

## PAPER

## ODONTOLOGY

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## Dental Shape Match Rates in Selected and Orthodontically Treated Populations in New York State: A Two-dimensional Study\*

**ABSTRACT:** Forensically identifying a suspect's dentition from a bitemark in an open population requires the supposition that every person's dental alignment is different. There have been few studies that have tested this claim. Four hundred and ten lower anterior dentitions from a selected population and 110 lower anterior dentitions from one that was orthodontically treated were measured using geometric morphometric analysis, allowing comparison of arch shape. Dental match rates of 1.46% and 42.7% of individuals were found in the respective populations, given an established measurement error. Orthodontic treatment had a strong effect on match rate suggesting that treated or naturally well-aligned dentitions may be indistinguishable. Sexual dimorphism was found to be only slightly significant. Principal shape variation in both populations was degree of arch curvature. Results of studying these populations show that dental matches can occur, and that statements of certainty concerning individualization in such populations should be approached with caution.

**KEYWORDS:** forensic science, forensic odontology, bitemarks, dental uniqueness, geometric analysis, morphometric analysis, orthodontic treatment

Bitemark analysis has received attention in the debate over reliability of forensic methodology (1). In disputed cases, there have been diametric disagreements between experts over the nature of the evidence. This prompts the question as to whether problems lay with the data in question or the fundamental principles that guide the interpretation. Bitemark analysis has continued to be introduced in the courtroom, and it appears very likely that more stringent examination of the scientific basis of bitemark evidence may be anticipated in the light of the current debate (1).

The primary tenets of bitemark analysis are that there are individualizing details in the dentition that transfer to and are recorded in the skin, allowing identification of the perpetrator. Current criticism of bitemark analysis focuses on the fact that the uniqueness of the dentition has not been established (1).

There are relatively few studies in the forensic odontology literature that investigate the issue of individuality of the human dentition. Those that have, either used flawed statistical treatments or argue uniqueness based on small differences in metric or shape measurements (2–4).

Rawson et al. in their much-cited 1984 study used a single point (x,y position and angle) to represent each anterior tooth, and by

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\*Presented at the 62nd Annual Meeting of the American Academy of Forensic Sciences, February 22–26, 2010, in Seattle, WA.

Received 8 Mar. 2010; and in revised form 3 May 2010; accepted 16 May 2010.

calculating possible tooth positions arrived at the conclusion that the “human dentition is unique beyond any reasonable doubt” (5, p. 252). Recently, Rawson et al.'s methodology has been revisited with consideration of nonuniform distribution and correlation of dental structure (6). Using the same measurement resolution as Rawson et al., significant numbers of dental matches were found within the data sets studied. This contrary finding is consistent with the intuitively sensible concept that as members of a single species, human dentitions fit within a defined biological shape space, and because this space has finite boundaries, there will be overlap (6). Indeed, it may be anticipated that as a dental database grows, the number of matches increases geometrically with database size (6). Other factors can lead to an increase in match rate, such as individuals who have received orthodontic treatment.

One result of orthodontic treatment is alignment of the anterior teeth. The anticipated effect of this is that there is less variation of tooth position in a treated population, with the teeth occupying a more restricted shape space. It may be further anticipated that such treatment will produce a higher dental match rate.

Other studies using a metric approach have measured mesial/distal tooth width, intercanine width, and tooth angulation. Two recent investigations with respective population sizes of  $n = 300$  and  $n = 410$  reported these measurements as falling into three categories: common, uncommon, and very uncommon (2,3). However, this approach did not address the issue of uniqueness of the dentition, nor did it provide any useful statistical comparison of dental shape.

In Bernitz et al.'s article, it was stated that “It is important to realize that when comparing the measurements of a suspect's dentition with the tooth marks present on the skin of the victim, an exact match will seldom be found” (2, p. 196). This raises the

question, *why make metric measurements if this is the case?* Although Bernitz et al. do not explain the basis of their statement, the concept is supported by recent empirical studies showing that due to distortion, exact metric dimensions of the dentition do not reliably transfer to human skin (7–10). The inherent qualities of the tissue, visco-elasticity, anisotropy, and nonlinear nature of skin all contribute to the distortion seen in a bitemark (7). The degree of distortion in a bite can exceed the measurement differences that distinguish one dentition from another and can result in an increased probability of more than one possible dental match (8,9).

If metric measurements are unreliable, it may be more pertinent to consider the arrangement of teeth in the arch and their relative alignment. By looking at the overall shape differences of the anterior dentition, we can study the frequency of a given dental shape or (mal) alignment pattern in a given population.

A well-developed method to describe shape variation between biological specimens is Geometric Morphometric analysis (11–13). Geometric Morphometric analysis involves placement of landmark points, curves or outlines on either two- or three-dimensional images. The landmark data can be extracted and analyzed statistically as a unit, removing rotation and size effects, but retaining shape. The size standardization is a scaling process rather than a removal of differences associated with biological form. Under this definition of shape, images that can be exactly overlaid are said to have the same shape. Subsequent to the alignment process of removing nonshape variation (the Procrustes Superimposition Process), shape variance analysis and statistical treatment of populations can be performed and match rates derived (11–13).

Among the tools available for statistical analysis is principal component analysis (PCA) with which the principal variations of shape can be plotted and visualized. This allows for determination of which shape aspect is responsible for the most variation. Canonical variate analysis (CVA) is another statistical tool that determines relationships between groups of variables. Shape information can be visualized by plotting landmark positions in superimposition. Procrustes distance is a measure of the closeness in shape of Procrustes superimposed specimens and is recognized as a general-purpose measure of specimen similarity in the geometric morphometrics framework. Procrustes distances can be used to summarize variations in populations, or express the degree of similarity of individual specimens, or means of populations.

Kieser et al. (4) were the first to use these tools in the forensic odontology context. That study involved landmark placement on six anterior teeth in 33 maxillas and 49 mandibles in an orthodontically treated population. A Procrustes distance between the two most similar maxillas was reported to be 0.0444 and the two most similar mandibles to be 0.0387. The differences in shape were thus very small. It was concluded, however, that this small difference in shape “supports the notion of the individuality of the human dentition.” Results suggested no sexual dimorphism and PCA determined that the principal shape variation in his population was curvature of the arch. A criticism of this study was that the sample size was limited, and that the measurement resolution (repeated measure error) was not reported (14). It was not shown whether the minimum observed Procrustes distance between specimens fell within measurement error of this study.

None of the prior studies investigated the issue of similarity of the dentition or the likelihood of finding a close match in a given population. Given consideration of the concept of increased matches as a function of database size, and that of human dentitions occupying a finite shape space, it was considered important to repeat analysis with a larger selected population and an expanded orthodontically treated population using the same Geometric

Morphometric methods. Thus, the goals of this study were first to reexamine the question of sexual dimorphism in a larger population, second to compare match rates between orthodontically treated and nontreated sets, and third to understand the dental causes of the principal shape variations.

## Materials and Methods

All necessary Human Subject Institutional Review Board protocols were completed for this project and exemption was granted. Three different model populations were obtained.

The first set consisted of 290 dental models (145 sets of maxillary and mandibular sets) were collected from the dental clinics at the State University of New York at Buffalo School of Dental Medicine. This group of models served as a test group to determine how relevant gender was in differentiating alignment pattern. The second group was comprised of 176 maxillary models and 265 mandibular models collected from the patient pools of several private practice dentists. These two groups were pooled for the purpose of shape comparison in a larger population resulting in 321 maxillary and 410 mandibular specimens. A third group of 110 maxillary and mandibular orthodontically treated patient models were collected from SUNY School of Dental Medicine.

The criteria for inclusion in all groups (University and private practice) were that there was a full complement of anterior teeth from canine to canine. Although both maxillary and mandibular models were collected and analyzed, this study reports only mandibular results as it was considered that fewer matches would result in the mandibles due to higher incidence of crowding and malalignment. In all cases, the sample size was one of convenience. The data sets may also be regarded as being selected, because of the criteria employed. Clearly the models are evidence that the patients had been under dental care and that they thus represented a certain cross-sectional demographic in New York State.

The models were scanned on a flat bed scanner at 300 dpi (Canoscan 8600F; Canon, Lake Success, NY) with an ABFO #2 scale in place for each scan, resulting in digital images of each arch. Fourteen Landmark points delineating mesial to distal extension of each anterior tooth (canine to canine) as well as the center point of each canine were placed using tpsDIG Freeware (15). Two additional landmark points were placed on the ABFO scale in each image, delineating a reference distance of 50 mm. The  $x/y$  coordinates of the landmarks were saved in data files that were statistically analyzed using IMP freeware (16).

Inter-operator error was measured by five operators placing landmarks on the same 15 dentition images. Intra-operator error was assessed with a single operator repeating landmark placement on the same set of images 10 times. This established a Procrustes distance threshold, that of the obtained measurement error, which was used to determine whether dentitions matched. When the Procrustes distance of two dentitions was equal to or less than this threshold the dentitions were considered a match. Procrustes plotting, PCA, and CVA were performed.

## Results

Inter- and intra-operator error measurement for landmark placement resulted in a Procrustes distance threshold of 0.03. This value is twice the root-mean-square of distances of specimens about their mean, which is analogous to a standard deviation measurement (but noting that these data were not normally distributed). This was taken as the minimum shape difference below which two samples were considered a match. Procrustes distances are dimensionless,

so to relate this distance to more familiar units, a translation was made that indicated that inter- and intra-operator error was approximately 1.2 pixels, or 102 microns (0.102 mm) per measured landmark coordinate. This seems intuitively reasonable as it makes the claim that the typical error made was a shift of roughly one pixel on a 300 dpi image. In other words, there was high accuracy and precision in landmark placement both between operators and on repeated measures with the same operator. A check of the distances among the repeated measures specimen indicated that 94% of the pairwise matches were within this resolution limit, very close to the familiar 95% confidence interval commonly used to indicate statistical significance.

### Gender Differences

Analysis of the test group of 58 male and 87 female participants for gender shape differences revealed a small difference between male and female participants in alignment of the mandibular anterior teeth. Figure 1 shows results of CVA analysis. The Procrustes distance between means was 0.0257, which was below our measurement error distance. Figure 2 is a Procrustes plot showing the comparison of the two as submitted to bootstrapped *F* test (testing the utility of our statistical method) revealing that the male and female data sets in general closely overlap. The difference in shape between genders was only slightly better than chance, thus male and female participants were combined into one group for the remainder of the study.

### Match Rates

For the open population of 410 mandibular models, three matched pairs of the lower anterior dentition were found, comprising six individual specimens, resulting in a match rate of 1.46% of this population. As the data set increased in numbers, the landmarks for each dentition overlapped with limited spread, as might be considered consistent with the concept of a common biological form. Clustering (nonuniform distribution) of the data points was strongly evident. Figure 3 is a histogram of distribution of the Procrustes distances between all 83,845 possible pairwise comparisons in the 410 mandibular dentitions. The histogram appears similar to

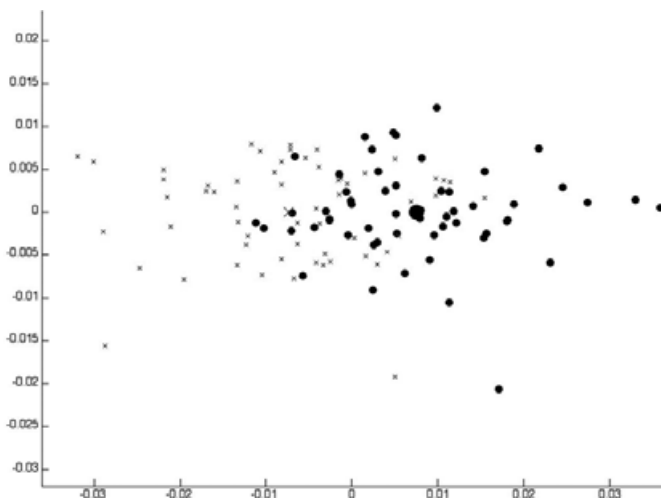


FIG. 1—CVA plot of male (dots) versus female subjects (crosses). The means of the populations are in large symbols. The distance between means was 0.0257, which was below our measurement error of 0.03. Had there been significant sexual dimorphism, the two sets of symbols would have been more separated.

a Poisson distribution, with few specimen pairs at very small distances, a large number at intermediate values and a long tail at large distances. The bold vertical line on the histogram indicates the error measurement threshold established as described. Clearly as measurement error increases, and the threshold moves to the right, large numbers of dentitions would be considered a match. The *x*-axis on the histogram is a measure of similarity, with most similar dentitions to the left, and less similar to the right.

Another way of understanding how similarity develops with data set size is to examine the mean nearest neighbor distance, a measure of the closeness in space of the data points (17). For the first 20 dentitions, the mean nearest neighbor was 0.081. When the data set had reached  $n = 400$ , the distance was 0.056. Further increase of the data set size would have the effect of this distance approaching our measurement resolution threshold (0.03), at which point each additional dentition would have a strong probability of

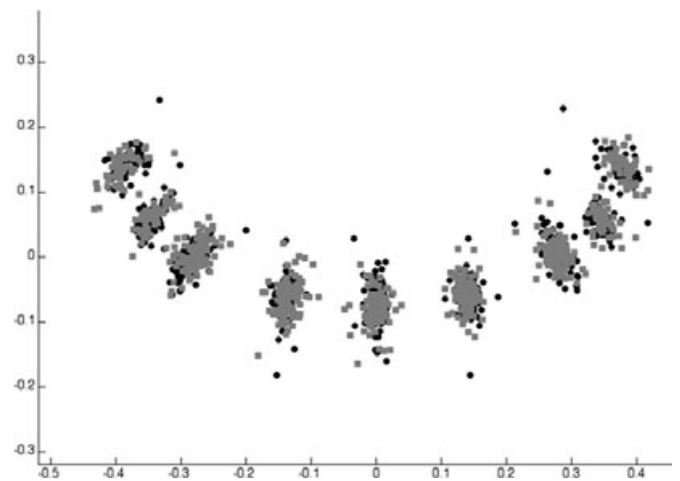


FIG. 2—Procrustes plot showing results of a bootstrapped *F* test (testing the utility of our statistical method) revealing that the male and female data sets in general closely overlap.

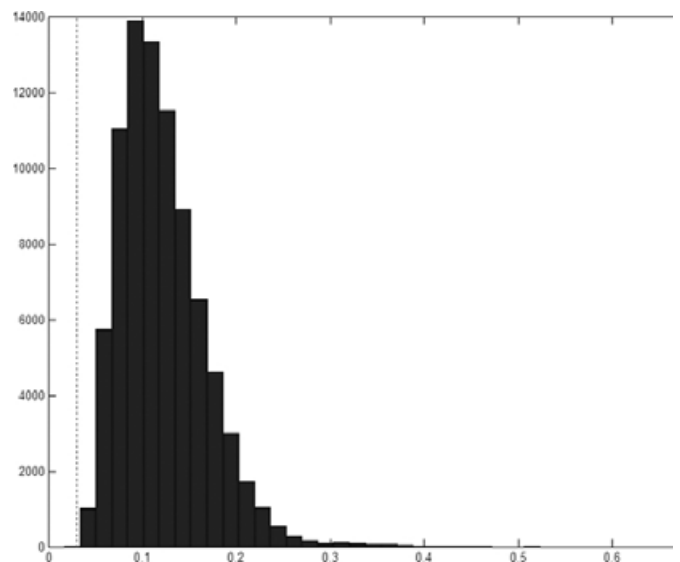


FIG. 3—Histogram of distribution of the Procrustes distance in the 410 mandibular dentitions. The *x*-axis on the histogram is a measure of similarity, with most similar dentitions to the left, and less similar to the right. The vertical line is our measurement error threshold. Clearly, as our error worsens and the line moves to the right, more dentitions would be considered a match.

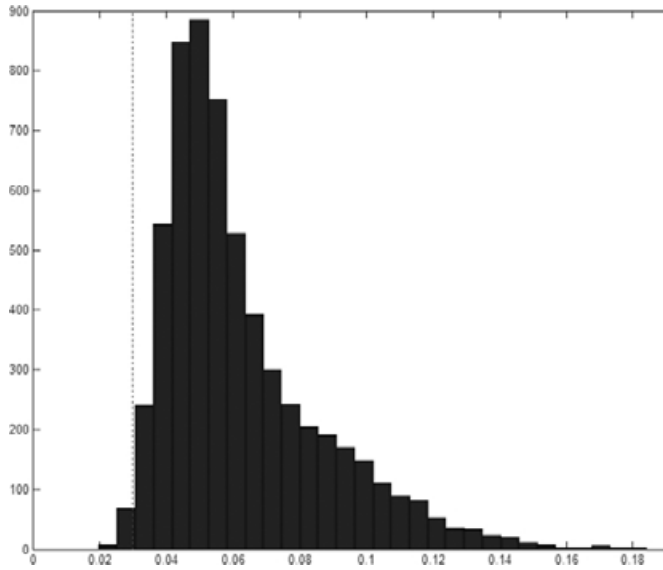


FIG. 4—Histogram of distribution of the Procrustes distance in the orthodontically treated population. Note horizontal axis units are an order of magnitude smaller than in Fig. 3, denoting a considerable increase in similarity. Comparison of the distance numbers shows that when the Procrustes distance approaches 0.1, large numbers of the general population will match, but nearly all of the orthodontically treated population will match.

matching an existing dentition. This effect will appear as the commonly occupied dental positions become more and more densely populated.

The match rate in the orthodontically treated mandibular data set ( $n = 110$ ) was 42.7% of the individuals, with 54 matches of paired specimens among 47 distinct individuals occurring using the established threshold. Unlike the nonorthodontically treated specimens, many specimens in this collection had more than one match to another individual. Figure 4 shows the histogram of distance distributions for the 5995 possible pairs of orthodontically treated mandibles. Note that now the peak of the distribution of pairwise distances has shifted downward, closer to the measurement error threshold, meaning that there is more similarity in these dentitions.

#### Dental Shape Analysis by PCA

PCA of the general population showed that arch width is the biggest variable. Figure 5 is a PCA plot in which the first axis is plotted horizontally, and the second axis vertically. The first axis explains 36% of the variance in shape, whereas the second vertical axis explains 12.9%. The position of the specimens from left to right represents degree of arch curvature, whereas the position on the vertical axis represents lingual movement of central incisors and labial displacement of lateral incisors. This can be visualized by plotting the relative shifts of points, as in Figs 6 and 7. In these figures, the arrows show the relative movements in shape space of the landmark points according to the PCA plot axes. This shows that the two principal dental variables for this collection of human mandibles are curvature of the arch, and lingual movement of central incisors and labial displacement of lateral incisors.

PCA of the orthodontically treated population shows a much higher percentage of variance explained by change in arch curvature, 50.6%. The second most significant variation in shape following orthodontic treatment is lateral movement of the anterior teeth, explaining 7% of the shape variance. In both populations studied, the third most significant shape variation is rotation of the canines (7.2 and 5.0% respectively).

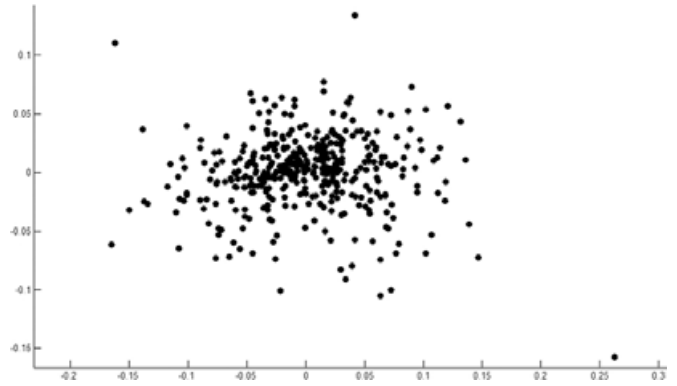


FIG. 5—PCA plot in which the first axis is plotted horizontally, and the second axis vertically. The first axis explains 36% of the variance in shape, whereas the second vertical axis explains 12.9%. The position of the specimens from left to right represent degree of arch curvature, whereas the position on the vertical axis represents lingual movement of central incisors and labial displacement of lateral incisors.

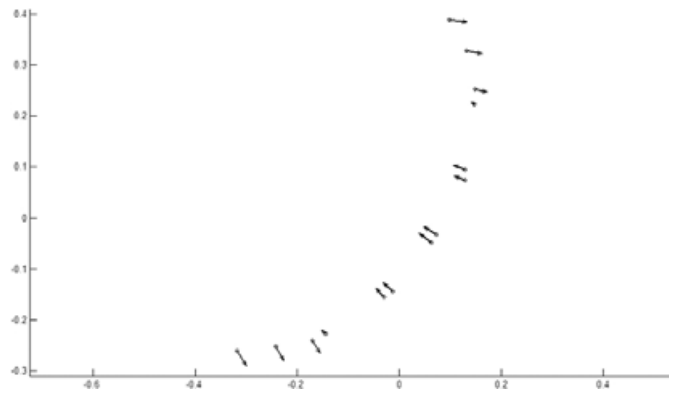


FIG. 6—Plot of landmark movement in the positive direction of the horizontal axis of Fig. 5, showing flattening of the arch.

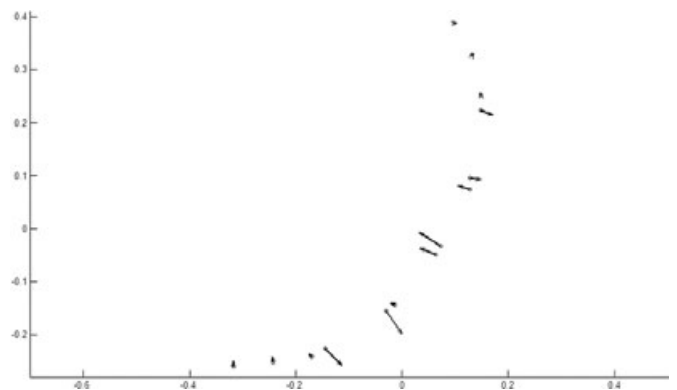


FIG. 7—Plot of landmark movement in the positive direction of the vertical axis of Fig. 5, showing lingual movement of central incisors and labial displacement of lateral incisors.

#### Shape Similarity

The shape variance within each group was calculated. The variance measure is the summed squared Procrustes distances of all specimens in a group from the mean of that group divided by  $(n-1)$ , where  $n$  is the number of specimens. The computation is thus very similar to the familiar univariate statistical approach. The variance for the general group was 0.00835, and the orthodontic



group 0.00224. In other words, there was much less variation in dental shape among the orthodontically treated group.

## Discussion

This study confirms earlier studies in finding only small shape differences between male and female participants (4). The implication of this finding is that in bitemark casework, statements concerning gender differences may have little basis. Effects of racial differences were not considered in this study.

The match rates reported here were based on a measurement error threshold developed under ideal laboratory conditions using measurements on dental casts. This resulted in a high level of accuracy and precision in landmark placement and thus description of dental shape, certainly higher than can be expected for bitemarks in skin. Under these laboratory conditions for assessing dental uniqueness, our general population showed a low but positive match rate (1.46%) given the threshold parameter derived from repeated measurement trials that we used to designate a match. The majority of the general population studied was known to have not received orthodontic treatment. If the measurement error had been higher, or had more of this population received orthodontic treatment, larger numbers of dentition would have been candidates for a match. Even so, given our measurement resolution, the dentition was found to be not unique.

As may be anticipated, orthodontic treatment had a very strong effect on dental shape similarity. The match rate in the known orthodontically treated set was 42.7% of individuals using the same threshold parameter in only 110 specimens. This confirmed that when orthodontically treated or naturally well-aligned, dentitions may be indistinguishable. This result is also a measure of how successful orthodontic treatment is at producing homologous dental arch shapes. The orthodontically treated human dentition is not unique, as measured here with high accuracy and precision.

The match rate in both populations was determined by the threshold, which in turn was determined by measurement error. As discussed above, dental metric detail is not transferred faithfully to the skin, so measurement of a bitemark in skin would result in an increase in measurement error. Thus, the match rates reported here for the lower anterior are minimal, and do not reflect the anticipated increase in match rate when considering skin distortion. Therefore, in circumstances in which comparison measurements are made on a diffuse bruise, one may expect reduced accuracy and precision. Thus, in a large population more (or the wrong) dentitions may be found to be match candidates. Adding the inevitable distortion of bitemark impression in skin, forming an opinion as to bitemark perpetrator identification with any degree of certainty when only a diffuse bruise exists, must be called into question.

The principal source of human dental shape variation is degree of curvature of the arch. This was true for both a general population and an orthodontically treated population. In the general population, the second cause of dental variation was displacement of the incisors (malalignment of the centrals), whereas in the orthodontically treated it was lateral movement of the teeth, as may be expected. The finding of central incisors displaced lingually to the lateral incisors can be related to eruption patterns, as these teeth tend to erupt lingually in the arch and drift forward. There are many variables that can affect this such as eruption sequence and size of the teeth versus room for eruption. Therefore, it is likely that this can be a common malalignment pattern.

The third principal shape variation was in angulation of the canines in both populations. Dental alignment patterns can also be affected by other parameters. There is an influence from

environmental factors with regard to malalignment, such as caries and trauma, that might affect the normal developmental sequence of eruption.

The shape similarity numbers derived here are quantitative measures of similarity of the dentition, and provide the first insight into the variability of the human dentition and the effect of orthodontic treatment. These findings are a step forward in understanding what constitutes shape difference in the human dentition, and therefore what might be the largest variables when considering how teeth may interact with the skin. It should be noted that this study only looked at matches in populations. It did not answer the question of the likelihood of matching a particular alignment pattern. Certain alignment patterns will obviously be more frequent than others.

This study was performed using a patient pool of convenience relevant only to the demographic locality. Extrapolation to other areas or countries in which dental care may be minimal or lacking entirely is not intended. In such regions there may be large proportions of the population with gross malocclusions and other dental defects that result in a broader range of possible individualizing dental characteristics. Furthermore, this study reports only mandibular results. The combination of matching both maxillary and mandibular shape deserves further investigation.

Due to so many variables, it could be argued that analysis procedures cannot be standardized due to the circumstances of the individual event that constitutes a bitemark. It can be stated now, however, that dental matches can occur, at least with regard to the anterior dentitions studied here. The shape variation of the human dentition, with regards to bitemarks, does not match the proposed level of individuality of fingerprints, and certainly can never be compared to statistical frequencies of molecular repeats that constitute DNA analysis.

## Acknowledgments

The authors would like to thank the two anonymous reviewers whose insight and perspective were greatly appreciated.

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