H41 Pair-Matching of Human Skeletal Elements: Evaluation of Morphological Features for Visual Examination and Statistical Tables for Metric Assessment

Richard M. Thomas, PhD, Federal Bureau of Investigation Laboratory, Trace Evidence Unit, Room 3210, 2501 Investigation Parkway, Quantico, VA 22135; Douglas H. Ubelaker, PhD, Department of Anthropology, NMNH - MRC 112, Smithsonian Institution, Washington, DC 20560; and John E. Byrd, PhD, 95-033 Hokuiwa Street, #51, Mililani, HI 96853-5530*

The goal of this presentation is to provide attendees with a better understanding of both the visual and metric techniques of the process of pair-matching human skeletal elements.

This presentation will impact the forensic science community by presenting a description of which morphological features of individual skeletal elements are most useful for making a visual pair match and by presenting a new statistic (M) that can be used to metrically assess whether homologous bones are a possible pair match.

The process of matching paired skeletal elements (e.g., left and right femurs) is a technique used in forensic anthropology, paleodemography, and other osteological studies to determine if two homologous bones could have originated from a single individual. It is commonly used to resolve commingling issues from mass graves or disaster scenes, but can also be used in individual forensic cases where partial remains are found in different areas or at different times. When dealing with a closed population (e.g., aircraft accident), pair-matching is an easier task for the anthropologist than when dealing with an open population, when the anthropologist must decide whether the skeletal homologs can be matched to the reasonable exclusion of all other individuals.

There are two methods of pair-matching: visual pair-matching, a subjective technique which uses gross visual evaluation of similarities in bone morphology and taphonomy to match pairs; and osteometric sorting, a quantitative technique which allows statistical evaluation of size similarities between homologs to evaluate possible matches. This presentation covers both methods.

Visual pair-matching has been discussed as a reliable process; however, the details of how the exercise of visual pair-matching is done and what skeletal features are used have been seldom explored. The work presented here evaluates discrete morphological features of the major postcranial paired skeletal elements as described by White and Folkens (2005). Examination of morphological features included pairwise comparisons of 26 skeletons (which led to 231 comparisons for each feature) from the Robert J. Terry collection, housed at the Smithsonian Institution's National Museum of Natural History. Postcranial skeletal elements were examined, including the clavicle, scapula, os coxa, and all long bones. Cranial bones as well as smaller and less diagnostic bones (i.e., ribs, patellae, hand and foot bones) were excluded from this study. This effort provides anthropological investigators with a list of features that are the most consistent between the left and the right side, which can be used for the identification of matched pairs. Perhaps more importantly, it also provides a list of features that show variation between the left and the right side, which should not be used as means for the exclusion of possible pair matches.

This presentation will also address metric evaluation of possible pair-matches. Previous studies have produced statistical tests to resolve commingling, which can be used for pair-matching purposes, but also apply to osteometric sorting of other skeletal elements, and therefore are more laborious than necessary for use in matching single pairs. These techniques usually require multiple measurements for each bone, which may be impossible in the case of fragmentary remains. Data from a database of standard skeletal measurements (Byrd and Adams 2003) are used to produce a statistic (M), which is designed to capture the range of variability between the left and right elements within human individuals to aid in the metric assessment of possible pair matches. This presentation will include an introduction to reference data tables that show the maximum value, as well as the 90th and 95th percentiles of the M-statistic. These values are shown for 52 standard measurements for paired elements and are applicable to fragmented bones. These tables allow a simple metric test of the null hypothesis that homologous bones originated from the same individual.

Pair-Matching, Osteometric Sorting, Commingling

** Presenting Author*