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Determination of sex from the proximal hand phalanges in a Thai population

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ABSTRACT

A sample of 249 skeletons (154 males, 95 females) from the Chiang Mai University Skeletal Collection was studied to investigate the potential of proximal hand phalanges as indicators of sex among individuals from the Chiang Mai province of Thailand. The sample ranged in age from 19 to 93 years. Six measurements were taken on each proximal phalanx: maximum length, medio-lateral base width, antero-posterior base height, medio-lateral head width, antero-posterior head height and maximum mid-shaft diameter. The measurements were then subjected to ROC analysis as well as binary logistic regression to assess the relative correct allocation accuracy for each bone, and for different combinations of measurements from each bone. All proximal phalanges from both sides exhibited greater than 87% correct allocation accuracy for at least one logistic regression equation that included only two or three measurements. When the sample was limited to individuals with no missing measurements ($n = 209$) in any of the phalanges, the most accurate equations for each proximal phalanx ranged from 87.6% to 92.3%, with the most accurate equation based on two measurements from the left 1st proximal phalanx, and the next most accurate from three measurements of the left 2nd proximal phalanx. The results suggest that proximal phalanges produce better allocation accuracies than metacarpals among modern individuals from Thailand.

1. Introduction

Studies concerned with the sexing potential of hand bones have become relatively common over the last two decades [1–10]. Most of these studies have focused on multiple measurements from individual metacarpals to create discriminant functions or logistic regression equations for determining sex in specific populations [1,4–7,10]. The metacarpals are probably favored over the phalanges in these studies because they are the largest and most easily identifiable bones of the hand. Typically, the equations with the highest accuracies from these metacarpal sexing studies range from 89 to 94% correct allocation. For those studies with sample sizes of at least 100 individuals, the highest allocation accuracies are 89–92% [4,5,7,10]. Considering results by bone, the median correct allocation accuracy among these studies is 89% for MC4, 88% for MC1, 87% for MC2 and MC5, and 86% for MC3.

Only three studies of sex determination from the hands have included measurements from one or more proximal phalanges [3,8,9]. The proximal phalanges are probably less commonly considered for this purpose because of perceived difficulties in determining the correct position and side of phalanges recovered in the field, and perhaps an assumption that the larger metacarpals will be subject to less measurement error than the somewhat smaller phalanges.

Recent work, however, indicates that complete phalanges are relatively easy to position and side [11–13], particularly if more than one is available for analysis, so this concern should not be a deterrent to their use. As for the effects of measurement error, a study by Varas and Thompson [13] of metric variation in the proximal phalanges found an intra-observer error rate for three caliper measurements ranging from an average of 0.13% for length measurements, to an average of 0.59% for head width measurements. This is a very similar range to that reported in a recent study of the sexing potential of the tarsals (0.08–0.60%) [11]. Furthermore, the average error rate for proximal phalanx length is slightly lower than the 0.17% reported for the 2nd metacarpal by Lazenby [6]. Therefore, it appears that the proximal phalanges can be measured with sufficient accuracy to be useful in sex determination.

Previous studies of the sexing potential of proximal phalanges have used quite different approaches, making the results difficult to compare. One study used six measurements of the first proximal phalanx to create a discriminant function equation with a tested accuracy of 78% [8]. The sample used to create the equation was somewhat small at 60 individuals, and the test sample was less

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than 20 bones. However, sexing equations were also calculated for the metacarpals in this same study, and the phalanx equation was at least as accurate as the metacarpal equations, with the exception of the one derived from the first metacarpal [8].

Another study used eight or nine measurements per proximal phalanx, depending on the digit, then combined the most sexually dimorphic measurements from all five phalanges into one sexing function for each hand [9]. The sample size in this study was quite large ($n = 160$), but it combined European immigrants, European-Americans, and African-Americans together, because part of the purpose of the study was to identify ancestry and sex simultaneously. The equation for the right hand required eight dimensions from among the first, second, third, and fifth phalanges for 78.6% accuracy, and the equation for the left hand required 10 dimensions from among the first, second, fourth, and fifth phalanges for 76.3% accuracy. Allocation accuracy was likely reduced in this study by the mixing of populations.

The third study that considered proximal phalanges for sex determination used a combination of length measurements from all of the proximal phalanges [3]. The sample was composed of 259 individuals of European-American descent. The right hand phalanges produced a correct classification accuracy of 82.7%, while the left phalanges produced an accuracy of 80.8%. The combined lengths from the proximal phalanges outperformed the combined lengths from the metacarpals by 1.2% in the left hand, and 4.8% in the right hand. However, to achieve this level of accuracy using lengths alone, a researcher must have at least three proximal phalanges available for measurement.

The purpose of this study is to test the utility of individual proximal phalanges for sex determination among a sample of Thai skeletons from the Chiang Mai province of Thailand. A recent study of the sexing potential of Thai metacarpals ($n = 249$) from the same sample produced highest pooled allocation accuracies that range from 85.2 to 88.9% in the right hand, and 83.2 to 89.8% in the left hand [5]. This study will examine whether the proximal phalanges exhibit similar levels of allocation accuracy, and will develop logistic regression equations for use in sexing of modern Thai individuals from the Chiang Mai province.

2. Materials and methods

The methods used in this analysis follow closely those described by Khanpetch et al. [5] to study Thai metacarpals for sex determination. The sample consists of 250 skeletons of Thai adults (155 males, 95 females) from the Chiang Mai University Skeletal Collection housed at the Department of Anatomy, Faculty of Medicine, Chiang Mai University, Thailand. The Chiang Mai collection is a documented sample of Thai citizens from the local area who died between 1990 and 2011. Age at death in our sample ranged from 19 to 93 years. Skeletons in this collection are self-donations and represent people from various socioeconomic backgrounds, including many professionals.

Only proximal phalanges that showed no pathology (e.g. perimortem trauma, fractures, or severe osteoarthritis) were measured for this study. Six measurements were taken from each proximal phalanx on both the left and right sides, including maximum length, maximum midshaft diameter, and width and height measures of the proximal and distal ends (Fig. 1). These measurements are identical to those described by Scheuer and Elkington for the first proximal phalanx [8], and follow the same approach for the remaining phalanges.

The naming convention for each measurement used in our study includes a three-letter abbreviation for the bone name, followed by a two-letter abbreviation for the measurement. The proximal phalanges are abbreviated ‘‘PP’’ followed by the ray in which they appear (e.g. PP1 for the thumb). Abbreviations for the measurements are: LG (length), BW (base width), BH (base height), HW (head width), HH (head height) and MD (midshaft diameter). Side is indicated, where necessary, by appending an ‘‘L’’ or ‘‘R’’ in front of the abbreviation. Thus, right third proximal phalanx head width would be abbreviated RPP3HW.

All measurements were taken by one of us (PK) to the nearest millimeter using non-digital vernier sliding calipers. Rounding to the nearest millimeter in this way reduces the impact of measurement error, but also reduces the number of unique data points in the measurement distribution. This restriction means that a single measurement is unlikely to be a good discriminator between the sexes, because of clustering of data points in the area of overlap between the male and female distributions at a particular integer value. However, measurement to the nearest millimeter also means that the measurements should be highly replicable, and all but the grossest of measurement error should be eliminated.

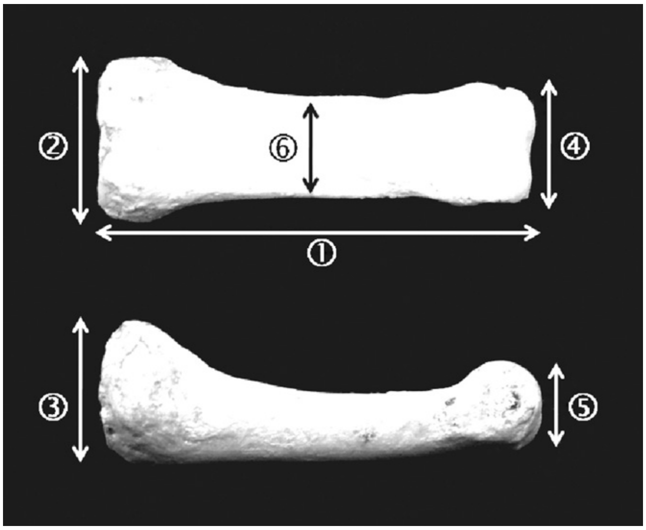

Fig. 1. Photo indicating the dimensions measured for this study: (1) length (LG), (2) base width (BW), (3) base height (BH), (4) head width (HW), (5) head height (HH), (6) midshaft diameter (MD). See Scheuer and Elkington [8] for a detailed description.

One male skeleton was removed from the data set because nearly all proximal phalanx measurements were four or five standard deviations below the mean. Thus, the final sample used for analysis consists of 249 individuals (154 males, 95 females).

Binary logistic regression analysis was performed on a subset of individuals with no missing data in either hand to determine which combinations of measurements from each individual proximal phalanx showed the greatest ability to correctly classify males and females. This subsample contained 209 individuals (127 males, 82 females) and was used to calculate the relative allocation accuracy of each regression equation for direct comparison between individual phalanges, and between the same dimensions on the left and right sides. Logistic regression is an appropriate choice because it has much more relaxed data requirements than discriminant analysis. It does not require the data to be normally distributed, and is less sensitive to high correlations among predictor variables and more tolerant of outliers than discriminant analysis [14,15].

ROC analysis was also conducted on the subset of 209 individuals with no missing data, in order to compare the performance of the various individual measurements, as well as their combinations in the logistic regression equations. ROC analysis is commonly used by clinicians to evaluate the quality of diagnostic decisions or the efficacy of clinical tests in identifying disease [16,17]. The method considers the performance of a particular diagnostic measure, such as a bone dimension, at each of the data points in the sample, rather than at just a single threshold value [18]. Thus, ROC analysis considers performance at the single sectioning point identified by logistic regression analysis, as well as at other sectioning points above and below that point throughout the data distribution.

The result of ROC analysis is a curve that represents a plot of the ‘‘true positive proportion’’ on the y-axis, against the ‘‘false positive proportion’’ on the x-axis. In our case, the true positive proportion might represent the male allocation accuracy – the number of males correctly identified divided by the total number of males in the sample. The false positive proportion might then represent the proportion of females mistaken for males, divided by the total number of females in the sample. The true positive proportion is called the ‘‘sensitivity’’ of the test, and the false positive proportion is denoted as ‘‘1 – specificity’’, where ‘‘specificity’’ is the proportion of females correctly identified.

ROC analysis allows comparison of different sexing techniques through comparison of the area under the curve (AUC). The larger the AUC value, the better the measurement at distinguishing male from female. The approach can be applied to logistic regression equations as well by using the logit values in place of measurements. One advantage of using ROC analysis is that it allows assessment of sexing performance at several different measurement values throughout the distribution. Thus, it may be possible to identify useful threshold values within individual measurements even when considerable overlap exists between the male and female distributions, as is the case in this study.

Statistical analyses were performed using SPSS version 18.0. For the logistic regression analysis, a forward conditional approach, which selects the most dimorphic measurement first, then assesses others for a significant additional contribution to the model, was applied to each metacarpal to select the best