Ancestry Assessment

1.0 Principle, Spirit, and Intent

Skeletal remains should be analyzed in a systematic manner for the purpose of assessing ancestry that may be relevant to human identification. The most appropriate technique(s) for assessing ancestry should be reliably and objectively applied. Methods should be documented to enable replication and verification.

2.0 Purpose and Scope

The following guidelines outline procedures for the assessment of ancestry from human skeletal remains. Many different methods are used in field and laboratory settings and may be population dependent. The intent is not to endorse one particular method, rather to establish valid assessment of ancestry.

Practitioners of forensic anthropology should implement these guidelines to the fullest extent as applicable, practical, and appropriate. In the absence of specific guidelines or procedures or in the case of conflicting procedures, the principle, spirit and intent should be met.

3.0 General Principles

Ancestry refers to the geographic region and/or the ancestral origin of a particular population group. Ancestry assessment of skeletal remains is important because it provides meta-data that can be used to narrow the list of potential matches from missing person's reports for DNA comparison, radiography comparison, or some other form of positive identification. Additionally, ancestry assessment will often affect estimates of other aspects of the biological profile.

Skeletal morphology is polygenic, reflecting genetic and environmental factors, and is highly heritable. Fundamentals of transmission genetics, evolutionary theory, quantitative variation, and human biological variation all provide support that skeletal morphology can be used to assess population relationships, even when considering environmental variation. Statistical methods of classification provide further mechanisms for assessing the relationship of an unknown individual (i.e. forensic anthropology case) to multiple reference groups for the purposes of ancestry assessment.

3.1 Human Variation

Modern human populations show more similarities than differences. Using genetic data or skeletal morphology, typically 85% of world-wide variation is found within populations and 15% between populations. Ancestry assessment involves classification and statistical methods and can maximize between-group variation to improve classification rates.

3.2 Classification

Because of the relatively high concordance between social race categories (e.g. U.S. Census Bureau race and ethnic categories) and skeletal morphology in the United States, social race categories can be used as a descriptor of group membership when writing a forensic report. In most forensic cases in the US, race will be a useful category to narrow down possible identifications, but further refinements may be necessary. For example, an ancestry of "East Asian" may not be specific or precise enough in some cases and distinctions between Vietnamese, Japanese, or Korean may be desirable. Depending on the country and region, local or national social race and/or ethnic categories may have low or high correlation to certain biological measures. When reporting a classification, do not state results in unequivocal terms. Even when probabilities indicate group membership is highly likely, it can still be incorrect in social terms because of the imperfect correlation between social race and biology. Biological answers do not always, no matter how strong, reflect the discrete race classification.

When craniometric data or trait frequencies for groups are assessed, there is no distinctive single trait that uniquely identifies any human group. Individuals may display skeletal traits that are “diagnostic” of different groups – and rather than concluding mixed ancestry, knowing and understanding the fundamentals of quantitative variation, the population frequencies of those traits, and the population structure and history of the groups in the analysis will aid in interpretation.

Complex groups (e.g. Hispanic) and individuals are expected to be difficult to correctly classify. However, using morphometric and morphological criteria with statistical methods should provide far better classification than random allocation.

4.0 Approaches

Reference samples/groups should be critically evaluated in terms of sample size, temporal period, geographic location, ethnicity, language, and other cultural parameters and activities such as dental modification. Sample sizes should be large enough to represent the natural variability present in all populations. Due to secular changes, reference samples should be comprised of forensically relevant individuals.

The statistical methods used provide measures of uncertainty in an overall classification (assessing the possibility that an ancestry can be correctly assessed) and to specific classifications (the probability that a correct classification into one group is far more probable than classification into a different group). There are no clear-cut or unambiguous indicators of ancestry. Rather, groups show differences in frequencies of traits or in means of measurements.

Selection and application of ancestry assessment methods depend on the skeletal elements available for examination, their condition, and the age and sex of the individual being examined. Analysis of skeletal remains for ancestry may involve different or multiple approaches, including morphological and metric traits. Generally these traits are analyzed separately, but they may also be analyzed together using certain statistical methods.

A single trait can rarely separate any two groups and the accuracy will be improved when using more traits. Also, there may be traits that suggest conflicting ancestries, but in a statistical classification method they will be properly weighted. Therefore, all traits of interest should be recorded. The most-often used statistical method is discriminant function analysis, but additional methods (e.g., nearest neighbor analysis and kernel probability density analysis) can be used and may be more appropriate than discriminant function analysis. Also, statistical methods provide ways to express uncertainty, for example, using posterior probabilities. For further details see the SWGANTH guidelines for Statistical Methods.

4.1 Morphological Traits

Morphological (non-metric) traits include discrete and morphoscopic traits/features of the skeleton, particularly the cranium, mandible, and teeth. Many non-metric traits are binary in nature, and recorded as present/absent. Morphoscopic traits, in comparison, represent ordinal grades of expression. When scoring non-metric traits, each trait should be scored independently of what the trait has traditionally implied for ancestry. For instance, a postbregmatic depression has traditionally implied African ancestry, although it is present in other groups.

Morphological traits can be used in ancestry assessment with 1) appropriate reference groups, 2) clear trait descriptions, and 3) appropriate statistical methods of classification.

4.2 Measurements

Measurements used in ancestry assessment generally involve cranial size and shape. Postcrania will also provide robust estimates. Appropriate measuring instruments, standards and/or software should be employed. As with morphological traits, multiple measurements and multivariate statistical techniques provide greater validity in ancestry assessments.

Measurements can be used in ancestry assessment with 1) appropriate reference groups, 2) clear measurement definitions, and 3) appropriate statistical methods of classification.

5.0 Best Practices

The following practices are recommended for ancestry assessment:

- Ancestry assessment should be made independently of suspected or presumptive identifications.
- Use methods based on large appropriate sex- and period-specific standards/samples with sufficient sample sizes and with objective ways of measuring and recording traits.
- Measurements and non-metric observations should always be recorded, even if samples for DNA analyses will be taken.
- Use adequate traits with appropriate statistical methods of classification. Express probability of certainty when reporting ancestry assessments, especially because ancestry assessments should never be given with 100% certainty as expressed in posterior probabilities.
- Use all appropriate and available groups for your case, but remember that the most appropriate reference samples may be unavailable for analysis.
- Know metric or non-metric trait definitions and be sure to understand how to score and record them.
- Understand the appropriate statistical methods employed in ancestry assessment and understand the interpretation of the results.
- Use terminology that is appropriate and widely accepted within the local vernacular, e.g. these remains likely represent a person who self- identified as Black during life.
- When comparing against reference groups, if the skeleton is complete and sex is unambiguous, perform a sex specific analysis, (i.e. if skeleton is clearly male, compare against male reference groups only).
- Anonymized raw data should be submitted to open-access anthropological data repositories to support future research and methodological improvement.

6.0 Additional Considerations

Pathological or taphonomic alterations may preclude the utilization of specific ancestry assessment techniques.

A major assumption in classifying an individual is that the unidentified individual comes from one of the populations represented by the reference groups. If one uses techniques for classifying an individual into two groups, for example, White and Black Americans, the technique can only classify into one of those groups even if the individual does not belong to either group.

7.0 Unacceptable Practices

The following practices are considered unacceptable and should be avoided when assessing ancestry.

- Basing conclusions on faulty samples (small, inappropriate temporal period, irrelevant geographic origins, arbitrary or uncertain classifications in reference groups).
- Basing conclusions on one or two morphological traits.
- Basing conclusions on methods that have not been validated.