A Pilot Study to Analyze the Uniqueness of Anterior Teeth Using a Novel Three-dimensional Approach

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Abstract: Anonymized upper and lower dental models of 20 patients who had completed orthodontic treatment with good clinical results were scanned by hand using an intra-oral three-dimensional scanner. The three-dimensional scans were then cropped to include only the incisal 2 mm of the six anterior teeth. The edited images were subsequently imported into the three-dimensional analysis software, and a best fit alignment analysis of test and reference scans was undertaken using approximately 10,000 reference points. The distance between each reference point of both scans was measured, and 0.1 mm was the threshold criteria used to accept as matches.

A pictorial map produced by the software illustrated both quantitative and qualitative data from 420 comparisons undertaken. The software was able to identify matches amongst different software files of the same scan and different scans of the same models. There was a complete mismatch between the scans of pre- and post-treatment models. There were no perfect matches amongst the different post-treatment three-dimensional scans. However, there were close similarities between four upper and seven lower models using the 0.1 mm threshold. Using stringent criteria, we have shown that the human anterior dentition is unique within this study population.

Introduction

The fundamental principle that underpins the forensic identification of unknown human remains and bite mark analysis is the uniqueness of the human dentition [1]. In addition, bite mark
analysis depends on an additional postulate—that the asserted specific characteristics of the anterior teeth are recorded in detail in the substrate [2].

The uniqueness of the human dentition is widely accepted in relation to the forensic identification of unknown human remains [3]. The dental features commonly utilized in forensic identification include, but are not limited to, the number of teeth and their arrangements, the number and type of restorations, variations in crown and root morphology, and other pathological conditions [1, 4].

In contrast, with respect to bite mark analysis, “The uniqueness of the [anterior] human dentition has not been scientifically established.” [5] Therefore, with respect to bite mark analysis, the postulate of the uniqueness of the anterior human dentition is controversial [2, 3, 6–8]. Bite mark (or tooth mark) analysis aims to confirm or exclude a possible biter on the basis of the class characteristics of the six anterior teeth (e.g., dimensions and shapes of the dental arch and relative positions of the teeth) and individual characteristics of the biting surfaces (e.g., fractures, fillings, and diastemas).

It is believed that the arrangement of the anterior teeth is specific to that individual and is influenced by (1) local factors such as oral musculature [7], the eruption of the canines, which will cause the displacement, rotation, and movement of adjacent teeth [9], as well as (2) external factors such as tongue thrusting or non-nutritive digit sucking [7]. The reduction in number of identifying features is partly why the principle supporting the uniqueness of the human dentition in forensic human identification cannot be extrapolated to bite mark analysis [8, 10].

Senn and Souviron [11] stated that the validity of any statistical and mathematical analysis of bite marks is suspect until the uniqueness of the human dentition is confirmed. This inability to express quantitatively the uniqueness of the human dentition [12] has led to doubts over the evidentiary value of bite mark analysis [5]. This is perhaps best illustrated by previous wrongful convictions in several countries [10, 11, 13–15]. There is, therefore, a need to investigate the axiom of the uniqueness of anterior teeth.

Because bite mark injuries in skin are three-dimensional patterns (i.e., the dimensions and relative positions of the teeth that might have made the mark, depth of indentations of the teeth into skin, bruising of the skin, and other inflammatory changes),
a true three-dimensional technique would allow an examiner to analyze more surface detail of a three-dimensional patterned injury [16] and thus avoid secondary distortion artifacts that are inherent in the two-dimensional analysis of a three-dimensional mark [17, 18]. Unfortunately, there are only a handful of studies that could be described as having utilized a true three-dimensional technique as part of their analysis [8, 16, 17, 19, 20]. The rest of the studies used flatbed scanners [22–27], two-dimensional analysis [22, 23, 28, 29], or pseudo three-dimensional analysis (e.g., three-dimensional analysis of two-dimensional images) [26, 27, 30].

The purpose of this pilot study was to use an intra-oral three-dimensional scanner and three-dimensional analysis software to investigate the uniqueness of the anterior human dentition amongst 20 patients who had completed orthodontic treatment to (1) determine the feasibility of a combined intra-oral three-dimensional scanner and three-dimensional analysis software approach to bite mark analysis; (2) determine whether the three-dimensional analysis software was able to detect the difference(s) between scans of different dental models; and (3) determine whether there were any matches in the scans of the study population.

Materials and Methods

Study Population

Anonymized dental stone models (upper and lower arches) of a convenience sample of 20 patients who had recently completed orthodontic treatment at the Dundee Dental Hospital and School, Scotland, United Kingdom, were selected. All of the dental stone models (Crystacal, British Gypsum, Loughborough, U.K.) were poured under the same laboratory conditions at the orthodontic laboratory of the Dundee Dental Hospital and School. Any inter-model variability was due to an actual difference between the different subjects and was not due to the impression or casting procedures.

These patients had been assessed as having a good clinical result (low peer assessment rating) [31]. Additional selection criteria were (1) good-quality models with minimal defects such as porosities and positive bubbles, (2) six sound anterior teeth, and (3) the absence of fixed orthodontic retainers. The peer assessment rating index was initially designed to measure the outcome of a patient’s orthodontic treatment [31, 32] and is also used for
audit and payment purposes in the National Health Service. The index measures the alignment of the anterior teeth, buccal segment occlusion, overjet, overbite, and midline deviations [33, 34]

Intra-Oral Three-dimensional Scanner

Forty-four dental models (20 post-treatment upper and lower models, and 2 pre-treatment upper and lower models) were scanned by hand using an intra-oral dental three-dimensional scanner [3M Lava Chairside Oral Scanner C.O.S (3M ESPE, St. Paul, MN)] (Figure 1). A systematic approach to scanning the entire arch of each model was undertaken to ensure (1) a similar focal distance from the model to the lens and (2) minimal overlapping passes of the scanner for each tooth surface (i.e., avoid multiple passes on the same surface). Care was also taken to ensure an accurate digitalization of the models (Figure 2) rather than relying on the scanning software to fill in small voids or to smooth the three-dimensional images.

Three-dimensional Manipulation Software

The three-dimensional scans were then exported as polygon file format (PLY) files to a three-dimensional manipulation software [MeshLab (v.1.3.2), Pisa, Italy] [35] (Figure 3). The images were then cropped to include only the incisal 2 mm of the six anterior teeth. In the majority of nonavulsive bite (or tooth) mark injuries, this is the portion of the teeth that make the mark (Figure 4).

Figure 1

*Dental models (right foreground) scanned using the 3M Lava Chairside Oral Scanner C.O.S. (left foreground). The three-dimensional scans would be subsequently transferred to a computer (visible in the background), where they would be downloaded and stored for three-dimensional analysis using Geomagic Control. In a routine clinical setting, these scans would be sent to 3M’s dental laboratory for fabrication of dental prostheses.*
Figure 2
A representative three-dimensional scan of a lower model produced by the 3M Lava Chairside Oral Scanner C.O.S (buccal view of the same model shown in Figure 1).

Figure 3
Buccal view of the three-dimensional scan of an upper model as seen in MeshLab (v.1.3.2).

Figure 4
Resultant three-dimensional scan after editing in MeshLab (upper 2 mm of the biting surfaces of the same model shown in Figure 3).
Three-dimensional Analysis Software

The edited three-dimensional scans were subsequently imported as PLY files into a commercially available three-dimensional analysis software (Geomagic Control, Morrisville, NC) [36] to analyze whether the characteristics of the anterior dentition in the study population were unique. Geomagic Control is an automated metrology software that allows manufacturers to inspect, measure, and compare accuracy of manufactured parts.

Two three-dimensional scans were initially orientated in completely different three-dimensional spatial orientations and positions to each other. As part of the best fit alignment analysis, approximately 10,000 reference points were assigned by the software to individual areas of both scans, far exceeding what is possible with manual reference point allocation [8, 16, 19, 21-27, 29, 30]. A fine superimposition was produced by matching each reference point on the “reference” scan onto a corresponding point on the “test” scan. The software then undertook a three-dimensional comparison that measured the distance between each reference point on the “test” scan relative to the corresponding point on the “reference” scan [20].

A threshold of 0.1 mm (100 μm) was used as the criteria to accept matches between the “test” and “reference” three-dimensional scans (i.e., any similarities below 0.1 mm were accepted as matches). By using the most stringent threshold of the software, it was possible to assess the accuracy of this novel combined intra-oral three-dimensional scanner and three-dimensional analysis software approach to bite mark analysis, as well as benchmark the collected data against other studies that used similar methodology and future studies that utilize the same methodology.

The analysis was depicted as a pictorial colored map that showed the amount of match for each area of the three-dimensional scans. This concurrently illustrated both the quantitative and qualitative analysis. The degree of match, or lack thereof, was shown qualitatively by the color of each individual area. Perfect matches were illustrated in green, whereas areas of complete mismatch were portrayed in grey. Overlaps in between both extremes were represented by either shades of yellow to red for positive differences or different shades of blue for negative differences. An accompanying colored scale to the map displayed the quantitative distances between reference points of both scans.
In addition, Geomagic Control analysis also generated various views of the pictorial colored map (buccal, palatal, occlusal, right and left lateral) as well as tables and histograms of the deviation distribution. The occlusal view was chosen because it most closely resembled a bite mark.

**Analysis**

To determine whether the method was feasible and accurate (objective 1), analyses were undertaken on different software files of the same scan (i.e., a single scan stored as two different software files) and different scans of the same upper and lower models obtained from scanning the models twice. Analyses were also undertaken on scans of the pre- and post-treatment models of the same patients to determine whether Geomagic Control was able to detect the difference(s) between those scans (objective 2).

After the veracity and utility of Geomagic Control was established, the study proceeded using the same threshold of 0.1 mm to investigate whether there were any matches in the scans of the post-treatment models of the study population (objective 3). This involved the analysis of one three-dimensional scan against all other three-dimensional scans of the same arch until all the possible analyses were exhausted. In total, 420 three-dimensional analysis reports (210 upper arches and another 210 lower arches) were generated.
Results

The comparison for different software files of the same scan (i.e., a single scan stored as two different software files) showed a complete overlap of the “test” and “reference” scans (objective 1) (Figure 5). On the other hand, the comparison between scans of pre- and post-treatment models of the same subject showed a mismatch (objective 2) (Figure 6).

The comparison of two different scans of the same upper and lower models obtained from scanning the same models twice (objective 1) obtained slightly less than 100% overlap (Figures 7, 8). This was validated by the deviation distribution histograms, which revealed a very slight deviation distribution between the reference points of the “test” and “reference” scans. [Note: The X axis of the deviation histograms shows the distance between reference points of the “reference” and “test” scans (units in mm). The Y axis shows the percentage of reference points on the “test” scan that match the corresponding point on the “reference” scan (units in percentage)]. All discrepancies between deviation points were less than 0.1 mm, as demonstrated by the low scales on the X axes of the histograms (Figures 7, 8). The results from the comparison of the different scans of the same models served as the benchmark against which the different post-treatment scans analyses were compared.

Within this population, using a threshold of 0.1 mm (100 μm), it was possible to classify all post-treatment dental models as unique because there were no perfect matches amongst the different three-dimensional scans (objective 3). However, there were some close similarities between four upper and seven lower models. Two of them from the upper models involved a single model. Amongst the lower models, six of the close similarities involved three models that were each similar to two other models. The results of the closest similarities amongst the upper models and lower models are shown in Figures 9 and 10.
**Figure 5**

Objective 1: Comparison of an upper model stored as two different software files (units in mm).

**Figure 6**

Objective 2: Comparison of pre- and post-treatment upper models of the same subject (units in mm).

**Figure 7**

Objective 1: Comparison of two different scans of the same upper model. Pictorial map shows the qualitative and quantitative results concurrently, whereas the histogram shows the deviation distribution.
Figure 8

Objective 1: Comparison of two different scans of the same lower model. Pictorial map shows the qualitative and quantitative results concurrently, whereas the histogram shows the deviation distribution.

Figure 9

Objective 3: Closest comparison of two different upper models. Pictorial map shows the qualitative and quantitative results concurrently, whereas the histogram shows the deviation distribution.

Figure 10

Objective 3: Closest comparison of two different lower models. Pictorial map shows the qualitative and quantitative results concurrently, whereas the histogram shows the deviation distribution.
Discussion

This study has demonstrated the utility and feasibility of a combined intra-oral three-dimensional scanner and three-dimensional analysis software approach to investigate the uniqueness of the anterior human dentition (objective 1). Not only should access to an intra-oral scanner be easier, presumably, operating one would also be more intuitive to a dentist than, say, an engineering-grade scanner. For example, compared to 30 minutes in a previous study [19], the average time taken to scan a complete set of upper and lower models with the 3M Lava Chairside Oral Scanner C.O.S was 8 minutes ± 2 minutes. Moreover, a forensic odontologist can also consider undertaking bite mark analysis by directly scanning the dentition of a suspected biter.

The very minor discrepancies between different three-dimensional scans of the same dental models (all deviation points were less than 0.1 mm) (Figures 7, 8) were unlikely to be due to errors arising from the 3M Lava Chairside Oral Scanner C.O.S. The manufacturer claims that the three-dimensional scans have an accuracy of ± 10 µm, and the resultant CAD/CAM prostheses have a remake rate of less than 1%, which is due to poor marginal fit [37]. Recent studies using the 3M Lava Chairside Oral Scanner C.O.S in their methodology had demonstrated its higher accuracy [38] and a better internal fit of CAD/CAM-fabricated prostheses [39]. The very minor discrepancies noted may be due to an accumulation of fine dust or some microscopic damage to the models because the two scans of the same models were taken on different occasions a few months apart (after completion of the scan for all the different post-treatment models). Nonetheless, results from the comparison of the different scans of the same models (objective 1) served as the benchmark against which the different post-treatment scans were analyzed (objective 3).

Stringent criteria were adopted (i.e., post-orthodontically treated subjects with a low peer assessment rating, plus a small threshold value of 0.1 mm as the criteria of accepting matches between scans) in order to investigate the uniqueness of the anterior human dentition in our study population. The uptake of orthodontic treatment is increasing in the general population and within such a post-treatment population, there should be minimal variations in class characteristics and one would expect to find matches between the different subjects. It has been argued that the uniqueness of the dentition could be proven
if one used an extremely small threshold [3, 6]. However, a stringent threshold was necessary in this study because the intention was to investigate the accuracy of a novel method (objective 1). Only then would it be possible to benchmark the findings against other studies that would use the same or similar methodology.

Thali et al. [17] also adopted a threshold of 0.1 mm in their three-dimensional analysis of an actual bite mark case and they were able to match the “biting surfaces and edges of each teeth” [sic] with the investigated bite mark. On the other hand, Bush et al. [25] found matches within their study population based on a threshold of 1mm (1000 μm). Unfortunately, the metric threshold to determine non-uniqueness in the human dentition has yet to be determined. For example, two other studies that found matches within their study population did not state what metric thresholds they had relied on [19, 23]. Theoretically, an examiner would no longer be able to determine any appreciable similarities or differences between different dentitions beyond a certain metric threshold value and this may presumably lie between 0.1 mm and 1 mm. Further work is needed to determine a statistically significant metric threshold or mathematical algorithm that would be of help to forensic odontologists in quantifying the certainty of associating or excluding a suspect with a bite (or tooth) mark.

The best fit alignment analysis of test and reference scans undertaken by Geomagic Control used approximately 10,000 reference points. This far exceeded what was possible with manual reference point allocation in earlier studies [8, 16, 21–27, 29, 30] where a range of 14 to 60 landmarks were used [8, 16, 19, 21, 22, 24, 26, 27]. Rather than just comparing selected individual points on the teeth, this study has compared the entire biting surfaces of the anterior teeth. Moreover, these reference points were assigned by the software as part of the best fit alignment analysis and thus reduced the subjectivity as well as variability inherent in the manual placement of reference points.

It was intended to report the findings in an intuitive fashion that would be easily understood by members and officers of the court. In the authors’ opinion, the colored pictorial maps, together with the deviation distribution histograms produced by Geomagic Control’s three-dimensional analysis, were sufficiently straightforward and yet scientifically robust. Therefore, no mathematical modeling was undertaken as part of this pilot
study. Full quantitative analysis of the data collected from this study will, however, be undertaken in the future.

Geomagic Control was able to identify matches amongst different software files of the same scan and different scans of the same models (objective 1) as well as detect the differences between scans of different dental models (objective 2). Using a stringent threshold of 0.1 mm (100 µm), it was determined that there were no perfect matches amongst the post-treatment scans of the study population (objective 3). The findings from this study show that the anterior human dentition within this study population was unique (the aim of this study).

The results of this pilot study therefore lend support to the basic tenant of uniqueness of the human dentition that underpins bite mark analysis. The individuality of anterior teeth had previously been demonstrated using two-dimensional geometric morphometric analyses by Kieser et al. [22] on a post-orthodontically treated population with unrestored teeth, as well as three-dimensional analysis by Al-Ali [40] on randomly selected dissimilar models compared with different bite impressions. However, there are differences of opinion in the literature regarding the asserted uniqueness of the human dentition [8, 21, 23, 25], and it is beyond the scope of this paper to discuss this.

There were some close similarities amongst some upper and lower arches of this population, and this supports the need for determining a metric threshold, if it exists, where differences between different dentitions can no longer be discernable. More close approximations were found amongst the lower than upper arches and this contrasted with earlier work that found proportionally more “matches” amongst the upper arches [8, 21]. Bush et al. [21] suggested that their findings might support the commonly held perception of a higher incidence of crowding in the lower arch—an issue unlikely to be present in the current study population. It is possible that the number of similarities amongst the different upper models may rise with an increase in study population size [23], however, this may not actually be as much as expected [8].

The finding of several close similarities amongst the upper and lower arches of the study subjects necessitates caution in bite mark analysis because this is not undertaken at such a level of accuracy. Therefore, there is a possibility of excluding the actual biter or including an innocent biter from a dental lineup of dentitions with similar arch widths and alignment patterns [24, 26, 28].
This is primarily because the human skin is a poor impression material with respect to recording the asserted unique characteristics of the anterior teeth [3, 6, 14, 15, 24, 26, 28, 29]. For example, studies have found a great deal of variation in the appearance of experimental bite marks in cadaver skin that were produced by a single dentition [24, 26, 29]. Moreover, Holtkötter et al. [27] found that in certain cases, certain features, such as the height and displacement of teeth, may actually be magnified in the bite mark compared to the dentition.

It is increasingly recognized that a three-dimensional analysis approach to bite mark analysis is a positive way forward to analyze bite marks [16, 17, 19, 21] particularly in the absence of any positive DNA assay from the victim’s skin swab as a result of cross-contamination, degradation, or insufficient DNA quantity. A bite (or tooth) mark is a three-dimensional patterned injury, and a three-dimensional approach allows an examiner to analyze more surface detail compared to a two-dimensional approach [16] and also avoids primary [28] and secondary distortion artifact(s) [16, 18]. Therefore, a three-dimensional approach to bite mark analysis could potentially result in a decrease in false positive matches [21].

**Conclusion**

At a stringent threshold level of 0.1 mm (100 μm), this study has shown that, within the study population, the human anterior dentition is unique because there were no perfect matches within the post-orthodontically treated upper and lower dental models. This finding therefore lends support to the basic tenant that underpins bite mark analysis— that the human dentition is unique.

However, the finding of several close similarities amongst the upper and lower arches within the study subjects should also serve as a warning of caution in bite mark analysis, because bite mark analysis is not undertaken at such a level of accuracy. In such an instance, the identity of the biter may not be discernable from a sample of similarly aligned dentitions. Hence, in order to improve the accuracy of bite mark analysis, one should consider a three-dimensional approach to bite (or tooth) mark analysis, particularly in the absence of viable DNA assays from the victim’s skin swab. Thus, the pilot results from using this combination of intra-oral three-dimensional scanner and commercially available three-dimensional analysis software are highly encouraging.
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