## H26 Non-Metric Assessment of Ancestry through Cranial Macromorphoscopics: A Validation of the Hefner Method

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After attending this presentation, attendees will learn the reliability and the validity of the newly proposed Hefner (2009) method.

This presentation will impact the forensic science anthropology community by assessing the validity of this method for ancestry estimation in human crania and will allow attendees to evaluate the utility of the method when applied to forensic cases and assess the method's ability to meet the *Daubert* requirements.

Ancestry estimation is essential for the construction of biological profiles for unidentified individuals found in forensic contexts. The human skull has historically been considered the best indicator of ancestry and has been analyzed in a number of metric and non-metric studies. Arguably, metric assessment of population affinity is primarily done with FORDISC 3.0 (Ousley and Jantz); although, non-metric methods of ancestry estimation continue to be employed and taught, as they are the suggested methods presented in a number of introductory osteology and forensic anthropology textbooks (cf. Bass, Byers).[1-3] The benefits of non-metric methods are numerous including ease of use, no need for specialized equipment, and relatively quick data collection.

Hefner (2009) presented a new method of ancestry estimation by creating ordinal scores with descriptions and corresponding illustrations for a set of 11 macromorphoscopic traits commonly, or historically, applied to ancestry estimation in the crania. The frequency distribution of those traits was analyzed in four populations (African, American-Indian, European, and Asian). Ten of the eleven traits analyzed by Hefner were found to be significantly different between groups and, when analyzed within a statistical framework, can reliably predict ancestry with accuracy rates ranging from 84-93% depending on the method applied and variables used. Also in the original study, tests of observer error were found to be low, suggesting that this method can be accurately applied for ancestry estimation.

Since publication, the Hefner method has been applied and cited in a number of actual forensic cases and has been incorporated into Osteoware (Smithsonian Institution), a free program developed for data collection and storage. However, in order for the Hefner method to be reliably applied for the estimation of ancestry, independent tests of both the reliability and validity of the method must be conducted by alternative observers and in populations not previously studied for scientific rigor.

Two observers, with some previous familiarity with the Hefner method, scored a sample of 84 crania from the Hamann-Todd (HTH) Collection. Two ancestral groups were analyzed: American whites (20 female, 21 made) and American blacks (22 female, 21 male). All crania used in this study had no apparent pathological conditions and were complete enough to score at least 14 of the 16 traits (the 11 traits originally used by Hefner 2009 and five additional traits included in the Osteoware 2011 package).[4,5]

The data were analyzed through linear discriminant function to examine ancestral affiliations. The variables for each analysis were forward stepwise selected. Analysis of inter-observer error was also conducted using Cohen's Kappa (K). Initial results provided accuracy results considerably lower than those found by Hefner with correct cross validated, classifications of 52.4% for observer one and 54.8% for observer two.[4] The Mahalanobis $D^2$ from WM and WF means were not significantly different, while the $D^2$ for BM and BF means were found to be significantly different in each of the observer's analyzes (*p-value* > 0.05). Intra-observer agreement was similarly lower than that found by Hefner.[4] Six of the traits had a moderate level of agreement (K=0.41–0.60), six traits showed a fair level of agreement (K=0.21–0.40), and four traits had only a slight level of agreement (K=0–0.20) based on Landis and Koch.[6]

Lower classification accuracies than those found by Hefner may be the result of less experience with the method and trait scores.[4] Additionally, some of the trait representations found in the HTH collection lacked corresponding descriptions and illustrations and were forced into the most similar score. Results from this study suggest that caution should be used when applying this method to samples other than the one with which it was created and suggest that this method may require extensive practical experience with the traits, scores and illustrations before being used for ancestry estimation.

**References:**

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**Ancestry Estimation, Cranial Non-Metric Validation, Discriminant Function Analysis**

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