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Three-dimensional analysis of the uniqueness of the anterior dentition in orthodontically treated patients and twins

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Dental uniqueness can be proven if no perfect match in pair-wise morphological comparisons of human dentitions is detected. Establishing these comparisons in a worldwide random population is practically unfeasible due to the need for a large and representative sample size. Sample stratification is an option to reduce sample size. The present study investigated the uniqueness of the human dentition in randomly selected subjects (Group 1), orthodontically treated patients (Group 2), twins (Group 3), and orthodontically treated twins (Group 4) in comparison with a threshold control sample of identical dentitions (Group 5). The samples consisted of digital cast files (DCF) obtained through extraoral 3D scanning. A total of 2.013 pair-wise morphological comparisons were performed (Group 1 n = 110, Group 2 n = 1.711, Group 3 n = 172, Group 4 n = 10, Group 5 n = 10) with Geomagic Studio® (3D Systems®, Rock Hill, SC, USA) software package. Comparisons within groups were performed quantifying the morphological differences between DCF in Euclidean distances. Comparisons between groups were established applying One-way ANOVA. To ensure fair comparisons a post-hoc Power Analysis was performed. ROC analysis was applied to distinguish unique from non-unique dentures. Identical DCF were not detected within the experimental groups (from 1 to 4). The most similar DCF had Euclidian distance of 5.19 mm in Group 1, 2.06 mm in Group 2, 2.03 mm in Group 3, and 1.88 mm in Group 4. Groups 2 and 3 were statistically different from Group 5 ($p < 0.05$). Statistically significant difference between Group 4 and 5 revealed to be possible including more pair-wise comparisons in both groups. The ROC analysis revealed sensitivity rate of 80% and specificity between 66.7% and 81.6%. Evidence to sustain the uniqueness of the human dentition in random and stratified populations was observed in the present study. Further studies testing the influence of the quantity of tooth material on morphological difference between dentitions and its impact on uniqueness remain necessary.

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1. Introduction

Forensic investigations on the uniqueness of the human dentition (UHD) increased considerably in the last few years [1–5]. Although the UHD is fundamental for forensic human dental identification and bite mark analysis, the increased prevalence of these investigations was mainly induced by the uncertainty surrounding the forensic bitemark practice [6–8]. It is estimated that more than 14 innocents were convicted or indicted based on misinterpreted bitemark evidences [8,9]. Accordingly, the American National Academy of Science included the unproven UHD amongst the most essential topics to be revisited scientifically [10].

Several studies in the field investigated the UHD in the context of bitemarks [1,5,11,12]. However, the outcomes reported were biased potentially based on methodological aspects [13]. Random sampling was one of the issues observed in these studies [1,2,14]. Establishing a methodological investigation on the UHD with a random population requires a representative and large sample size. Sample stratification arose as an option to reduce this issue. Stratification may be applied based on the presence of specific dental identifiers or using a specific population type [13]. Using specific dental identifiers enables the selection of subjects based on their particular dental traits, e.g. on specific tooth rotations or

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particular shape of dental crowns [15,16]. Evaluating a specific population type enables to filtrate subjects presenting similar dental morphology and arrangement, e.g. orthodontically treated patients and twins [11,12,14]. In practice, stratifying a sample on a specific dental identifier is extremely more difficult, than selecting individuals based on a specific population type.

Applied in previous studies, sample stratification based on a specific population type did not enable to support a complete proof of the UHD due to additional methodological limitations [11,12,14–16]. These limitations consisted of 2D image registration techniques used to compare 3D structures (human teeth); operator-depending procedures (landmarking); the lack of operator reproducibility control (intra-/inter-reliability tests); and the lack of proper data analysis (statistics) [13].

In fact, the UHD was not proved yet in the context of bitemarks impressed on human skin. These bitemarks often registers the indentations of the anterior dentition (six anterior teeth – from canine to canine). This is the reason why in the present research pair-wise superimpositions of dentitions were performed exclusively comparing the anterior dentition.

The present research aims to prove the UHD three-dimensionally (3D) comparing the dental crown morphology of the anterior dentition in stratified samples of orthodontically treated patients, twins, and orthodontically treated twins in relation to a threshold sample of identical dentitions. Additionally, a sample of random patients is included to prove and express the importance of sample stratification in the investigations on the uniqueness of the human dentition.

2. Material and methods

The present research was conducted after approval of the Committee of Ethics in Research (protocol number: 19575613.2.0000.0020).

Three groups of dental casts were sampled and 3D digitized. Group 1 was composed by 22 dental casts (11 mandibular and 11 maxillary) of randomly selected subjects (7 males and 4 females). Group 2 consisted of 59 maxillary dental casts of orthodontically treated patients (32 males and 27 females), collected after the removal of the orthodontic brackets. Group 3 included 344 dental casts (172 mandibular and 172 maxillary) of 86 pairs of twins, 39 were monozygotic (36 males and 42 females) and 47 were dizygotic (50 males and 44 females). Group 4 comprised 20 dental casts (10 mandibular and 10 maxillary) of 5 pairs of orthodontically treated monozygotic twins (2 males and 8 females) (Table 1).

All the dental casts included presented the permanent anterior teeth (from canine to canine). Dental casts with clinically visible supernumerary teeth in the anterior region, restorative or prosthetic dental treatment in the anterior teeth, and fixed orthodontic retainers were excluded. Specifically in Group 2, ahigh prevalence of orthodontic retainers was observed justifying the lack of analysis of mandibular dental casts. In Group 4, patients were also orthodontically treated but no orthodontic retainer was observed. In all the groups, the dental impressions were taken by the same operator (author) with alginate (Jeltrate Dustless®, Dentsply®, York, PA, USA) following the instructions of the manufacturer. These impressions were casted with plaster type IV (Durone®, Dentsply®, York, PA, USA) and digitalized using an automated motion device with angular laser scanning (XCADCAM Technology®, São Paulo, SP, Brazil) in resolution of $<20\ \mu m$. The obtained digital cast files (DCF) were stored in .STL format and imported for morphometric analyses and pair-wise comparison in Geomagic Studio® (3D Systems®, Rock Hill, SC, USA) software package (GS). To limit the comparisons to the anterior dentition, a standardized GS cropping procedure was established, placing on each DCF a cropping contour along the cemento–enamel junction of the anterior teeth based on 58 pre-cropping points.

Mean threshold values were established for the classification of two cropped DCF as identical or not. One examiner took impressions of 5 different subjects and repeated it after 7 days. The dental impressions were casted, digitized and prepared for analysis according to the procedures described previously. These DCF consisted of a reference group (Group 5). The mean threshold values were a measure of the comparative errors originating from the procedure to obtain the dental impressions, the casts, the DCF, the GS cropping procedure and the GS pair-wise morphometric comparisons.

Within random (Group 1) and orthodontically treated (Group 2) patients, all possible pair-wise DCF comparisons were performed, totalizing 110 (55 per dental arch) and 1711 (only maxillary arch) comparisons, respectively. Specifically in these groups, sub-sampling was necessary to randomly select only the independent pair-wise comparisons (in which the same DCF was not repeated). This procedure was repeated 250 times combining independent comparisons. Within twins (Group 3) and orthodontically treated monozygotic twins (Group 4), the DCF were pair-wise compared with their respective twin sibling DCF, totalizing 172 (86 for the mandible and 86 for the maxilla) and 10 (5 for the mandible and 5 for the maxilla) comparisons, respectively. Additionally in Group 3 mono- and dizygotic twin pair DCF were evaluated in function of the zygosity. In the reference sample (Group 5) the DCF of each subject obtained at moment 1 was pair-wise compared with the respective DCF at moment 2, separately for the maxilla and mandible, totalizing 10 comparisons. All the pair-wise comparisons were performed with the GS automated superimposition tool.

Table 1
Subject distribution per sampled group stratified on dental arch, zygosity and sex.

Dental arch	Group	Zygosity	Male (n)	Female (n)	Subjects (n)	DCF (n)
Maxillary	1	n/a	7	4	11	11
	2	n/a	32	27	59	59
	3	Monozygotic	36	42	78	78
	3	Dizygotic	50	44	94	94
	4	Monozygotic	2	8	10	10
	5	n/a	2	3	5	10
Mandibular	1	n/a	7	4	11	11
	3	Monozygotic	36	42	78	78
	3	Dizygotic	50	44	94	94
	4	Monozygotic	2	8	10	10
	5	n/a	2	3	5	10

DCF: digital cast files; Group 1: randomly selected subjects; Group 2: orthodontically treated patients; Group 3: twins; Group 4: orthodontically treated twins; Group 5: threshold; n/a: not applicable.

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