H60 A Simulation for Exploring the Effects of the "Trait List" Method's Subjectivity on Consistency and Accuracy of Ancestry Estimations

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After attending this presentation, attendees will have a clear understanding of the specific aspects of applying the trait list method that potentially incur bias. The sources of bias are tested by simulating the application of the trait list method, and the results will provide attendees with empirical information on the overall consistency of the trait list method.

This presentation will impact the forensic science community by providing a mathematical analysis of the bias embedded in a commonly used forensic anthropological method for assessing ancestry. The results of the analysis allow the authors to make specific conclusions regarding the consistency of the method, as well as recommendations for how to avoid bias when utilizing the trait list method.

The nonmetric "trait list" methodology is widely used for assessing ancestry of skeletal remains. Although, recent valid critiques have been made,[1-3] the method has endured because of its ease of application and the familiarity of traits to the anthropologist. For a given unidentified skeleton, a checklist of traits is completed, noting each trait's state of expression. The distribution of the trait states among three geographic ancestries (Asian, African, and European) are typically used in conjunction with additional lines of evidence (such as metric analysis) to arrive at an ancestry estimation for the unidentified skeleton. While the application seems straightforward, there are both theoretical and logistical issues with this approach. Trait states are not exclusive to a single ancestry; instead, the trait list method is grounded in the belief that individuals of a specific ancestry more often express a particular trait state than other ancestries. Because nonmetric traits are considered heritable, albeit to various degrees, genetic drift and gene flow must be considered when accounting for shifts in distributions of trait state expressions. The polygenic nature of nonmetric traits maintains a complex path for variation in expression. The evolutionary premise of trait state distribution within a population and the influential genetic nuances are often lost in the application of the trait list method, such as with the use of "mixed" or "admixed" ancestries.[4] This designation implicitly relies on the concept that trait states are unique to a given ancestry and that "Asian," "African," or "European" parental ancestries actually existed at some point in the past.[5]

Choosing to incorporate the admixture approach into their research, because whether this is a theoretically sound approach or not, it is an approach that has been generally practiced over the decades. Thus, this research is based on the typical application of the trait list method, not the theory-bound approach that has recently found support.[6,7] The effects of the method's embedded subjectivity on subsequent accuracy and consistency are largely unknown. Trait list ancestry assessment involves a series of decisions (how many and which traits to use) and interpretations (how to describe the ancestry based on the trait states), but there is no protocol.[4] For example, if 10 out of 10 observed traits express the Asian state, the associated skeleton would typically be classified as being of Asian ancestry, but what if only 9, 8, or 7 out of 10 are associated with Asian ancestry? What is the threshold for considering the conventional admixture estimations when using the "trait list" methodology?

Using a mathematical simulation that realistically represents the possible analytical variations of trait list ancestry estimation. The simulation explores: (1) trait selection; (2) number of traits employed; and, (3) ancestry choice thresholds affect the ancestry estimation of a skeleton. The relative accuracy of the trait list method in actual casework has not been comprehensively examined. The current study is a simulation of this accuracy, and tests how ancestry estimations for a given skeleton can differ from practitioner to practitioner when methodological choices vary. Using two temporally and geographically diverse samples comprising over 100 individuals, the simulation demonstrated that trait selection, quantity of traits, threshold choices, and the exclusion of high-frequency traits within a given sample had minimal effect on consistency in ancestry determination. For all datasets and

Runs, accuracy$_{AS}$ was maintained above 90%.

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Nonmetric Cranial Traits, Ancestry Estimation, Bias