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A study to determine the validity of mesiodistal dimensions of anterior teeth in dental identification

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ABSTRACT

Identification of deceased individuals is usually the most frequent role of a forensic dentist. The importance of teeth in human identification is well documented and established; however, there is a need for a simple method of identification to make dental identification more practical and user-friendly. The mesiodistal dimensions of teeth have been studied by various researchers in forensic dentistry, but none of these studies have used these measurements as an identification tool. This study was intended to find if mesiodistal dimensions can be used as an identification tool. A sample of 70 patients was taken, and mesiodistal diameter (m-d) of each tooth was obtained with digital calipers. A universal sequence for the mesiodistal widths of all anteriors was compared with the sequences obtained from the sample casts to check for uniqueness. The sequence of each sampling unit was significantly different from the universal sequence, as well as from each other. None of the sequences in the given data were similar to one another, and hence, we concluded that such a sequence can be used to identify an individual. Mesiodistal dimensions of teeth have been used in forensic dentistry for gender discrimination and as indicators of ancestry. Mesiodistal dimensions were utilized in our study to make a sequence which can be used to identify an individual. The use of dental metrics as a sequence for identification has been done for the first time ever, and the results suggest that this can be a very useful tool for dental identification.

Key words: Anterior teeth, calipers, dental identification, forensic dentistry, mesiodistal width

INTRODUCTION

Forensic dentistry is an applied branch of dental anthropology and forensic medicine, which includes population and demographic characteristics such as determination of sex and race, estimation of age, and personal identification to assign an unknown body to a specific person. Human identification is one of the most important aspects of forensic sciences, and identification of deceased individuals is usually the most frequent role of a forensic dentist.[1]

Dental identification of humans is usually employed in identification of bodies of victims of violent crimes, fires, motor vehicle accidents and work place accidents. Bodies of such victims can be disfigured to such an extent that identification by a family member is neither reliable nor desirable.[2] Persons who have been deceased for some time before discovery and those found in water also present unpleasant and difficult visual identifications. Most of the above-mentioned scenarios are also associated with the destruction of the soft tissues for the body, which makes the traditional method of identification using fingerprints very difficult.

Dental identification is preferred method for its ease and simplicity; however, the presence of antemortem records is required for dental identification. Antemortem records such as dental casts, radiographs, prosthetic, and orthodontic appliances are generally used, but obtaining these antemortem records transporting them to the site of identification is a tedious task. Moreover, systematic storing and maintenance of dental records are very rare in many countries. The importance of teeth in human identification is well documented and established,[3] but there is a need for a simple method of identification to make it more practical and user friendly.

The mesiodistal dimensions of teeth have been studied by various researchers as a tool for gender determination and to determine ancestry, but none of these studies have used these measurements as an identification tool.[4,5]

This study which is first of its kind was intended to find if individuals can be identified on the basis of the mesiodistal dimensions of anterior teeth when the measurements are considered as a complete sequence. These measurements will give us a unique identification number, which can be easily stored, retrieved, and can be compared easily.

MATERIALS AND METHODS

A sample of 70 patients was selected for this study from a dental institute in India. The inclusion criteria were fully erupted anterior teeth with no fillings or extractions, no crowns, no crowding of teeth, no fractured teeth or orthodontic apparatuses, and no developmental anomalies that could affect odontometric measurements. After obtaining informed consent from the patients, impression was taken using alginate and casts were poured with dental stone. After obtaining the casts, four casts were rejected due to the presence of air bubbles and damage

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to the cast during prying of the impression, and hence, the final sample size was 66.

Measurements were taken with a digital Vernier caliper giving two decimal points. Mesiodistal diameter (m-d) of each tooth was obtained by measuring the greatest distance between the proximal surfaces of the crown with the caliper held parallel to the occlusal and buccal surfaces according to methods outlined by Moorrees and Hillson.[6,7] To estimate intraobserver error, a second determination was made after 3 weeks by the same investigator. If the discrepancy between the two measurements was greater than ± 1.96 standard deviation, a new set of measurements was taken, and the nearest two measurements was averaged.

The measurements were taken starting from right maxillary canine and progressed onto left maxillary canine, and then, the measurement of mandibular teeth was taken starting from left canine and ending with the right mandibular canine.

Average mesiodistal width of all anterior teeth was taken from the textbook of Wheeler's Dental anatomy, physiology, and occlusion, which is considered as the gold standard for average mesiodistal dimension of teeth. This sequence obtained from wheelers was taken as a universal sequence and all the 66 sequences which were obtained from the patients were matched against this constant and against each other to check for the uniqueness of the sequence.

All the measurements were tabulated and statistically evaluated for the uniqueness of the sequence.

RESULTS

The magnitude of difference of each sequence obtained from the subjects was compared with that of the universal sequence of wheelers [Table 1], and if the given sequence matches with the wheelers sequence, then the magnitude of sequence should be equal to "0." None of the given sequences had the magnitude of difference as "0" and hence were not matching with the universal sequence [Table 2].

Some of the sequences had the same magnitude of difference with that of the universal sequence. Such sequences were clubbed together to check for matching of sequences and none among these scores have similar sequences though they have the same magnitude of difference [Table 3].

The sequence of each sampling unit was significantly different from an universal sequence, as well as the similar sum scores of magnitudes of difference from it when checked for any resemblance [Table 4]. It was found to be non-resembling, and thus, we conclude that no single sequence in the given data is similar to one another and such a sequence can be used to identify an individual.

DISCUSSION

The value of teeth in forensic dentistry is well established in many studies, as teeth are the hardest and chemically the most stable structures in the body and are resistant to mechanical, chemical, physical, and thermal types of destruction. Therefore, teeth are of great significance in mass disasters/natural calamities where bodies are damaged beyond recognition, and other means of forensic identification using bones are not possible due to fragmentation.[8-11]

The most important part of dental identification is that postmortem dental remains should be compared with the antemortem records such as study casts, radiographs etc, however retrieving antemortem records is a big challenge as many dental setups in many countries still do not have a systematic method of storing and filling records.[12,13] This is one of the greatest challenges of forensic dental identification, hence in this study we have studied the sequence generated by taking the mesiodistal width of all anterior teeth to identify an individual and it was found that such sequences were statistically unique for an individual and can be utilized for dental identification.

Identification using DNA is currently the most accurate method in human identification. However, it involves extraction of DNA and amplification of DNA using polymerase chain reaction, this requires equipment and trained experts, and this may not be easily available in many of the developing countries,[14] and hence, odontometry still remains the important method as it has an advantage of identification in large population as it is simple, reliable, easy to measure, and inexpensive.

Mesiodistal dimensions of teeth have been analyzed earlier in forensic dentistry for gender discrimination; most of these studies have reported that the mesiodistal width of teeth is sexually dimorphic and can be reliably used to determine the sex of an individual. The mesiodistal and buccolingual crown diameters showed statistically significant sex differences in all teeth, and a finding that agrees with the results found for others populations. Dental metrics have also been used to determine the ancestry in some studies and have found to be reliable indicators of ancestory as well, and the diameters of the Portuguese population (male and female) were found to be larger when comparing with other modern Caucasian populations.[15-21] Differences in teeth dimensions among the various populations could be related, in part, to the degree of ethnic mixing. O'Rourke and Crawford 27 concluded that the extent and direction of the microdifferentiation are reflections of differential amounts of mixing. These differences among populations and gender were utilized in our study to make a sequence which can be used to identify an individual. This is a novel study and the use of dental metrics as a sequence for identification has been done for the first time ever, and we would like to check the uniqueness and validity of such a method on a larger sample base to establish this method as a standard in dental identification.

Table 1: Legend: Universal sequence: Wheeler's textbook of dental anatomy and physiology

MXRC	MXRLI	MXRCI	MXLCI	MXLLI	MXLC	MDLC	MDLLI	MDLCI	MDRCI	MDRLI	MDRC
7.5	7	8.5	8.5	7	7.5	7	5.5	5	5	5.5	7

Table 2: Sum scores of magnitude of differences

Sequence	MXRC	MXRLI	MXRCI	MXLCI	MXLLI	MXLC	MDLC	MDLLI	MDLCI	MDRCI	MDRLI	MDRC	Sumof magnitude of differences
Universal sequence	7.5	7	8.5	8.5	7	7.5	7	5.5	5	5	5.5	7	
1	0.9	0.2	0.2	0.2	0.7	0.4	0.4	0	0	0.1	0	1	1.9
2	0.6	0.2	0.2	0.2	0.3	0.3	0.4	0.2	0.5	0.4	0.2	0.6	2.3
3	0.6	0.1	0.3	0.5	0.4	0.4	1.1	0.2	0.4	0.2	0.4	0.9	2.4
4	0.6	1	0.6	0.8	1.1	1.1	1.2	0.1	0.3	0	0.2	1.4	2.6
5	0.5	0.6	0.6	0.7	0.7	0.6	1.1	0.1	0.2	0.1	0.1	1	2.8
6	0.5	0.8	0.4	0.7	1.2	0.4	1.1	0.1	0.1	0.2	0.1	1.49	3.1
7	0.4	0.9	0.3	0.4	0.8	0.1	0.3	0.9	0	0.1	0.8	0.1	3.4
8	0.4	0.9	0.9	0.6	1	0.4	0.8	0.2	0.3	0.8	0.5	1.2	3.5
9	0.3	0.1	0.2	0.3	0.6	0.4	0.9	0.3	0.5	0.4	0.3	0.2	3.5
10	0.3	0	0.2	0	0.1	0.1	0.5	0.1	0.2	0	0.2	0.6	3.8
11	0.3	0.1	0.1	0	0.2	0.3	0.4	0.5	0	0.3	0.4	0.5	3.9
12	0.3	0.2	0.2	0	0.2	0.3	0.7	0.2	0.1	0.3	0.1	0.8	3.9
13	0.2	0.3	0.1	0	0.2	0.1	1.2	0.3	0.3	0.3	0.3	1.2	3.9
14	0.2	0.2	0.3	0.5	0.1	0.3	1.1	0.1	0	0.1	0.2	0.8	3.9
15	0.2	0.3	0.3	0.4	0.1	0.4	0.7	0	0.1	0.3	0.8	1	4
16	0.2	0.2	0.6	0.9	0.4	0.1	0.5	0.9	0.9	1	0.8	0.2	4.1
17	0.2	0	0.5	0.3	0	0.1	0.2	0.4	0	0.5	0.1	0.3	4.1
18	0.1	0.8	0.6	0.4	0.6	0.1	0.8	0.2	0.4	0.5	0	0.7	4.1
19	0.1	1.2	0.9	0.7	1.4	0.7	1.3	0.2	0.3	0.8	0.3	1.2	4.1
20	0.1	0.5	0.7	0.3	1	0.3	0.6	0	0.2	0.2	0.1	0.8	4.1
21	0.1	0.2	0	0.2	0.2	0.3	0	0.7	0	0.2	0.3	0.2	4.1
22	0.1	0.1	0.1	1.1	1.3	0.5	0.4	0.9	0.9	0.6	0.5	0.4	4.1
23	0	0.6	0.3	0.3	0.8	0.1	0.3	0.4	0	0.2	0.3	0.6	4.3
24	0	1.1	0.9	1	0.6	0.1	1.5	0.2	0.3	0.4	0.2	1.1	4.4
25	0	0.3	0.4	0	0.2	0.1	0.8	0.1	0.2	0.4	0.4	0.6	4.5
26	0	0.3	1.4	1.3	1	0.4	0.2	0.9	0.9	1.2	0.8	0.5	4.5
27	0	0.1	0.4	0.3	0.4	0.3	0.2	0.6	0.5	0.8	0.7	0.7	4.6
28	0.1	0.5	0.7	1	0.1	0.3	0.3	0.3	0.3	0.4	0.5	0.3	4.8
29	0.1	0.6	0.5	0.2	1	0.2	1.3	0.4	0.3	0.4	0.4	1.4	4.8
30	0.1	0.3	0.3	0.4	0.6	0.5	0.4	0.3	0.1	0	0.5	0.6	4.9
31	0.1	0.6	0.6	0.7	0.6	0	0.4	0.3	0	0.1	0	0.5	4.9
32	0.1	0.3	0.8	0.5	0.3	0.3	0.1	0.4	0.3	0.4	0.2	0.3	5
33	0.1	0.7	0	0.3	0.2	0.3	0.9	0.2	0	0	0.1	0.7	5.1
34	0.2	0.6	0.4	0.3	0.7	0.2	0.8	0	0.1	0.1	0.2	0.8	5.2
35	0.2	0.5	0.3	0.6	0.7	0.1	0.2	0.9	0.3	0.5	0.5	0.1	5.4
36	0.2	0.7	0.3	0.2	2.1	0	0.7	0	0.2	0.1	0.4	0.8	5.4
37	0.3	1.7	0.2	0.3	0.3	0.8	0.2	1.2	0.9	0.7	0.1	0.4	5.5
38	0.3	0.1	0.1	0.4	0	0.4	0.2	0.3	0.3	0.3	0.2	0.2	5.6

(Contd...)

Table 2: *(Continued)*

Sequence	MXRC	MXRLI	MXRCI	MXLCI	MXLLI	MXLC	MDLC	MDLLI	MDLCI	MDRCI	MDRLI	MDRC	Sumof magnitude of differences
39	0.3	0.6	0.4	0.3	0.1	1.1	0.4	0.5	0.8	0.8	0.7	0.2	5.7
40	0.3	0.2	0.4	0	0.2	0.6	0	0.5	0.5	0.4	0.6	0.1	5.7
41	0.3	0	0.1	0	0.3	0.1	0	0.3	0.1	0.2	0.2	0.3	5.8
42	0.3	0.9	0.3	0.3	0.4	0.4	0.2	0.7	0.7	0.1	0.9	0.5	6.2
43	0.3	0.1	0.3	0.4	0.3	0	0.5	0.3	0.5	0.5	0.3	0.4	6.3
44	0.4	0.3	0.3	0.1	0.3	0.1	0.1	0.2	0.6	0.7	0.3	0.7	6.4
45	0.4	1	1.4	1.3	0.2	0.4	0.1	1.4	0.6	0.3	0.8	0	6.7
46	0.5	0	0.6	0.3	0.2	0.3	0.5	0.2	0.6	0.5	0.3	0.1	6.7
47	0.5	0.2	1	1	0	1.7	0.5	0	0.1	0.2	0.1	0.3	6.7
48	0.5	0.5	0.6	0.4	0.1	0.3	0.1	0.9	0.5	0.6	0.7	0.2	6.8
49	0.5	0.2	0	0.3	0	0.9	0.3	0.5	0.9	0.7	0.2	0.4	6.8
50	0.6	0	0.4	0.5	0.5	0.8	0.1	0.8	0.2	0.9	0.9	0.1	6.9
51	0.6	0.5	1	1.1	1.2	0.3	0.7	0.1	0.2	0.2	0	0.9	6.9
52	0.6	0.5	0.6	0.4	0.1	1	0.4	0.7	0.7	0.7	0.6	0.4	7
53	0.6	0.3	0.6	0.2	0.2	0.5	0.9	0.5	0.1	0.4	0.9	1.5	7
54	0.6	0.1	0.3	0.7	0.1	0.2	0.2	1	0.4	1	0.4	0.4	7.1
55	0.7	0.5	0.2	0.1	0.5	0.8	0.2	0	0.2	0.1	0.1	0.7	7.4
56	0.7	0.2	0.9	0.5	0.4	0.7	0.2	0.7	0.5	0.7	0.8	0.1	7.9
57	0.7	1.2	0.7	0.6	0.9	0.3	0	0.8	0.5	0.7	0.2	0.3	7.9
58	0.8	1.1	0.2	0	1.2	0.4	0.2	0	0.2	0.1	0.1	0	8
59	0.8	0.5	0.9	0.6	0.8	0.6	0.1	0.7	0.4	0.8	0.6	0.2	8
60	0.9	0.7	0.3	0.5	0.6	0.6	1	0.9	0.6	0.5	0.8	0.6	8.4
61	0.9	1.2	1.2	1.1	1.1	1	0.2	0.8	1.2	0.7	1.1	0	8.9
62	0.9	0	1.1	0.9	0	0.8	0.9	1	0.8	1.1	1.2	0.2	8.9
63	1	0.4	1.4	1.3	0.6	0.1	0.7	0.9	0.9	1.3	0.8	1.2	9.1
64	1.1	0.6	1	0.8	0.2	1.3	0.9	0.7	0.4	1	0.9	0.9	9.8
65	1.1	0.6	0.1	0	0.7	0.7	0.1	0.1	0.2	0.1	0.3	0.1	10.5
66	1.3	0.4	0.7	0.6	0.7	0.6	0.1	0.7	1	0.8	0.6	0.4	10.6

Table 3: Sequences with similar magnitude of difference were clubbed together for evaluation of similarity I sequence

Sequence	MXRC	MXRLI	MXRCI	MXLCI	MXLLI	MXLC	MDLC	MDLLI	MDLCI	MDRCI	MDRLI	MDRC	Sum of magnitude of differences
11	0.3	0.1	0.1	0	0.2	0.3	0.4	0.5	0	0.3	0.4	0.5	3.9
12	0.3	0.2	0.2	0	0.2	0.3	0.7	0.2	0.1	0.3	0.1	0.8	3.9
13	0.2	0.3	0.1	0	0.2	0.1	1.2	0.3	0.3	0.3	0.3	1.2	3.9
14	0.2	0.2	0.3	0.5	0.1	0.3	1.1	0.1	0	0.1	0.2	0.8	3.9
16	0.2	0.2	0.6	0.9	0.4	0.1	0.5	0.9	0.9	1	0.8	0.2	4.1
17	0.2	0	0.5	0.3	0	0.1	0.2	0.4	0	0.5	0.1	0.3	4.1
18	0.1	0.8	0.6	0.4	0.6	0.1	0.8	0.2	0.4	0.5	0	0.7	4.1
19	0.1	1.2	0.9	0.7	1.4	0.7	1.3	0.2	0.3	0.8	0.3	1.2	4.1
20	0.1	0.5	0.7	0.3	1	0.3	0.6	0	0.2	0.2	0.1	0.8	4.1
21	0.1	0.2	0	0.2	0.2	0.3	0	0.7	0	0.2	0.3	0.2	4.1
22	0.1	0.1	0.1	1.1	1.3	0.5	0.4	0.9	0.9	0.6	0.5	0.4	4.1
25	0	0.3	0.4	0	0.2	0.1	0.8	0.1	0.2	0.4	0.4	0.6	4.5
26	0	0.3	1.4	1.3	1	0.4	0.2	0.9	0.9	1.2	0.8	0.5	4.5
28	0.1	0.5	0.7	1	0.1	0.3	0.3	0.3	0.3	0.4	0.5	0.3	4.8
29	0.1	0.6	0.5	0.2	1	0.2	1.3	0.4	0.3	0.4	0.4	1.4	4.8
30	0.1	0.3	0.3	0.4	0.6	0.5	0.4	0.3	0.1	0	0.5	0.6	4.9
31	0.1	0.6	0.6	0.7	0.6	0	0.4	0.3	0	0.1	0	0.5	4.9
35	0.2	0.5	0.3	0.6	0.7	0.1	0.2	0.9	0.3	0.5	0.5	0.1	5.4
36	0.2	0.7	0.3	0.2	2.1	0	0.7	0	0.2	0.1	0.4	0.8	5.4
39	0.3	0.6	0.4	0.3	0.1	1.1	0.4	0.5	0.8	0.8	0.7	0.2	5.7
40	0.3	0.2	0.4	0	0.2	0.6	0	0.5	0.5	0.4	0.6	0.1	5.7
45	0.4	1	1.4	1.3	0.2	0.4	0.1	1.4	0.6	0.3	0.8	0	6.7
46	0.5	0	0.6	0.3	0.2	0.3	0.5	0.2	0.6	0.5	0.3	0.1	6.7
47	0.5	0.2	1	1	0	1.7	0.5	0	0.1	0.2	0.1	0.3	6.7
48	0.5	0.5	0.6	0.4	0.1	0.3	0.1	0.9	0.5	0.6	0.7	0.2	6.8
49	0.5	0.2	0	0.3	0	0.9	0.3	0.5	0.9	0.7	0.2	0.4	6.8
50	0.6	0	0.4	0.5	0.5	0.8	0.1	0.8	0.2	0.9	0.9	0.1	6.9
51	0.6	0.5	1	1.1	1.2	0.3	0.7	0.1	0.2	0.2	0	0.9	6.9
52	0.6	0.5	0.6	0.4	0.1	1	0.4	0.7	0.7	0.7	0.6	0.4	7
53	0.6	0.3	0.6	0.2	0.2	0.5	0.9	0.5	0.1	0.4	0.9	1.5	7
56	0.7	0.2	0.9	0.5	0.4	0.7	0.2	0.7	0.5	0.7	0.8	0.1	7.9
57	0.7	1.2	0.7	0.6	0.9	0.3	0	0.8	0.5	0.7	0.2	0.3	7.9
58	0.8	1.1	0.2	0	1.2	0.4	0.2	0	0.2	0.1	0.1	0	8
59	0.8	0.5	0.9	0.6	0.8	0.6	0.1	0.7	0.4	0.8	0.6	0.2	8
61	0.9	1.2	1.2	1.1	1.1	1	0.2	0.8	1.2	0.7	1.1	0	8.9
62	0.9	0	1.1	0.9	0	0.8	0.9	1	0.8	1.1	1.2	0.2	8.9

Table 4: One sample *t*-test

One-sample statistics

Sequence scores	*n*	Mean	SD	SEM
	66	5.554545455000000	2.021741962000000	0.248859232000000

One-sample test

Sequence scores	Test value=0					
	t	df	Significant (2-tailed)	Mean difference	95% confidence interval of the difference	
					Lower	Upper
	22.32	65	0.000	5.55	5.057	6.051

SD: Standard deviation, SEM: Standard error mean

CONCLUSION

Dental identification is a very important aspect of forensic odontology and needs to be improved for faster and effective use during crime scene investigations and mass disasters. Our method of dental identification is easier and faster in storing and retrieving data for dental identification and needs to be validated using a larger sample size.

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