A GEOMETRIC MORPHOMETRIC ANALYSIS OF HOMINID

MAXILLAE AND MANDIBLES

An Undergraduate Research Scholars Thesis

by

JUDE JOSEPH MAGARO JR.

Submitted to Honors and Undergraduate Research
Texas A&M University
in partial fulfillment of the requirements for the designation as an

UNDERGRADUATE RESEARCH SCHOLAR

Approved by
Research Advisor: Dr. Darryl de Ruiter

May 2014

Major: Anthropology

TABLE OF CONTENTS

ABSTRACT

A Geometric Morphometric Analysis of Hominin Maxillae and Mandibles. (May 2014)

Jude Joseph Magaro Jr.
Department of Anthropology
Texas A&M University

Research Advisor: Dr. Darryl de Ruiter
Department of Anthropology

Fossil mandibular elements assigned to the taxon *Australopithecus sediba* were found at Malapa, South Africa. The mandibular elements have since been used to create a fully reconstructed version of the mandible of the animal. In order to better understand how fossil species separate with jaw bones an analysis will be done on extant species of great apes, gibbons, and humans. If the jaw bones do separate as expected it will be possible to then diagnose species based on jaw bone data, particularly if only data from one of the jaw bones is available.

DEDICATION

I wish to dedicate this work to my parents, my Aunt Rose, and my best friend Muhammad Ali Mendha without whom none of my academic success would have been possible. My father fostered a love of science and inquiry in me from the very beginning by sharing his passion for entomology with me as a child. My mother was always incredibly supportive of any undertaking I made and without her I doubt that I would have had the strength to come this far; even when her health was failing she always had a warm smile and bolstering wisdom for me. My Aunt Rose has always been a guiding force in my life and when my parents left this world she stepped in and kept me focused on my passions, without her I don't think I would have rediscovered my love of learning. Ali Mendha is my best friend and has been there for me throughout the good times and the bad. Ali and I have travelled the world together and I treasure our time and adventures together past, present, and future; he is always there for me and I could not ask for a better friend.

ACKOWNLEDGEMENTS

CHAPTER I

INTRODUCTION

One of the fundamental problems in palaeoanthropology is the separation of species due to the fragmentary nature of the fossil record (Sarmiento 1998). To address the problem the field has turned to detecting patterns in morphology that are not immediately visible with traditional measurement techniques (Slice 2007). The primary method used to detect these patterns are the statistical techniques known as geometric morphometrics. Geometric morphometrics allows the researcher to quantify shape and size in a very precise way such that even regional variation within a species is detectable (Hennessey et. al 2002). In application to the fossil record morphometrics has the ability to help repair portions of incomplete data that arise due to poor preservation of a specimen such as crushing during fossilization or breakage during excavation (Strauss et al. 2006). In this study geometric morphometrics has been applied to the study of living hominoid jaw bones to see if their morphology accurately separate species. The reason for performing this study on the living hominoids before applying it to the fossil record is to ensure that the method will perform as predicted. Using the living hominoids to model a method before application to the fossil record has great benefits in that a sufficient sample size is readily available for analysis, whereas in the fossil record some of the specimens we have are the only known representative of that species. Many other researchers have performed similar studies on other parts of hominoid anatomy in both extant and extinct species (Lague 1996, Francois 2000, Lockwood 2002, Couette 2010, Nicholson 2006). Our study focuses on the morphology of the maxilla and mandible of all of the specimens measured, because the morphology of the jaw bones tends to be diagnostic in the separation of species (Rosas & Bastir 2004). However, studies that have been previously been conducted focus on either the

maxillofacial complex or mandible exclusively, in this case we have combined data from both of the jaw bones to see if their collective data are species diagnostic. Performing this analysis is the preamble to performing further statistical operations that will reveal more about the exact relationship between the morphology of the jaw bones and the ways it can be applied to the fossil record. First though, it is necessary to see if the first ordination, meaning that the data points will cluster into groups, of maxillary and mandibular data do separate out species as predicted before the more advanced geometric morphometric methods can be applied.

CHAPTER II

METHODS

The data for this study was collected at the American Museum of Natural History (AMNH) in New York, NY, and the Forensic Anthropology Center at Texas State University (FACTS). A suite of fifty measurements were taken from each specimen, thirty from the mandible and twenty from the maxilla respectively. The measurements were taken using digital callipers to measure inter-landmark distances on each specimen. The total number of specimens is thirty-nine individuals consisting of great apes, gibbons, and humans. The number of males and females for each genus in the study was evenly divided except in the case of gorillas due to a limited number of female specimens. A complete specimen catalogue is included in Table 1. Once all of the data was collected a geometric morphometric analysis was then performed using the programs Excel and JMP.

The data was transferred into an excel spreadsheet where it was then linearized by using a natural log transformation so that the data could then be processed by the JMP program. In order to compensate for one missing maxillary data point in one of the human specimens, it was necessary to perform data imputation. In order to properly impute the missing data point, it was necessary to use both maxillary and mandibular data to account for covariance within the data set. The imputation process allows for the replacement of missing data points with mathematically neutral numbers that will not influence the rest of the data during analysis. The data imputation procedure requires that a design matrix be used with the linearized data in order to code which data belongs to certain discrete categories, in this case which genus of primate, and whether that specimen was male or female (Zelditch 2012). A design matrix consists of a list of ones and zeroes that code between two contrasted categories per column. Once the missing data point was imputed it was possible to begin performing matrix multiplication to generate variance and covariance between the data. Generating the variances

and covariances of the data first involves centering the data on the origin, which is done by multiplying the data sets and then subtracting the means of each column of the data, then that number must be squared and divided by the number of degrees of freedom available (Zelditch 2012). The number of degrees of freedom are calculated by the number of specimens you have minus one. In this case only one degree of freedom is lost due to the rotation of one of the data sets to allow multiplication of the other. The variances and covariance were then processed into eigenvectors and eigenvalues using the Jacobi function in excel. The eigenvectors describe in which direction the shape variation is occurring in morphometric space. The eigenvalues describe where most of the shape variation is actually occurring. Once the eigenvalues had been generated it was possible to compute principle component scores which allow compression of the data as well as describing the variance between the data (Zelditch 2012). The benefit of data compression was extremely necessary for this study as the number of specimens was less than the number of data points taken per specimen. The result of attempting to run these calculations without principle component analysis would result in calculation error. The canonical scores were saved from the analysis done with the principal components, and were then run together with the linearized data in another MANOVA test. The new test revealed which traits were contributing most heavily to the variation seen in the canonical axis. Finally, to see the strength of each variable in the analysis partial eta squared values were generated using the E and H matrices from the principal components MANOVA test (Tobler 2008). Partial eta squared values were generated for each variable that could be contributing to the variation in shape.

Species:	Males	Females	Facility
Gorilla gorilla	5	4	AMNH
Pan troglodytes	5	5	AMNH

|			
Hylobates mulleri a.	5	5	AMNH
Homo sapiens	5	5	FACTS

Table 1

CHAPTER III

RESULTS

The principal component scores revealed that 94.6% of the shape variation within our sample existed within the first twelve principle component scores. The results of the MANOVA test yielded a clear separation of species based on the data that was processed from the jaw bones of the specimens. The separation of species is clearly evident in the three dimensional representation of the canonical axes found in graph 1. The results of the MANOVA test also showed which variables were having a significant effect on the morphology of the specimens. In order to evaluate the strength of each effect a partial eta squared value was calculated. Only one interaction was dropped from the analysis due to the relatively low significance level it had on the morphology in the MANOVA test. The results of the calculation of the partial eta squared values can be found in table 3 along with the f and p values of each variable. The data show that the strongest effect on shape variation comes from the taxon variable, which is to be expected considering the taxa chosen to perform the analysis.

Variable	Partial η^2	f	p
Taxon	0.972005	3.302849	0.176824
Sex	0.560541	1.594406	0.194899
Taxon Sex	0.950328	1.819967	0.34825
LnGMS	0.742441	3.603263	0.010815
Taxon LnGMS	0.828277	0.458826	0.892656
Sex LnGMS	0.490855	1.205097	0.361019

Table 2
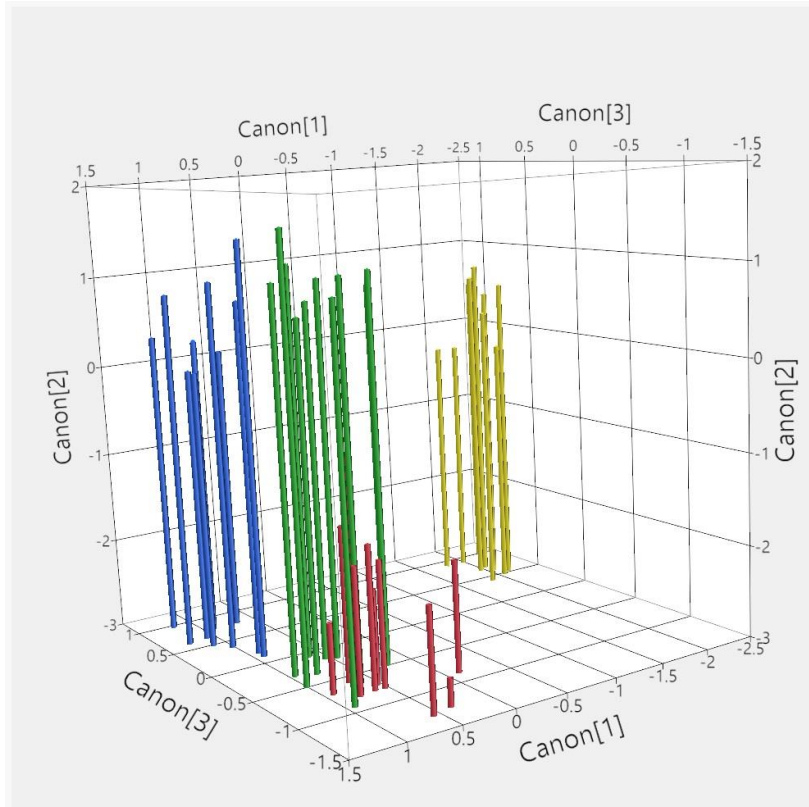
Graph 1

CHAPTER IV

DISCUSSION & CONCLUSION

The results of our data have shown that mandibular and maxillary morphology do accurately reflect the separation of both species and sexes that we expected in this study. The importance of this is that now it is certain that these collective morphologies are candidates for further study using more advanced statistical analyses. In the analysis of the partial eta squared values we see that the taxon variable has the strongest effect on the morphology of the specimen, which is the ideal result of this study given that the overall goal for future research is to use the methods being developed on the fossil record. The dataset with both maxillary and mandibular data show the possibility of separating species based on that data with complete data of known specimens. From our analysis future research goals will be to examine the same dataset with more advanced morphometric methods to see if there is a tight statistical link between the shapes of the maxilla and the mandible. If there is a tight link between the shapes of the jaw bones then we will proceed to try and mix and match complete data sets from the maxilla and mandible of different individuals to see if there is a statistical correlation between the morphology of the jaw bones on a species level. If future analysis does reveal that the suspected correlation between the shape of the mandible and maxilla, it may then be possible for a technique to be developed for dealing with fossil specimens of single or fragmentary jaw bones.

REFERENCES

Sarmiento, Esteban E. "Generalized quadrupeds, committed bipeds, and the shift to open habitats: an evolutionary model of hominid divergence. American Museum novitates; no. 3250." (1998).

Tobler, Michael, et al. "Toxic hydrogen sulfide and dark caves: phenotypic and genetic divergence across two abiotic environmental gradients in Poecilia mexicana." Evolution 62.10 (2008): 2643-2659.

Slice, Dennis E. "Geometric morphometrics." Annu. Rev. Anthropol. 36 (2007): 261-281.

Zelditch, Miriam Leah, Donald L. Swiderski, and H. David Sheets. Geometric morphometrics for biologists: a primer. Academic Press, 2012.

Lague, Michael R., and William L. Jungers. "Morphometric variation in Plio-Pleistocene hominid distal humeri." American journal of physical anthropology101.3 (1996): 401-427.

Marchal, François. "A new morphometric analysis of the hominid pelvic bone."Journal of human evolution 38.3 (2000): 347-365.

Lockwood, Charles A., John M. Lynch, and William H. Kimbel. "Quantifying temporal bone morphology of great apes and humans: an approach using geometric morphometrics." Journal of anatomy 201.6 (2002): 447-464.

Strauss, Richard E., and Momchil N. Atanassov. "Determining best complete subsets of specimens and characters for multivariate morphometric studies in the presence of large amounts of missing data." Biological Journal of the Linnean Society 88.2 (2006): 309-328.

Couette, Sébastien, and Jess White. "3D geometric morphometrics and missing-data. Can extant taxa give clues for the analysis of fossil primates?."Comptes Rendus Palevol 9.6 (2010): 423-433.

Nicholson, Elisabeth, and Katerina Harvati. "Quantitative analysis of human mandibular shape using three-dimensional geometric morphometrics."American journal of physical anthropology 131.3 (2006): 368-383.

Rosas, Antonio, and Markus Bastir. "Geometric morphometric analysis of allometric variation in the mandibular morphology of the hominids of Atapuerca, Sima de los Huesos site." The Anatomical Record Part A: Discoveries in Molecular, Cellular, and Evolutionary Biology 278.2 (2004): 551-560.

Hennessy, Robin J., and Chris B. Stringer. "Geometric morphometric study of the regional variation of modern human craniofacial form." American journal of physical anthropology 117.1 (2002): 37-48.