

A New Quantitative Method for Predicting Forensic Racial Identity Based on Dental Morphological Trait Analysis

Un Nuevo Método Cuantitativo para Predecir la Identidad Racial Forense Basada en el Análisis Rasgo Morfológico Dental

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SUMMARY: Few previous studies have demonstrated the likelihood of using the worldwide patterns of dental morphological variation in prediction of ancestry in the context of forensic dental anthropology. This paper introduces a new quantitative method for predicting forensic racial identity of individual specimens based on dental morphological trait analysis. In this study, the inter-population variation in the expression frequency of 16 non-metric tooth crown traits, manifested on the permanent dentition, was used for analysis. The method was developed from the notion that dental morphological characteristics, when viewed as sets of traits rather than isolated variables, can be utilized to calculate the relative probability that an individual belongs to a particular ancestry. This paper aimed at demonstrating that Mean Measure of Divergence analysis can be used to predict group membership of individual specimens into one of five ancestral categories: Western Eurasian, Sub-Saharan African, Sino-American, Sunda-Pacific, or Australo-Melanesian. Individuals were treated as artificially created groups defined by substituting the highest or lowest global frequencies for individual dichotomous values. Mean Measure of Divergence values were computed for every individual and the lowest score was the basis of the classification of individual specimens into one of five ancestral categories. This method was tested on individuals from a sample of living Jordanian Arabs (n 102), who were known to belong to the Western Eurasian ancestral category. Using this method, correct assignment of ancestry was made in 84.31% of cases. It is concluded that racial identification on the basis of dental morphology would be helpful in both forensic anthropology and historical archaeology.

KEY WORDS: forensic dental anthropology; non-metric tooth crown traits; racial identification.

INTRODUCTION

The relationship between dental morphological traits and ancestry have received the greatest amount of attention from dental anthropologists (Dahlberg, 1965, 1986; Edgar, 2005; Haeussler *et al.*, 1989; Irish, 1993, 1997, 1998, 2006; Lease & Sciulli, 2005; Scott & Turner, 1988, 1997; Stamfelj *et al.*, 2006; Turner, 1987 ; Turner & Hawkey, 1998; Ullinger *et al.*, 2005; and many others). However, the utility of inter-population variation in the expression frequency of dental morphological traits in assisting law enforcement officials with determining the ethnic affiliation or ancestry of individuals in forensic cases is not fully exploited (Schmidt, 2008).

In the absence of medical or dental records commonly used for determining the exact identity of isolated skeletal-dental remains of individuals, it is often challenging for law

enforcement officials to determine the ethnic affiliation or ancestry of the individual to whom such remains belong (Scott & Turner, 1997). When crania are well-preserved, discriminant function analysis of craniometric traits is usually the preferred method for racial diagnosis in forensic cases (Scott & Turner, 1997). In such cases, dental morphology would be a useful adjunct to craniometric analysis. However, in cases where crania are severely damaged to a degree that craniometric analysis could not be successfully performed, dental morphology is more useful in the identification of ancestry (Scott & Turner, 1997).

A number of studies have demonstrated the possibility of using the differences in the expression frequency of dental morphological characteristics among various ethnic groups in determination of ancestry in the context of forensic

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dental anthropology. Scott & Turner's (1997) approach for identifying the ethnic affiliation of isolated human remains is qualitative and based on a number of non-metric dental traits that are most or least likely affiliated with various racial groups. This approach is generally reliable if these traits are used as a set rather than isolated variables, so that the determination of racial affinity is broadly based (Schmidt).

Additional approaches to predict ancestry were more quantitative; they used multivariate statistics, such as logistic regression, to compare differences in both metric and non-metric dental traits among Euroamericans and Afroamericans (Edgar; Lease & Sciulli). Edgar found eight non-metric dental traits that successfully categorized a sample of 40 individuals as Euroamericans or Afroamericans in 90% of

Table I. A list of the traits chosen and their highest/lowest global frequencies used to substitute individual dichotomous values.

Trait name	Tooth observed	Grades of absence and negative expression	Lowest reported frequency	Breakpoint (positive expression grades)	Highest reported frequency
Winging	UI1	Grades 2-4 (unilateral winging, straight and counterwinging classes)	0.042 (SA)	Grade 1 (bilateral winging only)	0.500 (NSAI)
Shoveling	UI1	Grades 0-2 (none, faint and trace shovel classes)	0.000 (NG)	Grades 3-6 (Hrdlicka's semi- and full-shovel classes)	0.919 (NSAI)
Double shoveling	UI1	Grades 0-1 (smooth and faint ridging classes)	0.000 (KH & NG)	Grades 2-6	0.964 (JOR)
Interruption Grooves	UI2	Grade 0 (none)	0.104 (WA)	Grade 1 (presence)	0.650 (NWA)
Bushmen canine	UC	Grade 0	0.000 (NE & AA)	Grades 1-3	0.351 (KH)
Odontomes	UPMs & LPMS	Grade 0 (absence)	0.000 (NE, WA, KH, NG & JOR)	Grade 1 (presence)	0.065 (NWA)
3-cusped	UM2	Grades 2-5	0.033 (AUS)	Grades 0-1 (equivalent to 3 on Dahlberg scale)	0.306 (AA)
Carabelli's trait	UM1	Grades 0-4 (smooth surface, pit and groove forms)	0.019 (AA)	Grades 5-7 (tubercle and cusp forms only)	0.431 (JOR)
Cusp 5	UM1	Grade 0 (absence)	0.104 (NES)	Grades 1-5 (presence)	0.633 (JOR)
4-cusped	LM1	Grades 1-5 (cusp 5 presence)	0.000 (WA, NES, JOM, AA, NWA, NSAI & MI)	Grade 0 (cusp 5 absence; 4-cusped LM1)	0.100 (NE, NA)
4-cusped	LM2	Grades 1-5 (cusp 5 presence)	0.044 (NWA)	Grade 0 (cusp 5 absence; 4-cusped LM2)	0.844 (NE)
Y pattern	LM2	+ and X patterns	0.076 (CM)	Y pattern	0.719 (KH)
Cusp 6	LM1	Grade 0 (absence)	0.047 (KH)	Grades 1-5 (presence)	0.617 (AUS)
Cusp 7	LM1	Grade 0 and grade 1A	0.031 (JOM)	Grades 1-4 (presence excluding grade 1A)	0.437 (WA)
Deflecting wrinkle	LM1	Grades 0-2	0.038 (NG)	Grade 3	0.395 (NES)
Distal trigonid crest	LM1	Grade 0 (absence)	0.000 (WA & NG)	Grade 1 (presence)	0.187 (AA)

UI1: upper central incisor; UI2: upper lateral incisor; UC: upper canine; UPMs: upper first and second premolars; LPMS: lower first and second premolars; UM1: upper first molar; UM2: upper second molar; LM1: lower first molar; LM2: lower second molar; SA: South Africa; NSAI: North and South American Indians; NG: New Guinea; KH: Khoisan; JOR: Jordan; WA: West Africa; NE: Northern Europe; AA: American Arctic (Eskimo-Aleuts); NWA: Northwest North America (Na-Dene American Indians); AUS: Australian aboriginals; NES: Northeast Siberia; JOM: Jomon (prehistoric Japanese); MI:

the time. Likewise, Matis & Zewmer (1971) were able to develop discriminant function analysis for a combination of dental metric and non-metric traits that successfully distinguish Eskimos from American Indians about 90% of the time. Both Edgar's approach and that of Matis & Zewmer were quantitative and very successful. However, they were designed to distinguish specific groups, and their potential to be globally applied across diverse ethnic groups is uncertain. In addition, several recent studies have found statistically significant differences between sub-adult (deciduous) teeth of various ethnic groups, often combining metric and non-metric dental traits (Harris *et al.*, 2001; Liu *et al.*, 2001; Harris & Lease, 2005; Lease & Sciulli)

The objective of this study was to introduce a new quantitative method for discerning ethnicity depending on the idea that dental morphological features, when viewed as constellations of traits rather than isolated variables, can be utilized to calculate the relative probability that an individual belongs to a particular ancestral category (Scott & Turner, 1997). In addition, it aimed to demonstrate that Mean Measure of Divergence (MMD) analysis can be used to predict group membership of individual specimens into one of five ancestral categories: Western Eurasian, Sub-Saharan African, Sino-American, Sunda-Pacific, or Australo-Melanesian.

Table II. A list of the world samples used for comparative purposes and their corresponding ancestral categories (ranges of sample sizes in parentheses)

Ancestral category	Regional groupings
Western Eurasia	Western Europe (n= 154-308) Northern Europe (n= 46-319) North Africa (n= 175-545) Jordan (Middle Eastern Arabs; n= 360)
Sub-Saharan Africa	West Africa (n= 30-83) South Africa (n= 220-531) Khoisan (n= 46-155)
Sino-Americas (Sinodont)	China-Mongolia (n= 343-798) Japan (recent; n= 262-482) Jomon (prehistoric Japan; n= 136-292) Northeast Siberia (n= 43-192) South Siberia* (n= 92-272) American arctic (Eskimo-Aleuts; n= 155-569) Northwest North America (Na-Dene American Indians; n= 158-498) North and South American Indian (n= 1177-2756)
Sunda-Pacific (Sundadont)	Southeast Asia (prehistoric; n= 131-370) Southeast Asia (recent; n= 199-730) Polynesia (n= 274-632) Micronesia (n=78-186)
Sahul-Pacific (Australo-Melanesian; proto-Sundadont)	Australian aboriginals (35-643) Melanesia (n= 134-295) New Guinea** (n=30-197)

* South Siberian dental morphological pattern is generally viewed as a hybrid pattern between the Western Eurasian and the Sinodont patterns (Scott & Turner, 1997).

** The dental morphological pattern of New Guineans is similar to that of Western Eurasians. This is possibly explained by genetic drift or evolutionary random gene walk toward the Western Eurasian pattern, and away from the Australo-Melanesian pattern (Scott & Turner, 1997).

MATERIAL AND METHOD

A random stratified sample was obtained in 2009 by selecting 370 tenth grade school children (180 males and 190 females), from 12 schools representing the six regional directories of Amman, the capital of Jordan. Informed consents were obtained from the parents of all children who chose to participate in the study before they were subjected to dental examination or impression taking. The children were selected according to the following criteria: all subjects were apparently healthy with no history of serious childhood illnesses, have erupted second molars, showing well aligned arches with no supernumerary teeth and no history of orthodontic treatment, with normal appearing teeth, no large restorations or fixed replacements, and minimal marks of caries and/or attrition. All observations were performed on dental casts from a random representative subset (n= 102; 50 males and 52 females) of the original sample of 370 school children. This collection is housed at the museum of the Faculty of Dentistry of the University of Jordan.

For each individual, sixteen morphological tooth crown traits, that are observable on dental casts and commonly used for inter-population comparisons, were scored according to the

standard plaques of the Arizona State University (ASU) dental anthropology system (Turner *et al.*, 1991), and dichotomized according to Scott and Turner criteria (Scott & Turner, 1997). All observations were carried out under good lighting and using 10X hand lenses. The individual count method was used here to assign each individual positive expression vs. negative or no expression of the observed traits. According to this method, the antimere exhibiting the highest grade of trait expression is assigned to the individual (Scott & Turner, 1997). This method was chosen because it assigns each individual a phenotypic value that is thought to best represent the individual genotype (Scott & Turner, 1997). Root traits were left out since the data of the present study came from dental casts where root traits are unobservable. It is noteworthy that the 16 crown traits chosen here have been demonstrated to be largely independent of one another (Scott & Turner, 1997).

According to the method of the study, individuals were treated as artificially created groups defined by substituting the highest or lowest global frequencies for individual dichotomous values. For each trait the individual was assigned an expression frequency; if the individual exhibited positive expression forms for any of these traits, the highest reported expression frequencies for these traits were assigned to the individual, and if the individual exhibited absence or negative expression forms for any of these traits, the lowest reported frequencies for these traits were assigned (Table I). The biological distance values were measured between the individual (being treated as an artificially created group with assumed sample size equivalent to the sample size of the regional group) and 23 regional group from the five ancestral categories of humankind (Table II) using CAB Smith's MMD (Constandse-Westermann, 1972; Harris & Sjøvold, 2004) based on the variation in the expression frequencies of these 16 traits among these regional groups and the assigned frequencies for each individual. The MMD values were computed for every individual and the lowest MMD was the basis of the classification of individual specimens into one of five ancestral categories: Western Eurasian, Sub-Saharan African, Sino-America, Sunda-Pacific, or Australo-Melanesian.

This analysis was based on our own data for the frequencies of these traits among the living Jordanians (Alsoleihat & Khraisat, 2011) and on the data available in Scott and Turner (1997) regarding the frequencies of the same traits among the other 21 regional groups and the corresponding sample sizes. Anscombe's angular transformation formula was adopted here to transform frequencies into angles for calculating the Smith's MMD in order to stabilize sampling variances of binomial variables. Anscombe MMD transformation rather than the more commonly used Freeman & Tukey (1950), as discussed in Irish (2010), was chosen since this formula is the recommended angular transformation method by Rao (1952) for moderately large samples (Harris & Sjøvold, 2004). The MMD value between any two groups being compared was measured, as recommended by Harris & Sjøvold (2004), by calculating the differences between the two groups in angularly transformed frequencies of each trait, then this difference was squared, then the correction term $((1/n1k+0.5)+(1/n2k+0.5))$ was subtracted from this squared difference for each trait (hence the subscript k) to adjust for the overestimation of divergence between corresponding groups generated by the squared difference between two angular values, then the results were summed and divided by the number of traits (Harris & Sjøvold, 2004).

Table III. The classification matrix of Jordanian individuals into regional groups and large ancestral categories using the method of the study (number of individuals classified into a regional group or an ancestral category/total number of subjects in parentheses)

Predicted regional group or ancestral identity	Percent Males	Percent Females	Z-value	Percent (sexes pooled)
JOR	76.00% (38/50)	67.31% (35/52)	0.9790	71.57% (73/102)
NA	2.00% (1/50)	7.69% (4/52)	-1.3574	4.90% (5/102)
NE	4.00% (2/50)	11.54% (6/52)	-1.4428	7.84% (8/102)
WE	0.00% (0/50)	0.00% (0/52)	0.0000	0.00% (0/102)
WEuras*	82.00% (41/50)	86.54% (45/52)	-0.6301	84.31% (86/102)
SiAm	10.00% (5/50)	9.62% (5/52)	0.0645	9.80% (10/102)
SSA	4.00% (2/50)	1.92% (1/52)	0.6187	1.96% (2/102)
SP	2.00% (1/50)	1.92% (1/52)	0.0291	1.96% (2/102)
AM	2.00% (1/50)	0.00% (0/52)	1.0102	0.98% (1/102)
Non-WEuras*	18.00% (9/50)	13.46% (7/52)	0.6301	15.69% (16/102)

* Raw 6 = raw 2 + raw 3 + raw 4 + raw 5.

** Raw 11 = raw 7 + raw 8 + raw 9 + raw 10.

JOR: Jordanian; NA: North African; NE: Northern European; WE: Western European; WEuras: Western Eurasian; SiAm: Sino-Americas; SSA: Sub-Saharan African; SP: Sunda-Pacific; AM: Australo-Melanesians

Correct classification rate of Jordanian individual specimens into the Western Eurasian ancestral category was calculated by dividing the number of individuals who were classified, according to the method of the study, into any of the four regional groups included in the analysis and known to belong to Western Eurasia (MiddleEastern Arabs represented here by the Jordanian sample, North Africa, Northern Europe, and Western Europe) by the total number of tested individuals.

Z-value test was used to test any significant difference in the rates of classification between males and females of the Jordanian sample using software available on the following website: (<http://in-silico.net/statistics/ztest/two-proportion>).

RESULTS AND DISCUSSION

The classification matrix (Table III) displays predicted classification of the tested individuals from the living Jordanian Arabs using the classification method of this study. 84.31% of the Jordanian individuals were correctly classified as Western Eurasians. However, only 71.57% of the Jordanian individuals were accurately assigned to their correct regional group. The former result

reflects the strength of this approach for determining the ancestral category of humankind to which the individual belongs. However, the latter estimate does not appear highly accurate due to the fact that regional groups belonging to the same ancestral category generally exhibit a similar overall dental morphological pattern. Nonetheless, forensic dentistry is seldom expected to assign an individual to his/her correct regional group. Mostly, the need is to assign the remains to Western Eurasian, Sub-Saharan African, Sino-American, Australo-Melanesian, or Sunda-Pacific ancestry.

Table III showed that the rates of ancestral classification for Jordanian individuals are not sexually dimorphic. For example, Jordanian males and females were classified as Western Eurasian at 82.00% and 86.54% of the time, respectively, and this slight difference is statistically insignificant (z -value = -0.6301).

As mentioned earlier, Edgar's approach was successful in classifying Euroamericans vs. Afroamericans in 90% of the time, and that of Matis and Zwemer (1971) was successful in distinguishing Eskimos from American Indians about 90% of the time. Both of these approaches are quantitative and very successful. However, they are designed for distinguishing specific groups and their potential to be globally applied across diverse ethnic groups is uncertain. Similar to these methods, the method of this study is also quantitative. Although the classificatory accuracy of the method of the study is slightly lower than

the above mentioned methods (i.e. 84.31%), the method of the present study seems to have the potential to identify dental ancestry across diverse ethnic groups. In addition, the classificatory accuracy of this method could be enhanced by including non-metric dental root traits and more tooth crown traits known to exhibit inter-population variation.

The discrimination ability of the sixteen non-metric crown traits chosen in this study was assessed by calculating the difference in the resultant MMD value (Δ MMD) for the individual between two situations: (I) when each trait is entered as present (i.e. the highest expression frequency substituting positive expression grades) and (II) when the same trait is entered as absent (i.e. the lowest expression frequency substituting absence or negative expression grades). The traits with larger Δ MMD values are considered more discriminative among the five ancestral categories of humankind, and vice versa. It is noteworthy that the traits with wider global ranges of expression frequencies generally resulted in larger Δ MMD values. The analysis of the present study demonstrated that the traits chosen in this study exhibit variable degrees in discrimination ability between the five ancestral categories of humankind; with UI1 double shoveling, LM2 hypoconulid absence (4-cusped form), and UI1 shoveling being the most discriminant among these traits. While the following traits show intermediate discrimination ability among ancestral categories: UM1 cusp 5 (metaconule), UI2 interruption grooves, UM1 Carabelli's trait, UC Bushmen canine, LM2 Y groove pattern, UI1 bilateral winging, and LM1 cusp 6. The remainders of these traits are the least discriminant ones (i.e. UM2 hypocone absence (3-cusped form), premolar odontomes, LM1 deflecting wrinkle, LM1 distal trigonid crest, LM1 hypoconulid absence (4-cusped form), and LM1 cusp7) (Table IV).

Table IV. The differential discrimination ability of all chosen traits among the five ancestral categories of humankind.

Trait name	Tooth observed	Global range	Δ MMD
Double shoveling	UII	0.000-0.964	0.452
4-cusped LM2	LM2	0.044-0.844	0.182
Shoveling UII	UII	0.000-0.919	0.117
Cusp 5 UM1	UM1	0.104-0.633	0.087
Interruption Grooves	UI2	0.104-0.650	0.085
Carabelli's trait	UM1	0.019-0.431	0.083
Bushmen canine	UC	0.000-0.351	0.071
Y pattern LM2	LM2	0.076-0.719	0.067
Winging	UII	0.042-0.500	0.059
Cusp 6 LM1	LM1	0.047-0.617	0.053
3-cusped UM2	UM2	0.033-0.306	0.022
Odontomes	UPMs & LPMS	0.000-0.065	0.013
Deflecting wrinkle	LM1	0.038-0.395	0.009
Distal trigonid crest	LM1	0.000-0.187	0.009
4-cusped LM1	LM1	0.000-0.100	0.005
Cusp 7 LM1	LM1	0.031-0.437	0.003

UI1: upper central incisor; UI2: upper lateral incisor; UC: upper canine; UPMs: upper first and second premolars; LPMS: lower first and second premolars; UM1: upper first molar; UM2: upper second molar; LM1: lower first molar; LM2: lower second molar

CONCLUSIONS

The method of this study would be useful in forensic cases in multicultural countries such as North America, Australia and some European countries, where the primary concern is to determine whether the victim is of Western Eurasian, Sub-Saharan African, Sino-American, Sunda-Pacific, or Australo-Melanesian descent. The Assignment of individuals to their correct regional group by this method was less sensitive.

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RESUMEN: Pocos estudios previos han demostrado la posibilidad de utilizar los patrones mundiales de variación morfológica dental en la predicción de la ascendencia en el contexto de la antropología dental forense. Se presenta un nuevo método cuantitativo para predecir la identidad racial forense de muestras individuales basadas en el análisis del rasgo morfológico dental. En este estudio, se utilizó para el análisis la variación inter-población en la frecuencia de expresión de 16 rasgos morfológicos dentales no métricos, que se manifiesta en la dentición permanente. El método fue desarrollado a partir de la idea de que las características morfológicas dentales, cuando se ven como conjuntos de rasgos en lugar de variables aisladas, se puede utilizar para calcular la probabilidad relativa de que una persona pertenece a un linaje particular. Este documento está destinado a demostrar que la medida promedio del análisis de divergencia se puede utilizar para predecir la pertenencia a grupos de muestras individuales en una de cinco categorías ancestrales: Eurasia Occidental, África al sur del Sahara, sino-estadounidense, Sunda-Pacífico, o australo-melanesia. Los individuos fueron tratados como grupos creados artificialmente definidos mediante la sustitución de las frecuencias globales más altas o más bajas para los valores dicotómicos individuales. La media de los valores de medida de divergencia se calculó para cada individuo y la puntuación más baja fue la base de la clasificación de muestras individuales en una de cinco categorías ancestrales. Este método fue probado en individuos vivos de una muestra de árabes jordanos (n 102), que se sabe pertenecen a la categoría de ancestral Eurasia occidental. El uso de este método, y la asignación correcta de ascendencia se hizo en 84,31% de los casos. Se concluye que la identificación racial sobre la base de la morfología dental sería de gran ayuda, tanto en la antropología forense como en la arqueología histórica.

PALABRAS CLAVE: Antropología dental forense; Rasgos morfológicos dentales no métricos; Identificación racial.

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