 0.647 | 0.444 (30/54) |
| WF20 | | 8.5 | 0.108 | 0.496 | 0.488 | 0.650 (97/277) |
| EASF | | 8.6 | 0.103 | 0.506 | 0.479 | 0.263 (28/38) |
| BF20 | | 9.1 | 0.080 | 0.447 | 0.431 | 0.650 (28/80) |
| ZALF | | 9.4 | 0.069 | 0.429 | 0.405 | 0.391 (28/46) |
| TEIF | | 11.1 | 0.030 | 0.292 | 0.272 | 0.392 (31/51) |
| ZULF | | 11.5 | 0.024 | 0.265 | 0.244 | 0.234 (36/47) |
| BERF | | 11.6 | 0.022 | 0.253 | 0.234 | 0.241 (41/54) |
| SJAF | | 12.1 | 0.017 | 0.228 | 0.207 | 0.119 (37/42) |
| AUSF | | 13.4 | 0.009 | 0.163 | 0.147 | 0.120 (44/50) |
| MOKF | | 13.6 | 0.008 | 0.155 | 0.139 | **0.040 (48/50)** |
| HAIF | | 13.6 | 0.008 | 0.157 | 0.138 | 0.179 (32/39) |
| NJAF | | 13.6 | 0.008 | 0.159 | 0.137 | 0.152 (28/33) |
| AINF | | 14.9 | 0.004 | 0.109 | 0.094 | 0.128 (34/39) |
| TOLF | | 15.2 | 0.004 | 0.096 | 0.085 | **0.036 (53/55)** |
| MORF | | 15.8 | 0.003 | 0.082 | 0.071 | **0.038 (50/52)** |
| DOGF | | 15.9 | 0.003 | 0.078 | 0.068 | 0.075 (49/53) |
| BUSF | | 16.1 | 0.002 | 0.075 | 0.065 | 0.140 (43/50) |
| SANF | | 17.2 | 0.001 | 0.054 | **0.046** | **0.019 (51/52)** |
| GUAF | | 18.1 | 0.001 | **0.044** | **0.034** | **0.036 (27/28)** |
| ATAF | | 18.6 | 0.001 | **0.042** | **0.028** | 0.053 (18/19) |
| TASF | | 19.4 | 0.000 | **0.027** | **0.022** | **0.047 (41/43)** |
| ARIF | | 20.0 | 0.000 | **0.024** | **0.018** | **0.036 (27/28)** |
| ESKF | | 22.8 | 0.000 | 0.008 | 0.007 | **0.018 (55/56)** |
| PERF | | 23.5 | 0.000 | 0.007 | 0.005 | **0.018 (55/56)** |
| ANDF | | 23.6 | 0.000 | 0.007 | 0.005 | **0.028 (35/36)** |
| BURF | | 27.5 | 0.000 | 0.002 | 0.001 | **0.018 (54/55)** |

Current Case is closest to NORFs

# ATTACHMENT 3 - CASE FINDING - UMFC 63 – ADDENDUM, CONT.

## ADDENDUM X-6



# ATTACHMENT 4 - CASE FINDING - UMFC 75

**UMFC 75**
To: Dr. Skelton
From: Alexis Rizzolo, Anna Hampton
February 27th, 2019

**Chain Custody**

On February 27, 2019, a box containing skeletal remains to be analyzed was received by Alexis Rizzolo and Anna Hampton. Upon completion of the analysis, the box containing the skeletal remains was returned to the University of Montana Forensic Collection. No alterations to the remains were made upon completion of the analysis. The remains were returned on February 27th, 2019.

**Summary of Findings**

The individual was found to be a probable male, 23-57 years of age at the time of death, with the mean age around 35. The individual is estimated to have the stature of 60”-65” (5’0’’-5’5’’) with a mean height of 63” (5’3”).

**Inventory and Condition**

A portion of the skeletons was available for analysis. The cortical surface of the bone is not sun-bleached, and the integrity of the bone is not compromised by salt formations. Some portions of the bones exhibited postmortem fracturing due to handling and care of the remains. There was an absence of the crania, a portion of the left femur, the hyoid, 5 thoracic vertebrae, all the tarsals, all the foot phalanges, four right metatarsals, and five left metatarsals, coccyx, six carpals, two metacarpals for both the right and left hands, and 2 left hand phalanges and two right hand phalanges, both patellas, and lumbar vertebra one. There was an extra cervical vertebra that did not match the coloring or size of the other cervical vertebrae with these remains, so we have concluded it belongs to a different set of remains.

**Age**

Individual 75 is a middle adult between the ages of 35-50 years old based on the pubic symphysis (Suchey Brooks 1990). The pubic symphysis was determined to be a category IV 2. This ages range is from 23 to 57, with the mean being 35 years old. Looking at the fusion of the sacrum, S1 is completely unfused which is an indicator the individual age range is from 20-40 (Passalacqua 2009).

**Sex**

Sex estimation utilizing the pelvis indicates the postcranial remains to be male (Klales et al. 2012) (Addendum X-1). This determination was made by utilizing the Sub-pubic concavity, the ventral arch, and in addition to the angle of the sacrum and os-coxae. In addition, the mental eminence of the mandible was also estimated to have a probable male biological sex (Buikstra and Ubelaker 1994).

**Ancestry**

Ancestry estimation was not possible due to the lack of cranial remains.

# ATTACHMENT 4 - CASE FINDING - UMFC 75, CONTINUED

**Stature**

Utilizing the white male estimation with 20th century and Hispanic male statistics for the postcranial remains calculated by FORDISC stature was estimated (Jantz and Ously 2005) (Addendum X-2; X-3). Male Statistics estimates the individual's stature to be 60"-65" (5'0''-5'5'') with a mean of 63" (5'3").

**Skeletal Lesions, Trauma and Anomalies**

There is significant postmortem fracturing experienced by both the ribs and femur. Trabecular bone is present on almost every bone present in multiple locations, in addition to ossification of the epiphyseal ends of the long bones. Lumbar vertebra five was transected postmortem likely due to sampling for research. The right scapula was fractured post-mortem and the acromion, coracoid process, and supraspinous fossa was present. The vertebrae showed signs of possible spinal osteophytosis due to the lipping of the vertebra and ossification of the vertebral bodies (Roberts and Manchester 2007).

**Dental Inventory, Lesions, Wear, Anomalies**

The dental remains of Individual 75 consists of 4 erupted mandibular permanent teeth. The right first molar was lost antemortem and shows signs of reabsorption. There are no abscesses. The general wear of teeth is significant with wear scores ranging from five to eight per tooth/cusp. The teeth that were lost postmortem are the mandibular right and left central incisors, the left, canine, first and second premolars, first molar, second molar, and third molar, and the right mandibular first premolar.

Thank you for the opportunity to examine this case.

**Signatures**

*Alexis Rizzolo*
Alexis Rizzolo, BS/BA
Graduate Student, Forensic Anthropology

*Anna Hampton*
Anna Hampton, BA
Graduate Student, Forensic Anthropology

# ATTACHMENT 4 - CASE FINDING - UMFC 75, CONTINUED

**References**


Bass W. Human Osteology: A Laboratory and Field Manual. 5th ed. Missouri Archaeological Society. 2005.

Brooks, S. & Suchey, J.M. Hum. Evol. (1990) 5: 227. https://doi.org/10.1007/BF02437238

Buikstra JE, Ubelaker DH, editors. 1994. Standards: for Data Collection from Human Skeletal Remains. Arkansas Archeological Survey.

Jantz, R. L., & Ousley, S. D. 2005. FORDISC 3.1: personal computer forensic discriminant functions. Knoxville, TN: University of Tennessee.

Klales AR, Ousley SD, Vollner JM. 2012. A New Method of Sexing the Human Innominate Using Phenice's Nonmetric Traits and Statistical Methods. *American Journal of Physical Anthropology* 149:104-114.

Lovejoy, C.O., R.S. Meindl, R.P. Mensforth, and T.J. Barton, 1985. Multifactorial determination of skeletal age at death: A method and blind tests of its accuracy. Am. J. Phys, Anthrop. 68: 1-14.

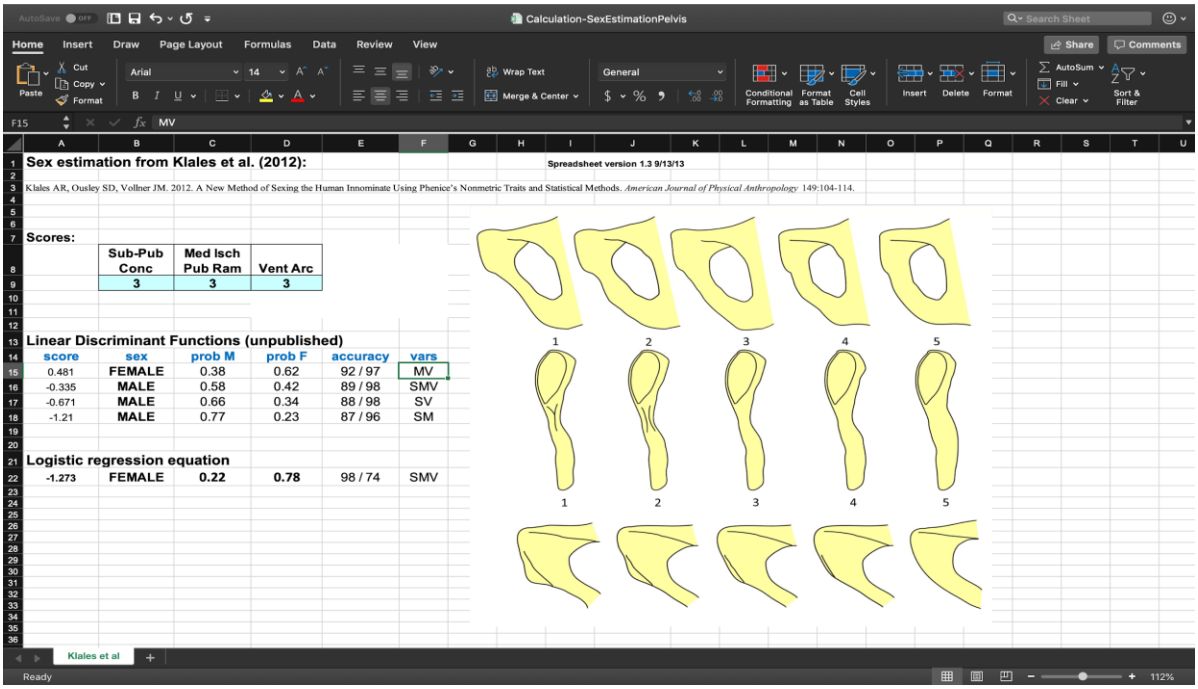
Roberts, C, Manchester K, 2007. The Archaeology of Disease. Cornell University of Press, New York. Pg 140-143.

Scott, E.C. 1979. Dental Wear Scoring Technique. American Journal of Anthropology. 51:213-218.

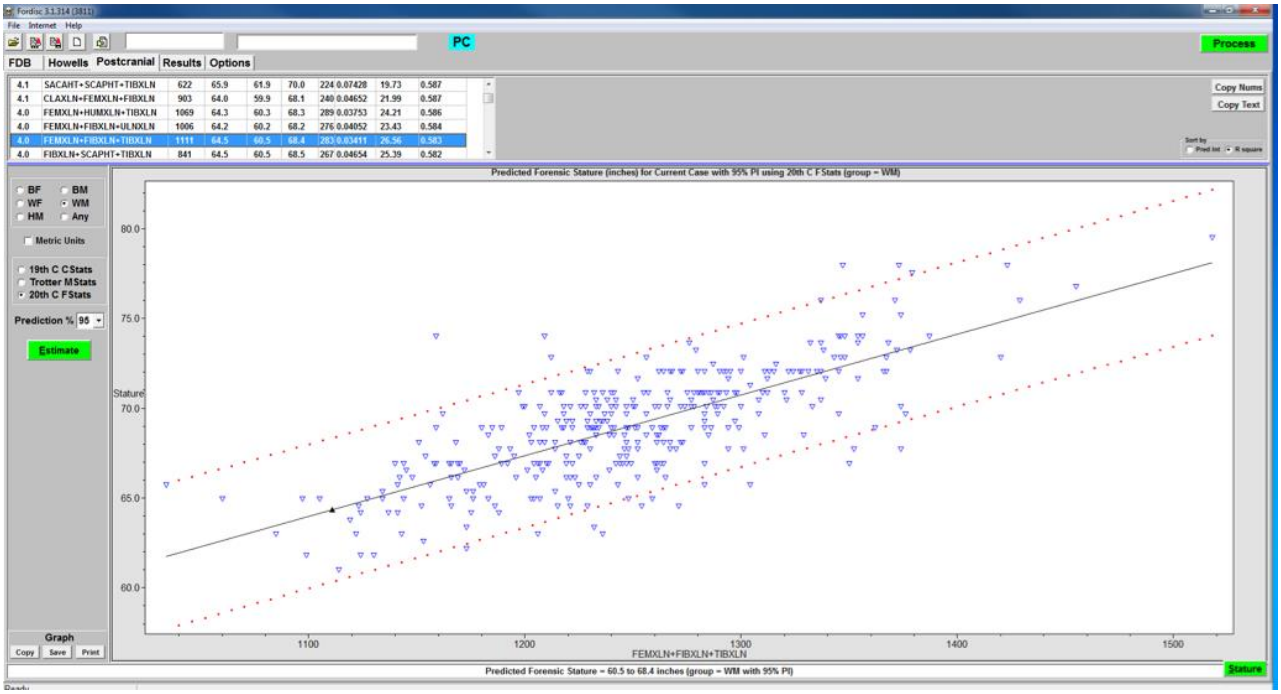
White, T., Folkens P., 2005. The Human Bone Manual. Elsevier Academic Press, Burlington.

# ATTACHMENT 4 - CASE FINDING - UMFC 75 – ADDENDUM

## ADDENDUM X-1

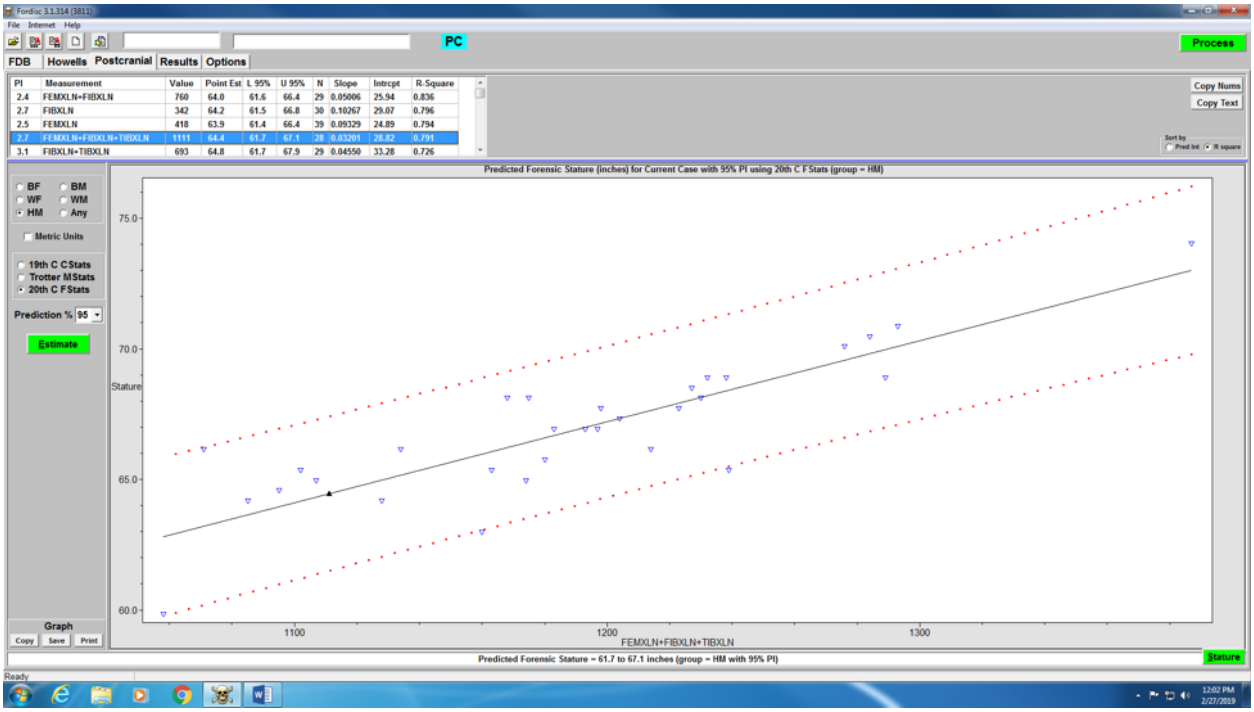



## ADDENDUM X-2



# ATTACHMENT 4 - CASE FINDING - UMFC 75 – ADDENDUM, CONT.

## ADDENDUM X-3



# ATTACHMENT 5 - CASE FINDING - UMFC 78

**UMFC 78**
To: Dr. Skelton
From: Alexis Rizzolo and Elizabeth Valentine
January 30th, 2019

**Chain Custody**

On January 16, 2019, a box containing a human cranium to be analyzed was received by Alexis Rizzolo and Elizabeth Valentine. Upon completion of the analysis, the box containing the cranium was returned to the University of Montana Forensic Collection. No alterations to the remains were made upon completion of the analysis. Remains were returned on January 30th, 2019.

**Summary of Findings**

The individual was probable male, of possible mixed ancestry, and 30+ years of age at the time of death.

**Inventory and Condition**

The only element present was the complete cranium. No post-cranial bones were present. The cortical surface of the bone is not sun-bleached.

**Age**

Individual 78 is a middle adult between the ages of 35-50 years old based on the cranial suture closure scores (Meindl and Lovejoy 1985). Sutures 1-7 created a composite score of 12 and was assigned to category S4 (Meindl and Lovejoy 1985). The mean age of this group is 45.2 with a standard deviation of 12.6 years.Sutures 6-10 created a composite score of 13 and resulted in the assignment of category S7 (Meindl and Lovejoy 1985). The mean age of this group is 56.2 years with a standard deviation of 8.5 years. Mild dental wear is consistent with an age of a middle adult, 35-50 years old (Scott 1979).

**Sex**

The probable male estimation is based on the morphology of the cranial remains. Walkers (2008) regression is split between male and female. The features suggesting the individual is a probable female rather than a probable male include the gracile nuchal crest, glabella, and left mastoid process (Buikstra and Ubelaker 1994; Bass 2005). The mental eminence suggests the remains are male (Buikstra and Ubelaker 1994; Bass 2005).

**Ancestry**

Ancestry estimation was determined to be of African ancestry (Gill, 1995; Rhine 1990). The cranium exhibits complex sutures with 5 wormian bones, 4 along the lambdoid suture and 1 along the sagittal suture. The features present suggesting African ancestry include a hyperbolic palatine, curved zygomaticomaxillary sutures, an arched palatine suture, and cranial index. The cranium is low and sloping, which is present in both Asian and African ancestry. The features present suggesting Asian ancestry include wormian bones, zygomatic tubercles, flaring zygomatics, complex sutures, and medium nasal aperture (Gill, 1995; Rhine, 1990). FORDISC 3.1 suggest the individual is Japanese male (Jantz and Ously 2005) (Addendum X-1), while Howell's

data set suggest the individual is of Teita Africans Ancestry (Addendum X-2). Due to the remains being identified as an anatomical specimen, ancestry is known to be "peoples of India".

**Stature**

Stature estimation was not completed due to the unreliability of stature estimation utilizing the human cranium.

**Skeletal Lesions, Trauma and Anomalies**

There is recent taphonomic trauma of the remains which resulted in fracturing of the teeth postmortem. The cranium has been sawed apart proximal of the eye orbits, due to the medical examiner creating this for an anatomical specimen. The upper eye orbits experienced thinning and postmortem fracturing most likely due to the manner in which it was handled. Hardware was facetted to the skull to reattach the skull cap, in addition to the mandible having springs attached for the anatomical placement of the cranium.

**Dental Inventory, Lesions, Wear, Anomalies**

The dental remains of Individual 78 consists of 30 erupted mandibular and maxillary permanent teeth. No teeth were lost antemortem and there are no abscesses. There was post-mortem fracturing of the teeth; a sealant was applied to maintain the integrity of the teeth. There are five carious lesions: maxillary left second premolar, maxillary right second premolar, maxillary right second molar, mandibular right first premolar, and mandibular right first molar. The general wear of teeth is mild with wear scores ranging from one to three per tooth/cusp. However, the mandibular second premolars experienced serious wear receiving a score of 7. Three teeth were lost postmortem: maxillary right canine, maxillary right central incisor, and left maxillary 2$^{nd}$ premolar.

Thank you for the opportunity to examine this case.

**Signatures**

*Alexis Rizzolo*

Alexis Rizzolo, BS/BA
Graduate Student, Forensic Anthropology

*Elizabeth Valentine*

Elizabeth Valentines, BA
Graduate Student, Forensic Anthropology

# ATTACHMENT 5 - CASE FINDING - UMFC 78, CONTINUED

**References**

Bass W. Human Osteology: A Laboratory and Field Manual. 5th ed. Missouri Archaeological Society. 2005.

Buikstra JE, Ubelaker DH, editors. 1994. Standards: for Data Collection from Human Skeletal Remains. Arkansas Archeological Survey.

Jantz, R. L., & Ousley, S. D. 2005. FORDISC 2.0: personal computer forensic discriminant functions. Knoxville, TN: University of Tennessee.

Lovejoy, C.O., R.S. Meindl, R.P. Mensforth, and T.J. Barton, 1985. Multifactorial determination of skeletal age at death: A method and blind tests of its accuracy. Am. J. Phys, Anthrop. 68: 1-14.

Rhine, S. 1990. Non-metric skull racing. In: Gill, G., and Rhine, S. (eds) Skeletal Attribution of Race: Methods for Forensic Anthropology. Pp. 9-20. Albuquerque, New Mexico: Maxwell Museum of Anthropology, Anthropological Papers Number 4.

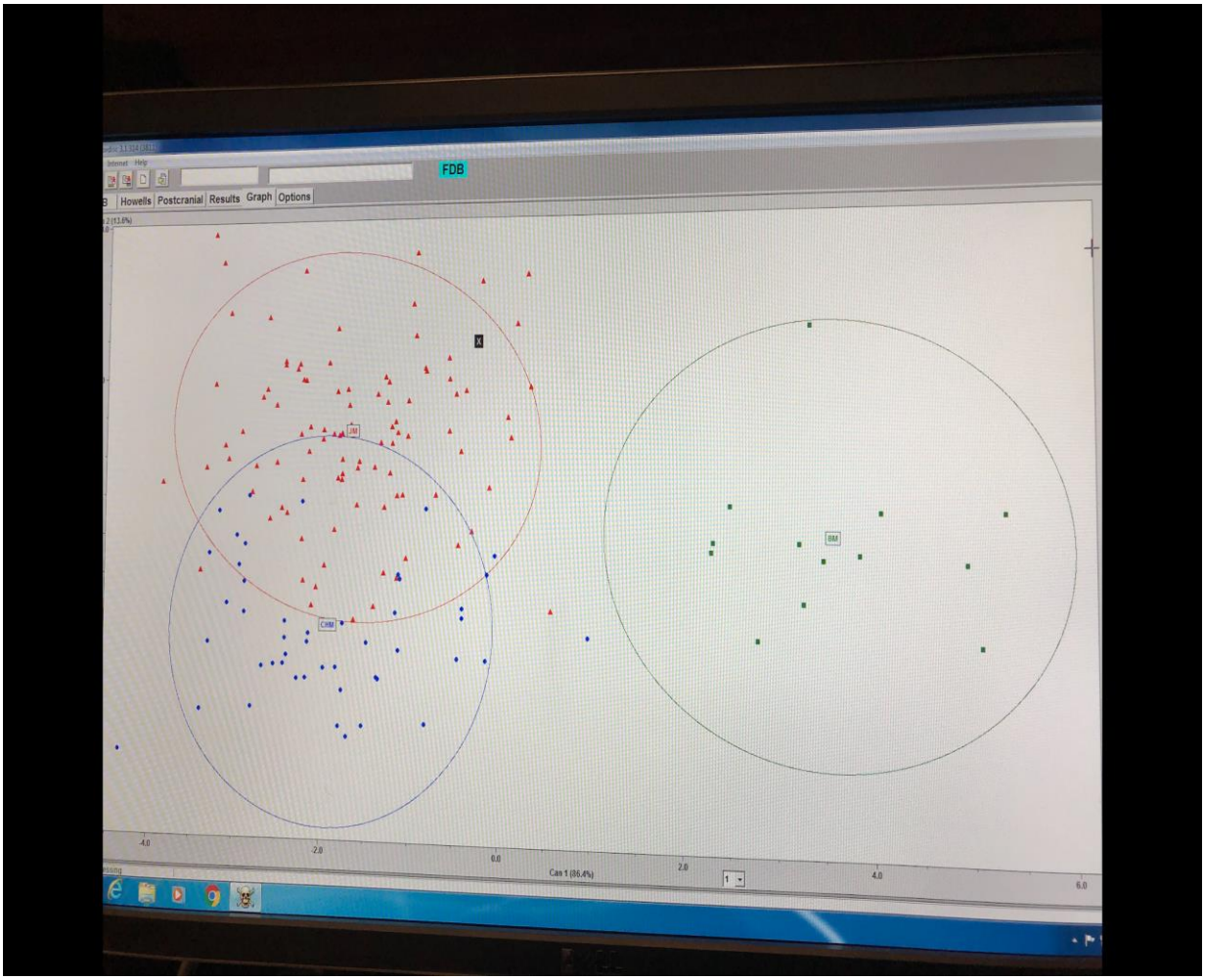
Scott, E.C. 1979. Dental Wear Scoring Technique. American Journal of Anthropology. 51:213-218.

Walker PL. Sexing skulls using discriminant function analysis of visually assessed traits. American Journal of Physical Anthropology 2008;136(1):39–50.

White, T., Folkens P., 2005. The Human Bone Manual. Elsevier Academic Press, Burlington.

# ATTACHMENT 5 - CASE FINDING - UMFC 78 – ADDENDUM

## ADDENDUM X-1

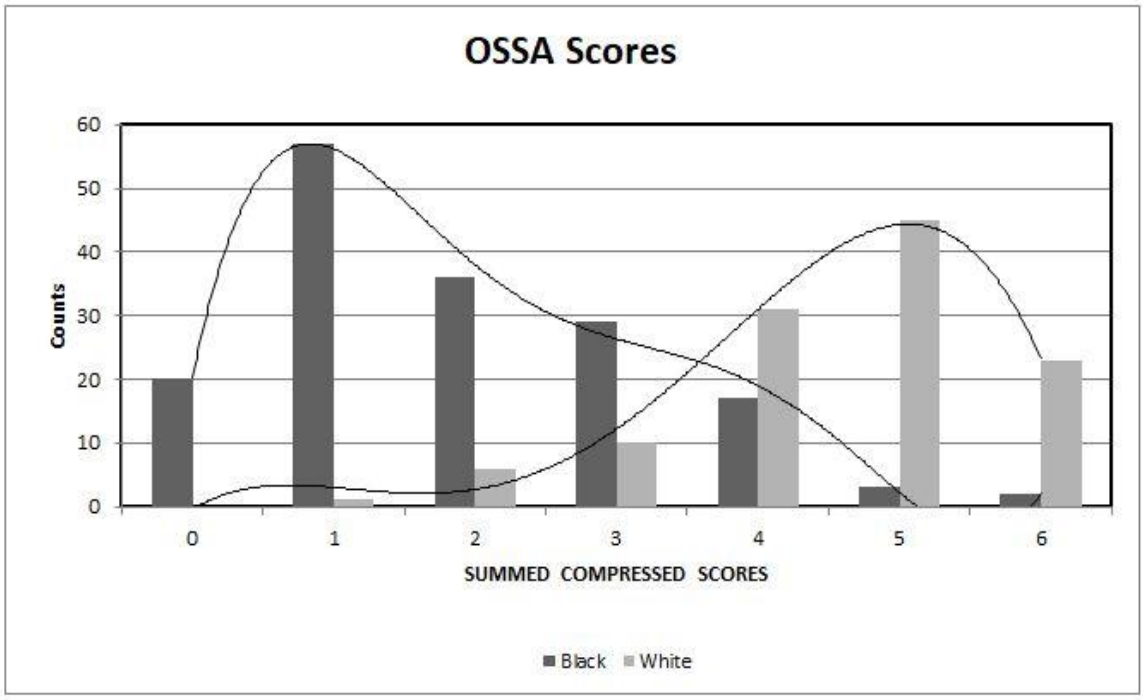


# ATTACHMENT 5 - CASE FINDING - UMFC 78 – ADDENDUM, CONT.

## ADDENDUM X-2

# ATTACHMENT 5 - CASE FINDING - UMFC 78 – ADDENDUM, CONT.

## ADDENDUM X-3




PREDICTED ANCESTRY

**Black**

# ATTACHMENT 6 - CASE FINDING - UMFC 85

UMFC 85
To: Dr. Skelton
From: Elizabeth Valentine, Nohely Gonzalez & Alexis Rizzolo
27 February 2019

**Chain of Custody**

On 13 February 2019, a box containing human remains to be analyzed was received by Elizabeth Valentine, Nohely Gonzalez and Alexis Rizzolo. Upon completion of analysis, the remains consisting of a nearly complete skeleton were returned to the University of Montana Forensic Collection (UMFC). No alterations were made during analysis of the remains. The remains were returned to the UMFC on 20 February 2019.

**Summary of Findings**

The individual is a probable male of possible Chinese or Indian ancestry with an estimated stature of 5 ft 1 in and older than 23 years of age at the time of death.

**Inventory and Condition**

The remains consisted of a nearly complete skeleton. The elements missing from the individual are as follows: the left clavicle, the nasals, the lacrimals, the mandibular left third molar, the left foot phalange, both zygomatics, two left ribs and a left distal hand phalanx. Furthermore, there is evidence of post-mortem damage due to the handling and care of the remains.

**Age**

Cranial suture closure scores could not be complied on the individual due to the condition of the crania. Determination of age was further difficult as paint and glue was applied to the epiphysis. However, it is estimated that the individual is a middle to old adult based on the extreme dental wear. All post cranial and cranial sutures are fused, and the third molars have erupted indicating that the individual is at least 23 years of age at the time of death.

# ATTACHMENT 6 - CASE FINDING - UMFC 85 - CONTINUED

**Sex**

The probable male estimation for this individual is based on morphological features of the crania. According to the Walker (2008) sex estimation, the nuchal crest, mastoid, orbital sockets, glabella and mental eminent non-discriminate measurements all estimate the individual to be a probable male (Addendum X-1).

**Ancestry**

The ancestry of the individual is determined to be of probable Chinese or Indian ancestry due to the individual being an anatomical specimen.

**Stature**

As ancestry needs to be determined in order to estimate stature using the Trotter (1970) method, stature estimates on the femur was conducted under all available ancestries in order to obtain a more holistic and non-biased stature estimate for this individual (Addendum X-2). Utilizing the Trotter Method stature equation for European-American males, the estimated stature for this individual is 5 ft 1 in, with an overall stature range of 5 ft 0 in to 5 ft 2 in. Alternatively, employing the Trotter Method's equation for African American males, the estimated stature for this individual is 5 ft 0 in, with an overall stature range of 4 ft 9 in to 5 ft 2
in. Lastly, using the same method for East Asian males, the estimated stature for the individual is 5 ft 2 in, with an overall stature range of 5 ft 0 in to 5 ft 3 in. Therefore, we conclude that the estimated stature of this individual is probably 5 ft 1 in.

**Trauma**

There is no distinguishable perimortem or antemortem trauma to the individual.

# ATTACHMENT 6 - CASE FINDING - UMFC 85 - CONTINUED

**Taphonomy**

There is postmortem damage to the remains due to the handling and care of the individual. Specifically, there is postmortem damage to the lateral incisors, both canines, the left first and second premolars and the right third molar.

**Pathology**

There is no distinguishable pathology to the individual.

Thank you for the opportunity to examine this case.

**Signatures**

*Elizabeth Valentine*
Elizabeth Valentine, BA
Graduate Student, Forensic Anthropology

*Nobely Gonzalez*
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# ATTACHMENT 6 - CASE FINDING - UMFC 85 - CONTINUED

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# ATTACHMENT 6 - CASE FINDING - UMFC 85 – ADDENDUM

**ADDENDUM X-1**

**Sex estimation from Walker (2008)**

Table 9. Logistic Regression Equations

**Scores:**

| nuchal | mastoid | orbit | glabella | mental |
|---|---|---|---|---|
| 4 | 3 | 3 | 3 | 5 |

**Sex estimations:**

| score | sex | prob Male | prob F | accuracy | vars |
|---|---|---|---|---|---|
| -4.302 | **MALE** | 0.99 | 0.01 | 88 / 86 | gl-ma-me |
| -1.647 | **MALE** | 0.84 | 0.16 | 85 / 83 | gl-ma |
| -4.628 | **MALE** | 0.99 | 0.01 | 87 / 82 | gl-me |
| -5.008 | **MALE** | 0.99 | 0.01 | 70 / 84 | me-ma |
| -6.253 | **MALE** | 1.00 | 0.00 | 78 /78 | or-me |
| -2.148 | **MALE** | 0.90 | 0.10 | 77 / 83 | nu-ma |

# ATTACHMENT 6 - CASE FINDING - UMFC 85 – ADDENDUM

**ADDENDUM X-2**

European American Male

2.38 x FEM + 61.41 ± 3.27 = 2.38 x 39.5 + 61.41 ± 3.27

= 155.42 ± 3.27

= 61.1 in

152.15 – 158.69 inches  Estimate = 5‘1“
59.9 – 62.4 inches  Range = 5‘0“- 5‘2“

African American Male

2.11 x FEM + 70.35 ± 3.94 = 2.11 x 39.5 + 70.35 ± 3.94

= 153. 70 ± 3.94

= 60.5 inches

149.75 – 157.63 inches  Estimate = 5‘0“
59.0 – 62.0 inches  Range = 4‘9“- 5‘2“

East Asian Male

2.15 x FEM + 72.57 ± 3.80 = 2.15 x 39.5 + 72.57 ± 3.80

= 157. 49 ± 3.80

= 62.0 inches

153.69 – 161.29 inches  Estimate = 5‘2“
60.5 – 63.5 inches  Range = 5‘0“- 5‘3“

# ANTY 510: SEMINAR IN HUMAN VARIATION AND EVOLUTION

Exploration of historical and current theories that form the foundation for biological and molecular anthropology were applied to research papers with a focus on migration through a genetic perspective of peoples in different regions. The individual reports were then combined to create the final paper below.

## ATTACHMENT 7 - MIGRATIONS THROUGH A GENETICS PERSPECTIVE

### CARIBBEAN

Migration of *Homo sapiens* into the Caribbean occurred recently in contrast with other regions of the world. Prehistoric migrations in the Caribbean are straightforward, with people coming from South America and populating some of the closer islands. The majority of historic migrations were populated by Africans brought over for slave labor. The prehistoric peopling of the Caribbean is composed of Native American origin. However, the historic peopling of the Caribbean region will be explored, utilizing disease, mtDNA, and Y-Chromosome analysis which is ultimately primarily composed of African American origin due to the slave trade.

There were two major and two lesser movements in the Caribbean. The first major movement was by people who used flake stones and inhabited Cuba and Hispaniola around 5000 BCE (Bellwood 2015). However, some anthropologists argue that the Caribbean migration occurred around 7kya, and the flake stones were directly associated to the chert quarrying industry in Belize (Harcourt 2016). The second major movement occurred around 2.5kya and the people came from the northern part of South America (Bellwood 2015). Again, there are many debates

that this second movement in fact did not involve the movement from South America, but from the Southern Lesser Antilles to Trinidad (Harcourt 2016, Lalueza-Fox et al. 2003).

The first lesser movement occurred around 5000 BCE and was based on the Arawak-speaking people who moved within the Caribbean and introduced pottery and agriculture throughout (Bellwood 2015). Additionally, a different stance for the first lesser migration is that these tools could have easily been exchanged from mainland Central America and as a result should not indicate any new movement into the Caribbean (Harcourt 2016). The second lesser movement of Caribbean peoples occurred with the movement of peoples into the lesser Antilles prior to the Europeans, and there was no timeframe associated with this. (Bellwood 2015).

The tools found in the Caribbean that date back to the prehistoric movement cannot be radio-carbon dated due to the abysmal environmental conditions preserving the chemical materials to be analyzed could lead to debate and should be backed by another source of evidence (Harcourt 2016). Another thought process for the second lesser migration is one that migrations continued after the movement of people from the northern area of South America (Harcourt 2016). Unfortunately, there is lack of genetic evidence when it comes to these early migrations. This is due to environmental conditions which affected the genetic material. The Caribbean region is very hot and humid, and surrounded by water, which results in the degradation of ancient DNA. Water and heat are prominent factors that break down the chemical bonds of DNA (Schanfield 2007). However, when genetic material is collected from modern humans that occupy the Caribbean region, it is possible to track back the lineages by looking at haplotypes of the individuals.

The original population of the Caribbean were called the Taino group. Skeletal remains were found in the Bahamas that lived around 500 years before European contact. Through the

sequencing of an individual's DNA, the researchers determined it was a female. After the sequencing of the mitogenome this individual had the haplotype B2, which is one of the founding lineages of the Americas (Schroeder et al. 2018).

Peopling of prehistoric Cuba gives insight to those who may have been the first to inhabit this land. DNA from ancient remains revealed that the mtDNA C and D haplogroups were the most prevalent among prehistoric human remains in Cuba (Lalueza-Fox et al. 2003). Genetic variation for the Caribbean region occurred within the region and results in little to no new diversity introduced into this area of the region (Lalueza-Fox et al. 2003). In addition, there is less heterogeneity when compared to South American populations (Lalueza-Fox et al. 2003). Overall, this information can be used to determine a possible country of origin for the prehistoric peopling of Cuba. A South American entrance into Cuba is more feasible than a Central or North American one because South America through to Cuba had a very short distance and as a result required less aquatic technology (Lalueza-Fox et al. 2003). Cuba was most likely populated by multiple waves of people from the Lower Orinoco Valley in South America during the Prehistoric migration (Mendizabal et al, 2008). The first group of individuals arriving to Cuba is around 5000 B.C. and the latest around 100 B.C. (Mendizabal et al. 2008).

Migrations occurring throughout the period of colonialism have been categorized into the following three groups: long-stay residence, short-stay, and return migration (Thomas-Hope 2013). Two of these groups can have an effect on genetic admixture in the societies in which they integrate to. For long-stay residence, the individuals that are new to the population can introduce genetic diversity within the population if they mate with someone who originally resided in that area.

## CARIBBEAN, CONTINUED

The Caribbean has an interesting composition when it comes to modern colonization. The population of these islands' immigrants were brought from Europe, Africa, and Asia over the Last 500 Years (Vilar et al. 2014). As a result, it is hard to determine genetic lineage due to the vast amount of admixture with the introduction of the Europeans, Native Americans, and Africans. Through mtDNA, researchers have found similarities with Native American, African, and West Eurasian haplogroups among its inhabitants (Torres et al. 2015; Vilar et al. 2014).

HIV-1B can be used to possibly track a migration route throughout the Caribbean. Through genetic tracking it is suggested that the spread of the disease originated within Puerto Rico (Pagan and Holguin 2013). This could also represent the historic migration of peoples within the Caribbean. The spread of this disease progressed from Puerto Rico to Antigua and continued to spread throughout the Caribbean, before ultimately reaching Dominica (Pagan and Hologuin 2013). This study found that the migration of peoples can be closely related to distance as people are more likely to travel through short-distance movements. These movements can be broken into two separate groups, the Greater Antilles, and the Lesser Antilles. The Greater Antilles movement follows an East to West diffusion, where the Lesser Antilles movement followed a North-South diffusion (Pagan and Hologuin 2013).

However, one study has found that when comparing ancestry proportions in the X chromosome versus the autosomes, Native American ancestry has a higher proportion throughout all of the Caribbean in the X chromosome (Moreno-Estrada et al. 2013). around 33% of Cuban mtDNA is of Native American origin (Mendizabal et al. 2008). The main Native American haplogroup is A2, which accounts for around 67% of the Native American mtDNA gene pool, with the other two haplogroups represented being D1 and C (Mendizabal et al. 2008). There were no Native American Y-Chromosome lineages in the samples analyzed (Mendizabal et al. 2008). This can be representative of the decreasing numbers of indigenous Cubans after the Spanish came and colonized the country. Puerto Rican individuals are comprised of mtDNA haplogroups A2 and C1, accounting for most of the lineages. In addition, there are distinct HVS1 and CR haplotypes (Vilar et al. 2014). Among the maternal lineage in the HVS1 haplotype, the haplogroup A2 was the most common, indicating that this haplogroup has Native American origins (Toro-Labrador et al. 2003, Vilar et al. 2014) Respectively, this haplotype and haplogroup combination is deemed the founder group and represents the prehistoric migration group that first entered the region from South America (Vilar et al. 2014). This group has undergone two nucleotide pair transitions at 16,083 and 16,236. As a result, this new haplogroup is called A2z (Vilar et. Al 0214). This group is unique to the Caribbean island peoples. The haplogroup A2z is only found in modern day Puerto Ricans and Cubans (Vilar et al. 2014). Looking into the historic peopling of Jamaica, it had many different regions of the world contribute to its genetic diversity. Before the colonization by Spanish peoples in 1509 AD, there were few indigenous peoples living on the island (Deason et al. 2012). Peopling of both Trinidad and Saint Vincent are similar in some regards, yet distinct in others. Trinidadian and Saint Vincent populations both are primarily composed of the A2 and C1

haplogroups, which are indicative of the founding Native American mitochondrial haplogroups (Torres et al. 2015). These groups have different percentages of the two haplogroups represented in the total mtDNA's of each population. The Trinidadian population has haplogroup A2 representing around 42% and C1 representing 17% of the total mtDNA composition of this group. Whereas A2 comprises around 16% and C1 represents 21% of the mtDNA composition in Saint Vincent (Torres et al. 2015). Determining which haplogroup was the oldest is the next step in determining which group came before the other. The A2 haplotypes are older dating to 8489ybp, whereas C1 is dated to 2452ybp (Torres et al. 2015). In addition to these Native American haplogroups, these populations also exhibited maternal lineages from other regions as well. No Native American haplogroups were observed in the Haitian group sample (Wilson et al. 2012). In Aruba Haplogroups A, B, C, D, and X represent Native American origin (Toro-Labrador et al. 2003). The Native American origins are representative of the prehistoric migrations and indicate that individuals travelled through South America before coming to the Caribbean region.

## EUROPEAN ORIGINS

When looking at admixture within the populations of the Caribbean, the best model for the populations suggest that the time estimates of initial contact between Native Americans and Europeans is older than what was previously thought by anthropologists (Moreno-Estrada 2013). Some of the time estimates can occur as late as seventeen generations ago to as recently as 16 generations or approximately five hundred years ago. Cuba's initial contact is estimated to be about 17 generations ago, however Puerto Rico, the Dominican Republic and Haiti, all have estimates for the first initial contact between Native Americans and Europeans of approximately 16 generations ago.

Cuba and Puerto Rico comprise a part of the Greater Antilles. Based on their proximity, they were some of the first islands to have been colonized by the Europeans. More specifically, they were colonized by Spain (Harcourt 2016). The historic migration of Cuba has an interesting history. When the Spanish arrived, the native population was already in decline, due to disease (Mendizabal et al. 2008). The mtDNA of Cubans has around 22% of the mtDNA sequences of West Eurasian origins, more specifically Europe and the Middle East (Mendizabal et al. 2008). The haplogroup of the Cuban mtDNA is H, which represents European origins (Mendizabal et al. 2008). Looking at the Y-Chromosome lineages, it has a reverse effect from mtDNA. In the Y-Chromosome haplogroups, the majority of the results can be traced back to the west Eurasian gene pool to about 79% (Mendizabal et al. 2008). This could be indicative that more European males were impregnating African females than vice versa, which is a high occurrence throughout the slave era.

The genetic composition of Puerto Rico is very diverse. Puerto Rico had multiple countries lay claim to colonies within their country as well as others in the Caribbean region. Britain, France,

Holland, and Spain all tried to lay claim to this region (Vilar et al. 2014). These countries while mating with the indigenous peoples created the following mutations off of the founder group haplotype, T17896 and A3856G. The T haplogroup is indicative of Caucasian origin (Toro-Labrador et al. 2003). This represents the Europeans genetic contribution within the Puerto Rican region historically. This mutation resulted in the new formation of the HVS2 haplotype known as the haplotype indicative of modern populations (Vilar et al. 2014). This new formation, in addition to the A2z, has only been found in modern day populations. Of the Puerto Rican paternal lineages, around 84% of the individuals were of European or West Eurasian origin (Vilar et al. 2014). The majority of the individuals belong to the haplogroup R1b, which is most commonly found among European populations the second most common haplogroup is the E1b1b. The E1b1b haplogroup is also frequently found among European populations, more specifically the Mediterranean portion of the European region, as well as North Africa. This can be indicative of the Europeans coming to Puerto Rico and colonizing it while bringing along African slaves to mine resources that were only found in the islands (Deason et al. 2012, Torres et al. 2012, Toro-Labrador et al. 2003, Wilson et al. 2012). Around the early 17$^{th}$ century, the English seized Puerto Rico from the Spanish and introduced a large number of African slaves into this region (Deason et al. 2012).

While the Greater Antilles represents the spread of the Prehistoric Native Americans as they moved across the lands, the north to south Lesser Antilles movement shows Europeans moving throughout all the countries in search of precious resources. Aruba, which is located in the Lesser Antilles has haplogroups E, F, and G present. These haplotypes represent Asian origins (Toro-Labrador et al. 2003). In addition, haplogroups H, K, I, J, T, U, V, W, and X represent

## EUROPEAN ORIGINS, CONTINUED

European origins (Toro-Labrador et al. 2003). African and Caucasian haplogroups are indicative of the colonization of Aruba by European settlers and their slaves (Toro-Labrador et al. 2003).

## AFRICAN ORIGINS

When looking at individual countries, for example, Cuba has a significantly higher proportion of African ancestry on the X chromosome (Moreno-Estrada et al. 2013). Along with the Spanish's arrival in Cuba they brought along with them African slave trade (Mendizabal et al. 2008). After analyzing the mtDNA of modern-day Cubans, the mean pairwise differences are high, but the weakly interacting massive par value is low (Mendizabal et al. 2008). This indicates that the sample is composed of distantly related haplogroups with low to moderate internal diversity (Mendizabal et al. 2008). Around 45% of the mtDNA sequences in Cubans are of African origin (Mendizabal et al. 2008).

The haplotypes associated with the African lineages are primarily composed of the L haplogroup, with a small amount of the U6 haplogroup (Mendizabal et al. 2008). The L haplogroup is associated with Sub-Sharan Africa, whereas the U6 haplogroup is associated with Northern Africa (Deason et al. 2012, Mendizabal et al. 2008, Torres et al. 2015, Toro-Labrador et al. 2003).

The breakdown of mtDNA haplogroups reveal that the Spanish and African slaves had a huge impact in genetic diversity. Looking at the Y-Chromosome lineages, it has a reverse effect from mtDNA. In the Y-Chromosome haplogroups the African fraction accounts for around 20% (Mendizabal et al. 2008). Looking into modern Jamaicans mtDNA, the peopling of this region can be estimated as a majority of the haplogroups studied from the group of modern Jamaicans are allocated to the L haplogroup, which is most closely associated with Sub-Saharan Africa (Deason et al. 2012). The L2a1 profile has been found nine times in Jamaica, which suggests that there were discrete genetic drift episodes experienced on this island (Deason et al. 2012). This occurred through mutations within the L haplotype and introduced new diversity into this region. Performing an admixture analysis of the L haplogroup, a specific region of Sub-Saharan Africa

was identified as being the parental population. This population came from the Gold Coast and resulted in being the most consistently prolific group to populate Jamaica throughout the slave era (Deason et al. 2012).

Both Saint Vincent and Trinidad had maternal lineages from Africa, belonging to haplogroups L0, L1, L2, and L3 (Torres et al. 2015). Similar to the difference in composition, Trinidad, and Saint Vincent both have different compositions of each haplogroup for the African lineages. The African influence can be seen in both lineages in the Trinidad and Saint Vincent population and are due to the number of African slaves introduced into the countries (Torres et al. 2015). Trinidadians most common haplogroups are the haplotype L, L2 and L3, whereas for Saint Vincent the most common haplotype is L2. In addition to the African haplotype, there are also South Asian haplotypes seen within the Trinidadian population. The haplogroup M33a belongs to the Trinidadian population, and it is a lineage commonly seen in Northeastern India (Torres et al. 2015). As a result, this shows that the Trinidadians exhibited higher gene diversity than those from Saint Vincent. Saint Vincent and Trinidad have similar genetic diversity to Puerto Ricans and comparative populations; however, these groups all showed signs of lower diversity compared to other populations within the Lesser Antilles, with the exception of Dominica (Torres et al. 2015).

Looking at the Y-Chromosome diversity in Saint Vincent and Trinidad helps one to gain a fuller picture of the peopling of this area of the Caribbean region. African, European, and Native American haplogroups were present in the Y-chromosome (Torres et al. 2015). This is similar to the mitochondrial DNA haplotypes. More than 80 percent of the haplotypes of the Y-Chromosome were non-indigenous to the Americas (Torres et al. 2015). When looking at Saint Vincent populations and Trinidadian populations the composition of lineages varied. Saint Vincent Y-

Chromosome lineages were comprised of half-African and half-European, whereas the lineage for Trinidadians showed a higher frequency, about 80 percent, for African than European (Torres et al. 2015). This is due to the Trinidadian population being composed of more Africans than Europeans, as the area was most likely settled by the Africans rather than the Europeans.

Analyzing the mtDNA of two rural communities in Haiti, researchers were able to gain a better insight to the population history of this country. After analyzing the mtDNA, the majority of the results belonged to 32 different mtDNA derived haplogroups based on HSV-1 polymorphism motifs (Wilson et al. 2012). Haplogroups L2a1, L11, and L2c2 were the most frequent, and predominantly originate in Sub-Saharan Africa (Wilson et al. 2012). These haplogroups are a result of the high number of slaves brought into the region (Deason et al. 2012, Torres et al. 2015, Wilson et al. 2012). The Haitian group can be split into Northern and Southern subgroups, and as a result there is little haplotype sharing between these two subgroups (Wilson et al. 2012). Overall, 13 haplogroups are Pan-African and two are European, which suggests that there was a European female founder of the modern-day Haitian. Overall, this study concluded that genetic differentiation exists between the maternal lineages from Haiti are in fact in line with historical recounting (Wilson et al. 2012).

Examining the mtDNA of those living in Aruba shows the diversity of the Caribbean peopling of this region. Haplogroups, A, B, F, H K, U, V, W, X, C, D, E, G, I, J, K, and L were all present within the mtDNA (Toro-Labrador et al. 2003). Haplogroups L and U represent African origins (Toro-Labrador et al. 2003).

After examining the prehistoric and historic migration of peoples within the Caribbean there are few debates. The main debate for the prehistoric migration is the actual dates that people

arrived in the Caribbean. Date estimations for the time that the Caribbean was first inhabited ranges anywhere from 8,000 - 2,000 years ago. However, for historic migration, the debates are centered around who modern Caribbean peoples are descendants of and how they migrated within the region. These debates will never truly be resolved, due to the environmental conditions that account for the lack of preserving ancient DNA.

Historic migrations cannot be attributed to one specific movement like the prehistoric movement of the Caribbean region. This results in creating more migration patterns, that cannot be easily traced. Little data has been collected on every island within the Caribbean, but as more data is collected these debates are likely to intensify.

Many different countries in this region have vastly different mtDNA makeups. Each region has its own unique circumstances. Due to the lack of ability to travel to the Caribbean by foot, boats were used to transport individuals to many of the different regions that were significantly farther away. Without the use of these watercrafts, these foreign regions of the Caribbean would not have otherwise had a way to interact with peoples of the Caribbean. They continued to return to these islands for resources which were not available in their own regions. In order to extract these resources, they used slaves brought from Africa. These slaves ended up remaining in the areas and contributed to their historic genetic makeup. Due to the lack of documentation of where the slaves came from specifically within Africa, in addition to the lack of information for every other nation that came to these countries, results in a large amount of debate over who contributed most to the genetic diversity of each country.

Overall, the pre-historic migration of peoples to the Caribbean region occurred from South America. The historic migration of peoples within the Caribbean is more complex. This is due to

the variety of regions conquering and colonizing certain islands, in addition to the influx of Africans brought into the region for slave labor. Each country has their own unique haplogroup compositions, which makes the Caribbean a very diverse region.

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# ANTY 418: EVOLUTION AND GENETIC VARIATION IN HUMAN POPULATIONS

I examined and explained human variation from a biological perspective, including how variation arises among humans, and how studies of human variation influence society both past and present. I chose to do a 1 hour and 20-minute lecture presentation to my peers which included genetic, phenotypic, sex, and behavioral differences among humans, as well as the theory, methods, and ethics involved in scientific studies of humans.

# ANTY 513: SEMINAR IN BIOARCHAEOLOGY AND SKELETAL BIOLOGY

I took an in depth look into the world of Bioarchaeology including its future. I selected a topic to pursue for the entire semester and wrote a proposal, presented research, conducted analyses, and discussed my findings with the class. My final paper begins on the following page.

# ATTACHMENT 8 – FINAL PAPER

Exploring the current methods for biological sex determination there are two widely used methods: visual assessment, which is a qualitative form, and the metric method, FORDISC, which is a quantitative method. Both methods are used when it comes to determining biological sex. This project is looking to see which method has the higher accuracy rate. Having a high accuracy rate is imperative to ensure that the results for biological sex determination whether visual or metric is accurate in the identification of remains.

The first research question I will address is: What is the error rate utilizing the known sex of the teaching collection between both visual and metric methods? A good error rate would be less than 15%, based on the average of error rates found by Garvin (2012), Stewart (1979), and Walker (2008). The second question this research aims to answer is what is the percent difference between the raw numbers of males and females through the sex determination that FORDISC assigns and the sex that visual assessment provides from the University of Montana Forensic Collection (UMFC) cases? If the error rates for the data collected agree with the accuracy rates of Stewart (1979) and Garvin (2012), then the error rate will have no effect on the applicability of the method to accurately determine biological sex. These research questions allow for a complete understanding of the implications of utilizing each method and will allow current and future researchers to become aware of their pitfalls.

This research will directly impact how we use and implement different sex determination methods. For example, if we know that the visual method may have a lower accuracy for certain teaching collection skulls maybe we can find an underlying cause as to why this method may not

work. Maybe there is a difference based on ancestry as to why the visual assessment may work better for some populations versus others then we may be able to adjust when we utilize the visual assessment method. Subsequently, there is the possibility that the metric method may reveal some inaccuracies, and if that is the case, we can consider the possibility that more cranial measurements are needed to increase accuracy. This would result in the addition of new known-sex cases to the forensic database within the FORDISC software. Additions to the database may provide a better picture for sex determinations or they may illuminate the need for a new system to be developed in order to generate a more accurate computational sex assessment determination.

These direct impacts will have broader implications that will affect the larger scientific community as well as law enforcement by allowing them to understand the limitations of sex determination methods within forensic anthropology, in addition to allowing the scientific community to find or create a better method of sex determination. When creating and utilizing the best method, it may allow the criminal justice system to have more confidence in identifying missing or unidentified remains, which will provide closure to family members who have no clue what has happened to their missing loved ones. Known error rates are also useful to increase accuracy so that sex-based differences can be assessed in Bioarchaeology.

## LITERATURE REVIEW

Currently, the primary methods utilized for cranium sex estimations are qualitative (non-metric) and quantitative (metric). Craniums vary in forms and dimensions and are heterogeneous based on populations. There are five commonly employed non-metric traits of skull morphology utilized for determining the sex of craniums, which are the nuchal crest, mastoid process,

supraorbital margin, glabella, and mental eminence. Females have less prominent traits and are considered to be more gracile, whereas male traits are more defined with a protuberance of the bone and considered to be robust (White 2011).

Visually scoring the non-metric features introduces a degree of subjectivity based on the observer. Subjectivity can come in various forms, such as the difference of final sex determinations between observers and interobserver, which are not ideal (Walker 2008, Walrath et al. 2004, Williams and Roger 2006). Individual examiners can look at the same set of remains, and they each can have drastically different final determinations. In forensic anthropology, obtaining an accurate sex estimation is based heavily upon the reliability and precision of the methods (Langley et al. 2017). One final form of subjectivity occurs when the observer gives a trait a score of 2-4. Buikstra and Ubelaker (1994) fail to state what deems a ranking of 2-4 for any of the traits, which means it has a high degree of variability based on the lack of information to accurately observe the differences between a score of two, three, or four.

To obtain the rate of accuracy this research is utilizing three observers determine sex on known skeletal collections. Observers often misidentify or fail to identify the sex of skeletal remains collected. Overall, accuracy rates for sexing skulls range from a percentage of 70 to the high 80s, but most of the higher accuracy rates can be attributed to the experience of the anthropologist conducting the analysis (Stewart 1979). When determining sex, the baseline accuracy rate is 50%, because there is always a 50/50 chance of accurately determining the sex by just guessing between males and females. When determining male, female, or indeterminate then the baseline accuracy rate decreases to 33.3%.

# ATTACHMENT 8 – FINAL PAPER, CONTINUED

## LITERATURE REVIEW, CONTINUED

Metric analysis is multivariate analyses of cranial metrics, which produces correct classification rates between 90-90.3% (Spradley and Jantz 2011). Utilizing multivariate analysis, cranial dimensions will capture some shape changes in the skull (Garvin 2012). However, characteristics such as ancestry can also influence the shapes that are expressed and subsequently measured by the metric methods. As a result, many multivariate analyses revert to utilizing the Buikstra and Ubelaker's five standard traits. When using the standard five traits for determining sex, based on the shape of craniums, the multivariate analysis rate decreases to an 87.4% accuracy (Garvin 2012). This accuracy rate shows there is no improvement in the accuracy of nonmetric analysis when sexing craniums. When visually assessing craniums and determining sex, it can be a clear guessing game due to the inability to provide written differentiation between scores of 2-4.

## MATERIALS AND METHODS

This dataset is comprised of 44 craniums which is split between both an unknown and known collection. 17 craniums are from the teaching collection and 27 are form an unknown collection. A known collection is a collection that has biological sex known for each of the craniums. The known collection is a teaching collection located at the University of Montana. The teaching collection consists of casts with tags associated to them indicating their demographic information. The unknown collection is a collection where no information is provided for the craniums. There are some site records, and autopsy reports but these individuals are unidentified, therefore they are unknown. There are five commonly employed traits of skull morphology utilized for determining the sex of craniums. These features include the nuchal crest, mastoid process, supraorbital margin,

# ATTACHMENT 8 – FINAL PAPER, CONTINUED

## MATERIALS AND METHODS, CONTINUED

glabella and mental eminence, shown in Figure 1. Females have less prominent traits and are considered to be more gracile, whereas male traits are more defined with a protuberance of the bone and considered to be robust (White 2011). According to the *Standards for Data Collection from Human Skeletal Remains* (Buikstra and Ubelaker 1994) to sex a cranium a composite score is utilized which is derived from the five aspects listed above. Each one is given a ranking scale for the following:

- 0 - insufficient skeletal material
- 1 - female
- 2 - most likely female
- 3 - indeterminate
- 4 - most likely male
- 5 – male

# ATTACHMENT 8 – FINAL PAPER, CONTINUED

## MATERIALS AND METHODS, CONTINUED

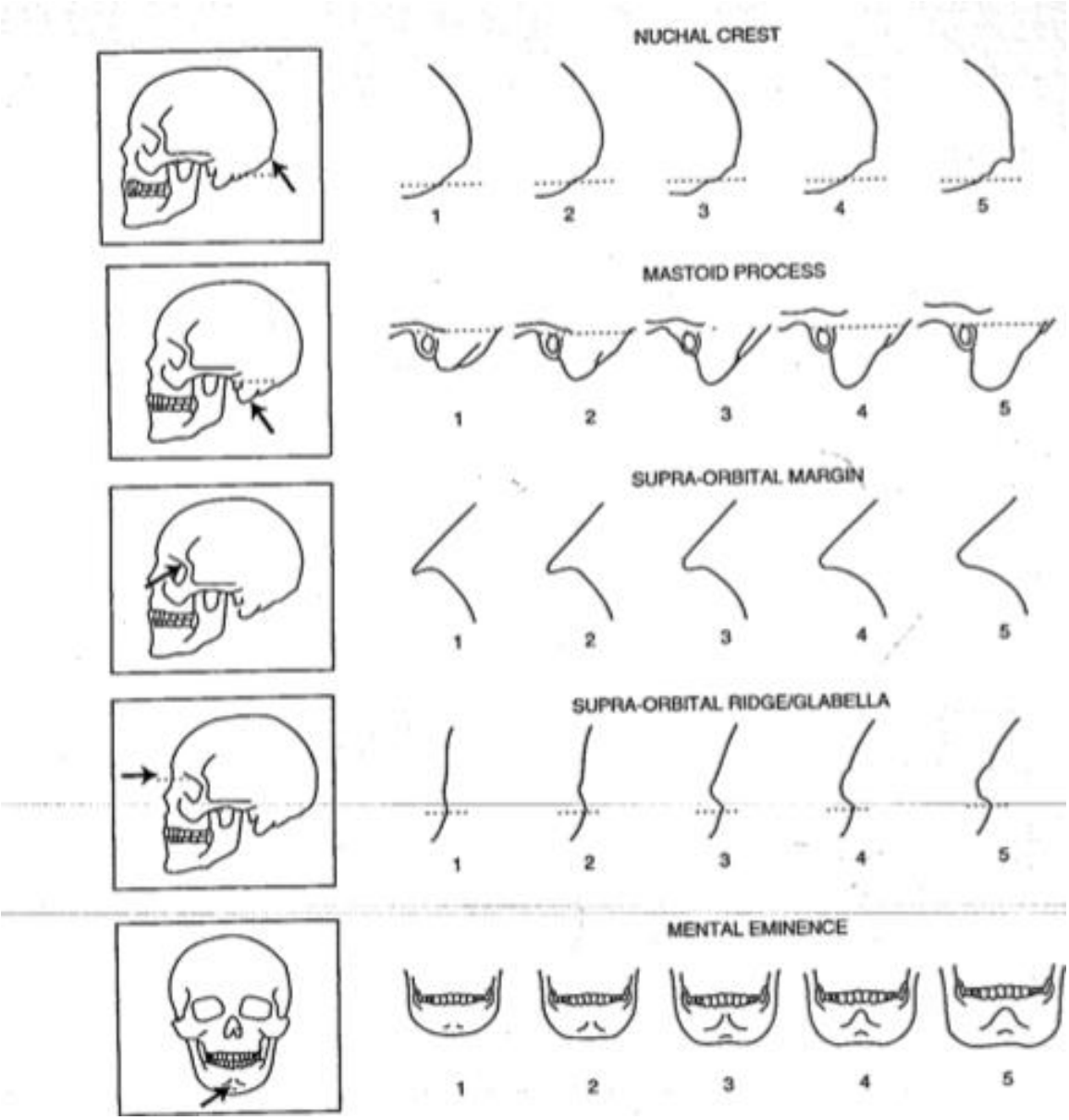


Figure 1: Non-metric cranial traits (Buikstra and Ubelaker 1994, pg 74-78) Positioning the cranium properly to determine the rank can be difficult and should be followed exactly as described by Buikstra and Ubelaker to ensure that the proper traits are being observed. To properly obtain the most accurate score, the skull must be positioned a few inches above the trait being observed. In addition to the positioning, the distance should be around an arm's length away from the observer and adjusted for each of the traits in Figure 1, Image 1 - 3.

# ATTACHMENT 8 – FINAL PAPER, CONTINUED

## MATERIALS AND METHODS, CONTINUED

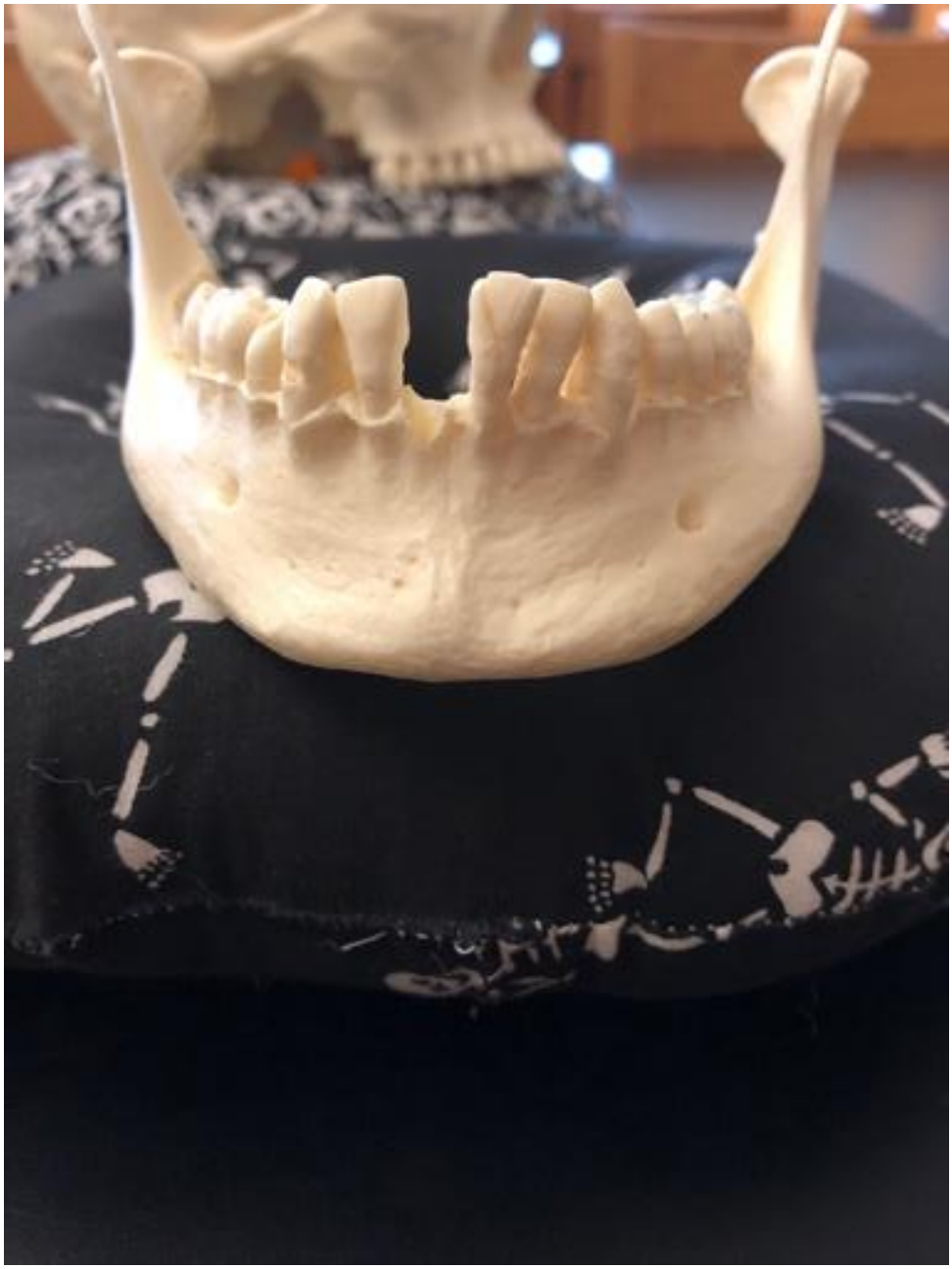

Image 1: Positioning of Mandible at arm's length

# ATTACHMENT 8 – FINAL PAPER, CONTINUED

## MATERIALS AND METHODS, CONTINUED

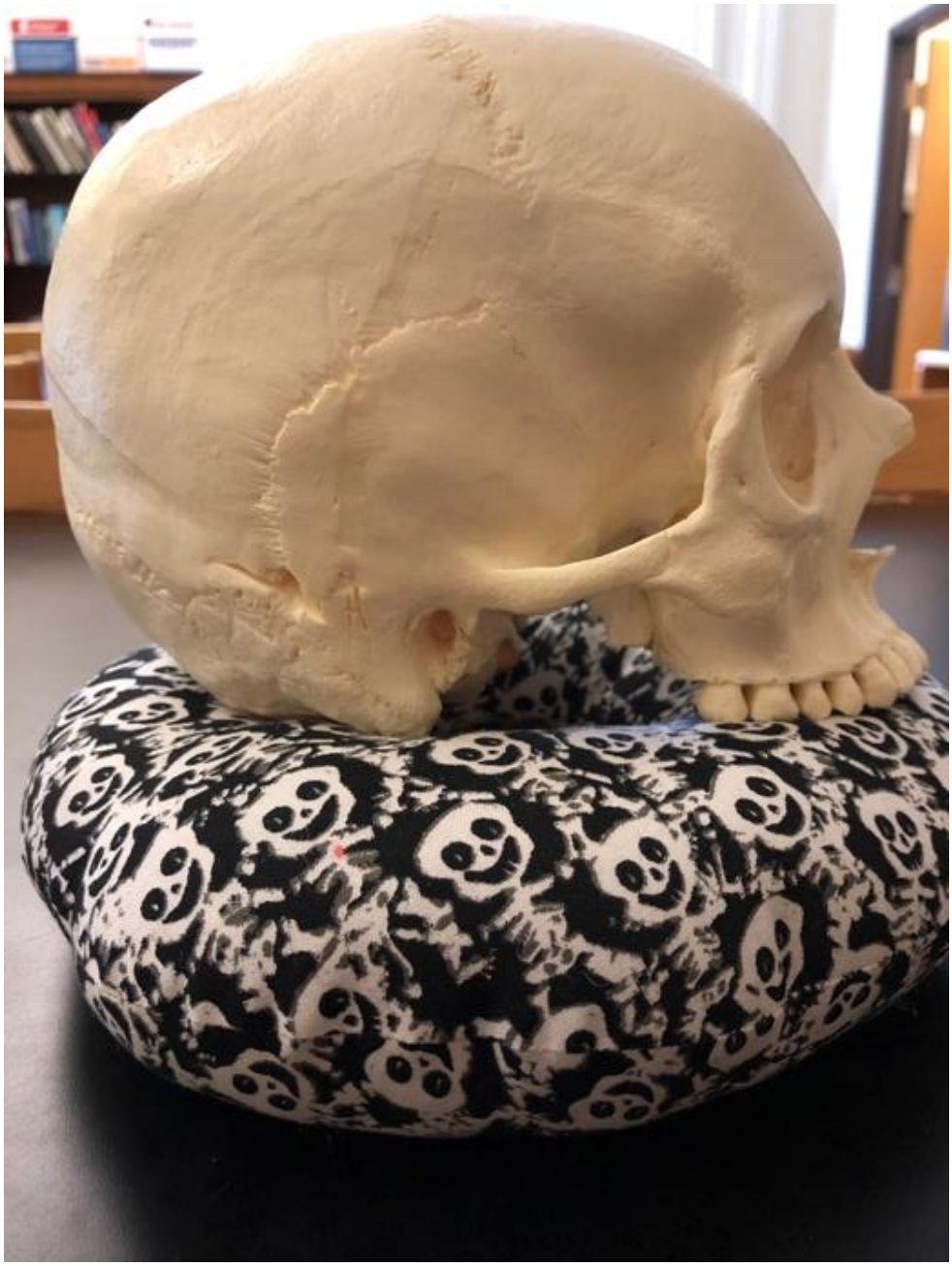

Image 2: Positioning of Glabella and Mastoid Process at arm's length.

# ATTACHMENT 8 – FINAL PAPER, CONTINUED

## MATERIALS AND METHODS, CONTINUED

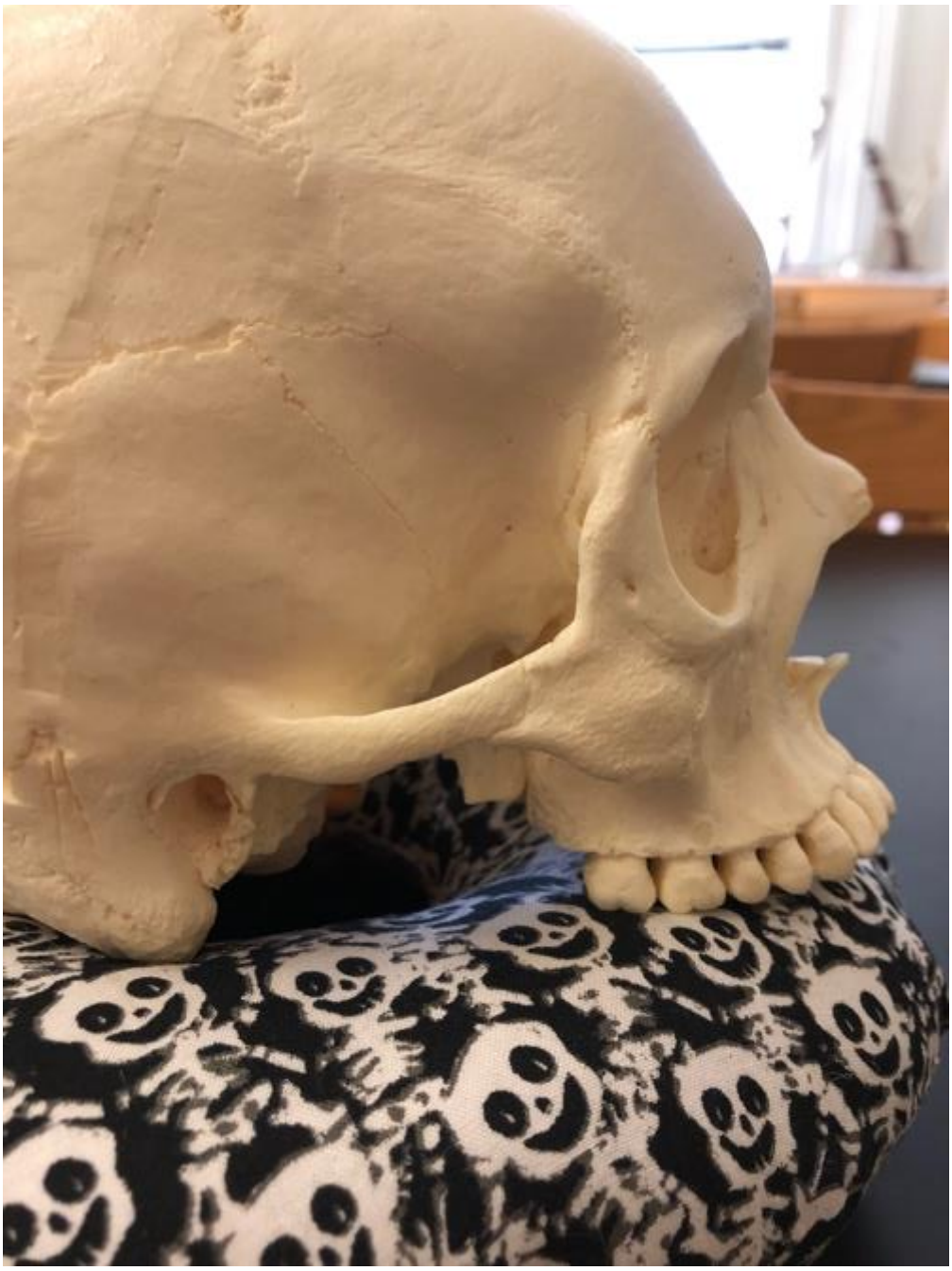

Image 3: Positioning of Nuchal Crest and Mastoid Process at arm's length

# ATTACHMENT 8 – FINAL PAPER, CONTINUED

## MATERIALS AND METHODS, CONTINUED

Metric Analysis occurs through following the measurements listed within *Standards for Data Collection from Human Skeletal Remain,* located within Chapter Seven, and are measurements numbers 1-34. Once the measurements are collected, they are then input into FORDISC 3.1 (Jantz and Ousley 2005). FORDISC then determines a biological sex to be either male or female, while providing a confidence interval. FORDISC utilizes a discriminant function analysis, as described in the manual this is a grouping of statistical procedures. This grouping allows for both the separation and classification of unknown's individuals through measurements (Jantz and Ousley, 2017).

The most common statistical procedure utilized within the discriminant function analysis is the linear discriminant function (Jantz and Ousley, 2017). This procedure allows for the differentiation of inter-group differences through a linear combination of measurements. Other statistical procedures utilized within the Discriminant Function Analysis grouping is the canonical variates analysis. This allows for classification among multiple axes' or dimensions (Jantz and Ousley, 2017).

For this research, the following equations were used to calculate error rates, accuracy rates, and average error rates between observers:

- $\frac{Number\ of\ Misidentified\ Individuals}{Number\ of\ Total\ Individuals} \times 100 = Accuracy\ Rate$
- $100 - Accuracy\ Rate = Error\ Rate$
- $\frac{(Group\ 1\ Error\ Rate)+(Group\ 2\ Error\ Rate)+\cdots}{Number\ of\ Groups} = Average\ Error\ Rate$

# ATTACHMENT 8 – FINAL PAPER, CONTINUED

## MATERIALS AND METHODS, CONTINUED

The Accuracy rate will inform the percentage for which the method will accurately get the biological sex correctly identified. This will allow researchers to understand out of 100 individuals analyzed how many will be properly identified. Conversely, the error rate informs the researcher how many will be misidentified. So out of every 100 individuals the percentage corresponds to how many will be misidentified. Finally, the average error rate will inform the researcher utilizing the method the overall error rate between multiple observers employed throughout this study. This will inform future researcher that there is a variance between observers, and they will be able to understand that the error rate can change when utilizing multiple observers. Again, it will tell on average out of 100 individuals how many will be misidentified.

## RESULTS

Based on the data collected a known Percentage of Error for the visual assessment was calculated, through the use of the error rate formula, at 23.5%, based on utilizing the known sex and comparing it to the sex determined by each observer (Table 1). Also, a known Percentage of Error for the metric assessment is 82.4% based on utilizing the known sex and comparing it to the sex determined by FORDISC 3.1 (Table 1). When looking at the UMFC collection at the University of Montana, there is a 68.2% difference between metric and visual assessment sex determinations. With these known error rates, it can then be assumed that out of the 44 UMFC individuals analyzed, 36 individuals will be incorrectly classified for sex utilizing the metric assessment through FORDISC as well as, 10 out of the 44 individuals sex determination utilizing

## RESULTS, CONTINUED

visual assessment would be incorrectly identified. This is due to the fact that there is no known collection to base the accuracies off of for this unknown collection, therefore a known set was created through using the visual assessment. The visual assessment was chosen over the metric assessment, because in the known collection the visual assessment had the higher accuracy percentage compared to the metric assessment.

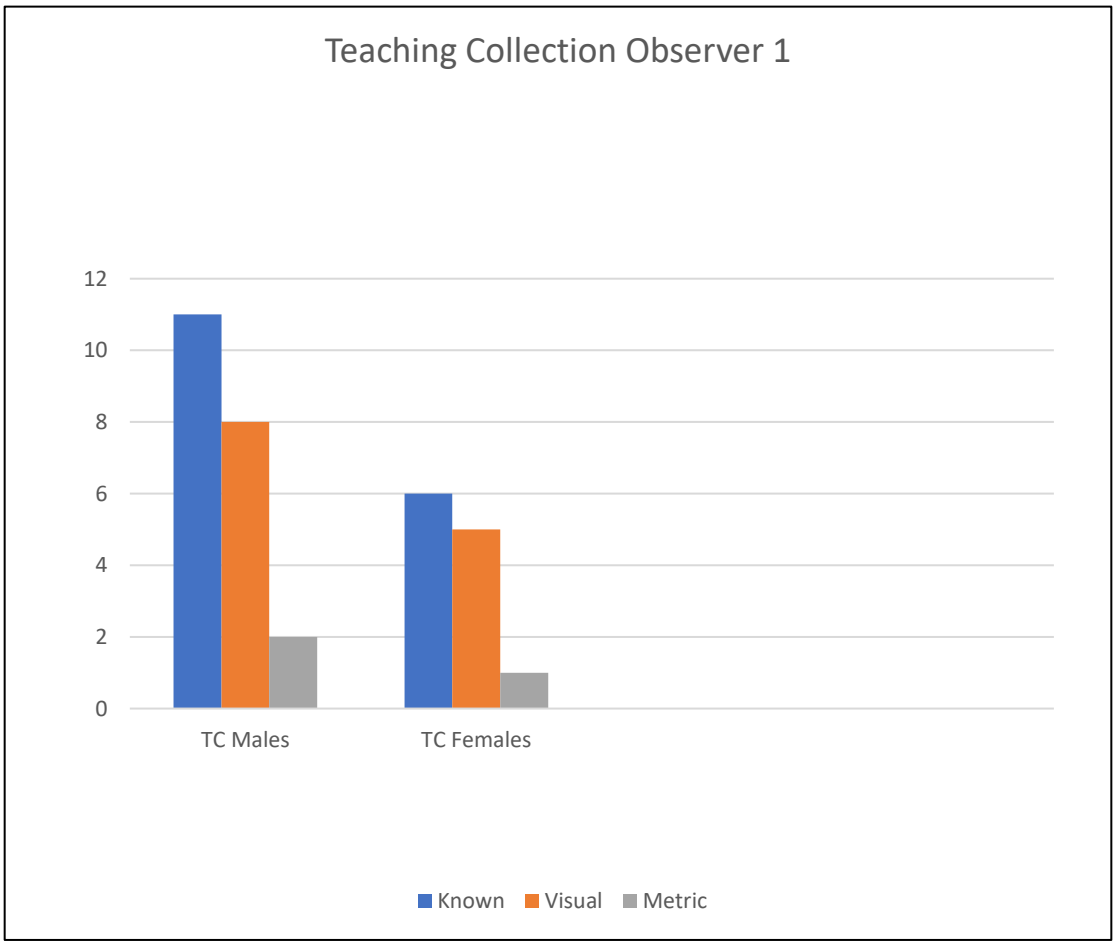


Table 1: Identifications of Observer 1's Visual and Metric Assessment

# ATTACHMENT 8 – FINAL PAPER, CONTINUED

## RESULTS, CONTINUED

Table 2 shows how the subjectivity of the visual scoring system can create issues with determining biological sex. Six out of 11 males (54.5%) were successfully identified and 4 out of the 6 females (66.6%) were successfully identified. The error rate for the visual assessment completed by Observer 2 is 34.4%, which results in an accuracy rate of 65.6% The Percent Error Rate utilizing metric assessment for Observer 2 was 87.5%. Between Observer 1 and 2 there was only a 5.1% difference between the metric assessment results which, when both error rates are averaged, brings the overall percent error rate for the metric assessment method to 85%, which results in an accuracy rate of 15%.

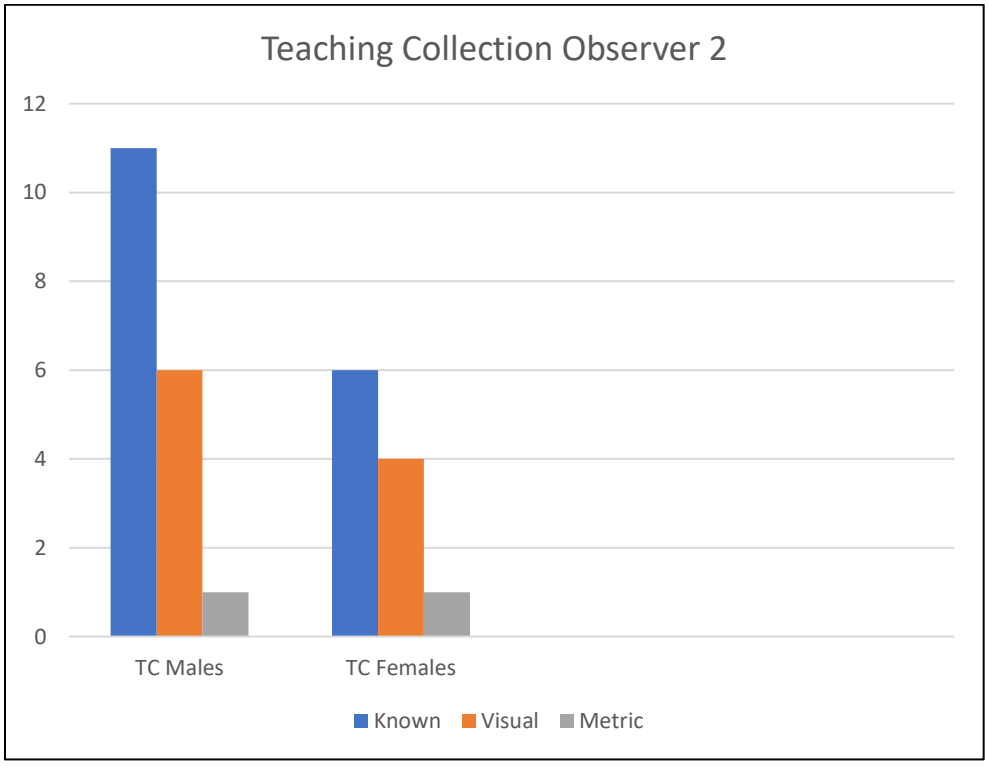


Table 2: Identifications of Observer 2's Visual and Metric Assessment

# ATTACHMENT 8 – FINAL PAPER, CONTINUED

## RESULTS, CONTINUED

Table 3 shows the number of identified males and females for Observer 3. The error rate Observer 3 had for the visual method was 33.3%. This observer had an accuracy rate of 69.7%. Between Observers 1-3, there is a difference of 10.9% in the error rate. As a result, the average percent error rate of visual assessment is 30.4%. Which in turn generates an accuracy rate of 69.6% for the visual assessment method.

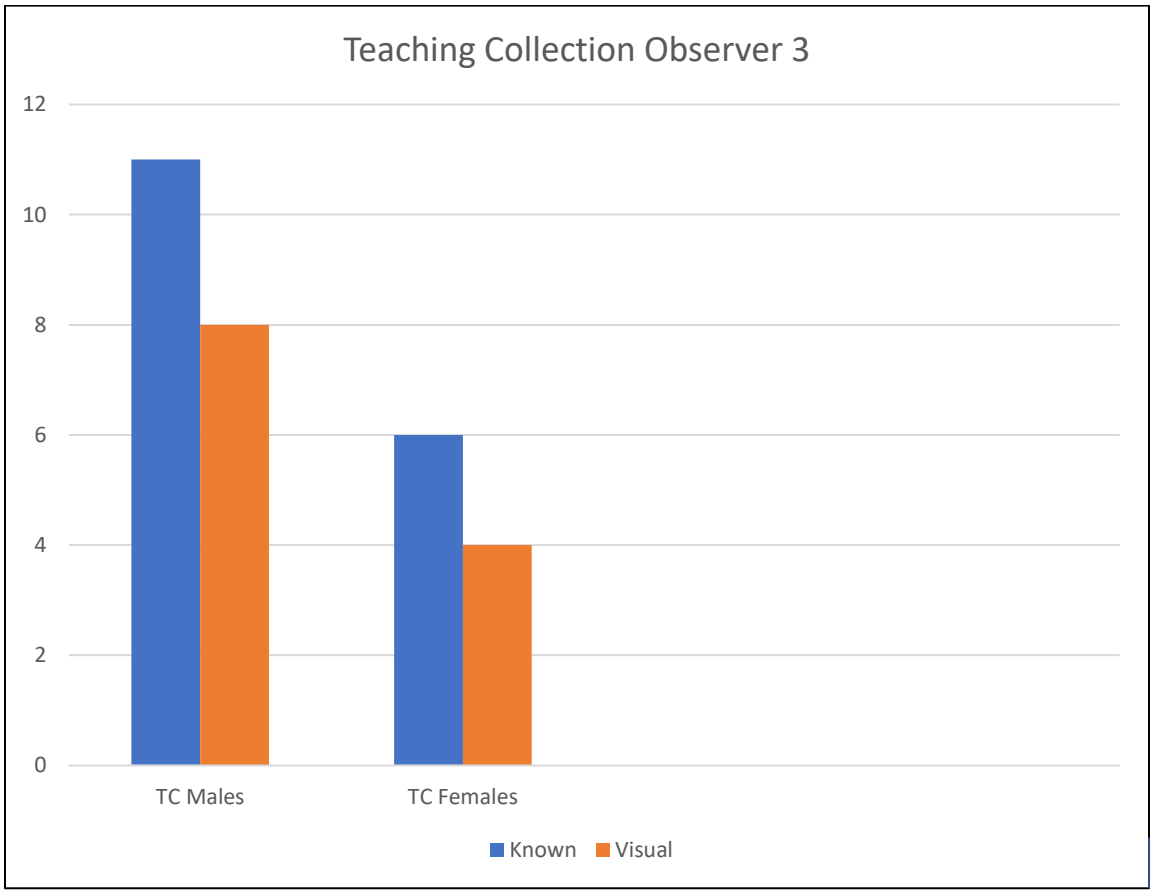


Table 3: Identifications of Observer 3's Visual and Metric Assessment

# ATTACHMENT 8 – FINAL PAPER, CONTINUED

## RESULTS, CONTINUED

The accuracy for the metric assessment of UMFC collection is based on the visual assessment, with the expectation that the percent error for visual assessments is around 24%. The accuracy is based off of the visual assessment because there is demographic information for the UMFC collection because it is comprised of unidentified individuals. Therefore, based off of the data for the known teaching collection, the visual assessment yielded the higher accuracy rate when compared to the visual. Therefore, the visual assessment was substituted for the known to create an error rate for the metric assessment for the UMFC collection. Figure 2 shows how each observer scored each individual.

| | FDB M/F/I | Known | Observor 1 | Observor 2 | Observor 3 |
|---|---|---|---|---|---|
| JMFC 78 | F | | M | | |
| JMFC 18 | F | | M | | |
| ΓC 52 | F | M | M | I | M |
| ΓC 19 | I | F | F | F | F |
| ΓC 10 | I | F | F | F | F |
| ΓC 15 | M | M | I | M | I |
| ΓC 9 | I | F | F | I | I |
| ΓC 11 | I | F | F | F | F |
| ΓC 17 | I | M | M | M | I |
| ΓC 8 | I | M | M | M | M |
| ΓC 16 | F | M | M | M | M |
| ΓC 48 | F | M | M | M | M |
| ΓC 114 | I | M | M | I | M |
| ΓC 21 | I | F | I | I | I |
| ΓC 12 | F | M | I | I | M |
| ΓC 33 | F | M | I | I | I |
| ΓC 13 | F | M | M | I | M |
| ΓC 14 | F | F | F | F | F |
| ΓC 18 | M | M | M | M | M |

Figure 2: Visual assessment scores from each Observer

# ATTACHMENT 8 – FINAL PAPER, CONTINUED

## RESULTS, CONTINUED

Table 4 shows that there were 12 indeterminate remains identified through the visual assessment and of those seven were determined indeterminate through metric assessment as well. However, there were a total of 20 indeterminate determinations through the use of FORDISC (Table 5). Table 4 shows the representation of male, female, and indeterminate sex determination of the metric assessment through FORDISC. Twenty individuals were determined to be indeterminate, five individuals are male, and 19 are female. Overall, this shows how likely an observer is to get a correct sex determination out of utilizing the metric method, and which biological sex is more commonly identified correctly if any.

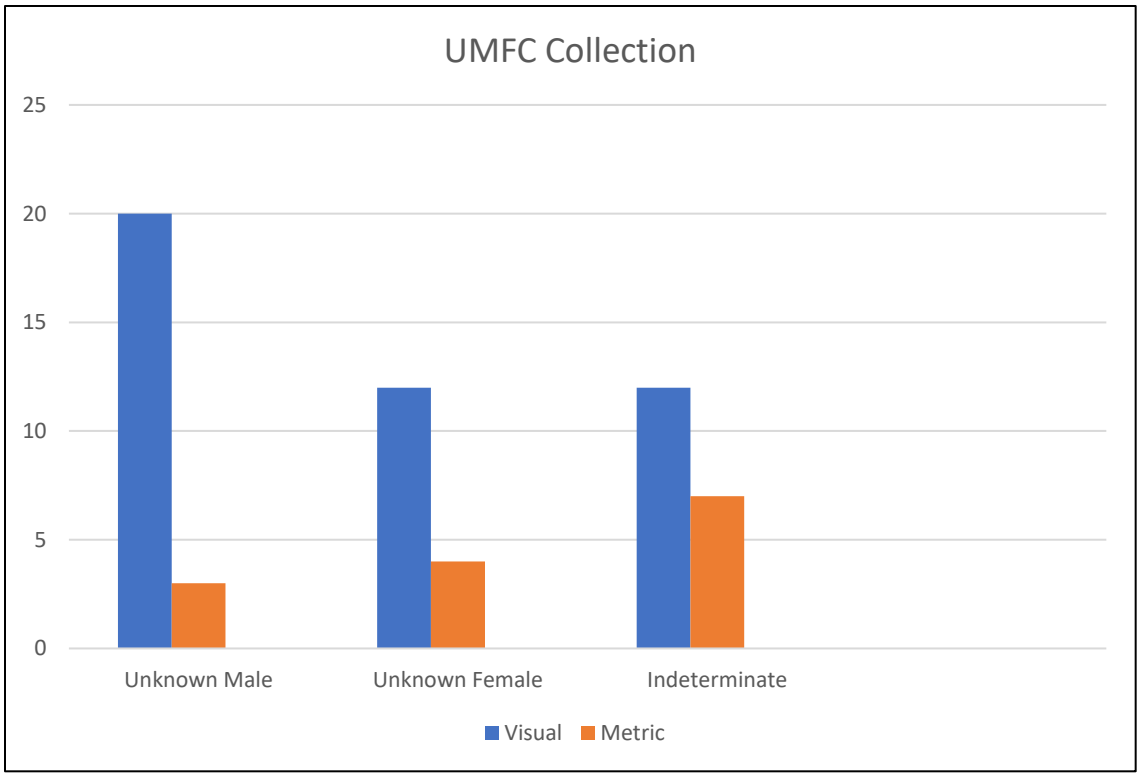


Table 4: Comparison of the UMFC results for the visual assessment and the metric assessment that had the same result

## ATTACHMENT 8 – FINAL PAPER, CONTINUED

### RESULTS, CONTINUED

Table 4 shows that when using the two methods to assess an unknown collection it becomes extremely hard to determine the accuracy rate. This is because there is not a known collection to create an accurate accuracy rate. Therefore, the visual assessment is being substituted as the known reference to determine the accuracy rate of the metric analysis. The error rate for the metric analysis of females is 33.3%, for indeterminate individuals its 58.3%, and for males it is 15% (Table 4). The overall average error rate for the metric assessment of unknown individuals is 35.5% (Table 4).

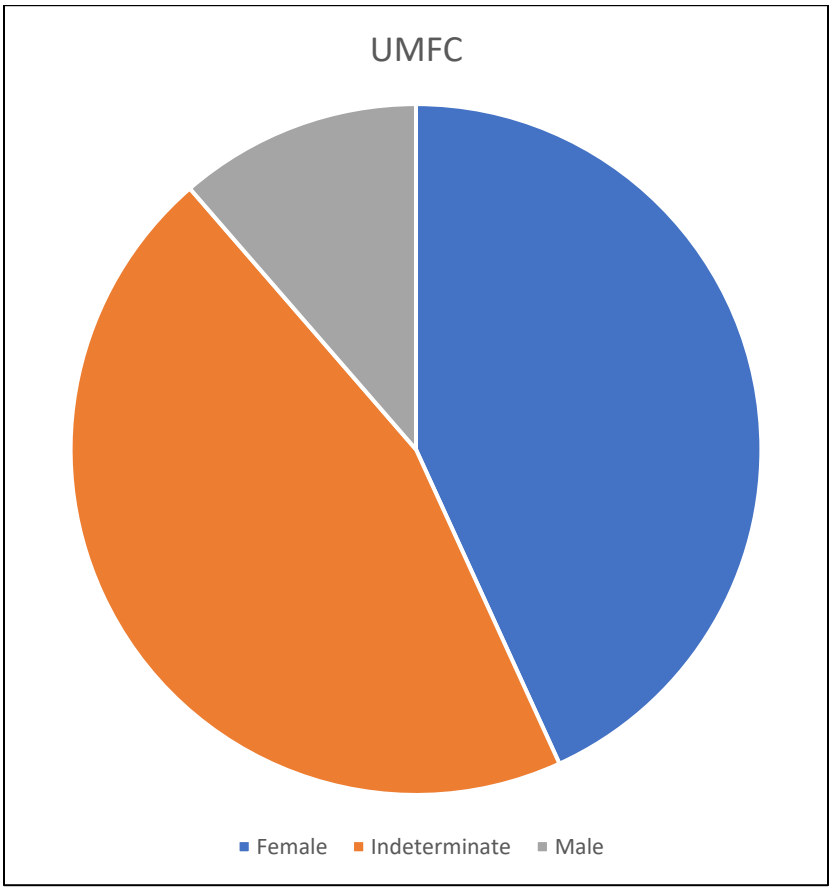


Table 5: FORDISC 3.1 results of all measurements collected of the UMFC

# ATTACHMENT 8 – FINAL PAPER, CONTINUED

## DISCUSSION

This study gives evidence towards both known issues of observer and interobserver errors for the visual method. This study revealed that the interobserver rate can range between 30.5%. When there are high interobserver rates like this that means that the reproducibility of this method is difficult. Therefore, it may be necessary to either adjust the current method in order to eliminate the large interobserver error rate or create a new method all together.

These error rates can arise based on the educational background and experience of each observer. Currently, there is no standard training on how to utilize both metric and visual biological sex assessment. It is possible that some observers never receive training before attempting to utilize these methods. In addition, different methods are taught based on the professor's way that they were most likely taught resulting in different points of view. Therefore, one method can have different interpretations and as a result those interpretations could influence how each observer implements the method. Overall, to counteract this, there should be a formal training in which observers are trained in how to properly utilize the method.

When reviewing the method itself, it should have full instructions to not allow for drastic observer interpretations. The current visual method created by Buikstra and Ubelaker, fails to write out in detail what the cranium should look like to obtain a score of 2, 3, or, 4 (1994). This also allows for the interpretation of what a score of 3 means. Walker (2008) determined that a score of 3 indicated male instead of indeterminate. This goes against what Buikstra and Ubelaker (1994) stated, "When creating a method is it best to have an option of indeterminate or should the observer force it into a specific category. This debate is one that is going to take time to address but should be addressed in the future."

# ATTACHMENT 8 – FINAL PAPER, CONTINUED

## DISCUSSION, CONTINUED

The metric assessment method allows for observer error and differential educational training to affect the way in which the measurements are taken. Similar to the issues with interpretations of the method that visual assessments have, the measurements can have different interpretations as well. Based on the educational training and experience one receives, the individual's ability to understand the location of the pivotal landmarks on the skull that allow for the metric measurements to be taken may vary. Without the proper measurement taken the result of the metric biological sex assessment will be inaccurate.

FORDISC is consistent with its accuracy rate. However, due to FORDISC's low accuracy the method needs to undergo some revisions. One revision might include not forcing the sex determination into one category or another other. This could be implemented by utilizing the posterior probability and determining a point where if the posterior probability is at or below a certain percent then the measurements for the individual is determined to be indeterminate. Even though this doesn't improve the accuracy rate, it assists in the broader impacts of not narrowing a criminal investigator search for the identity to a possibly wrong sex and resulting in a nonidentification of the remains. A possible way to make FORDISC more accurate is to import more skeletal data from worldwide populations to have a larger and more accurate sample. If more samples are included into the sample the accuracy rate can increase because it provides a larger range of what is possible for each biological sex.

### Conclusion

Overall, each method provides its own set of issues. If utilizing one method over the other the visual method has a higher likelihood of providing an accurate biological sex determination

# ATTACHMENT 8 – FINAL PAPER, CONTINUED

## DISCUSSION, CONTINUED

### Conclusion, continued

due to the low percentage of error rate. However, based on the previously mentioned hypothesis neither method provides a good accuracy rate under 15%. More research needs to be completed in trying to find alternative methods where there is less subjectivity that plays a role in the determination of biological sex and that provides consistently low error percentage rate.

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# ANTY 515: THEORY AND METHODS IN BIOLOGICAL ANTHROPOLOGY

As a result of the final paper produced, my foundation in graduate level theory and methods of physical/biological anthropology were broadened. The application of methods learned were applied to sets of data, interpretation of results in light of theories, familiarity with terminology and basic principles of evolution at the population (microevolutionary) and species (macroevolutionary) levels are contained within the following attachments. Competency with a variety of techniques, approaches, and methods of analysis, including the use of common software were achieved. Confidence and skill in interpreting the results of analyses within theoretical frameworks, and interpretation and presentation of those results provided a professional foundation for future graduate level research papers. Approaching anthropological phenomena at the level of process (why they are the way they are) rather than the level of description (what are they) was achieved. The following pages demonstrate my accomplishments.

# ATTACHMENT 9 – ANALYSIS OF CRANIA HISTORY OF MALES WORLDWIDE

Alexis Rizzolo
Dr. Skelton
ANTY 515
September 20, 2018

## MATERIALS

Utilizing data provided by Dr. Skelton, via Microsoft Excel, enabled the analysis of crania history of males worldwide. Data sets provided by W. W. Howells: *Skull shapes in maps, Who's who in skulls: Ethnic identification of crania from measurements,* and *Cranial variation in man* added to the scope of this study (1973, 1989, 1995).

A selection of ten groups, which represents a sampling of worldwide male population, was selected from the data set (Howells 1989). The selection consists of three groups from Africa (Bushman, Dogon, and Egypt), two groups from the America's (Arikara and Peru), one group form Polynesia (Mokapu), one group from Oceania (Australia), two groups from Asia (Anyang and Anadmanls), and one group from Europe (Zalavar). A total of 515 individuals were examined from all ten groups.

One hundred and fifty individuals of the 515 sampled were obtained from Africa. The Bushman group sample contained forty-three individuals from collections in South Africa and Europe. Another collection, from the South African Museum in Cape Town, encompassed "Bushman victims of a smallpox epidemic in 1866" (Howells 1989). The Bushman people spoke NIIng a language derived from the Tuu language family (Wikipedia 2018a). The Dogon sample "collected in 1934" (Howells 1989) east of the Niger at the coordinates of 14°30'N 30°30'W, consisted of 49 individuals, and dates back approximately 230 years ago (Howells 1989).

# ATTACHMENT 9 – ANALYSIS OF CRANIA HISTORY OF MALES WORLDWIDE, CONTINUED

## MATERIALS, CONTINUED

The language family to which their pre-colonial predecessors spoke was known as the Dogon language (Wikipedia 2018b). A sampling was obtained of 58 Egypt males "located south of the Gizeh pyramids" Howells 1989). There is no known recovery date indicated for these specimens; however, the population existed between 600-200 B.C. (Howells 1989).

For this study North and South America are combined and designated as the Americas. The North America group, Arikara, excavated in South Dakota is comprised of 43 males. This sampling was recovered during the "summer seasons of 1957, 1958, 1961, and 1962 (Howells 1989) and they existed between 1600 to 1750 A.D. Their spoken language, Arikara, is from the Caddoan language family (Wikipedia 2018c).

Descending from South America is the Peru group, involving 75 males. The first known location of this collection, post-excavation, was the National Museum of Anthropology and Archaeology in Lima, Peru, and dates back to 1890. (Howells 1989). There is no information as to when the sample was excavated or the time in which these males inhabited South America. The absence of information regarding the language family resulted in an unknown spoken language of pre-colonial times.

The Mokapu thrived within a region of Polynesia located on the Mokapu peninsula. These 54 sets of male remains were excavated between 1938 to 1940 and date back to 1400 and 1790 A.D. (Howells 1989). There is no information on the language family, or the pre-colonial language spoken for this group.

ATTACHMENT 9 – ANALYSIS OF CRANIA HISTORY OF MALES WORLDWIDE, CONTINUED

**MATERIALS, CONTINUED**

The group Australia, part of the Oceania region consists of 52 male individuals. These individuals were excavated from a cemetery located at Swanport in 1911 (Howells 1989). There is no information available to ascertain the dates in which these individuals lived. The language family spoken within this group is the Ngarrindjeri dialects during pre-colonial times (Wikipedia 2018d).

Two groups, the Anyang and Andamanls, will be analyzed from Asia. The Anyang group is made up of forty-six male individuals. This group lived during the times of the Shang Dynasty and were buried within sacrificial pits located in the Shang Dynasty Tombs (Howells 1995). The language family for this group is unknown; therefore. we have no idea of the language spoken pre-colonially during this time. The Andamanls specimens consisting of thirty-six individuals derived from the Andaman Islands. There is no information to where the population was excavated or to when the population lived. In addition, there is a lack of information on the language family spoken during pre-colonial times.

The Zalavar group originated from the region of Europe, more specifically the country of Hungary and consisted of fifty-eight individuals. This population lived during the 9$^{th}$ and 11$^{th}$ century A.D. The excavation site was located in western Hungary around 16km from the western shore of Lake Balaton and the remains exhumed from 1948-1952 (Howells 1989). The language family is Indo-European during the pre-colonial times for these individuals (Wikipedia 2018e).

# ATTACHMENT 9 – ANALYSIS OF CRANIA HISTORY OF MALES WORLDWIDE, CONTINUED

## MATERIALS, CONTINUED

Seventy-nine cranial measurements were collected and are listed below (Howells 1989):

| | |
|---|---|
| GOL | Glabello-Occipital Length |
| NOL | Nasio-occipital Length |
| BNL | Basion-Nasion Length |
| BBH | Basion-Bregma Height |
| XCB | Maximum Cranial Breadth |
| XFB | Maximum Frontal Breadth |
| STB | Bistephanic Breadth |
| ZYB | Bizygomatic Breadth |
| AUB | Biauricular Breadth |
| WCB | Minimum Cranial Breadth |
| ASB | Biasterionic Breadth |
| WCB | Minimum Cranial Breadth |
| ASB | Biasterionic Breadth |
| BPL | Basion-Prosthion Length |
| NPH | Nasion-Prosthion Breadth |
| NLH | Nasal Height |
| OBH | Orbit Height Left |
| OBB | Orbit Breadth Left |
| JUB | Bijugal Breadth |
| NLB | Nasal Breadth |
| MAB | Palate Breadth |
| MDH | Mastoid Height |
| MDB | Mastoid Width |
| ZMB | Bimaxillary Breadth |
| SSS | Zygomaxillary Subtense |
| FMB | Bifrontal Breadth |
| NAS | Nasio-Frontal Subtense |
| EKB | Biorbital Breadth |
| DKS | Dacryon Subtense |
| DKB | Interorbital Breadth |
| NDS | Naso-Dacryal Subtense |
| WNB | Simotic Chord |
| SIS | Simotic Subtense |
| IML | Malar Length Inferior |
| XML | Malar Length Maximum |
| MLS | Malar Subtense |
| OCA | Occipital Angle |

| | |
|---|---|
| WMH | Cheek Height |
| SOS | Supraorbital Projection |
| GLS | Glabella Projection |
| FOL | Foramen Magnum Length |
| FRC | Nasion-Bregma Chord |
| FRS | Nasion-Bregma Subtense |
| FRF | Nasion-Subtense Fraction |
| PAC | Bregma-Lambda Chord |
| PAS | Bregma-Lambda Subtense |
| PAF | Bregma-Subtense Fraction |
| OCC | Lambda-Opisthion Chord |
| OCS | Lambda-Opisthion Subtense |
| OCF | Lambda-Subtense Fraction |
| VRR | Vertex Radius |
| NAR | Nasion Radius |
| SSR | Subspinale Radius |
| PRR | Prosthion Radius |
| DKR | Dacryon Radius |
| ZOR | Zygoorbitale Radius |
| FMR | Frontomalare Radius |
| EKR | Ectochonchion Radius |
| ZMR | Zygomaxillare Radius |
| AVR | M1 Alveolus Radius |
| NAA | Nasion Angle, ba-pr |
| PRA | Prosthion Angle, na-br |
| BAA | Basion Angle, na-br |
| NBA | Nasion Angle, ba-br |
| BBA | Basion Angle, na-br |
| BRA | Bregma Angle |
| SSA | Zygomaxillare Angle |
| NFA | Nasio-Frontal Angle |
| DKA | Dacryal Angle |
| NDA | Naso-Dacryal Angle |
| SIA | Simotic Angle |
| FRA | Frontal Angle |
| PAA | Parietal Angle |

# ATTACHMENT 9 – ANALYSIS OF CRANIA HISTORY OF MALES WORLDWIDE, CONTINUED

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# ATTACHMENT 10 - HUMAN DIASPORA OF HOMO SAPIENS

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October 31, 2018

## INTRODUCTION

The human diaspora of homo sapiens has been highly debated. The main concept of the travel from region to region is widely agreed upon; however, the exact timeframes and entrance and exit routes between each region is highly contested. The main expansion route of homo sapiens originates in Africa and ends in the Pacific Island region. I will show how varied time estimates are when dealing with arrival dates of modern humans into and out of the seven specific regions which encompass the worldwide human diaspora.

The movement out of Africa is one area of the human diaspora that is widely argued, as some believe the migrations occurred in waves while others deem it to have been in one mass exodus. The first wave of human migrations out of Africa ensued about 85kya and followed the coasts through the middle east into southern Asia. The next migration occurred around 40-12kya and brought humans northward into Europe. These dates were based on the analysis of H. Pylori and the D loop region of mtDNA (Kundu et al. 2014). H. Pylori is a type of bacteria that exhibits phylogeographical differentiation and therefore can be used a predictor of human migration patterns. The D-loop region of mtDNA is where most mutations occur and therefore experience more environmental changes as they continue migrating out of Africa. An opposing view is the movement out of Africa occurred between 50,000 – 100,000 years ago, neither archaeological, genetic, or fossil evidence can distinguish the exit route taken (Luca Pagani et al. 2015). One main issue with this particular viewpoint is that it goes onto further explain the two possible routes that

# ATTACHMENT 10 - HUMAN DIASPORA OF HOMO SAPIENS, CONTINUED

## INTRODUCTION, CONTINUED

could have been taken. The first is the northern route, which exits through Egypt and Sinai. The second route is the southern route which exits through Ethiopia, the Bab el Mandeb strait, and the Arabian Peninsula. Utilizing the whole genome sequence, this article concluded that the northern route is the exit route taken, because of the genome and haplotype frequency most closely resembling non-African populations. If genetic evidence is not used to obtain an exit route, it is not plausible to then state that based on sequencing of human genome that the most likely route taken was the northern route.

Another viewpoint is the route went out of Africa through the Persian Gulf and this opinion was based on the analysis of H. Pylori (Harcourt 2016). This out of Africa movement occurred 70kya into Eurasia, and Oldowan stone tools were utilized by these individuals. This movement can be tracked through where these tools have been discovered (Bellwood 2015). I will discuss one final viewpoint with respect to the variability in paths, time ranges, and expansion out of Africa which occurred anywhere between 45 to 60kya. As groups exited from Africa there is a clear decline in genetic diversity, evident from H. Pylori (Henn et al. 2012).

When attributed to the Dogon, Bushman, and Egyptian groups within the data set from W. W. Howells: *Skull shapes in maps, Who's who in skulls: Ethnic identification of crania from measurements*, and *Cranial variation in man* the movement of these groups is less frequently debated (1973, 1989, 1995). The hierarchy of movement of the Dogon, Bushman, and Egyptian groups are Bushman to Dogon and finally Egyptian. The Bushman people resided in Southern Africa from as early as 100kya. This date estimation is based on mtDNA, and archaeological

# ATTACHMENT 10 - HUMAN DIASPORA OF HOMO SAPIENS, CONTINUED

## INTRODUCTION, CONTINUED

evidence from the Border Cave. Archaeological remains of four individuals were discovered within the Border Cave dating to around 120 to 90kya (Deacon 1992).

The first arrival of the Dogon peoples was around 1430 AD. Oral traditions told attribute the Dogon people's arrival to somewhere between 1230 -1332 AD. Many of the Dogon traditions and history were passed down orally through time. Evidence of the Dogon people are derived from the evolution of their language, potsherds, and charcoal fragments. In rural areas, the Dogon's language remained primitive, yet in Mali where the Dogon people are centrally located their language is developed and intricate. The potsherds and charcoal fragments have been radiocarbon dated to a time range of 1490-1640AD (Mayor et al. 2005).

Sequencing of mtDNA shows that the Egyptians first entered Southwestern Asia and later moved on to Europe through North Africa from 45-40kya. The mtDNA markers that prove this are movement and time frame and are referred to as haplogroups M1and U6 (Olivieri et al. 2006).

Modern humans were first discovered within Eastern Asia around 40kya; however, genetic analysis suggests dates from as early as 60kya, and around 40kya for Japan (Harcourt 2016). They arrived via a southern coastal route (Moodley et al. 2009). The phylogenetic tree analysis of the study confirms a southern coastal route as well. This study is based on the fact that both Northeast and Southeast Asians have distinct clusters. (Jin and Su 2000). The early migration of peoples entering Asia were referred to as Mongoloids. They entered through Southeastern Asia (Hrdlička 1921).

# ATTACHMENT 10 - HUMAN DIASPORA OF HOMO SAPIENS, CONTINUED

## INTRODUCTION, CONTINUED

Using mtDNA, the haplogroups of M31 and M32 were identified as genetic markers of the Andaman Islands people, which suggests a recent population of these islands. Direct descendants of this early migration demonstrate distinctive languages and a history of isolationism. The major haplogroup M represents the majority of the Andaman lineages, and suggests they are of Southeast Asian origin (Barik 2008).

Australia once was part of a continent called Sahul. Sahul was comprised of four countries: Australia, Tasmania, New Guinea, and the Aru Islands. Australia was inhabited around 45kya, with Tasmania following 10kya later despite there being no land barrier between them (Harcourt 2016, Henn et al. 2012). Homo sapiens landed in Mainland Sahul, known today as Australia, around 50-60kya. Based on the mtDNA of modern-day aboriginals', archaeologists can assume that the movement of these people involved the use of sound watercrafts, the capacity to adapt to different landscapes, all while indicating that these individuals came from Southeast Asia.

In Australia utilizing luminescence analysis of sand grains in rock shelters, researchers can date artifacts back to 50-60kya and all the way up to 20kya. The mtDNA from the oldest skeleton found in Australia, dates to about 43kya and has mtDNA that is still present in modern day aboriginals. Another way that can be used to date the movement of humans is megafauna, however it can be very unreliable. (Bellwood 2015). This indicates that there was one large movement to the continent of Sahul.

Using *Helicobacter Pylori* researchers were able to distinguish a specific strain of bacteria that is attributed to another movement on the continent of Sahul. This specific strain of H. Pylori

# ATTACHMENT 10 - HUMAN DIASPORA OF HOMO SAPIENS, CONTINUED

## INTRODUCTION, CONTINUED

is only found is this specific region of Sahul. The Australia H. Pylori strain is called hpSahul and indicates the time range of arrival on the continent of Sahul to around 37-31kya. In addition, the migration route can be tracked using the Y chromosome markers (Moodley et al. 2009).

Arrival of modern humans to Europe dates to around 44kya for Southern Italy, and 43kya for Southern Britain. As a result of the Ice Age, humans were forced to retreat from Northern Europe to the Basque of Spain and they did not return until 10kya (Harcourt 2016). A huge debate among the peoples of Europe is "Which country was the first to have been populated?"

Currently the oldest modern human remains in Europe came from Tuscany, Italy. This conclusion is based on mtDNA sequencing, where they researchers found the greatest amount of haplotype diversity (Francalacci et al. 1996). A molecular marker of mtDNA is U5, and it can be used to estimate the time frame for when modern humans entered into Europe. The timeframe of this movement occurred sometime around 55-30kya (Malyarchuk 2010).

The human diaspora within the America's is another highly debated topic among anthropologists. An allele combined with a single blood group is ubiquitous among both native American and Amerindian populations which is also evident in eastern Siberians. This indicates that a small population of Siberians populated to the America's (Harcourt 2016). The migration to the America's originated in south-western Europe to north-eastern North America via the Bering Land bridge that connected Siberia to Alaska. The Clovis culture is attributed to the migration of this group of peoples. (Llamas et al. 2017).

# ATTACHMENT 10 - HUMAN DIASPORA OF HOMO SAPIENS, CONTINUED

## INTRODUCTION, CONTINUED

Most genetic data for North America suggests there was a single migration with relatively few individuals that occurred around 25-15kya., with the migration route going down the pacific coast, or through the Laurentine and Cordilleran Glaciers. For this migration to have occurred in the Laurentine and Cordilleran Glaciers there was thought to have been an ice-free corridor 12,550 years ago (Lewis 2007).

Through the extraction of mtDNA, remains excavated from Arikara sites date to the time around 1600-1832AD. The Arikara spoke Caddoan a language family which split from the Pawnee around 1450-1650AD. The Arikara were approximately 30,000 strong, once exposed to European diseases their population experienced a serious decline in numbers (Lawrence et al. 2010).

In South America there is both archaeological and genetic evidence to suggest that this continent was populated around 14kya. This evidence is based on the analysis of mtDNA HV1 data (Lewis 2007). A topic highly debated within the people of South America is the number of migrations that occurred to this area of the region. Based on the mtDNA HV1 data the Peruvian populations were clustered closely to the Chilean populations. These populations are separated by around 2,000-3,000km (Lewis 2007). This significant amount of distance between the two populations suggests a similar line of descent, or perhaps they were populated by a group that was based on a Founder Effect from the Chilean group.

There were two major and two lesser movements in the Caribbean. The first major movement was by people who used flake stones and inhabited Cuba and Hispaniola around 5000 BCE. The second major movement occurred around 2.5kya and the people came from northern

# ATTACHMENT 10 - HUMAN DIASPORA OF HOMO SAPIENS, CONTINUED

## INTRODUCTION, CONTINUED

part of South America. The first lesser movement occurred around 500 BCE and was based on the Arawak-speaking people who moved within the Caribbean and introduced pottery and agriculture throughout. The second lesser movement that Keegan discussed was the movement of Caribbean peoples into the lesser Antilles prior to the Europeans, and there was no timeframe associated with this. (Bellwood 2015).

Another first major viewpoint is that the Caribbean migration occurred around 7kya, and the flake stones were directly associated to the chert quarrying industry in Belize. An alternative viewpoint to the second major is that migration occurred from the Southern Lesser Antilles to Trinidad. Additionally, a different stance for the first lesser migration is that these tools could have easily been exchanged from Mainland Central America and as a result should not indicate any new movement into the Caribbean. The fact that the tools cannot be used, could lead to debate, and should be backed by another source of evidence. Another thought process for the second lesser migration is one that migrations continued after the migration of people from the northern area of South America. (Harcourt 2016).

The migration through the Pacific Islands is a recent one and occurred around 5kya. Using *Helicobacter Pylori* there were able to distinguish the migration route of the Pacific Islanders and labeled the specific strain of H. Pylori to represent this. This strain is called hpMaori and represents the migration through Taiwan that eventually diverged into the subgroups Melanesia and Polynesia around 5kya.

# ATTACHMENT 10 - HUMAN DIASPORA OF HOMO SAPIENS, CONTINUED

## INTRODUCTION, CONTINUED

This migration route can also be tracked through the dispersal of the Austronesian language family (Moodley et al. 2009). The language family of the Polynesian groups are Malayo-Polynesian, which is a sub-group of the Austronesian language families. When looking into the other subgroups of the Austronesian language family, it is primarily spoken in Taiwan (Moodley et al. 2009). This suggests that the dispersal of the Austronesian language family originated in Taiwan and spread from there. A human genetic marker of this route is spread through the mtDNA, HV1 motif of lineage B4a1a. This is found at high frequency among Melanesians, Polynesians, and Taiwanese modern-day populations (Moodley et al. 2009).

Knowing that the Austronesian language spread from Taiwan would mean that the migration route of modern humans began in Taiwan and based on the mtDNA genetic markers travelled through Polynesia and Melanesia. The order in which this migration occurred, has yet to be figured out. However, some evidence from the spread of the language family indicates that it might have went to Micronesia before Polynesia (Bellwood 1980). This would suggest that the migration route occurred from Taiwan, went through Micronesia, and ended in Polynesia.

The Human Diaspora is highly debated throughout the anthropological community as many regions want to claim that they have the oldest modern human. I hypothesize that cranial measurement among the worldwide males' dataset will show a reduction is size based on the distance of migration from the original origin of Africa.

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# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS

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## METHODS

Performing a Principal Components Analysis, a scatter plot was created using PAST in order to investigate clustering of groups. Additionally, a Principal Component Table was created after performing the Principal Component Analysis in PAST. This was used to investigate which components had the greatest percent of variance within the Worldwide dataset. Conical Variance Analysis was performed using PAST, and a scatter plot was utilized to investigate the clustering between groups within the Worldwide dataset. A Principal Coordinates Analysis was performed in PAST utilizing the Euclidean distance matrix and resulted in the formation of a scatter plot. This scatter plot is used to investigate the clustering between groups. Utilizing the K-Means clustering Analysis performed using PAST, a K Means Table was created to investigate which individuals within a certain group was assigned to what cluster, and to determine the overall percentage of each group's clustering. A Cluster Percent Graph was created using Excel in order to investigate what percentage of individuals in a group are assigned to a cluster. The $F_{ST}$ Calculation was created using RMET with a Heritability rate of 0.55 in order to investigate the measure of divergence of populations from an original founding population. The Relethford Blangero Analysis was created using RMET with a Heritability rate of 0.55 and is used in order to investigate the phenotypic variation of each population and the resulting gene flow between groups. A Principal Coordinates Analysis was done utilizing RMET with a Heritability rate of 0.55 and used to investigate the clustering between groups. A Hierarchal Clustering Dendrogram was created utilizing PAST with a Euclidean distance matrix. This dendrogram is used to investigate

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## METHODS, CONTINUED

relationships between groups. A Means Analysis was done utilizing Instat+ to create the information needed to perform an Unpaired Group Means Arithmetic (UPGMA) analysis. The information from Instat+ was then utilized within PAST with a Euclidean distance to investigate the relationships between groups within the Worldwide dataset to determine a possible migration pattern through the creation of a UPGMA dendrogram. Finally, a Neighbor Joining phylogram was created using PAST with a Euclidean Distance matrix to investigate the relationships and distances shared between each group within the Worldwide dataset to determine a possible migration pattern.

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS

Figure 1 is the Principal Components Analysis Scatter plot. This is showing that the Bushman group is clustered on the left-hand side of the Y-Axis. Other than the distinctiveness of the Bushman group, there is no significant clustering between any other group.

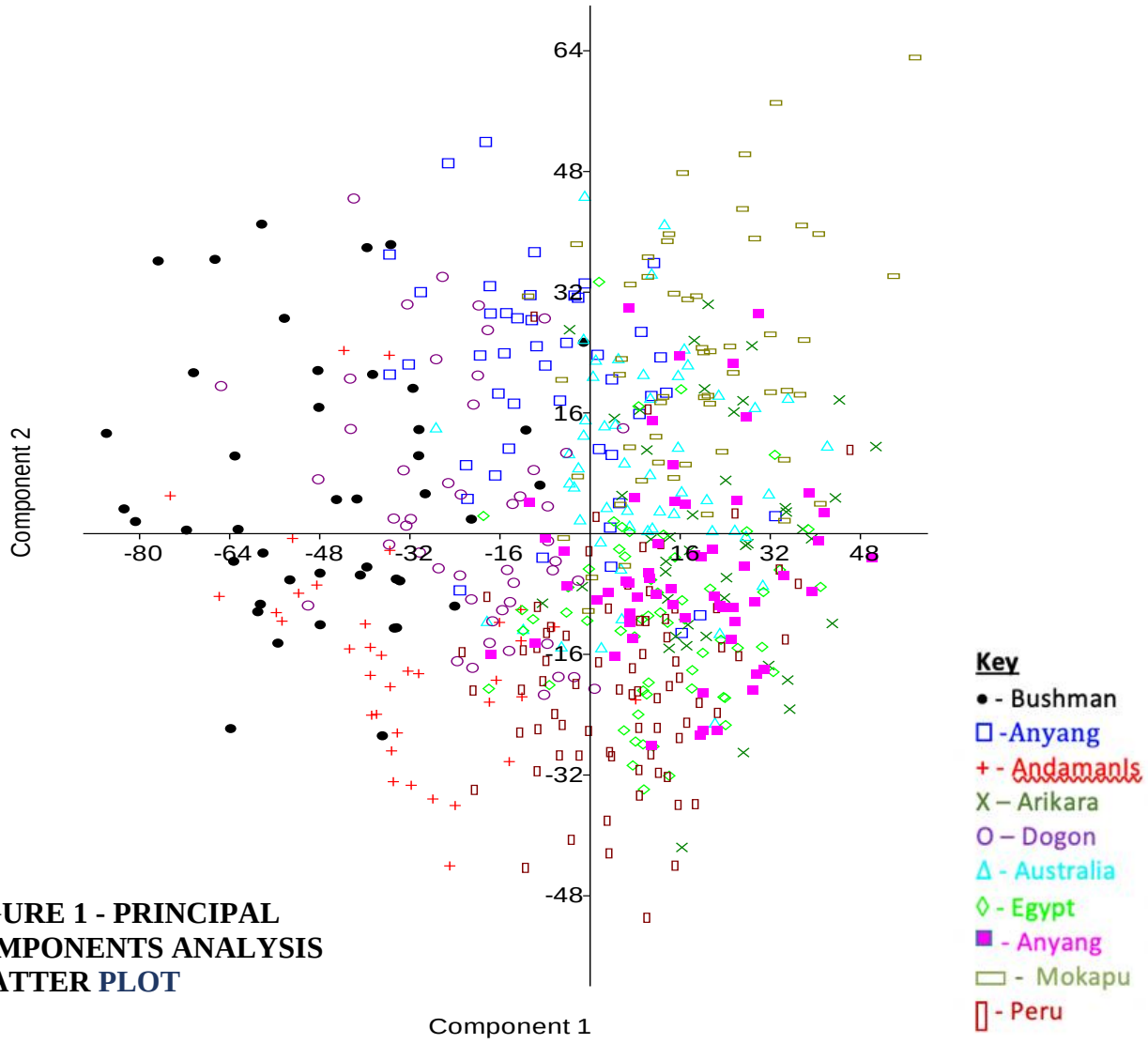



**FIGURE 1 - PRINCIPAL COMPONENTS ANALYSIS SCATTER PLOT**

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

In Table 1, you will find that principle components 1-7 have around seventy-six percent variance:

### PRINCIPLE COMPONENT TABLE

| PC | Eigenvalue | % Variance | PC | Eigenvalue | % Variance | PC | Eigenvalue | % Variance |
|---|---|---|---|---|---|---|---|---|
| 1 | 665.411 | 31.866 | 16 | 18.846 | 0.90252 | 31 | 4.941 | 0.23662 |
| 2 | 400.389 | 19.174 | 17 | 16.5367 | 0.79193 | 32 | 4.84446 | 0.232 |
| 3 | 180.64 | 8.6507 | 18 | 14.9809 | .071742 | 33 | 3.73576 | 0.1789 |
| 4 | 127.477 | 6.1048 | 19 | 14.1755 | 0.67885 | 34 | 3.57193 | 0.17106 |
| 5 | 92.2051 | 4.4156 | 20 | 13.6318 | 0.65281 | 35 | 3.15271 | 0.15098 |
| 6 | 70.9132 | 3.396 | 21 | 10.283 | 0.49244 | 36 | 2.87191 | 0.13753 |
| 7 | 67.7094 | 3.2425 | 22 | 9.80612 | 0.46961 | 37 | 2.82839 | 0.13545 |
| 8 | 59.1057 | 2.8305 | 23 | 9.33414 | 0.447 | 38 | 2.46199 | 0.1179 |
| 9 | 49.3515 | 2.3634 | 24 | 8.69896 | 0.41658 | 39 | 2.38785 | 0.11435 |
| 10 | 38.687 | 1.8528 | 25 | 8.38863 | 0.40172 | 40 | 2.17465 | 0.10414 |
| 11 | 31.9677 | 1.5309 | 26 | 7.73228 | 0.37029 | 41 | 2.01989 | 0.09673 |
| 12 | 27.0412 | 1.295 | 27 | 7.28747 | 0.34899 | 42 | 1.68826 | 0.080849 |
| 13 | 24.7636 | 1.1859 | 28 | 6.36041 | 0.30459 | 43 | 1.63255 | 0.078181 |
| 14 | 23.0095 | 1.1019 | 29 | 6.12793 | 0.29346 | 44 | 1.6182 | 0.077494 |
| 15 | 21.9226 | 1.0499 | 30 | 5.10855 | 0.24464 | 45 | 1.41186 | 0.067613 |

**TABLE 1**

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

**PRINCIPLE COMPONENT TABLE, CONTINUED**

| PC | Eigenvalue | % Variance | PC | Eigenvalue | % Variance |
|---|---|---|---|---|---|
| 46 | 1.18554 | 0.056774 | 61 | 0.0817255 | 0.0039138 |
| 47 | 1.17689 | 0.05636 | 62 | 0.0752289 | 0.0036026 |
| 48 | 1.11513 | 0.053402 | 63 | 0.0715135 | 0.0034247 |
| 49 | 0.883844 | 0.042326 | 64 | 0.0619858 | 0.0029684 |
| 50 | 0.839234 | 0.04019 | 65 | 0.0567194 | 0.0027162 |
| 51 | 0.643284 | 0.030806 | 66 | 0.0423358 | 0.0020274 |
| 52 | 0.542366 | 0.025973 | 67 | 0.0385259 | 0.001845 |
| 53 | 0.441036 | 0.021121 | 68 | 0.0372494 | 0.0017838 |
| 54 | 0.414693 | 0.019859 | 69 | 0.0342074 | 0.0016382 |
| 55 | 0.390697 | 0.01871 | 70 | 0.0241577 | 0.0011569 |
| 56 | 0.259915 | 0.012447 | 71 | 0.0102649 | 0.00049158 |
| 57 | 0.174191 | 0.0083418 | | | |
| 58 | 0.130349 | 0.0062423 | | | |
| 59 | 0.106306 | 0.0050909 | | | |
| 60 | 0.0891307 | 0.0042684 | | | |

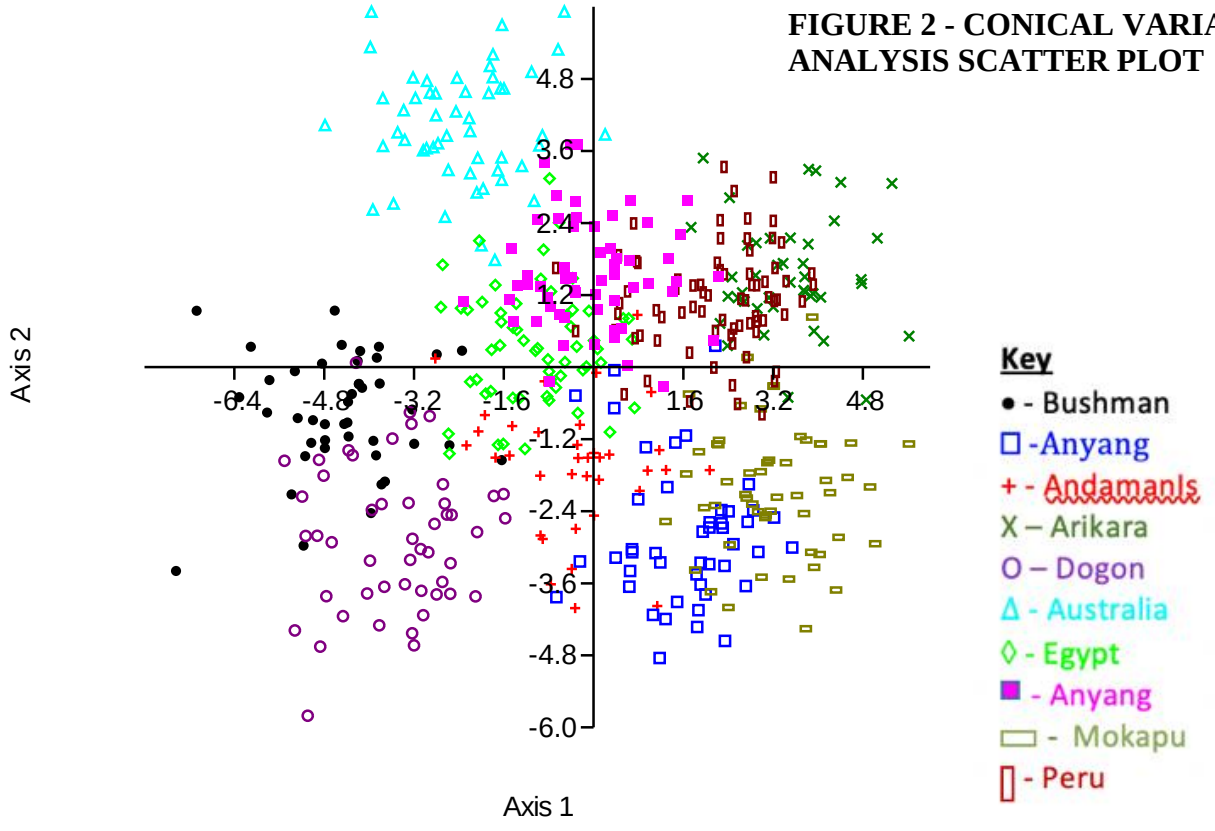
**TABLE 1, CONTINUED**

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

The Conical Variances Analysis Scatter Plot, Figure 2 (below), shows groupings based on quadrants formed by the Y-Axis and X-Axis. Quadrant one is located above the X-Axis and to the left of the Y-Axis. The second quadrant is located above the Y-Axis and to the right of the X-Axis. The third quadrant is located below the X-Axis and to the left of the Y-Axis. The fourth quadrant is located below the X-Axis and to the right of the Y-Axis. Quadrant One shows that the Australia and Egypt groups are clustered together. Quadrant Two clusters Zalavar, Peru, and the Arikara groups together. Quadrant three clusters the Bushman, Dogon, and Andaman Islands together. Finally, Quadrant four clusters the Mokapu and Anyang groups.

**FIGURE 2 - CONICAL VARIANCES ANALYSIS SCATTER PLOT**



# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

A Principal Coordinate Analysis Scatter plot, Figure 3, shows that there is no clustering between the groups.

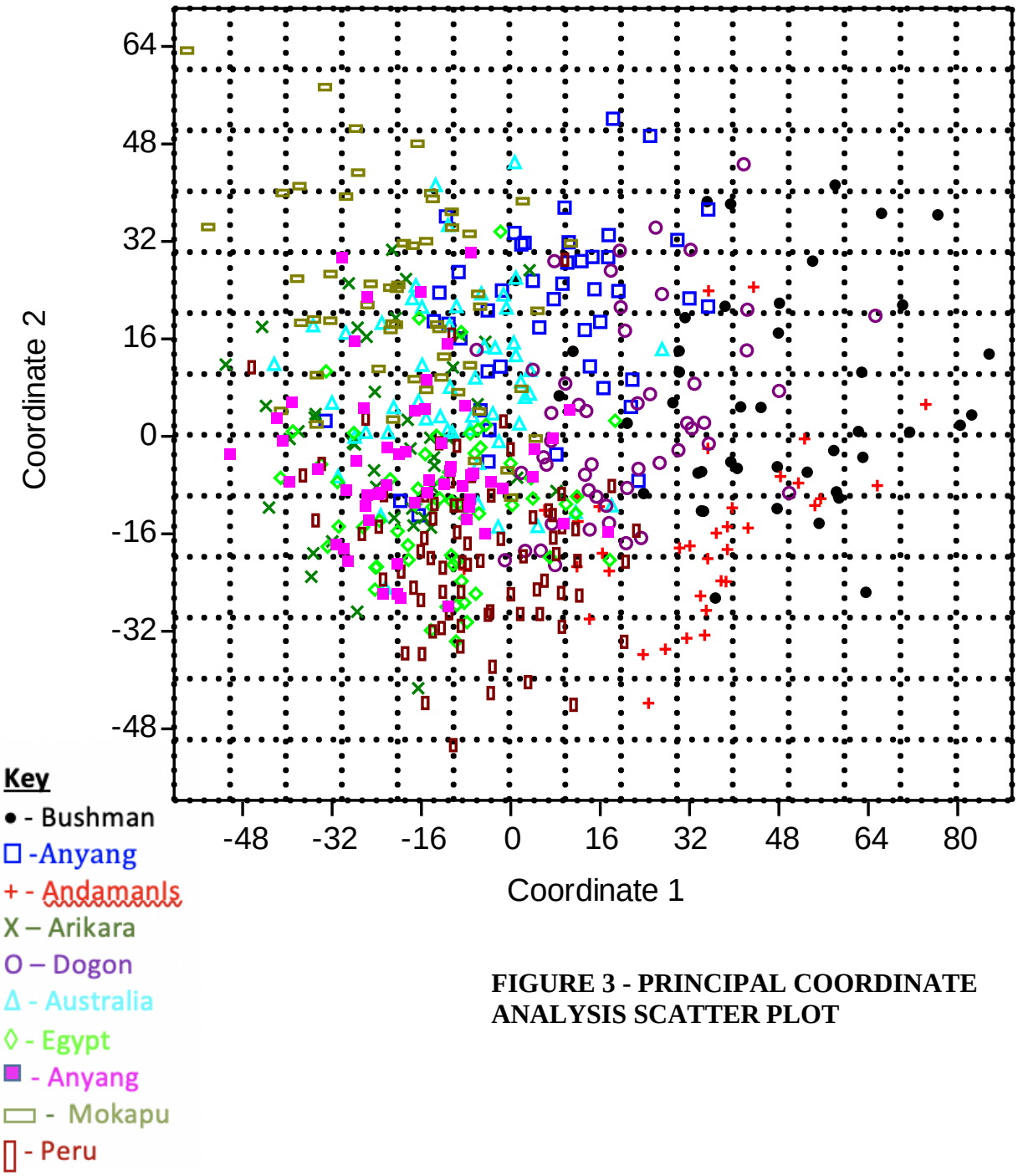



**FIGURE 3 - PRINCIPAL COORDINATE ANALYSIS SCATTER PLOT**

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

The individuals from the Bushman group in the K Means Cluster Table, Table 2, show that the majority of the individuals belong to cluster one. In addition, cluster one also has the majority of the AndmanIs and Dogon individuals. In Cluster Two is the majority of the Anyang, Australia, and Mokapu individuals. Cluster three contains the majority of the Arikara, Egypt, Peru and Zalavar individuals.

**K-MEANS 3 CLUSTERING TABLE - TABLE 2**

| Item | Cluster | Item | Cluster | Item | Cluster | Item | Cluster |
|---|---|---|---|---|---|---|---|
| Bushman | 1 | Bushman | 1 | Bushman | 1 | Bushman | 1 |
| Bushman | 1 | Bushman | 2 | Bushman | 1 | Bushman | 1 |
| Bushman | 1 | Bushman | 1 | Bushman | 1 | Bushman | 1 |
| Bushman | 1 | Bushman | 1 | Bushman | 1 | Bushman | 1 |
| Bushman | 1 | Bushman | 1 | Bushman | 1 | AndamanIs | 1 |
| Bushman | 1 | Bushman | 1 | Bushman | 1 | AndamanIs | 3 |
| Bushman | 1 | Bushman | 1 | Bushman | 1 | AndamanIs | 3 |
| Bushman | 1 | Bushman | 1 | Bushman | 1 | AndamanIs | 1 |
| Bushman | 1 | Bushman | 1 | Bushman | 1 | AndamanIs | 1 |
| Bushman | 1 | Bushman | 1 | Bushman | 2 | AndamanIs | 1 |
| Bushman | 1 | Bushman | 1 | Bushman | 1 | AndamanIs | 1 |
| Bushman | 1 | Bushman | 1 | Bushman | 1 | AndamanIs | 3 |
| Bushman | 2 | Bushman | 1 | Bushman | 1 | AndamanIs | 1 |

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

### K-MEANS 3 CLUSTERING TABLE – TABLE 2, CONTINUED

| Item | Cluster | Item | Cluster | Item | Cluster | Item | Cluster |
|---|---|---|---|---|---|---|---|
| AndamanIs | 1 | AndamanIs | 3 | Anyang | 1 | Anyang | 2 |
| AndamanIs | 3 | AndamanIs | 1 | Anyang | 2 | Anyang | 2 |
| AndamanIs | 1 | AndamanIs | 1 | Anyang | 2 | Anyang | 2 |
| AndamanIs | 1 | AndamanIs | 1 | Anyang | 2 | Anyang | 2 |
| AndamanIs | 1 | AndamanIs | 1 | Anyang | 1 | Anyang | 2 |
| AndamanIs | 3 | AndamanIs | 1 | Anyang | 2 | Anyang | 2 |
| AndamanIs | 1 | AndamanIs | 1 | Anyang | 2 | Anyang | 2 |
| AndamanIs | 1 | AndamanIs | 1 | Anyang | 3 | Anyang | 2 |
| AndamanIs | 1 | AndamanIs | 1 | Anyang | 2 | Anyang | 2 |
| AndamanIs | 1 | AndamanIs | 1 | Anyang | 3 | Anyang | 2 |
| AndamanIs | 1 | AndamanIs | 1 | Anyang | 2 | Anyang | 3 |
| AndamanIs | 1 | AndamanIs | 1 | Anyang | 1 | Anyang | 2 |
| AndamanIs | 1 | AndamanIs | 1 | Anyang | 2 | Anyang | 2 |
| AndamanIs | 1 | AndamanIs | 1 | Anyang | 2 | Anyang | 2 |
| AndamanIs | 1 | Anyang | 1 | Anyang | 1 | Anyang | 1 |
| AndamanIs | 1 | Anyang | 2 | Anyang | 3 | Anyang | 1 |

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

### K-MEANS 3 CLUSTERING TABLE – TABLE 2, CONTINUED

| Item | Cluster | Item | Cluster | Item | Cluster | Item | Cluster |
|---|---|---|---|---|---|---|---|
| Anyang | 3 | Arikara | 3 | Arikara | 3 | Arikara | 3 |
| Anyang | 2 | Arikara | 2 | Arikara | 3 | Arikara | 3 |
| Anyang | 2 | Arikara | 3 | Arikara | 3 | Arikara | 3 |
| Anyang | 2 | Arikara | 3 | Arikara | 3 | Arikara | 3 |
| Anyang | 3 | Arikara | 3 | Arikara | 3 | Arikara | 2 |
| Anyang | 2 | Arikara | 2 | Arikara | 2 | Arikara | 3 |
| Anyang | 1 | Arikara | 2 | Arikara | 2 | Arikara | 3 |
| Anyang | 2 | Arikara | 3 | Arikara | 2 | Australia | 2 |
| Anyang | 2 | Arikara | 3 | Arikara | 2 | Australia | 2 |
| Anyang | 2 | Arikara | 2 | Arikara | 3 | Australia | 2 |
| Anyang | 2 | Arikara | 3 | Arikara | 2 | Australia | 2 |
| Anyang | 1 | Arikara | 3 | Arikara | 3 | Australia | 3 |
| Arikara | 3 | Arikara | 3 | Arikara | 2 | Australia | 2 |
| Arikara | 3 | Arikara | 3 | Arikara | 2 | Australia | 2 |
| Arikara | 3 | Arikara | 3 | Arikara | 2 | Australia | 2 |
| Arikara | 3 | Arikara | 3 | Arikara | 2 | Australia | 2 |

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

### K-MEANS 3 CLUSTERING TABLE – TABLE 2, CONTINUED

| Item | Cluster | Item | Cluster | Item | Cluster | Item | Cluster |
|---|---|---|---|---|---|---|---|
| Australia | 2 | Australia | 3 | Australia | 3 | Dogon | 2 |
| Australia | 3 | Australia | 2 | Australia | 3 | Dogon | 1 |
| Australia | 2 | Australia | 3 | Australia | 3 | Dogon | 1 |
| Australia | 3 | Australia | 2 | Australia | 3 | Dogon | 1 |
| Australia | 3 | Australia | 3 | Australia | 2 | Dogon | 1 |
| Australia | 2 | Australia | 2 | Australia | 2 | Dogon | 2 |
| Australia | 3 | Australia | 3 | Australia | 2 | Dogon | 1 |
| Australia | 2 | Australia | 3 | Australia | 3 | Dogon | 1 |
| Australia | 3 | Australia | 2 | Australia | 2 | Dogon | 2 |
| Australia | 2 | Australia | 1 | Australia | 3 | Dogon | 1 |
| Australia | 2 | Australia | 2 | Australia | 3 | Dogon | 3 |
| Australia | 2 | Australia | 3 | Dogon | 1 | Dogon | 1 |
| Australia | 3 | Australia | 2 | Dogon | 1 | Dogon | 1 |
| Australia | 2 | Australia | 3 | Dogon | 1 | Dogon | 1 |
| Australia | 2 | Australia | 1 | Dogon | 3 | Dogon | 2 |
| Australia | 2 | Australia | 3 | Dogon | 1 | Dogon | 3 |

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

### K-MEANS 3 CLUSTERING TABLE – TABLE 2, CONTINUED

| Item | Cluster | Item | Cluster | Item | Cluster | Item | Cluster |
|---|---|---|---|---|---|---|---|
| Dogon | 1 | Dogon | 1 | Egypt | 3 | Egypt | 3 |
| Dogon | 1 | Dogon | 1 | Egypt | 3 | Egypt | 3 |
| Dogon | 3 | Dogon | 3 | Egypt | 3 | Egypt | 3 |
| Dogon | 1 | Dogon | 1 | Egypt | 2 | Egypt | 3 |
| Dogon | 1 | Dogon | 1 | Egypt | 3 | Egypt | 3 |
| Dogon | 1 | Dogon | 2 | Egypt | 3 | Egypt | 3 |
| Dogon | 1 | Dogon | 3 | Egypt | 3 | Egypt | 2 |
| Dogon | 1 | Dogon | 3 | Egypt | 3 | Egypt | 3 |
| Dogon | 3 | Dogon | 1 | Egypt | 3 | Egypt | 3 |
| Dogon | 1 | Dogon | 1 | Egypt | 3 | Egypt | 3 |
| Dogon | 2 | Dogon | 1 | Egypt | 3 | Egypt | 3 |
| Dogon | 1 | Dogon | 1 | Egypt | 3 | Egypt | 3 |
| Dogon | 1 | Egypt | 3 | Egypt | 1 | Egypt | 3 |
| Dogon | 1 | Egypt | 3 | Egypt | 3 | Egypt | 2 |
| Dogon | 2 | Egypt | 3 | Egypt | 3 | Egypt | 3 |
| Dogon | 3 | Egypt | 3 | Egypt | 1 | Egypt | 3 |

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

### K-MEANS 3 CLUSTERING TABLE – TABLE 2, CONTINUED

| Item | Cluster | Item | Cluster | Item | Cluster | Item | Cluster |
|---|---|---|---|---|---|---|---|
| Egypt | 3 | Egypt | 2 | Mokapu | 2 | Mokapu | 2 |
| Egypt | 3 | Egypt | 3 | Mokapu | 2 | Mokapu | 2 |
| Egypt | 3 | Egypt | 3 | Mokapu | 2 | Mokapu | 2 |
| Egypt | 3 | Egypt | 3 | Mokapu | 2 | Mokapu | 2 |
| Egypt | 3 | Egypt | 3 | Mokapu | 2 | Mokapu | 2 |
| Egypt | 3 | Egypt | 3 | Mokapu | 2 | Mokapu | 2 |
| Egypt | 3 | Mokapu | 2 | Mokapu | 2 | Mokapu | 2 |
| Egypt | 3 | Mokapu | 2 | Mokapu | 2 | Mokapu | 2 |
| Egypt | 3 | Mokapu | 2 | Mokapu | 2 | Mokapu | 2 |
| Egypt | 3 | Mokapu | 2 | Mokapu | 2 | Mokapu | 3 |
| Egypt | 3 | Mokapu | 2 | Mokapu | 2 | Mokapu | 2 |
| Egypt | 3 | Mokapu | 2 | Mokapu | 2 | Mokapu | 2 |
| Egypt | 1 | Mokapu | 3 | Mokapu | 2 | Mokapu | 2 |
| Egypt | 3 | Mokapu | 3 | Mokapu | 2 | Mokapu | 2 |
| Egypt | 3 | Mokapu | 2 | Mokapu | 2 | Mokapu | 2 |
| Egypt | 3 | Mokapu | 2 | Mokapu | 2 | Mokapu | 2 |

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

### K-MEANS 3 CLUSTERING TABLE – TABLE 2, CONTINUED

| Item | Cluster | Item | Cluster | Item | Cluster | Item | Cluster |
|---|---|---|---|---|---|---|---|
| Mokapu | 2 | Peru | 3 | Peru | 3 | Peru | 3 |
| Mokapu | 2 | Peru | 3 | Peru | 3 | Peru | 3 |
| Mokapu | 2 | Peru | 3 | Peru | 3 | Peru | 3 |
| Mokapu | 2 | Peru | 3 | Peru | 3 | Peru | 3 |
| Mokapu | 3 | Peru | 3 | Peru | 3 | Peru | 3 |
| Mokapu | 2 | Peru | 3 | Peru | 3 | Peru | 3 |
| Mokapu | 3 | Peru | 3 | Peru | 3 | Peru | 3 |
| Mokapu | 2 | Peru | 3 | Peru | 3 | Peru | 3 |
| Mokapu | 3 | Peru | 3 | Peru | 3 | Peru | 3 |
| Mokapu | 2 | Peru | 3 | Peru | 3 | Peru | 3 |
| Mokapu | 2 | Peru | 3 | Peru | 3 | Peru | 3 |
| Mokapu | 3 | Peru | 1 | Peru | 3 | Peru | 2 |
| Peru | 3 | Peru | 3 | Peru | 3 | Peru | 1 |
| Peru | 2 | Peru | 3 | Peru | 3 | Peru | 3 |
| Peru | 3 | Peru | 3 | Peru | 3 | Peru | 3 |
| Peru | 3 | Peru | 1 | Peru | 3 | Peru | 3 |

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

### K-MEANS 3 CLUSTERING TABLE – TABLE 2, CONTINUED

| Item | Cluster | Item | Cluster | Item | Cluster | Item | Cluster |
|---|---|---|---|---|---|---|---|
| Peru | 3 | Peru | 1 | Zalavar | 3 | Zalavar | 3 |
| Peru | 3 | Peru | 3 | Zalavar | 3 | Zalavar | 3 |
| Peru | 3 | Peru | 3 | Zalavar | 3 | Zalavar | 3 |
| Peru | 3 | Peru | 3 | Zalavar | 3 | Zalavar | 3 |
| Peru | 3 | Peru | 3 | Zalavar | 1 | Zalavar | 3 |
| Peru | 3 | Peru | 3 | Zalavar | 3 | Zalavar | 3 |
| Peru | 2 | Peru | 3 | Zalavar | 3 | Zalavar | 3 |
| Peru | 3 | Zalavar | 3 | Zalavar | 3 | Zalavar | 3 |
| Peru | 3 | Zalavar | 3 | Zalavar | 3 | Zalavar | 3 |
| Peru | 3 | Zalavar | 2 | Zalavar | 3 | Zalavar | 3 |
| Peru | 3 | Zalavar | 2 | Zalavar | 2 | Zalavar | 3 |
| Peru | 3 | Zalavar | 3 | Zalavar | 3 | Zalavar | 3 |
| Peru | 3 | Zalavar | 3 | Zalavar | 2 | Zalavar | 3 |
| Peru | 3 | Zalavar | 3 | Zalavar | 3 | Zalavar | 3 |
| Peru | 3 | Zalavar | 3 | Zalavar | 2 | Zalavar | 3 |
| Peru | 3 | Zalavar | 3 | Zalavar | 3 | Zalavar | 2 |

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

### K-MEANS 3 CLUSTERING TABLE – TABLE 2, CONTINUED

| Item | Cluster | Item | Cluster | Item | Cluster | Item | Cluster |
|---|---|---|---|---|---|---|---|
| Zalavar | 3 | Zalavar | 3 | Zalavar | 3 | Zalavar | 1 |
| Zalavar | 3 | Zalavar | 3 | Zalavar | 3 | Zalavar | 3 |
| Zalavar | 3 | Zalavar | 3 | Zalavar | 3 | Zalavar | 3 |
| Zalavar | 3 | Zalavar | 3 | Zalavar | 2 | Zalavar | 3 |
| | | | | | | Zalavar | 3 |

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

### CONTINGENCY CHART

The Contingency Chart in Figure 4 show that the groups associated with the blue color are located within Sub-Saharan Africa. The Bushman, AndamanIs, and Dogon groups are the groups within the Worldwide dataset. The Mokapu, Anyang, and Australia groups are represented by the color of orange are associated with the southern migration route. Finally, the Arikara, Egypt, Peru, and Zalavar groups are associated with grey color, and represent the northern route.

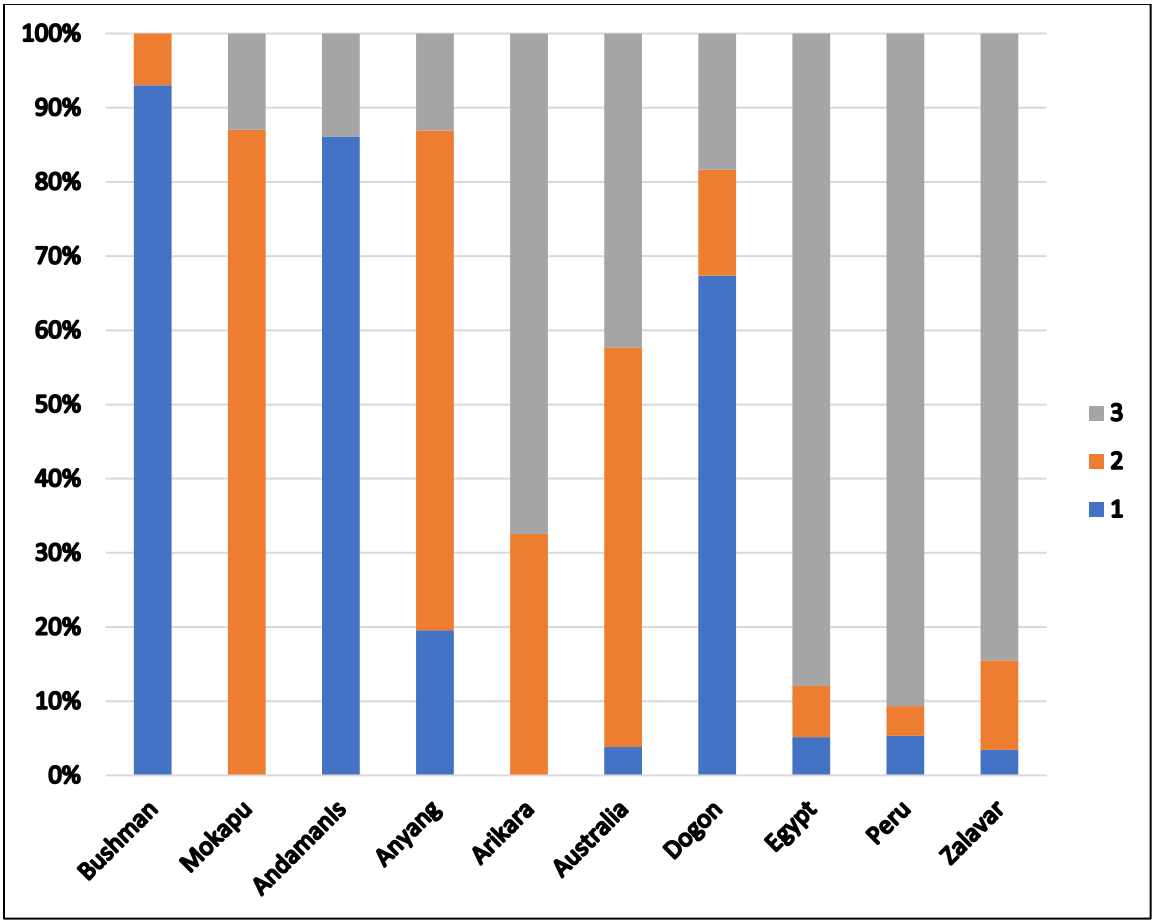



**FIGURE 4**

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

In Table 3 (below), the FST value indicates that a little over 22 percent of the variance is due to variation between populations.

**DIAGONALS OF THE R MATRIX:**

| **POPULATION** | **BIASED r(ii)** | **UNBIASED** r(ii) | **SE** |
|---|---|---|---|
| BUSHMAN | 0.350041 | 0.338413 | 0.013246 |
| ANDAMANIS | 0.182352 | 0.168463 | 0.010449 |
| ANYANG | 0.207791 | 0.196922 | 0.009867 |
| ARIKARA | 0.239985 | 0.228357 | 0.010968 |
| AUSTRALIA | 0.338023 | 0.328408 | 0.011837 |
| DOGON | 0.284115 | 0.273910 | 0.011179 |
| EGYPT | 0.166824 | 0.158204 | 0.007874 |
| MOKAPU | 0.302227 | 0.292968 | 0.010983 |
| PERU | 0.166655 | 0.159988 | 0.006920 |
| ZALAVAR | 0.110510 | 0.101890 | 0.006408 |

**TABLE 3**

**Fst = 0.234852**

**Unbiased Fst = 0.224752**

**se = 0.002466**

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

## THE RELETHFORD-BLANGERO ANALYSIS

In Table 4 (below), the results of The Relethford-Blangero Analysis are that there is a little more than .64 percent of variance between the Mean Within-group Phenotype. Six out of the ten groups are less variable than expected. Whereas four out of the ten groups are more variable than expected.

MEAN WITHIN-GROUP PHENOTYPIC VARIANCE = 0.646

**WITHIN-GROUP PHENOTYPIC VARIANCE**

| POPULATION | r(ii) | OBSERVED | EXPECTED | RESIDUAL |
|---|---|---|---|---|
| BUSHMAN | 0.338413 | 0.778 | 0.551 | 0.227 |
| ANDAMANIS | 0.168463 | 0.544 | 0.693 | -0.149 |
| ANYANG | 0.196922 | 0.644 | 0.669 | -0.025 |
| ARIKARA | 0.228357 | 0.612 | 0.643 | -0.031 |
| AUSTRALIA | 0.328408 | 0.598 | 0.560 | 0.038 |
| DOGON | 0.273910 | 0.712 | 0.605 | 0.107 |
| EGYPT | 0.158204 | 0.646 | 0.701 | -0.055 |
| MOKAPU | 0.292968 | 0.683 | 0.589 | 0.094 |
| PERU | 0.159988 | 0.620 | 0.700 | -0.080 |
| ZALAVAR | 0.101890 | 0.622 | 0.748 | -0.126 |

**TABLE 4**

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

In Figure 5 there are five clusters of groups. The first cluster occurs with H and C. The second clustering occurs with groups B, G, and J. The third clustering occurs with groups D and I. The fourth clustering occurs with groups F and A. Finally, the last clustering Group is group E.

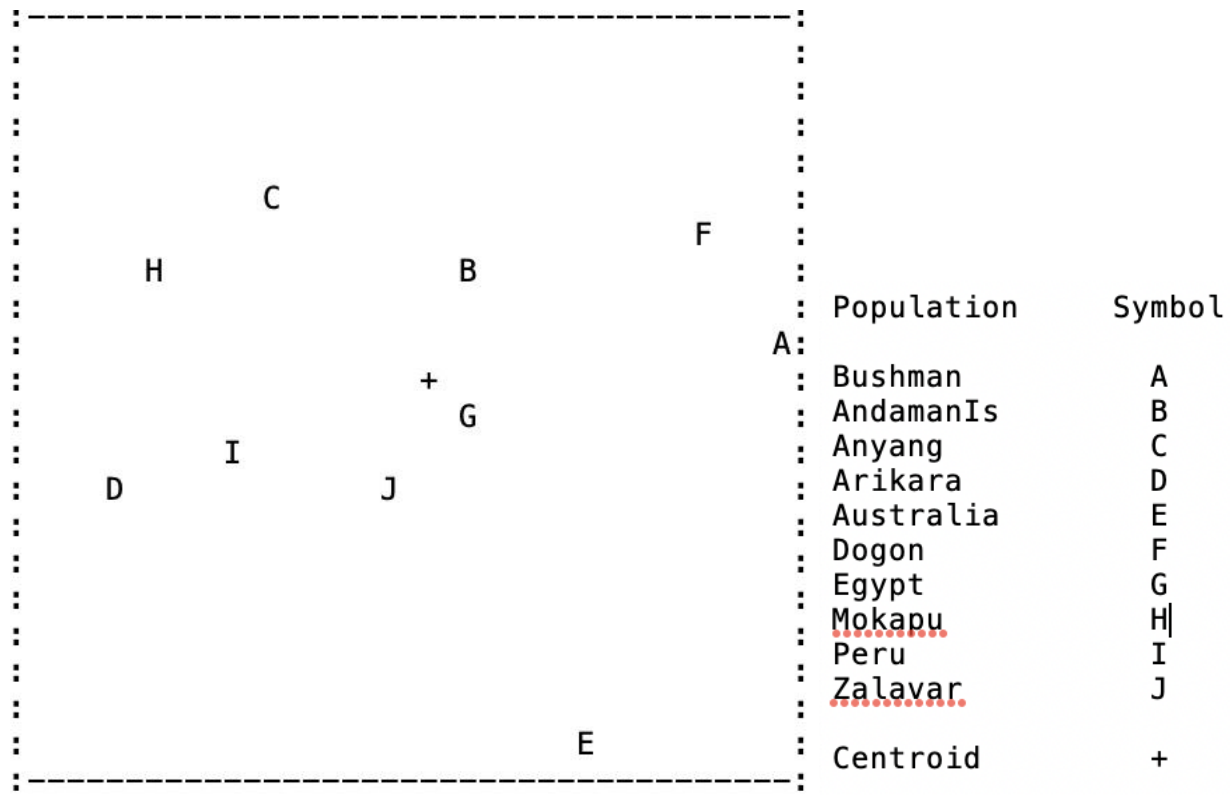



**FIGURE 5**

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

Table 5 (below) indicates that the majority of the groups have gene flow within the groups. However, there are some anomalies where the groups have a positive R-Matrix which indicates that there is gene flow outside of the groups.

**R MATRIX:**
(standard errors in parentheses)

| POPULATION | r(ii) | STANDARD ERRORS |
|---|---|---|
| BUSHMAN | 0.338413 | (0.013246) |
| ANDAMANIS | 0.168463 | (0.010449) |
| ANYANG | 0.196922 | (0.009867) |
| ARIKARA | 0.228357 | (0.010968) |
| AUSTRALIA | 0.328408 | (0.011837) |
| DOGON | 0.273910 | (0.011179) |
| EGYPT | 0.158204 | (0.007874) |
| MOKAPU | 0.292968 | (0.010983) |
| PERU | 0.159988 | (0.006920) |
| ZALAVAR | 0.101890 | (0.006408) |

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

**RESULTS, CONTINUED**

**GENE FLOW WITHIN THE GROUPS**
(standard errors in parentheses)

| GROUP 1 | GROUP 2 | r(ii) | STANDARD ERRORS |
|---|---|---|---|
| BUSHMAN | ANDAMANIS | -0.003493 | (0.008674) |
| BUSHMAN | ANYANG | -0.032048 | (0.008188) |
| BUSHMAN | ARIKARA | -0.129344 | (0.008599) |
| BUSHMAN | AUSTRALIA | 0.017170 | (0.008867) |
| BUSHMAN | DOGON | 0.068942 | (0.008608) |
| BUSHMAN | EGYPT | -0.024925 | (0.007309) |
| BUSHMAN | MOKAPU | -0.142459 | (0.008532) |
| BUSHMAN | PERU | -0.100221 | (0.006785) |
| BUSHMAN | ZALAVAR | -0.003663 | (0.006809) |
| ANDAMANIS | ANYANG | -0.019709 | (0.007243) |
| ANDAMANIS | ARIKARA | -0.037838 | (0.007666) |
| ANDAMANIS | AUSTRALIA | -0.080662 | (0.008336) |
| ANDAMANIS | DOGON | 0.028346 | (0.007911) |
| ANDAMANIS | EGYPT | -0.000235 | (0.006474) |
| ANDAMANIS | MOKAPU | -0.026013 | (0.007964) |
| ANDAMANIS | PERU | -0.003554 | (0.006168) |
| ANDAMANIS | ZALAVAR | -0.039194 | (0.005786) |

**TABLE 5**

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

**RESULTS, CONTINUED**

**GENE FLOW WITHIN THE GROUPS, CONTINUED**
(standard errors in parentheses)

| GROUP 1 | GROUP 2 | r(ii) | STANDARD ERRORS |
|---|---|---|---|
| ANYANG | ARIKARA | 0.030008 | (0.007359) |
| ANYANG | AUSTRALIA | -0.125145 | (0.007818) |
| ANYANG | DOGON | -0.013471 | (0.007492) |
| ANYANG | EGYPT | -0.067567 | (0.006233) |
| ANYANG | MOKAPU | 0.057745 | (0.007492) |
| ANYANG | PERU | 0.000022 | (0.005869) |
| ANYANG | ZALAVAR | -0.037625 | (0.005679) |
| ARIKARA | AUSTRALIA | -0.031358 | (0.008199) |
| ARIKARA | DOGON | -0.162775 | (0.007874) |
| ARIKARA | EGYPT | -0.056401 | (0.006573) |
| ARIKARA | MOKAPU | 0.041981 | (0.007863) |
| ARIKARA | PERU | 0.089574 | (0.006175) |
| ARIKARA | ZALAVAR | 0.016168 | (0.006012) |
| AUSTRALIA | DOGON | 0.000144 | (0.008162) |
| AUSTRALIA | EGYPT | -0.023081 | (0.006978) |
| AUSTRALIA | MOKAPU | -0.058305 | (0.008065) |
| AUSTRALIA | PERU | -0.039961 | (0.006446) |

**TABLE 5**

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

**RESULTS, CONTINUED**

**GENE FLOW WITHIN THE GROUPS, CONTINUED**
(standard errors in parentheses)

| GROUP 1 | GROUP 2 | r(ii) | STANDARD ERRORS |
|---|---|---|---|
| AUSTRALIA | ZALAVAR | 0.003174 | (0.006546) |
| DOGON | EGYPT | 0.017628 | (0.006689) |
| DOGON | MOKAPU | -0.065937 | (0.007848) |
| DOGON | PERU | -0.082253 | (0.006224) |
| DOGON | ZALAVAR | -0.074740 | (0.006209) |
| EGYPT | MOKAPU | -0.044032 | (0.006688) |
| EGYPT | PERU | -0.023416 | (0.005241) |
| EGYPT | ZALAVAR | 0.055203 | (0.005076) |
| MOKAPU | PERU | -0.021112 | (0.006192) |
| MOKAPU | ZALAVAR | -0.044096 | (0.006253) |
| PERU | ZALAVAR | 0.014264 | (0.004840) |

**TABLE 5**

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

## HIERARCHICAL CLUSTERING DENDROGRAM

Due to the large amount of information on the Hierarchical Clustering Dendrogram, Figure 6 (below), it is difficult to read. As a result, a UPGMA and a neighbor joining tree was created using the means of the groups allowing for an easier read of the groups.

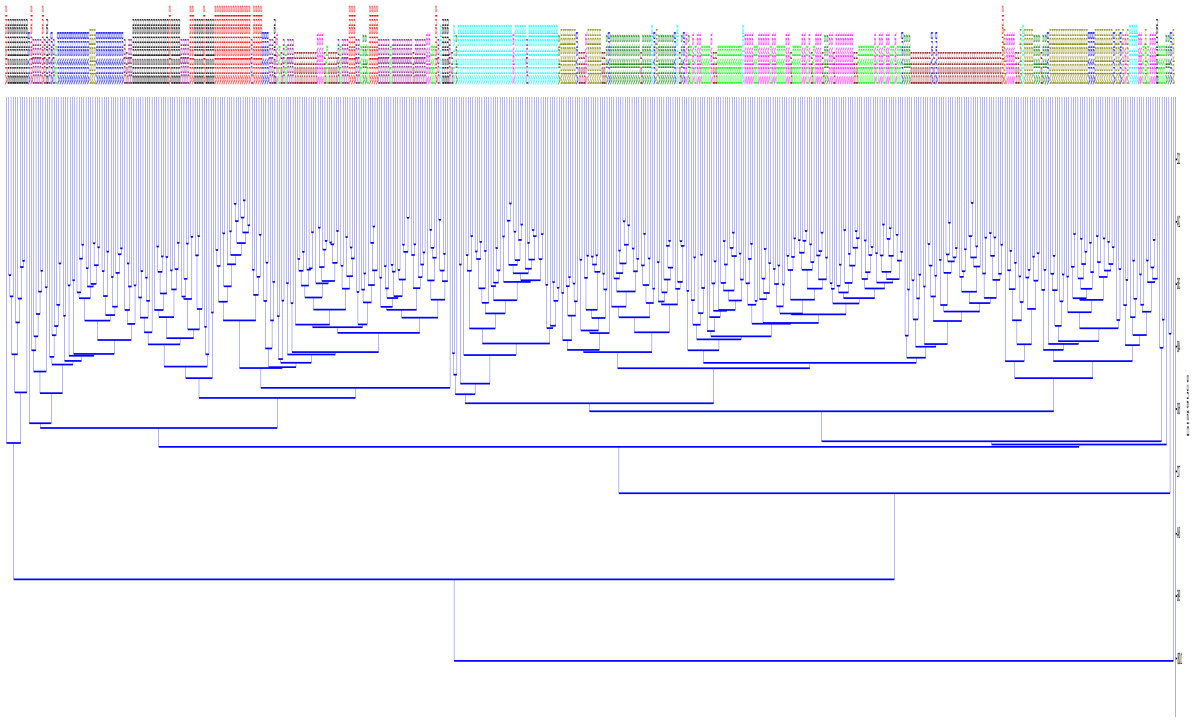


**FIGURE 6**

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

### UPGMA DENDROGRAM

The UPGMA Dendrogram, Figure 7 (below), shows the Andaman, Dogon, and Bushman to be closely related. This grouping is the most distant. In addition, the Anyang and Mokapu groups are closely related. The next groups that are closely related are the Arikara, Egypt, Peru, Zalavar, and Australia.

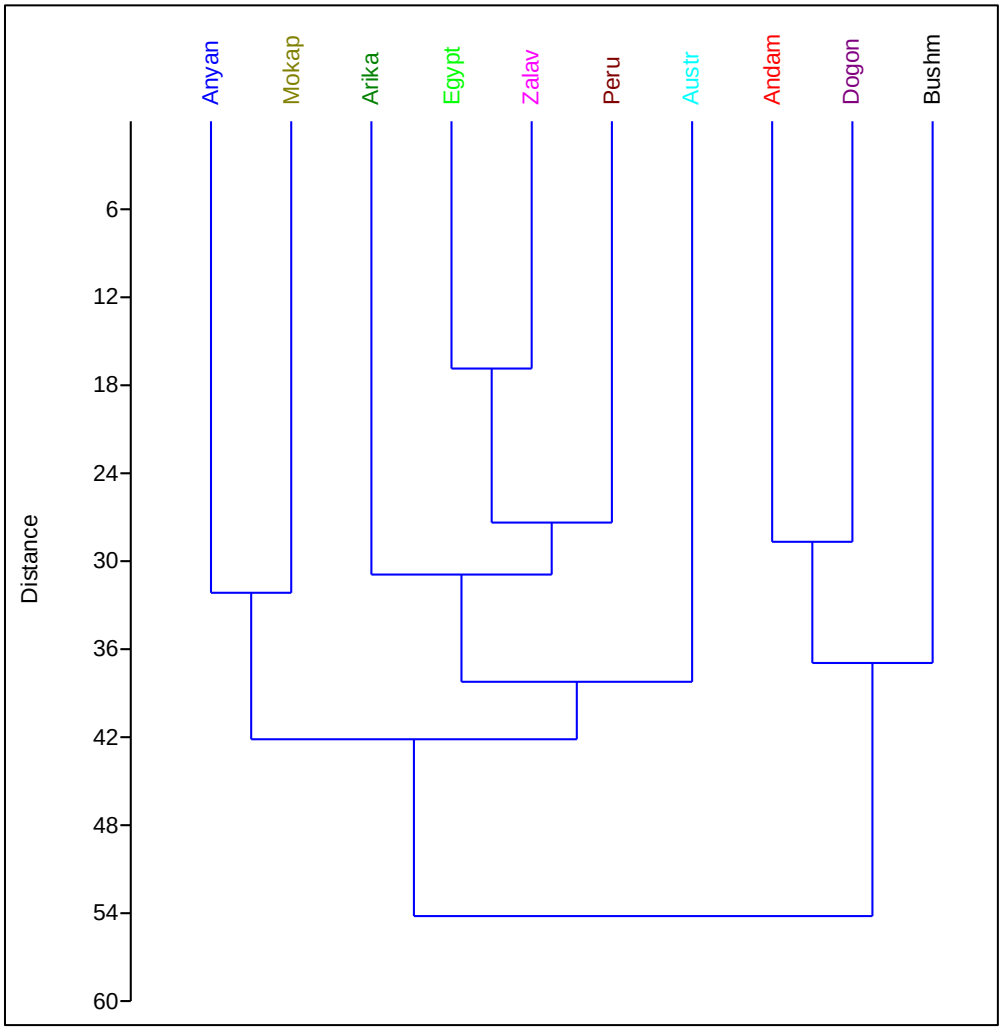



**FIGURE 7**

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

## NEIGHBOR-JOINING TREES

Figure 8 and 9 are both Neighbor-Joining Trees, where Figure 8 is unrooted, and Figure 9 is rooted. Both Figure 8 and 9 shows the Bushman group to be the outgroup of all ten groups within the Worldwide Dataset. It all shows the Bushman, AndamanIs, and Dogon groups to be most closely related, while being the most distantly located. Figure 8 and 9, then goes on to group the Anyang, Mokapu, and Australia groups together. The final branching of Figure 8 and 9's phylogram is the Arikara, Peru, Zalavar, and Egypt groups.

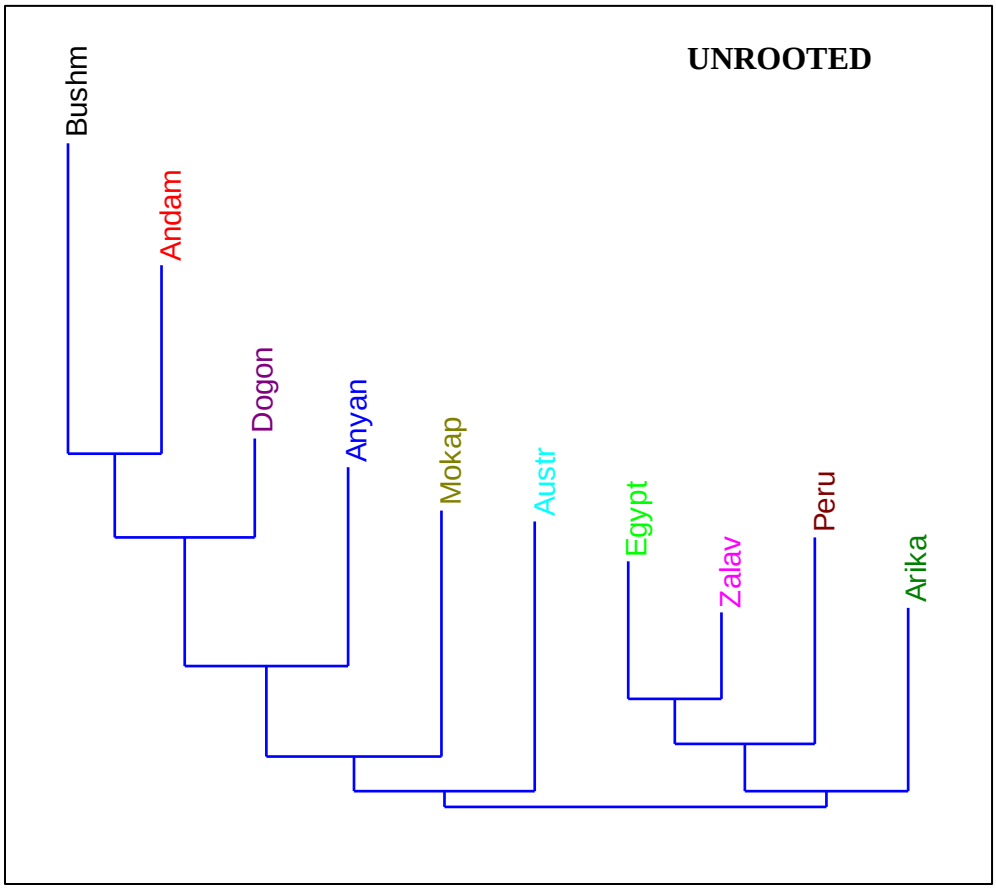



**FIGURE 8**

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

## RESULTS, CONTINUED

### NEIGHBOR-JOINING TREES, CONTINUED

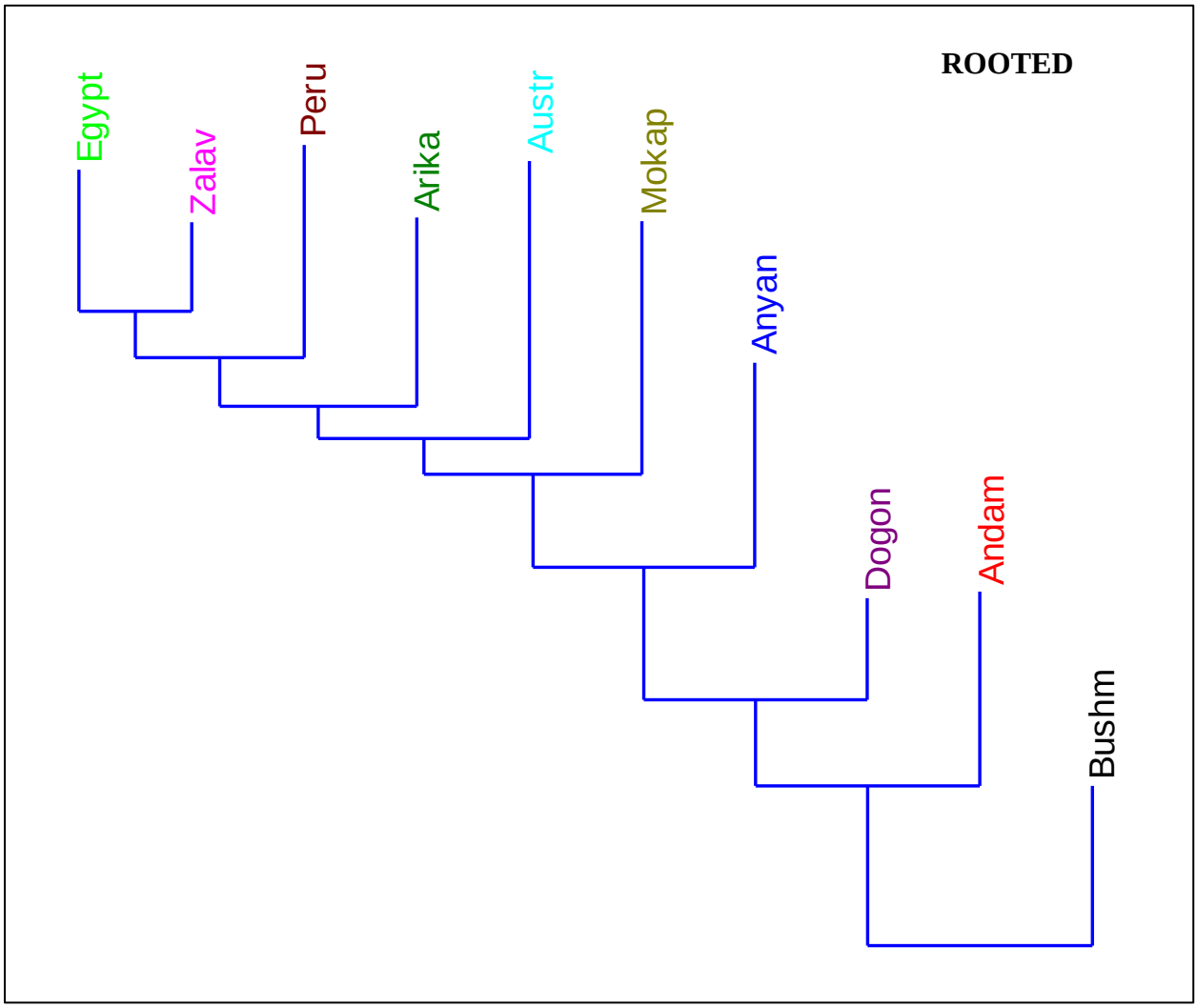



**FIGURE 9**

# ATTACHMENT 11 - A PRINCIPAL COMPONENTS ANALYSIS, CONTINUED

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Hammer, Ø., Harper, D.A.T., Ryan, P.D. 2001. PAST: Paleontological statistics software package for education and data analysis. Palaeontologia Electronica 4(1): 9pp. http://palaeo- electronica.org/2001_1/past/issue1_01.html

Written by John H. Relethford, available at http://employees.oneonta.edu/relethjh/programs/

Statistical Services Centre, University of Reading, UK, 2004. Instat+ an interactive statistical pack- age. http://www.reading.ac.uk/ssc/resource-packs/ICRAF_2007-11-15/InStat/Instat.html.

# CJUS 488: FORENSIC SCIENCE THE CRIME LAB AND BEYOND

During this course as demonstrated in the paper below, I applied the fundamental theories and practices of forensic science. I broaden my skill set in areas such as: how to draw conclusions from forensic evidence, the roles of forensic scientists, police officers, attorneys, and others in a criminal investigation, types of questions and analyses addressed by forensic sciences, the existence and nature of new and emerging forensic sciences, and the application of forensic sciences to a variety of modern problems, such as wildlife and conservation, national security, organized crime, and history.

## ATTACHMENT 12 - FORENSIC ANTHROPOLOGY

Forensic Anthropology is a way to provide identity to the otherwise unidentifiable remains and embodies the applications of both knowledge and methodology of anthropology while applying it to medico-legal issues (Ubelaker 2017). Forensic Anthropology utilizes both the biological and archaeological aspects of applied anthropology. I will provide a brief look into the history of forensic anthropology as well as examining the required qualifications/certifications, and the types of court cases these anthropologists are utilized in.

Historically physical/biological anthropologists were hired by law enforcement agencies to assist with the identification of unknown remains (Traithepchanapai et al. 2016). This paved the way to create a specific field called Forensic Anthropology where an individual specialized in both physical and biological anthropology. Forensic Anthropology gained its start in the late 19$^{th}$ and early 20$^{th}$ centuries (Steadman 2103, Ubelaker 2017). A Forensic Anthropologist's role is to assist in the review of skeletal remains and to determine identity through biological characteristics such

## ATTACHMENT 12 - FORENSIC ANTHROPOLOGY, CONTINUED

as sex, age, stature, and ancestry (Steadman 2013, Traithepchanapai et al. 2016). In addition, these anthropologists look for time of death, possible trauma related injuries, and/or review pathology that led to death (Steadman 2013, Traithepchanapai et al. 2016). For these methods most scholars tend to agree that they are population specific (Traithepchanapai et al. 2016). Forensic Anthropology can be broken down into three periods: Formative, Consolidation, and Modern (Tersigni-Tarrant and Shirley 2013). The Formative Period occurred during the early 1800s and ended in 1938 (Tersigni-Tarrant and Shirley 2013). This Formative Period came into being when Oliver Wendall Holmes and Jefferies Wymann utilized their knowledge of osteology to discern who killed Dr. George Parkman; however, the first avid practitioner of Forensic Anthropology was Thomas Dwight (Tersigni-Tarrant and Shirley 2013). Thomas Dwight is considered the father of Forensic Anthropology (Stewart 1979). He earned this title for being the first American to discuss utilizing human skeleton remains to ascertain information to support identification (Tersigni-Tarrant and Shirley 2013).

There is debate as to the who the actual founding father of American Forensic Anthropology was during the Formative Period. Some consider Ales Hrdlicka to be the founding father of American Forensic Anthropology by W.M. Krogman (1976). Hrdlicka was the founder of the American Association of Physical Anthropology and the American Journal of Physical Anthropology (Tersigni-Tarrant and Shirley 2013). His studies focused on quantitative measurements of the human skeleton (Tersigni-Tarrant and Shirley 2013). Many Forensic Anthropologists during the Formative Period were practicing anatomists or physical anthropologists (Tersigni-Tarrant and Shirley 2013). There is one exception to this, Harris H. Wilder created a notable contribution to Forensic Anthropology when it came to identification.

## ATTACHMENT 12 - FORENSIC ANTHROPOLOGY, CONTINUED

Wilder was originally a Zoologist who based on interest became a Physical Anthropologist. The title of Physical Anthropologist was given to him because Forensic Anthropology had not been identified at this time, so as result they had no name for these practices. (Tersigni-Tarrant and Shirley 2013).

The end of the Formative Period and beginning of the Consolidation Period was based on the publishing of Wilton Marion Krogmans' *Guide to the Identification of Human Skeletal Material* in the Federal Bureau of Investigations Law Enforcement Bulletin in 1939. This became the primary text for Physical Anthropologists doing Forensic Anthropology at that time. These guidelines made it accessible for all physical anthropologist to learn how to identify human skeletal materials. (Tersigni-Tarrant and Shirley 2013). The Consolidation Period occurred from 1939 to 1971 (Tersigni-Tarrant and Shirley 2013).

The Modern Period began in 1972 and is still ongoing today (Tersigni-Tarrant and Shirley 2013). The founding of the physical anthropology section of the American Academy of Forensic Sciences is often referred to as the beginning of the Formative Period (Tersigni-Tarrant and Shirley 2013). It was also at this time when the term Forensic Anthropology first began to be used on a regular basis to refer to practitioners in this field (Tersigni-Tarrant and Shirley 2013). Modern-day Forensic Anthropology applies not only to single cases, but also war crime cases and mass disasters (Cattaneo 2006). Historically, Forensic Anthropologists reviewed remains that were brought to them. Modern-day, Forensic Anthropologists are involved in the search and retrieval of human remains (Cattaneo 2006). Present-day Forensic Anthropologists need to be trained for the archaeological techniques needed to perform a proper retrieval of remains to collect all evidence

## ATTACHMENT 12 - FORENSIC ANTHROPOLOGY, CONTINUED

(Cattaneo 2006). In addition to being fully trained in archaeological techniques, Forensic Anthropologists are trained in the techniques to perform a proper search for buried human remains as well as surface scattered remains (Cattaneo 2006). As a result of searching and retrieving human remains, Forensic Anthropologists determine what species the remains belong to through visual or DNA analysis looking for specific protein compositions. (Cattaneo 2006). Previously Post-Mortem Interval was conducted through microscopic and macroscopic methods looking for soft tissue residues, however modern-day methods utilize soil and test for volatile fatty acids, cations, and anions that soak into the soil during decomposition (Cattaneo 2006). Overall, as more research is done in the field of Forensic Anthropology the more the methods will change and the accuracy more precise.

Each country has a different history when it comes to the utilization of Forensic Anthropologists. The development of this discipline depends on history, status of education, legislation, and forensic practice (Traithepchanapai et al. 2016). I will discuss a few countries to show the differences between the utilization of Forensic Anthropologists amongst nations. In 1930, Mr. Sankas of Thailand was considered to be the founder of Forensic Anthropology (Traithepchanapai et al. 2016). A recent Thailand skeletal collection, created between 1993 and 1996, allowed for researchers to figure out age, sex, ancestry, and stature found within their country's population (Traithepchanapai et al. 2016). When investigating unnatural deaths in Thailand, the police force is in charge of victim identification and establishing manner of death (Traithepchanapai et al. 2016). These officers obtain reports from forensic pathologists who write the autopsy reports, details of injuries, and cause of death (Traithepchanapai et al. 2016). In

## ATTACHMENT 12 - FORENSIC ANTHROPOLOGY, CONTINUED

addition to all the previously aforementioned tasks, forensic pathologists also conduct all Forensic Anthropologists' duties (Traithepchanapai et al. 2016).

Forensic Anthropology within Australia had a similar yet distinct start, when compared to the United States. Originally in Australia, similar to the start in the United States, anatomists were called upon by police investigators whenever skeletal remains were present that required the expertise of someone with extensive osteological knowledge (Mallett and Evison 2017). The first true acknowledgement of Forensic Anthropology in Australia occurred after a presentation was given by two American Forensic Anthropologists, William Bass and Diane France (Mallett and Evison 2017). Forensic Anthropology within Australia grew notably from 1996 to 2000 (Mallett and Evison 2017). Due to Forensic Anthropologists clear recognition of casualties from many mass atrocities and disasters in Australia, they are now recognized for their attributes and requested to aid in the judicial process (Mallett and Evison 2017). The role of Forensic Anthropologists is similar around the world, they all aid in the identification of human remains in both single death cases as well as mass fatality incidents. In addition, Forensic Anthropologists around the world aid in the search and recovery of human remains. Over the past five years in Australia, research, training, and teaching In Forensic Anthropology have advanced considerably (Mallett and Evison 2017). However, throughout Australia, Forensic Anthropology is still not acknowledged as a core forensic competency (Mallett and Evison 2017).

For Forensic Anthropologists obtaining board certification is a way for them to be identified as qualified experts. This American Board of Forensic Anthropology certification is obtained through an examination that contains rigorous educational and experience requirements (Ubelaker 2017). To be eligible to go through the certification process you must meet a few

## ATTACHMENT 12 - FORENSIC ANTHROPOLOGY, CONTINUED

requirements. This first is to be a permanent resident of either the United States, Canada, or their respective territories ( http://theabfa.org accessed December 1st, 2018). In some circumstances, if you are not a permanent resident of these nations or territories a petition can be made to the board of directors (Ubelaker 2017). In addition, the individual desiring certification must have their doctoral degree in physical/biological anthropology or its equivalent, along with three years of experience in forensic anthropology after receipt of the degree (http://theabfa.org accessed December 1st, 2018). The applicant must also have letters of recommendation from at least two different institutions and include one American Board of Forensic Anthropology diplomate (http://theabfa.org accessed December 1st, 2018). The final requirement which must be met is to include three redacted forensic cases with supporting documents (http://theabfa.org accessed December 1st, 2018). If the applicant qualifies through all the aforementioned requirements, then they must successfully complete a multiple choice and practical examination (http://theabfa.org accessed December 1st, 2018). As of 2016, only 80 board certified anthropologists were active (Bethard 2017). Whereas in 2017, there are now 119 Forensic Anthropologists certified by the American Board of Forensic Anthropology (Ubelaker 2017).

Becoming certified in Europe has similar, yet entirely different criteria and different levels of certification. The Forensic Anthropology Society of Europe initiated a certification program that includes educational and experience requirements with successful completion of an examination (Ubelaker 2017). This is similar to the American Board of Forensic Anthropologists. The Forensic Anthropology Society of Europe consists of two levels of certification. Level One certification requires both proof of degree, either MD or PhD in a relevant field of study, along with 5 years of experience after receipt of the degree

## ATTACHMENT 12 - FORENSIC ANTHROPOLOGY, CONTINUED

(http://forensicanthropology.eu/activities/fase-certification/ accessed December 1st, 2018). In addition, the applicant must submit 20 case reports after the receipt of the degree (http://forensicanthropology.eu/activities/fase-certification/ accessed December 1st, 2018). Obtaining a level two certification requires a Master's degree or the equivalent in a relative field, in addition to training and casework experience (http://forensicanthropology.eu/activities/fase-certification/ accessed December 1st, 2018). Both certification levels require an intensive examination that the applicant must successfully pass (http://forensicanthropology.eu/activities/fase-certification/ accessed December 1st, 2018). In addition, the Forensic Anthropology Society of Europe has an awards honoris causa certification for those who working as a Forensic Anthropologist with at least 15 years of practice who are deemed worthy by the Board of Directors (http://forensicanthropology.eu/activities/fase-certification/ accessed December 1st, 2018).

Another certification system for Forensic Anthropologists is based within the United Kingdom and is sponsored by the Royal Anthropological Institute, the British Association of Forensic Anthropology, and the Office of Forensic Science regulation (Ubelaker 2017). This system offers three levels of certification, with similar requirements of education and experience as well as an examination (Ubelaker 2017).

One final certification system for Forensic Anthropologists is based in Latin America and is sponsored by the Latin American Association of Forensic Anthropology (Ubelaker 2017). Similar, to all the other certification programs, this one also involves education and experience requirements in addition to an examination (Ubelaker 2017). This association differs from others in that it holds online meetings for its certified members. This is done for member convenience

while allowing for collaboration of casework and research experience among the certified anthropologists (Ubelaker 2017).

Unfortunately, there is a lack of Board certification for Forensic Anthropologists located in the Australasian region; however, accreditation is currently being discussed by the Forensic Anthropology Scientific Working Group, approved by the Australia New Zealand Policing Advisory Agency and the National Institute of Forensic Science (Mallett and Evison 2017).

Currently there are many certifications for tons of Forensic Sciences in the Australasian region http://www.anzpaa.org.au/forensic-science/resources/affsab Accessed December 1st, 2018). As of right now, this means that anyone can claim to be a Forensic Anthropologist. As a result, it makes it very difficult for Police to have ways to check the suitability of that person to practice and provide evidence in forensic cases (Mallett and Evison 2017).

Utilizing Forensic Anthropology can be seen in criminal cases throughout the legal system. When human remains are usually discovered, the primary objective in the investigation is to identify the victim and determine cause and manner of death (Grisbaum and Ubelaker 2001). If the remains are usually found relatively soon after death, then these objectives are usually accomplished by the law enforcement agency and forensic pathologist (Grisbaum and Ubelaker 2001). When the remains are not discovered until long after death, then a Forensic Anthropologist is needed (Grisbaum and Ubelaker 2001). The job of the Forensic Anthropologist is to establish a profile of age, ancestry, sex, and stature and provide an assessment of trauma (Grisbaum and Ubelaker 2001).

I will examine utilization of Forensic Anthropology within a few cases, to give a greater understanding of the relationship between the Criminal Justice Court Systems and Forensic

## ATTACHMENT 12 - FORENSIC ANTHROPOLOGY, CONTINUED

Anthropology. A case in Germany illustrates the importance of the role of the Forensic Anthropologist in providing an identity to an otherwise unidentifiable individual. Partially skeletonized remains were found in Germany, based on the unusual, flexed position of the individual as well as the fact that the skeleton was hidden underneath a slab of concrete, readily implied foul play (Kemkes-Grottenthaler 2001). To aid the police in their criminal investigation, a biological profile was made to effectively narrow the police investigator's search parameters (Kemkes-Grottenthaler 2001). In addition, DNA was extracted from the femur to provide some more insight as to who the individual was (Kemkes-Grottenthaler 2001). In this specific case, the biological profile, which included age, ancestry, stature, and unique anomalies aided the police investigators in finding a positive match to a missing person to link the remains with (Kemkes-Grottenthaler 2001).

Looking at a case that was completed in New York City can show how Forensic Anthropology relies on other forensic analysts to assist in figuring out the identity of skeletal remains. For this investigation, investigators and the medical examiner took the key roles, but specialists like Forensic Anthropologists, radiologists, and molecular biologists all worked together to form the identity of the remains (Ubelaker et al. 2003). The radiologist was needed to exclude possible victims, and as a result greatly facilitated the investigation (Ubelaker 2003). In addition to radiologists excluding victims, radiologists combined with the Forensic Anthropologist were able to pinpoint the age at death and sex of the individual (Ubelaker 2003). The Forensic Anthropologist also drew attention to a healed fracture and other unique anatomical features that aided in identification of the human skeletal remains (Ubelaker 2003). The Forensic

## ATTACHMENT 12 - FORENSIC ANTHROPOLOGY, CONTINUED

Anthropologist was able to articulate three of the segments showing they originated from one individual (Ubelaker 2003). The Molecular Biologist performed an analysis and was able to match the probable identification of the individual to the human remains (Ubelaker 2003). As a result of the conclusions derived from the forensic scientists, the authorities were ultimately convinced that the identification was indeed accurate and found to be the remains of a missing thirteen-year-old girl (Ubelaker 2003). The authorities listed the cause of death as trauma of undetermined etiology, and the case never went to trial due to lack of evidence to convict the suspect (Ubelaker 2003). Overall, these forensic scientists aided in the criminal investigation, and as a result they can be called to court as expert witnesses if deemed necessary.

A final set of cases to show the role of the Forensic Anthropologist in the legal system are cases that were submitted to the Smithsonian Institution by the Federal Bureau of Investigations. The cases that the Federal Bureau of Investigation sent to the Smithsonian were sent to the Bureau from local law enforcement agencies (Grisbaum and Ubelaker 2001). These cases represent a variety of patterns (Grisbaum and Ubelaker 2001). The observed variation in all the cases can be explained in relation to the growth of the discipline (Grisbaum and Ubelaker 2001). As more Forensic Anthropologists emerged the less cases were being sent to the Federal Bureau of Investigations, which in turn resulted in less need for a major overseer of the discipline. As the number of Forensic Anthropologists increased their local involvement increased as well (Grisbaum and Ubelaker 2001). The cases studied in the Federal Bureau of Investigation encompass a wide variety of demographic ranges, and have exhibited varied forms, including antemortem, perimortem, and postmortem (Grisbaum and Ubelaker 2001). The Federal Bureau of Investigations provided many services to local agencies including demographic profiling,

## ATTACHMENT 12 - FORENSIC ANTHROPOLOGY, CONTINUED

assessment of trauma and attempts at obtaining a positive identification (Grisbaum and Ubelaker 2001). The largest origins of these cases seen were from the South and West (Grisbaum and Ubelaker 2001). This could be due to the large populations in these areas of the United States. In addition to the South and West being the largest origin of cases, May through November are significant months for recovery of remains. This is due to the increased human activities in rural areas along with greater visibility during the summer months (Grisbaum and Ubelaker 2001).

Forensic anthropology was founded around the late 19$^{th}$/early 20$^{th}$ centuries. There are multiple ways to become a certified Forensic Anthropologist, however they all contain education and experience requirements in addition to the successful completion of an examination. Forensic Anthropologists when used within the legal systems are used in criminal context. Forensic Anthropology represents a dynamically evolving complex discipline utilizing both Forensic Science and Biological/Physical Anthropology.

# ATTACHMENT 12 - FORENSIC ANTHROPOLOGY, CONTINUED

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# ANTY 500: CONTEMPORARY ANTHROPOLOGICAL THOUGHT

Several in-class presentations were completed that dealt with major theoretical frameworks that are important to today's anthropology. I delved into numerous sub-disciplines of anthropology such as biological, socio-cultural, linguistic, and archaeological and engaged in readings and discussions inclusive of evolution, ecology, and multiple social theoretical paradigms.