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A Validation Study Examining Hefner's "Cranial Nonmetric Variation and Estimating Ancestry"

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ABSTRACT

Nonmetric cranial trait analysis in forensic anthropology has traditionally been a valuable tool in assessing ancestry in medico legal investigations. However, it can be argued that an accurate analysis of these traits largely lacks scientific merit. This study aims to use refined morphoscopic trait definitions along with less ambiguous line drawings produced by Dr. Joseph Hefner through his original research on this topic (2009). The current study uses the 11 morphoscopic traits Hefner describes in his research in order to test the validity of his statistical method of mophoscopic ancestry classification. The range in variation between and among the traits traditionally assigned to African- and European-derived populations provides some insight into the benefits of multi-variable trait use in ancestry classification. With the use of a statistical framework, morphoscopic traits can be analyzed more scientifically, as well as used in a medico legal context under the existing Daubert Guidelines (1993). The current study supports some of Hefner's findings while also examining modern populations and possible changes in current trait expression in ancestrally-derived groups.

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INTRODUCTION

Ancestry estimation from non-metric cranial traits has been used for many years by forensic anthropologists to identify unknown human remains. While these analyses have been used in many cases and contexts, questions regarding standardization and general accuracy in estimation have been continually raised. Since morphological trait analysis has not yet been standardized, it largely relies on the observer's experience and expertise with recognizing and assessing traits associated with various populations and ancestrally-derived groups, which makes it more of an "art" and less of a science. This level of expertise is not easily attainable and leaves the method open to possible high error rates. Dr. Joseph Hefner sought to apply a standard scoring method to 11 of the most commonly used non-metric cranial traits for ancestry estimation in order to attempt to make the method more scientific, and therefore more acceptable for use in medico legal cases under the current Daubert Guidelines (*Daubert v. Merrell Dow Pharmaceuticals, Inc.* 1993; Hefner 2009).

This statistical framework also provides an insight regarding the level of individual variation that exists in any given population. This variation is essential when assessing non-metric traits and estimating ancestry based on these traits. Through a more thorough analysis of the statistical trends present in the current United States population, more accurate estimations can be made. In addition, trait lists for ancestrally-derived groups can be revised to better reflect the current expressions of each significant trait in the present population. In this way, the application of statistical methods can greatly increase the overall accuracy of non-metric cranial analysis and move the science of anthropology forward.

The purpose of this study is to test Hefner's method of nonmetric cranial ancestry estimation using his line drawings, revised descriptions and definitions, and data entry program

for analysis. Replicating the study will determine the validity of results obtained by a less experienced observer, which will test the standardization of the method and provide an analysis of the use of morphoscopic cranial traits in ancestry estimation.

METHODS AND MATERIALS

Sample

A sample of 60 individuals from the William M. Bass Donated Skeletal Collection was selected for analysis. Ten American Blacks and fifty American Whites were sampled, all from a modern population group. This sample population was chosen with careful consideration of the African American individuals that Hefner selected from the W.M. Bass Collection for his 2009 publication. None of the individuals selected for this study were used in Hefner's original research, which limited the number of individuals available for analysis in the current study.

The two populations will be grouped together for analysis based on self-reported ancestry. Table 1 displays the sex distribution and ancestry for the sample size.

TABLE 1 – *Male and female samples from the W.M. Bass Collection separated by ancestry.*

Sample	American Whites	American Blacks
Male (*n*)	27	9
Female (*n*)	23	1
Total (*n*)	50	10

Morphoscopic Traits

Data collection was accomplished with the use of a data entry program created by Hefner and downloaded from the Osteoware website hosted by the Smithsonian National Museum of Natural History (Hefner 2009). Line drawings and definitions are included in this software for each trait that was analyzed. Hefner compiled the definitions and refined line drawings from multiple sources regarding previous research on morphoscopic trait analysis (see Hauser and De

Stefano 1989; Brues 1990; Rhine 1990; Burns 1999; Byers 2001 as cited in Hefner 2009). Figure 1 shows a screen-capture of the computer program used in the current study.

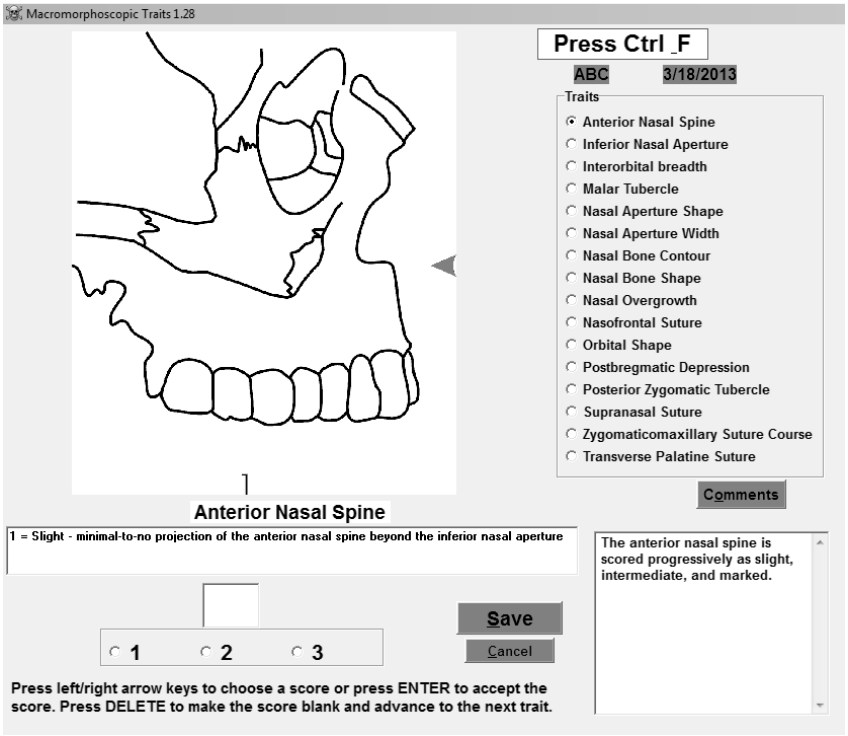

FIG. 1 – *Morphoscopic trait collection computer program screen-capture* (Hefner 2009).

Table 2 contains a list of the 11 morphoscopic traits used in the current study. For full descriptions and definitions of each trait, as well as scoring criteria, see Hefner (2009).

Table 2 – *Morphoscopic traits used in the current study from Hefner* (2009).

Trait	Abbreviation
Anterior Nasal Spine	ANS
Inferior Nasal Aperture	INA
Interorbital Breadth	IOB
Malar Tubercle	MT
Nasal Aperture Width	NAW
Nasal Bone Contour	NBC
Nasal Overgrowth	NO
Postbregmatic Depression	PBD
Supranasal Suture	SPS
Transverse Palatine Suture	TPS
Zygomaxillary Suture	ZS

Figures 2-12 provide illustrations of the modified line drawings Hefner created for his original research. Scores for individual trait expressions are included with each illustration (Hefner 2009).

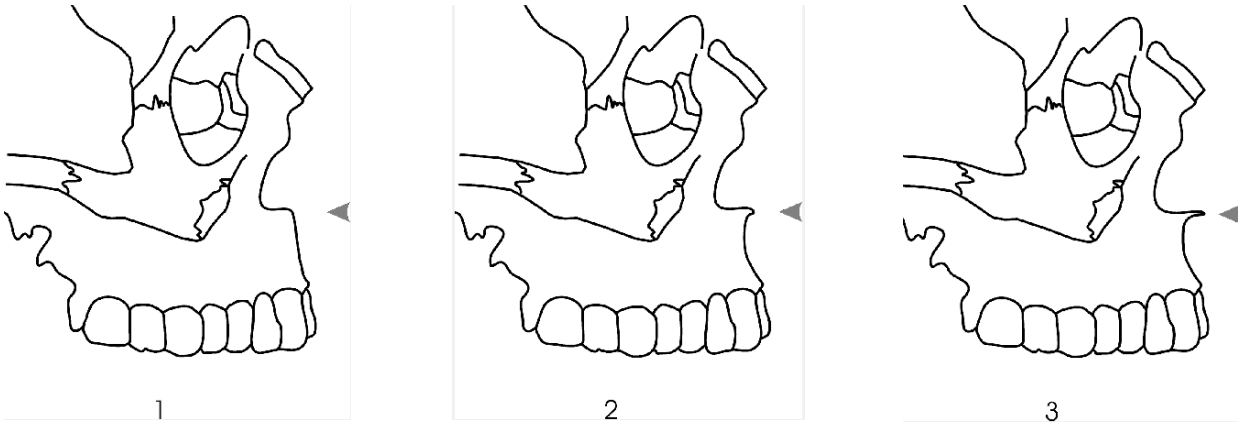

FIG. 2 – *Line drawings for the anterior nasal spine* (Hefner 2009).

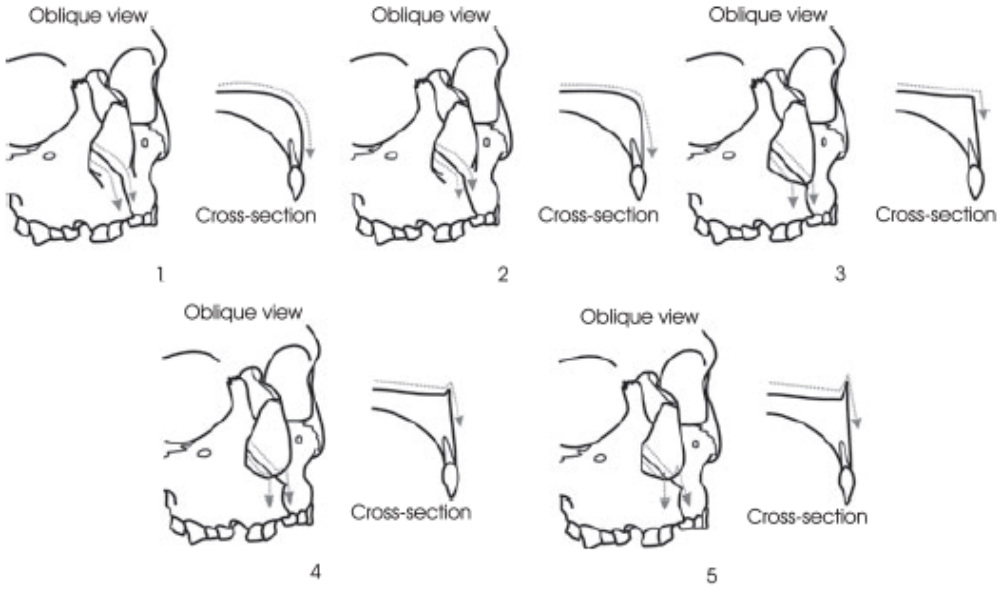

FIG. 3 – *Line drawings for the inferior nasal aperture* (Hefner 2009).

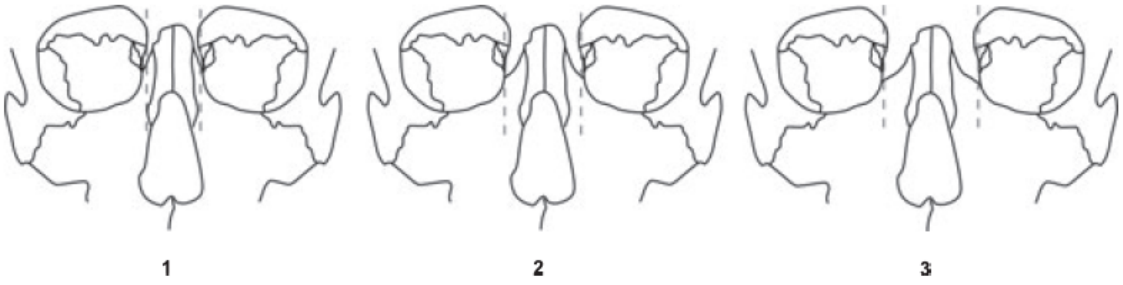

FIG. 4 – *Line drawings for the interorbital breadth* (Hefner 2009).

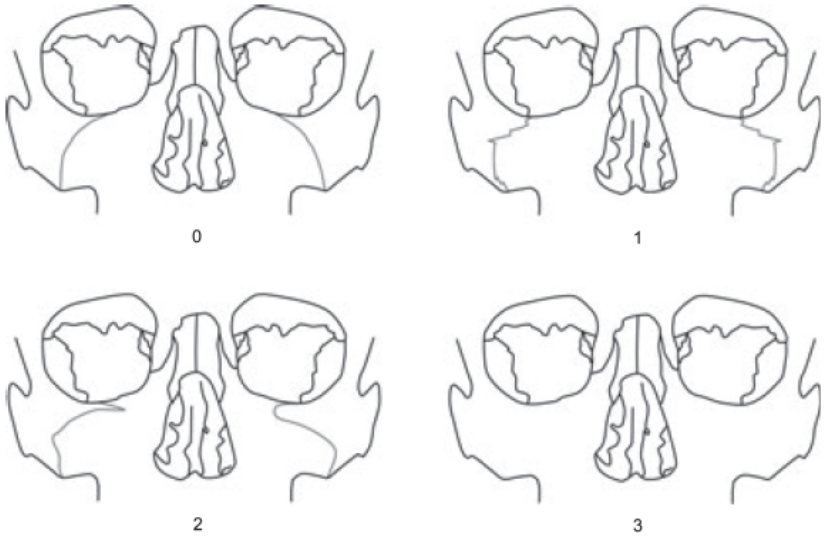

FIG. 5 – *Line drawings for the malar tubercle* (Hefner 2009).

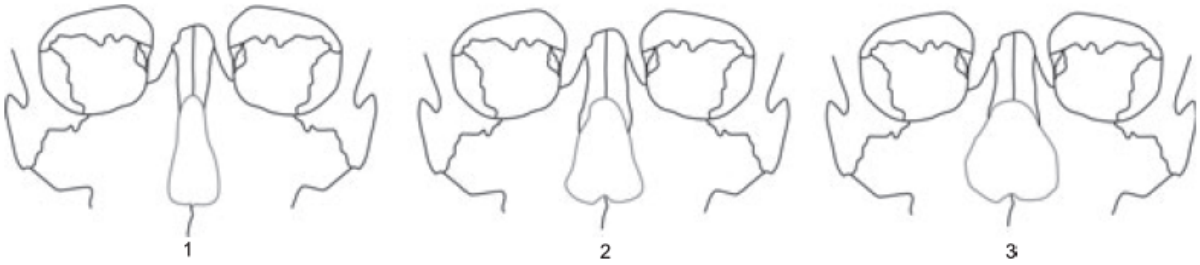

FIG. 6 – *Line drawings for the nasal aperture width* (Hefner 2009).

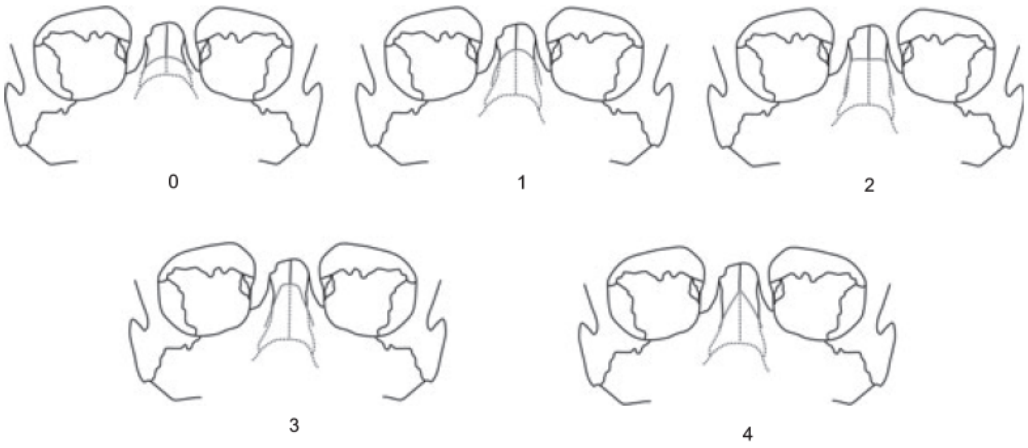

FIG. 7 – *Line drawings for the nasal bone contour* (Hefner 2009).

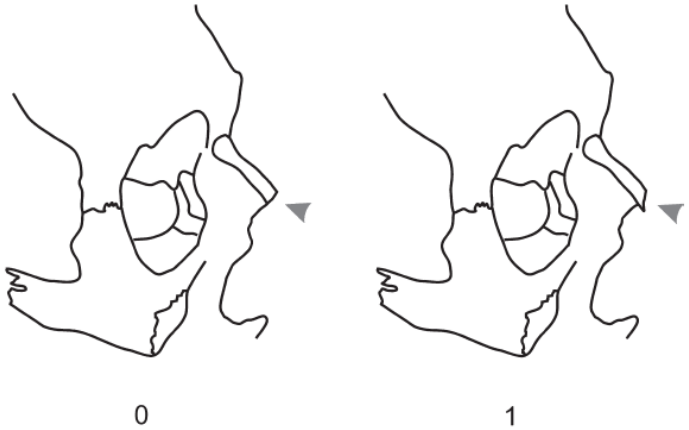

FIG. 8 – *Line drawings for the nasal overgrowth* (Hefner 2009).

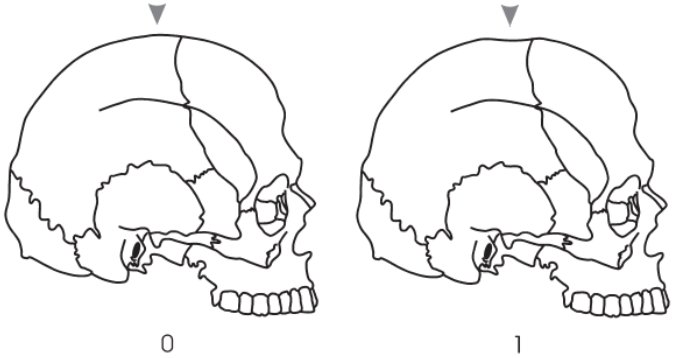

FIG. 9 – *Line drawings for the postbregmatic depression* (Hefner 2009).

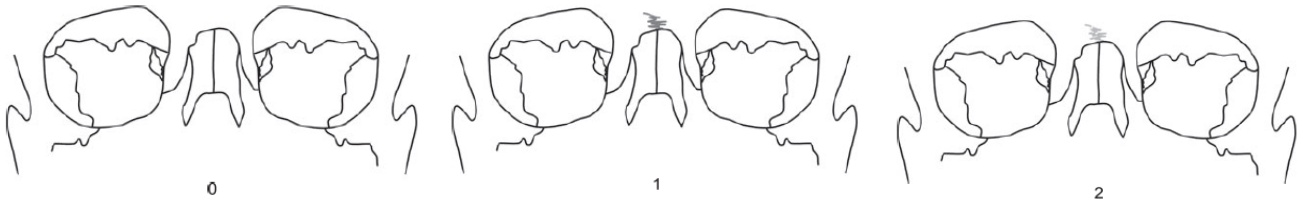

FIG. 10 – *Line drawings for the supranasal suture* (Hefner 2009).

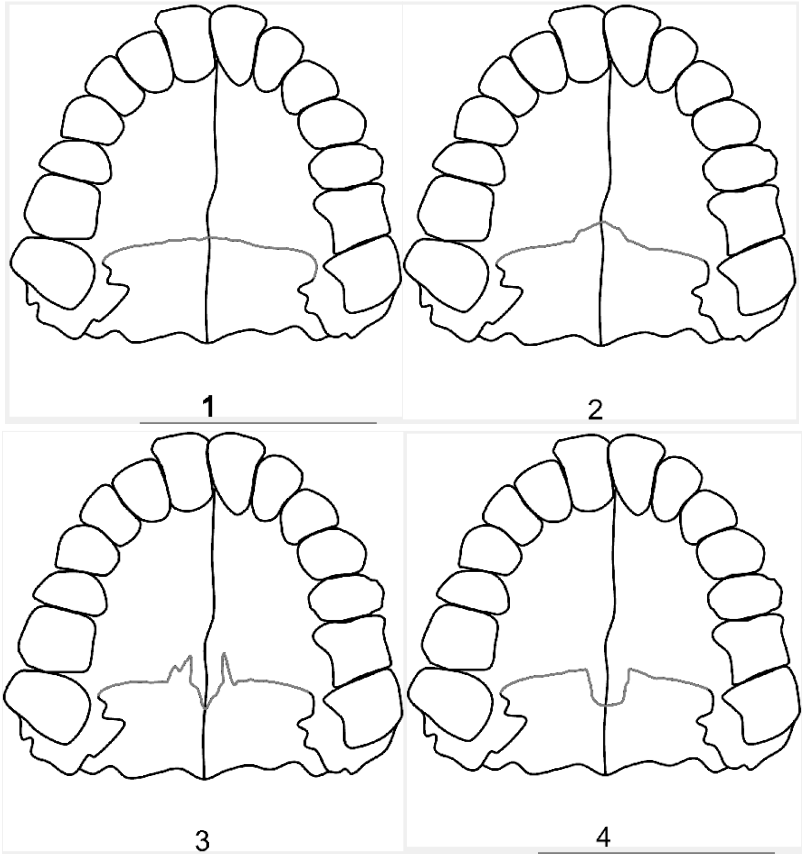

FIG. 11 – *Line drawings for the transverse palatine suture* (Hefner 2009).

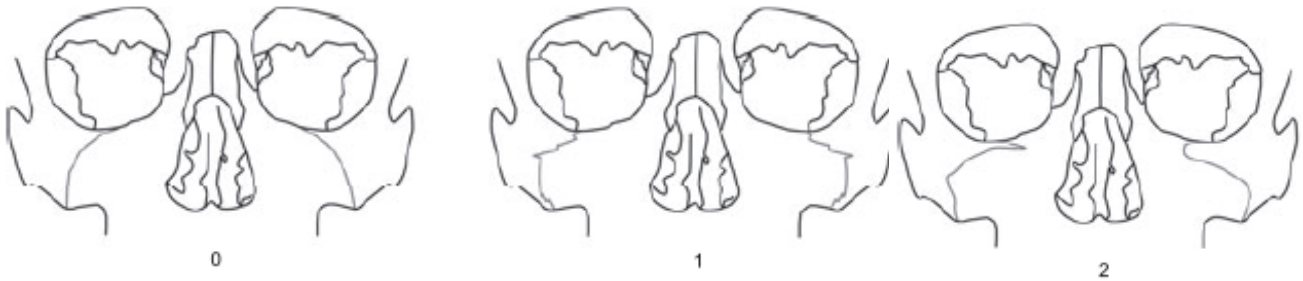

FIG. 12 – *Line drawings for the zygomaxillary suture* (Hefner 2009).

Statistical Methods

Frequency Distributions – JMP Pro 10.0 was used to calculate frequency distributions for the 11 morphoscopic traits analyzed (2012).

Correlations – Correlation coefficients were calculated for each of the 11 morphoscopic traits analyzed in this study. These calculations were performed in order to show the associations between traits that can potentially be used for better ancestry estimation. JMP Pro 10.0 (2012) was used to calcuate all correlation coefficients for the data analyzed.

RESULTS

Frequency Distributions

The frequency distributions presented in tables 3-13 indicate the variation that is present within the two ancestral groups studied, as well as the comparable groups from Hefner's study (2009). All individuals studied showed some deviation from the trait lists traditionally associated with each ancestral group. While individual variation within each population must be taken into account, these results could indicate a change in the trait expression of the modern American population. It should also be noted that frequency distributions for the small sample size of 10 American Blacks in the current study must be carefully considered and cannot be used for making generalizations about the African American population as a whole.

TABLE 3 – *Frequency distribution comparison for anterior nasal spine (ANS).*

	American Black (N = 10)	Hefner's African sample (N = 218)	American White (N = 49)	Hefner's European sample (N = 146)
ANS	%	%	%	%
1	30	69.7	4.1	36.3
2	60	20.2	44.9	26
3	10	10.1	51	37.7

TABLE 4 – *Frequency distribution comparison for inferior nasal aperture (INA).*

	American Black (N = 10)	Hefner's African sample (N = 218)	American White (N = 49)	Hefner's European sample (N = 146)
INA	%	%	%	%
1	0	29.4	0	0.7
2	60	28.9	4.1	3.4
3	20	21.6	38.8	24
4	10	13.3	30.6	41.1
5	10	6.9	26.5	30.8

TABLE 5 – *Frequency distribution comparison for interorbital breadth (IOB).*

	American Black (N = 10)	Hefner's African sample (N = 218)	American White (N = 50)	Hefner's European sample (N = 146)
IOB	%	%	%	%
1	10	9.6	26	30.8
2	70	34.4	56	63
3	20	56	18	6.2

TABLE 6 – *Frequency distribution comparison for malar tubercle (MT).*

	American Black (N = 10)	Hefner's African sample (N = 218)	American White (N = 50)	Hefner's European sample (N = 146)
MT	%	%	%	%
0	30	50.5	38	51.4
1	20	27.5	54	32.2
2	50	14.7	6	12.3
3	0	7.3	2	4.1

TABLE 7 – *Frequency distribution comparison for nasal aperture width (NAW).*

	American Black (N = 10)	Hefner's African sample (N = 218)	American White (N = 50)	Hefner's European sample (N = 146)
NAW	%	%	%	%
1	0	3.7	42	54.1
2	60	40.8	52	32.9
3	40	55.5	6	13.1

TABLE 8 – *Frequency distribution comparison for nasal bone contour (NBC).*

	American Black (N = 10)	Hefner's African sample (N = 218)	American White (N = 50)	Hefner's European sample (N = 146)
NBC	%	%	%	%
0	20	52.3	2	7.5
1	10	22.9	28	15.8
2	20	10.1	4	18.5
3	40	10.6	24	25.3
4	10	4.1	42	32.9

TABLE 9 – *Frequency distribution comparison for nasal overgrowth (NO).*

	American Black (N = 10)	Hefner's African sample (N = 207)	American White (N = 50)	Hefner's European sample (N = 146)
NO	%	%	%	%
0	80	68.1	94	52.7
1	20	31.9	6	49.2

TABLE 10 – *Frequency distribution comparison for postbregmatic depression (PBD).*

	American Black (N = 10)	Hefner's African sample (N = 218)	American White (N = 50)	Hefner's European sample (N = 184)
PBD	%	%	%	%
0	80	52.8	80	82.9
1	20	47.2	20	17.1

TABLE 11 – *Frequency distribution comparison for supranasal suture (SPS).*

	American Black (N = 10)	Hefner's African sample (N = 215)	American White (N = 50)	Hefner's European sample (N = 146)
SPS	%	%	%	%
0	40	42.8	36	39
1	10	31.2	8	39
2	50	26	56	22

TABLE 12 – *Frequency distribution comparison for transverse palatine suture (TP).*

	American Black (N = 10)	Hefner's African sample (N = 180)	American White (N = 49)	Hefner's European sample (N = 145)
TP	%	%	%	%
1	20	18.3	12.2	29
2	40	47.2	22.4	27.6
3	20	25	53.1	33.8
4	20	9.4	12.2	9.7

TABLE 13 – *Frequency distribution comparison for zygomaxillary suture (ZS).*

	American Black (N = 10)	Hefner's African sample (N = 177)	American White (N = 50)	Hefner's European sample (N = 135)
ZS	%	%	%	%
0	50	5.1	40	1.5
1	30	31.6	22	37
2	20	49.7	38	42.2
3	0	13.6	0	19.3

Correlations

Table 14 presents the correlational analysis with significance values for the 11 traits analyzed. These calculations represent the relationships among the morphoscopic traits analyzed in the current study. The postbregmatic depression and the zygomaxillary suture are the only two morphoscopic traits that did not present a significant correlation with any of the other traits studied. As Hefner found in his research, the majority of the mid-facial traits were most strongly correlated with one another (2009). The current study found that interorbital breadth, nasal aperture width, and nasal bone contour correlated the most often with other traits.

TABLE 14 – *Correlation coefficient analysis for the morphoscopic traits analyzed in this study.*

	ANS	INA	IOB	MT	NAW	NBC	NO	PBD	SPS	TPS	ZS
ANS	-										
INA	0.411	-									
IOB	-0.055	-0.121	-								
MT	-0.077	**-0.172**	0.121	-							
NAW	**-0.352**	**-0.296**	**0.577**	**0.222**	-						
NBC	0.070	0.023	**-0.274**	-0.073	**-0.252**	-					
NO	0.021	-0.003	**0.211**	-0.166	0.110	**-0.239**	-				
PBD	0.006	-0.075	-0.091	0.080	-0.078	-0.025	0.000	-			
SPS	**0.279**	0.086	**0.318**	0.176	0.043	-0.082	0.134	-0.053	-		
TPS	0.036	0.097	0.157	-0.061	-0.062	**-0.333**	0.066	0.113	0.137	-	
ZS	-0.090	0.134	-0.065	0.163	0.091	-0.078	0.092	-0.057	-0.127	0.106	-

ANS, anterior nasal spine; INA, inferior nasal aperture; IOB, interorbital breadth; MT, malar tubercle; NAW, nasal aperture width; NBC, nasal bone contour; NO, nasal overgrowth; PBD, postbregmatic depression; SPS, supranasal suture; TPS, transverse palatine suture; ZS, zygomaxillary suture.

Bolded values are significant at the $p < 0.05$ level.

The frequency distributions presented above, in conjunction with the correlational analysis, suggest that in order to achieve an accurate representation of an individual's traits for ancestry estimation, multiple traits are necessary for analysis. Previous research using multiple traits in addition to statistical methods has been shown to improve estimation results in metric analyses (Jantz and Ousley 2005). The current study provides evidence that the success seen in statistical methods for metric analyses could also be applied with comparable results in non-metric trait analyses.

DISCUSSION

This research, in conjunction with Hefner's original study, provides some evidence to support the use of statistical morphoscopic trait analysis in ancestry estimation (Hefner 2009). However, both studies present some flaws that should be carefully considered. For example, Hefner groups a large sample of 19th century American Blacks with a medium-sized sample of

contemporary American Blacks and a small sample of native Africans; this grouping provides a large range of trait expressions due to the different populations represented in the same group. By placing a historic population in the same category as a modern population, the analysis of trait expression may be skewed for use in contemporary forensic analysis. A historic African population cannot be expected to present the same trait expressions that a modern African American population presents, especially when individuals have lived in the United States and intermarried with other African Americans for multiple generations. While determining trends in the ancestral group is important and presents valid and useful data that can also be applied to modern populations, grouping the three populations together for the purpose of statistical categorization that can be used in a modern forensic analysis could present a problem with the state of the United States' current "mixed" ancestry population.

The frequency distributions from Hefner's study as compared with the current study provide some insight into this issue; however, as noted above, the small sample size of American Blacks used in the current study must be considered in these comparisons. For example, Hefner rates the majority of Africans (almost 70%) as having a slight anterior nasal spine projection, while the current study found that 60% of the African American sample presented an intermediate ANS (Hefner 2009). Furthermore, the discrepancies in findings regarding the malar tubercle in African ancestry populations are notable. Hefner's sample is classified as a 2 mm or less projection 50% of the time, while the current study found that the malar tubercle presented as a 2-4 mm projection 50% of the time (2009). Hefner's study also found that a postbregmatic depression was absent in 53% of his sample, but the current study found that this trait was absent in 80% of individuals studied (2009). While these discrepancies could be attributed to the small

sample size used in the current study, they are worth considering in an overall evaluation of the method.

Hefner asserts that the use of individual morphoscopic traits is problematic and that previous literature often cites admixed populations as a reason for difficulty with or improper identification based on single trait analysis. However, when these traits are carefully defined and placed in a statistical framework, classification becomes more accurate (Hefner 2009). Although these claims are somewhat supported by Hefner as well as the current study, more research is necessary to determine the proper traits to be used in such multi-level statistical analyses, as well as to note the changes in traits associated with African- and European-derived groups represented in the current United States population. The individual variation found in ancestral groups in both studies offers further cause to take multiple traits into account when classifying ancestry based on morphoscopic traits alone. The mid-facial traits generally provided the highest correlation in both studies; however, further research would be beneficial to determine which traits correlate most significantly in the modern American population (Hefner 2009).

Although there are some discrepancies between the two studies regarding correlations and frequency distributions, both studies support that there are significant differences between American Whites and Blacks that can be assessed nonmetrically. Further research regarding the changing trends in trait expression for current populations is necessary to determine the traits that are most statistically significant. For example, the current study found that the malar tubercle correlated significantly with the inferior nasal aperture and nasal aperture width, but Hefner's study did not find the malar tubercle to be significantly correlated with any other traits (2009). While the small sample size of the current study could be a factor in the results of the statistical analysis, the trends of modern populations could also be changing from the historical population

norms, as found in metric analyses of changes in craniofacial morphology in modern populations by Jantz and Meadows Jantz (2000) and Wescott and Jantz (2004).

The use of standard drawings and definitions for the purposes of trait scoring offers a more reliable analysis for ancestry classification. The previous use of vague, and sometimes even differing, definitions and line drawings that rely on an observer's training and experience makes the scoring of morphoscopic traits susceptible to high rates of error. Inexperienced observers are also more likely to make errors with previous methods. The computer software program Hefner created for his 2009 study reduces these errors and makes data collection easier, especially for inexperienced observers. The software presents each trait with scoring criteria that includes full definitions for each score as well as line drawings together on the same menu. The current study found this method to be especially helpful when making score determinations for traits such as the zygomaxillary suture and transverse palatine suture that present many possible variations between individuals.

By combining morphoscopic trait scores into a methodical statistical analysis, more accurate classifications can be achieved (Ousley and Hefner 2005; Hefner and Ousley 2006). Given proper standardization, the application of statistical methods to non-metric trait analysis could potentially yield results close to the accuracy currently observed in metric ancestry estimation. The current study suggests that trait combinations are more reliable than single trait analysis, as seen in the high degrees of variability in frequency distributions for individual traits. While the current study, as well as Hefner's original research (2009), have found valuable statistical trends for the samples studied, further research on modern population trends and general trait analysis will be necessary to determine the optimal traits for selection to be used in such standardized statistical models for ancestry classification in modern populations.

CONCLUSIONS

The current study provides further support for Hefner's statistical analysis of morphoscopic trait analysis in ancestry estimation. However, the discrepancies in statistically significant correlations, as well as the differences in frequency distribution between and among ancestral groups should be noted and studied in further research. It is possible that these differences could be attributed to changes in the expression of these traits in modern populations in the United States (Jantz and Meadows Jantz 2000; Wescott and Jantz 2004).

The most significant limitations of the current study include small sample size and an inexperienced observer. The overall sample consisted of 60 individuals, only 10 of which were of African-derived ancestry. A larger, more representative sample of African Americans would be necessary to make generalizations about the entire African American population with regard to morphoscopic ancestry trait analysis. The European-derived sample, while larger than the African-derived sample could also be expanded in order to track variances in trait expression. In addition to the small sample size, the inexperience of the observer could have an impact on the error rates of the current study. While the use of carefully defined traits and clearer line drawings than previously available contributed to a more accurate scoring of traits, a more experienced observer would most likely classify traits more accurately.

Although further analysis of the trends of current trait expression between ancestral groups is necessary, the current study finds that multivariate statistical analysis is a valuable tool in ancestry estimation using morphoscopic traits. Employing multiple statistical analyses for each trait, as well as overall analyses for trends between and among groups will provide more accurate classifications. Additionally, relying less on the "art" of morphoscopic trait analysis and

more on quantitative data collection will make nonmetric trait analysis more acceptable for use in medico legal cases under the Daubert Guidelines (1993).

In conclusion, the current study finds some support for Hefner's statistical methods, but calls for further research and analysis of overall trends of trait expression in modern American populations. Studying the changing trends in cranial trait expression, in conjunction with correlations and frequency distributions between and among different ancestrally-derived groups, could provide valuable insights into the application of morphoscopic trait analysis in a medico legal setting. As the modern American population continues to change with respect to demographic make-up and increasingly admixed populations (United States Census Bureau 2010), the science of forensic anthropology must evolve and adapt to account for all possible ancestry combinations.

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