Resolving Commingled Human Remains

1.0   Principle, Spirit and Intent

Skeletal remains should be recovered and analyzed in an organized manner for the purpose of resolving commingling. The most appropriate technique(s) should be reliably and objectively applied for segregating remains and determining the number of individuals present. Tests should be documented in a manner conducive to the documentation, replication, and verification of the work performed.

2.0   Purpose and Scope

Commingling of human remains is a common component of certain types of incidents, such as mass graves or mass disasters, and it is often the role of the forensic anthropologist to attempt to document and resolve commingling. This section presents acceptable methods to utilize with commingled human remains in both field recovery and laboratory analysis.

With forensic investigations, commingling should be resolved to the greatest extent possible in order to increase the identification potential for the decedents, to return the remains to the next of kin, and for overall investigative success. Practitioners of forensic anthropology should implement these guidelines to the fullest extent as applicable, practical and appropriate. In the absence of specific guidelines or in the case of conflicting procedures, the principle, spirit and intent should be met.

3.0   General Principles

During field recovery, it is important to thoroughly document the provenience (three-dimensional location) of human remains and associated evidence so that this information is maintained and is available for use during the laboratory analysis.

During laboratory analysis, it is important to consider whether or not the remains of more than one individual are potentially intermixed. When commingling is present it is necessary to implement acceptable techniques to segregate the remains into specific individuals and determine the number of individuals represented. For some situations it may also be necessary for a forensic anthropologist to segregate non-human remains that are commingled with human remains. It is acknowledged that segregation of all remains will not always be possible.

As the number of individuals increases, so does the complexity of the forensic investigation and the skills needed for case resolution. Body fragmentation adds an even further level of difficulty since each separate fragment has to initially be treated as a separate individual until an association can be established. DNA sampling adds significant power to the resolution of commingling of fragmented remains.

4.0 Best Practices

Methods to be employed to resolve commingling and estimate the number of individuals are divided into three general categories in this document: Recovery, Sorting, and Number of Individuals. For each category, techniques will vary depending upon the remains available for examination and their overall condition. As the condition of the remains declines (e.g., fragmentation or poor preservation), the complexity of the recovery and/or analysis increases. The degree of commingling can vary widely from situations that are relatively straightforward (intact remains and a small number of individuals) to very challenging (large number of individuals and/or extensive fragmentation).

4.1 Recovery

The process of resolving commingling begins in the field. The field context can prove critical to the laboratory analysis and decedent identification process. For details concerning best practices in field recovery, consult the appropriate SWGANTH guidelines.

The components of a recovery effort that are critical to the ultimate resolution of commingling include:

- The discovery and recognition of remains and other evidence *in situ*.

- The capture of accurate site data, with spatial relationships of remains and material evidence mapped to an appropriate level of detail. This should include the development of necessary and sufficient field notes (including maps, unique identifiers of plotted specimens, photographic documentation, etc.). This recovery information should be transferred to the laboratory and considered during the analysis of the remains.

  o Site data should be gathered at a level of detail that captures all necessary probative information. The level of detail included in field documentation will vary depending on the complexity of the site and the available resources. For example, it is often necessary to piece plot individual bone elements when they are disarticulated and encountered as isolated finds. However, when whole sections of bodies are still in anatomical position (e.g., limbs or torsos), piece plotting individual bone elements (versus the

whole part) may not necessarily contribute to the subsequent identification process.

- o An appropriate field labeling and collection strategy should be used to ensure that remains/evidence are documented and linked to a scene map. Remains/evidence should be collected in a manner to ensure that inadvertent commingling does not occur during transport. Remains/evidence should retain these labels when they are received in the laboratory.

- ▪ The successful transfer of remains along with the recovery information to laboratory personnel charged with sorting the commingled remains.

4.2   Sorting

In general, the sorting process should take place in the laboratory. The complexity of the sorting process is dependent on the overall number of individuals involved in the incident and the preservation of the remains. When preservation is good, the sorting techniques used in the resolution of commingling may include visual pair-matching, articulation, process of elimination, osteometric comparison, and taphonomy. These techniques, when used in conjunction with each other, provide a solid basis for the association of most skeletal elements. These sorting procedures should be reliably and objectively applied and are most appropriate for instances of small-scale commingling. They may also be useful for large-scale commingling situations, but the discriminating power is likely to be reduced as the number of individuals grows (i.e., differences in size and shape may not be as apparent when the number of individuals increases). Large-scale commingling may introduce logistical problems, such as data management and analytical space, which need to be considered as part of laboratory analysis. Although not an anthropological technique, DNA profiles also provide a powerful means of segregating or linking remains.

With all of the procedures described, greater confidence is granted to results that lead to exclusions than those that show consistencies. In other words, just because two remains show consistency with each other does not mean with certainty that they originated from the same person. On the other hand, remains showing incompatibility with each other (i.e., exclusions) can be segregated with confidence. Analysts should be cognizant of pathological conditions that may affect size and shape.

The majority of the sorting procedures are not stand-alone techniques. For best results they should be used in conjunction with each other and with the scene information. It is important that systematic procedures are utilized and appropriately documented.

For very fragmentary remains, DNA testing may be the only reliable method for re-association. Since DNA testing is destructive, the sampling should take place after anthropological examinations are completed. Cross-sectioning of bones for DNA sampling should be avoided whenever possible to eliminate additional fragmentation and

potential disassociation of remains. Protocols should be developed to standardize sampling locations so that potentially important skeletal features are not removed (e.g., a fracture site that could potentially be used to conjoin with another fragment).

When using DNA profiles as a basis for sorting, it is important to be cognizant of random match rates for the profiles obtained from the remains. Random matches are not uncommon when working with mtDNA sequence data and it must be recognized that commingled cases can potentially involve large numbers of pairwise comparisons. The forensic anthropologist utilizing DNA profiles should always consult with the DNA testing laboratory as to the risks of random matches in light of the commingling problem. Furthermore, precautions should be used during sampling and handling to minimize the risk of cross-contamination of DNA profiles. An anthropological review of DNA based reassociations should be completed in order to confirm consistency.

The re-association of some commingled remains may be impossible to determine with certainty using these techniques. In these instances, the analyst should assign the unassociated elements to some type of "group" category.

4.2.1   Field Recovery Information

Upon receiving a case in the laboratory, the field recovery documentation (e.g., written documentation, photographs, and site maps) should be reviewed to investigate possible associations with adjacent elements and/or material evidence. Photographs and maps may also provide laboratory personnel with relevant *in situ* information that could assist with their analysis. Finally, three dimensional map data may be mined for information of possible associations using spatial relationship analysis.

4.2.2   Inventory and Reconstruction

The first steps of the laboratory sorting process involve an analysis of any available documentation from the field recovery and the determination of element representation. It is important to label bones and bone fragments to maintain any provenience information collected during the recovery effort as this may become critical during the analytical process. Furthermore, elements that were articulated at the time of recovery should be maintained as a unit throughout the analytical process, but their association should be confirmed in the laboratory.

Fragmentary remains should be conjoined (i.e., reconstructed) to the greatest extent possible as this will assist in the overall segregation process. An inventory of the remains including element, side, and developmental status should be completed.

4.2.3   Visual Pair-matching

Visual pair-matching refers to the comparison of antimeres (i.e., left-right) of the same element based on morphological features. It is important that preservation is adequate to allow this type of comparison. To facilitate pair-matching, bones should be sorted by

element type, side, and size (e.g., all right femora should be organized from most gracile to most robust). Grouping elements by age criteria (e.g., lack of epiphyseal fusion) may also be helpful at this stage of the sorting process. Greater confidence with pair-matching is granted to results that lead to exclusions than those that show consistencies.

Visual matching of different skeletal elements (e.g., a humerus and a femur) based on morphology is not recommended in most instances due to the subjective nature of the procedure. (Visual matching of different element types may be possible with cases that involve a limited number of individuals who exhibit marked skeletal variation.)

4.2.4   Articulation

Articulation indicates that a bone forms a congruent joint or juncture with another bone and, depending on the elements compared, can provide an acceptable means for associating remains. Poor articulation between elements may also be a basis for segregating remains. This sorting procedure offers a reliable assessment, but the strength of association varies depending on the element considered and the demographics of the population. Laboratories should establish standards for the confidence that will be placed in various articulations (i.e., a rank order from high confidence to low confidence). Problems with articulation arise from the lack of a close fit between some elements. Through articulation it may be possible to systematically group a significant portion of the skeleton, especially in instances of small-scale commingling involving well-preserved remains. Articulation is not advised when remains are extremely fragmented, or when articular surfaces are missing or damaged. Caution should be applied when the commingled population is large and homogeneous (e.g., all 17-19 year old White males). Greater confidence with articulation is granted to results that lead to exclusions than those that show consistencies.

4.2.5   Process of Elimination

Process of elimination may be very useful, especially in instances of small-scale commingling, but as the number of individuals increases it usually becomes problematic to narrow the list of potential candidates to a single individual. In most cases, it is preferable to complete the articulation and pair-matching process prior to the process of elimination step. After articulation and pair-matching are completed, duplicated elements may remain that can be associated with a specific individual through the process of elimination.

4.2.6   Osteometric Comparison

Osteometric comparison is a technique that uses statistical models to objectively compare size and shape relationships between elements. Osteometric comparison removes subjective judgment calls and provides a solid statistical basis for segregation. The strength of this technique is that it can be used to segregate remains that could not be segregated through other means, such as pair-matching and articulation. It is also amenable to situations in which the remains are fragmentary; however, extensive cortical

erosion could produce biased results. It is important to realize that the real strength of osteometric comparison is to recognize *inconsistent* relationships which lead to exclusionary sorting (i.e., consistency between elements alone is not sufficient evidence for association). In most instances it is not possible to osteometrically segregate individuals with similar body size and build.

4.2.7   Taphonomy

Taphonomic patterning refers to similarities and differences in preservation (e.g., color and staining). Analysis of taphonomic similarities or differences should not be considered a primary sorting technique in most instances. Taphonomic patterns can be very individualizing, especially due to idiosyncratic circumstances such as when a rust stain from a zipper crosses adjacent bones. However, there may also be drastic taphonomic differences present on the remains of the same individual due to disarticulation and a variable burial context. Care should be used when considering taphonomic factors, such as color, since traumatic disarticulation (such as may occur from an aircraft crash) may disperse portions of a single individual into very different contexts.

4.3   Number of Individuals

When working with commingled human remains, it is important to develop a quantitative estimate of the total number of dead. These results could have implications on the identification process and for possible criminal investigations. In some instances it may be useful to generate number estimates prior to completing the entire sorting process outlined above.

Generally, discussions concerning number estimates with commingled human remains focus on the Minimum Number of Individuals (MNI). One of the reasons for the popularity of the MNI is its ease of calculation. Other options include the Lincoln Index (LI) or a slight modification to the LI called the Most Likely Number of Individuals (MLNI). These alternatives to the MNI can potentially provide more analytical power when dealing with commingled remains.

There are two critical components to consider when determining the appropriate quantification technique: 1) bone taphonomy (e.g., preservation and fragmentation); and 2) scale of the incident. Extremely fragmentary or poorly preserved remains may not be amenable to any meaningful quantification technique.

Most commingled sites can be considered to be either small-scale or large-scale. Everything else being equal, it will generally be easier to determine the number of individuals with small-scale incidents. Large-scale scenarios become more complicated from both an analytical and logistical perspective.

4.3.1   Minimum Number of Individuals (MNI)

For interpreting population size from a skeletal assemblage, the MNI presents the minimum estimate of the number of individuals that contributed to the sample. The most common method of the MNI used for the analysis of human remains is calculated by sorting the bones by side, element, and developmental status (e.g., infant, adolescent, adult) and then taking the greatest number as the estimate. In other words, the MNI is the number of the most repeated element after sorting by element, side, and developmental status. In order to deal with fragmentary remains, specific segments of an element (e.g., distal femur) can be used for the calculation of the MNI. Every fragment must share a specific landmark to ensure that fragments do not originate from the same skeletal element. The basic principle of an MNI estimate is to avoid counting the same individual twice.

4.3.2   Lincoln Index (LI) and the Most Likely Number of Individuals (MLNI)

The Lincoln Index (LI) and the Most Likely Number of Individuals (MLNI) are quantification techniques that potentially improve the statistical accuracy of the estimates when compared to the MNI. These techniques are used to estimate the *actual* number of individuals, as opposed to the *minimum* number. Both of these techniques are calculated based on the number of paired and unpaired bones (as opposed to the MNI which usually is not dependent on pair-matching). With both the LI and MLNI preservation must be good as it is critical that elements can be accurately pair-matched. Errors in pair-matching can result in the calculation of very misleading estimates.

While both the LI and the MLNI will provide very similar results in most situations, it is recommended that MLNI should be used since it was derived specifically in order to remove bias from the estimate. For single elements, the MLNI is calculated as: $MLNI = [(L+1)(R+1)/(P+1)]-1$; where L= total number of lefts, R= total number of rights, and P= total number of pairs.

5.0   Other Considerations

At the onset of any analysis involving commingled remains it is important to establish baseline parameters and protocols (e.g., the scope of DNA testing and the disposition of unidentifiable remains). While these decisions may fall outside the purview of the anthropologist, they will have a significant impact on the analyses performed for sorting and reassociating commingled remains.

6.0   Unacceptable Practices

The following practices should be avoided when working with commingled human remains:

- Uncritical combining of elements in the field based strictly on proximity
- Not preserving contextual information in sorting the remains
- Assuming that MNI estimates represent the actual number of individuals in a scene/situation as opposed to the minimum
- Naïve utilization of DNA profile data, especially with regards to mtDNA sequence data. Failure to consult with a DNA specialist as to the risk of random matches
- Failing to document the sorting process
- Using unscientific procedures to sort commingled remains
- Working in the laboratory without review and consideration of available field recovery documentation.
- Over reliance on a single sorting method without consideration of other techniques