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The Diversity of Adult Dental Patterns in the United States and the Implications for Personal Identification

ABSTRACT: Few would argue about the individuality of dental radiographs for forensic identification, but when an antemortem/postmortem comparison is based strictly on dental treatment notes and/or charts it becomes less certain. In the past, attempts to validate the high diversity of dental patterns created by combinations of missing, filled, and unrestored teeth have been based on unfounded statistical assumptions. The goal of this research is to present a statistically valid method of assessing dental pattern diversity for the identification of missing individuals. Empirical observation of large reference datasets was found to be the best technique for assessing dental diversity. This technique is nearly identical to the procedure used for mitochondrial DNA casework. For the research presented in this paper, two large datasets were used, one composed of U.S. military personnel and one composed of U.S. civilians. Dental patterns were found to be very diverse on a scale that is comparable to mtDNA. In addition, it was found that the diversity values remain very consistent regardless of the level of detail present in the treatment records. Overall, combinations of missing, filled, and unrestored teeth were found to be very individualistic and an excellent source for forensic identification.

KEYWORDS: forensic science, diversity, dental patterns, forensic odontology, human identification, NHANES III, TSCOHS, mitochondrial DNA

The comparison of antemortem and postmortem dental characteristics is a commonly employed technique to establish personal identification in the forensic sciences. The key pieces of evidence needed for a dental comparison are twofold, the presence of dental remains and accurate antemortem dental records. With the proper evidence, forensic odontologists can make dental identifications very rapidly and with a high degree of certainty due to the inherent variability within the human dentition. Typical antemortem dental records may include radiographs, dental charts (odontograms), both intra- and/or extraoral photographs, dental casts, and notes. Certainly dental radiographs are one of the most desirable pieces of antemortem evidence, but, unfortunately, they are not always available, and the comparison of antemortem and postmortem characteristics must occasionally be based on handwritten charts and notes. This research is specifically concerned with nonradiographic dental comparison. Specifically, this research examines the variability of the adult dentition (combinations of missing, filled, and unrestored teeth) as noted and charted in nonradiographic formats. The reader should realize that this research acknowledges the power of radiographic comparison, an area that does not need to be tested.

The use of dental charts and notes for forensic identification is based on the number of possible dental characteristics that can be derived from combinations of missing, filled, and unrestored teeth. Statistically, there are trillions of possible combinations within the adult mouth, suggesting that an individual's dental health pattern should often be of sufficient uniqueness to be used for identification. This is a point of view that has been stressed by many in the field of odontology (1–8). While the core theory of this argument is correct, the statistics that have been used to justify the diversity of dental patterns are often erroneous and inappropriate. For this reason there is a clear need for the diversity of dental patterns formed by missing, filled, and unrestored teeth to be explored in more detail.

Previous Statistical Arguments for Dental Pattern Diversity

The number of *theoretically* possible combinations of filled, missing, and unrestored teeth can be calculated as C^n, where C is the number of possible characteristics and n is the number of teeth considered. If only three possible characteristics for each tooth are utilized (e.g., unrestored, filled, or missing) the number of possible combinations with 32 teeth would be 3^{32}, or 1 853 020 188 851 841 different patterns. If the possible combinations of filled surfaces are considered (mesial, occlusal, distal, facial, and/or lingual) along with the missing and virgin states, the number of possible characteristics for each tooth is 33 since there are 31 possible combinations of filled surfaces for each tooth. The expression would then be 33^{32}, or about 3.91×10^{48} different combinations. Even if only the posterior teeth are considered, the number of possible combinations with three characteristics is 3^{20}, or 3 486 784 401 different combinations. If the 33 possible character states are considered, the expression then becomes 33^{20}, or about 2.35×10^{30} different possibilities for the posterior teeth alone. Obviously the statistical values generated for any of these scenarios present sufficient numbers of possible variations to be of discriminating value if, indeed, this variation is truly expressed in the population. Statistical arguments of this type regarding the possible number of combinations of missing and filled teeth have been especially stressed by Keiser-Nielsen and Sognnaes for forensic purposes (9–11); *unfortunately, these types of statistics are improperly applied, misleading, and should be avoided.*

Sognnaes (9) discussed the uniqueness of the individual human dentition and the diversity created by various character states. He provided an example in which it is calculated that four missing teeth create 35 960 possible combinations in the mouth. Of the 28 remaining teeth, four of these have fillings, which is calculated as an additional 20 475 possible combinations. Sognnaes treated these characteristics independently and multiplied the values to arrive at a figure of 730 281 000 possible combinations of four missing and four filled teeth. A very similar example is also presented by Keiser-Nielsen (10,11). This type of statistical assessment suggests that all of the various combinations of missing and filled teeth occur randomly and that they are equally probable in the population, an assumption that is not valid.

Furthermore, it is recommended by Keiser-Nielsen (10,11) that the frequencies of individual dental characteristics can be assumed to occur independently, and that these values can be multiplied in order to produce an expected frequency for a combined occurrence. He wrote (Ref 11, p. 69) that when considering six features, each with a frequency of 10%, that this combination ". . . would make the person in question one out of at least one million people, all of them missing and all of them with a physical possibility of ending up at the site of recovery." Again, the assumption of independence is inappropriate in this situation, a criticism that has been mentioned by Lorton and Langley (12).

The main error of the statistical computations presented above is that they incorrectly apply the law of independence and assume that dental treatment occurs randomly throughout the mouth. If this were true, dental pattern diversity would be comparable to nuclear DNA diversity. Dental morphology will dictate that molars, based on their large surface area, will be more susceptible to decay than other teeth, such as canines or incisors. While the number of combinations presented by Keiser-Nielsen and Sognnaes are theoretically possible, some are, in actuality, unlikely to ever be found in an individual. For example, while it is theoretically possible for an individual to have an alternating pattern of missing and filled teeth throughout the oral cavity, this would be unlikely to ever occur. Other more far-fetched examples could easily be imagined.

Another flaw of these arguments is that each of the possible dental patterns cannot be considered to be equiprobable; otherwise, there would not be any dental patterns that occur more frequently than others. If all patterns were equiprobable, then the expected frequency of any dental pattern would be (1/total number of possibilities). In the case of 32 teeth with three possible characteristics, the expected frequency for a specific pattern would be 1/1 853 020 188 851 841 which is certainly not the case. Individuals with all unrestored teeth, or perhaps only filled molars, are likely to be observed much more frequently in the overall population. As such, the theoretical values do not represent a valid number of dental patterns that can be expected to be observed in the population as a whole, and use of these figures in a court of law could be difficult to defend and potentially misleading.

Mertz (Ref 13, p. 64) writes that, "Many forensic odontologists believe mathematical theories on variable probabilities could be questioned in a court of law." In reference to situations in which there are only a few points of concordance, he goes on to state (Ref 13, p. 65), "Perhaps in the future, as the state of art improves, a well-trained biostatistician will be able to provide weighted values for each identifying characteristic and help to clear up some of these problem areas." This attitude is also echoed by Sognnaes (14), who recognized that future research might provide more sophisticated quantitative techniques to address the issues involved with antemortem-postmortem concordance.

The goal of this research is to utilize an appropriate technique for exploring the diversity of dental patterns formed by missing, filled, and unrestored teeth and to assess the validity of dental pattern matches for forensic identification purposes. It is recommended that *empirical comparison* is the most appropriate method available. The method used for the empirical assessment of dental pattern diversity is nearly identical to the technique used for mitochondrial DNA (mtDNA) casework.

Dental Patterns and mtDNA Sequences

In many respects it is appropriate to compare the diversity of dental patterns formed by combinations of missing, filled, and unrestored teeth with the diversity of mtDNA sequences formed by combinations of variants at multiple polymorphic sites within the mtDNA sequence. The comparison of these techniques is relevant because many properties of mtDNA variation are similar to dental pattern variation, and the relatively well-developed system for assessing the significance of mtDNA matches in forensic casework provides an excellent frame of reference for considering the identification potential available from dental data. Several points show that dental information and mtDNA share some of the same strengths and weaknesses.

Unlike nuclear DNA, neither the character states comprising a dental pattern nor the various nucleotide positions comprising a mtDNA sequence can be considered to occur independently. The entire mtDNA molecule is a single nonrecombining locus, so that any single mutation/polymorphism is permanently associated with other mutations on the molecule. Similarly, decay on teeth is not a random event that occurs equally throughout the mouth. This means that dental patterns and mtDNA sequences must be evaluated in relation to the frequency of the patterns/sequences in the population (not all dental patterns or mtDNA sequences are equiprobable in the population and random matches may occur). Some mtDNA sequences and some dental patterns are more likely to occur than others.

Depending on the format considered, dental variants are at least as abundant as the number of mtDNA variants. If detailed surface information is utilized for dental fillings, in combination with missing and unrestored conditions, each tooth will express one of 34 variable states (i.e., missing/unreplaced, missing/replaced, virgin, and any combination of mesial, occlusal, distal, facial, or lingual restoration). Consideration of strictly generic dental codes, including only a single code for fillings, provides four variable states for each tooth (i.e., virgin, restored, missing/unreplaced, and missing/replaced). With mtDNA there are four possible nucleotide bases (adenine, guanine, cytosine, and thymine) for each polymorphism (15). Clearly the detailed dental characteristics provide a vast range of possible combinations that surpass mtDNA, although if all 610 positions of the two hypervariable regions are considered the theoretical variation possible within mtDNA still exceeds that of the teeth.

MtDNA is maternally inherited without recombination, with the result that maternally related individuals have matching sequences (barring infrequent mutation). It is actually this very fact that allows for mtDNA to be of great use in many forensic comparisons. For instance, the sequence derived from a set of remains believed to be of a specific individual can be compared to a family reference sample (e.g., blood or saliva) obtained from family members separated by even multiple generations from the missing individual. Perhaps one of the most publicized identifications based in large part on mtDNA evidence was the identification of the Vietnam soldier from the Tomb of the Unknowns (16). Dental patterns of off-

spring, on the other hand, cannot be accurately predicted based on the dental health of their parents, although some degree of genetic influence may be present. In essence, the family reference sample used for mtDNA comparison can be considered to be analogous to an antemortem dental record. Problems locating a family reference sample for mtDNA are comparable to the difficulty of locating antemortem dental records. Dental identification is useful only if there are antemortem records available, while mtDNA can be used even in the absence of samples from the decedent (provided they are available from maternally related individuals).

It is possible for the mtDNA sequences of maternal relatives to differ slightly from each other due to a mutation event, and it is possible for more than a single mtDNA type to occur within an individual (a condition known as heteroplasmy) as a result of a recent mutation event in the individual or the individual's matriline. For dental patterns it is possible for dental conditions to be present in the postmortem record that are not expressed in the antemortem files due to undocumented treatment (e.g., a tooth was filled subsequent to the date of the available documentation, so the files show the tooth to be unrestored, but the postmortem analysis shows the tooth to be filled). With both mtDNA and dental patterns it is possible for these types of "explainable discrepancies" to exist. In both instances it is important to acknowledge that these slight variations may occur and that they are not evidence for exclusion. Perhaps the greatest danger in either mtDNA or dental comparisons is a false exclusion due to contamination. For mtDNA the contamination may result from the introduction of exogenous DNA, while serious charting errors may inadvertently "contaminate" a dental comparison.

Both mtDNA and dental pattern comparison are limited in their utility for forensic identification when common sequences/patterns are encountered. This problem has been addressed by sequencing outside of the hypervariable regions with mtDNA (17). Edentulous individuals and those with perfect teeth present the greatest challenges to nonradiographic dental identification.

Through the use of large, representative datasets it is possible to assess the overall diversity of mtDNA sequences for identification purposes. By performing all pairwise comparisons of the sequences, it is possible to present the overall frequency that they match one another in a database. From these comparisons it is possible to derive an assessment of the overall diversity of the sequences, as well as the probability of a random match between two individuals. This type of analysis has been utilized in support of the high population diversity observed for mtDNA sequences (16,18), and it is also very appropriate for the analysis of dental patterns. Use of these statistics provides the framework for empirical observation of dental patterns

and is an appropriate assessment of their true diversity. Analysis of these values provides an indication of the overall utility of dental pattern matches for personal identification.

Materials and Methods

In order to empirically address the issue of diversity for dental patterns, large datasets are needed for analysis. By empirically observing the frequencies of dental patterns from large, representative datasets, it is possible to accurately estimate the diversity of the population as a whole. Due to their size and scope, data from two modern dental health studies provided an excellent source of information and were therefore utilized for the diversity assessment. Only permanent teeth were considered during this research, excluding third molars.

NHANES III Data

The first sample is comprised of a large number of adults from the civilian U.S. population that was originally compiled as part of the Third National Health and Nutrition Examination Survey (NHANES III). The NHANES III is a cross-sectional survey that was conducted by the National Center for Health Statistics and the Centers for Disease Control and Prevention in collaboration with a large consortium of federal agencies, including the National Institute of Dental Research. The NHANES III study is a multifaceted health examination survey that was conducted between 1988 and 1994 in the United States to collect data on the civilian, noninstitutionalized population (19). For the dental component of this study, oral health examinations were conducted in Mobile Examination Centers that traveled to 88 locations across the United States. In total, dental information was collected for 31 311 individuals aged two months to over 90 years, and these data are available to the general public for research purposes via a website (http://www.cdc.gov/nchs/about/major/nhanes/datalink.htm). As the NHANES III dataset contains information on a range of individuals from infants to the elderly, a subset of data was extracted in order to observe the diversity of adult dental patterns. A sample of 9730 individuals was selected that consisted of only individuals between the ages of 17 and 50 years. The demographic composition of this sample is presented in Table 1.

TSCOHS Data

The second dataset is composed of a modern sample of 19 422 U.S. military personnel. The data were originally collected in 1994 and 2000 as part of two phases of the Tri-Service Comprehensive

TABLE 1—*Sample size and demographic composition of the NHANES III data.*

	NHANES III Dataset (*N* = 9730)					
	White		Black		Other	
Age	Male	Female	Male	Female	Male	Female
17–19	305	344	183	204	18	19
20–24	490	553	236	324	43	33
25–29	487	518	231	282	39	26
30–34	435	527	234	313	30	32
35–39	365	472	214	286	23	33
40–50	731	817	355	438	43	47
Total	2813	3231	1453	1847	196	190

TABLE 2—*Sample size and demographic composition of the TSCOHS data.*

	TSCOHS Dataset (N = 19 422)					
	White		Black		Other	
Age	Male	Female	Male	Female	Male	Female
17–19	2116	474	521	192	468	119
20–24	3652	673	980	281	642	123
25–29	2137	331	562	133	294	43
30–34	1736	171	416	85	218	18
35–39	1230	143	297	42	135	11
40–61	799	77	154	26	112	11
Total	11 670	1869	2930	759	1869	325

Oral Health Survey (TSCOHS). The dental health data representing the TSCOHS population were generously provided for this research by the Tri-Service Center for Oral Health Studies, which is affiliated with the Uniform Services University of the Health Sciences, Bethesda, Maryland. The raw data from this study were originally gathered by the Tri-Service Center for Oral Health Studies as part of an ongoing project to observe dental health throughout the active duty and recruit population of the U.S. military. The 1994 data are composed of detailed dental conditions of active duty and recruits from all branches of the service and from different military installations across the continental United States. The year 2000 phase of TSCOHS considered all branches of the military, but only in regard to recruits. These data represent the first military oral health study to be conducted on a tri-service level. The study design was created to be comparable to large-scale civilian dental health studies, such as NHANES III. The data were collected from airmen, sailors, and soldiers by clinical examination and with radiographs. Additional information regarding TSCOHS can be found at their website (http://www.usuhs.mil/tscohs). The demographic composition of the TSCOHS data is listed in Table 2.

Data Format

The data from both the NHANES III and the TSCOHS studies contained detailed codes regarding the conditions of the individual teeth. In order to examine the effect that coding has on the diversity estimates, the original codes used in the NHANES III and TSCOHS studies were converted for use in the present research. Both datasets were analyzed in a *generic* and a *detailed* format. The only difference between the two was the manner in which restorations were documented. The *detailed* format provides specific surface information concerning the location of a restoration on any combination of the mesial, occlusal, distal, facial, or lingual surfaces. The *generic* format disregards the surface information and simply designates the tooth as restored. Active decay was ignored for this analysis and was treated as a virgin tooth or tooth surface. A similar recommendation regarding the coding of active decay was presented by Friedman and colleagues (20).

Detailed Format

A dataset of detailed information was constructed to record the specific locations of restorations on the tooth surfaces (i.e., mesial, occlusal, distal, facial, and lingual). Multiple restorations on a single surface (e.g., two distinct occlusal restorations on the maxillary right 1st molar) were only assigned a single code. Furthermore, there is no differentiation between a single restoration that affects multiple surfaces and distinct restorations on different surfaces of the tooth. For example, in the database it would be impossible to differentiate between a tooth that had two restorations, one on the occlusal surface and one on the facial surface, and a tooth that had a single restoration that was present on the occlusal surface and wrapped onto the facial surface. For the posterior teeth (Universal #s 2–5, 12–15, 18–21, and 28–31) five tooth surfaces were considered for each tooth and restorations could be any combination. Due to the original format of the NHANES III and the TSCOHS data, only four surface codes were assigned to the anterior teeth (Universal #s 6–11 and 22–27). For the anterior teeth the occlusal, or incisal, surface was ignored. Unique codes were not utilized for teeth with crowns. Due to the data format, it was not possible to distinguish between teeth that have restorations present on all surfaces and teeth with crowns. Missing teeth without replacement were differentiated from missing teeth that were replaced by a prosthesis (denture or bridge). Teeth with only active caries were considered to be "virgin," the same as teeth with neither decay nor fillings. If a tooth was both carious and filled, it was only considered in regard to the filling, as this was deemed to have greater utility for forensic identification. On occasion, individuals were found to possess a deciduous tooth that had been retained in the place of a permanent tooth. In these situations the deciduous tooth was treated in the same manner as a permanent tooth.

Generic Format

In the simplified datasets all filled surfaces were considered as only generically restored and the surface information was ignored. Similarly, teeth with crowns were simply considered to be restored. It would not be possible to differentiate a single occlusal restoration and a full crown in the generic format of the data. The remaining codes were the same for missing, decayed, and unrestored teeth.

Diversity of Dental Patterns Based on Empirical Comparison

In order to test the overall diversity of dental patterns, a FORTRAN program written by Dr. Lyle Konigsberg at the University of Tennessee, Knoxville, performed pairwise comparisons of the NHANES III and TSCOHS datasets and generated the total number of pattern matches. In addition, both of the datasets were pooled and the same pairwise comparisons were performed. This analysis was performed for both of the datasets in the *detailed* and *generic* formats. Based on the values derived from this program, it was possible to calculate diversity and random match probability values. Both of these values are related to each other and can be used for

comparison to diversity figures used in the discussion of mtDNA studies (16,18).

Two different criteria were used for the diversity values, one based on the total sample (total diversity) and one that is conditional upon having some substantive dental states other than "perfect" teeth or no teeth (conditional diversity). In both instances, the numerator reflects the number of mismatches encountered during the pairwise comparisons. The larger the numerator, the closer the diversity value is to 1 (an overall value of 1 would indicate that all patterns present within the data are distinct, a value of 0 would indicate that all are the same). The total diversity measure was calculated as:

$$\frac{\sum_{i>j} \delta_{ij}}{\left(\frac{N(N-1)}{2}\right)}$$

where $\delta_{ij} = 1$ when individuals i and j have different patterns and 0 when they share the same pattern.

For the conditional diversity measure, matches based on individuals with no missing or filled teeth ($MF = 0$) or individuals with all of their teeth missing ($M = 28$) were not considered. The reason for treating these conditions differently ("perfect teeth" and edentulousness) is because they represent an acknowledged problem for dental identification. The frequencies of individuals with perfect teeth and edentulous individuals are presented in Table 3 for each of the datasets. Although these individuals represent an identification problem, based on the frequency information in Table 3, it can be seen that if an unidentified individual is encountered with perfect teeth then a substantial percentage of the population can still be excluded, which may be useful information. Clearly the individuals with perfect teeth will have a larger effect on the diversity estimate than the edentulous ones simply due to the sample size (Table 3). The conditional diversity was calculated as:

$$\frac{\left(\sum_{i>j} \delta_{ij}\right) + XY}{\left(\frac{Y(Y-1)}{2} + XY\right)}$$

TABLE 3—*Frequency of individuals with perfect teeth and edentulous individuals.*

Dataset	Total Number	Perfect Teeth	Edentulous
TSCOHS	19 422	2397 (12.34%)	2 (0.01%)
NHANES III	9730	1325 (13.62%)	161 (1.65%)
Pooled Data	29 152	3722 (12.77%)	163 (0.56%)

where $\delta_{ij} = 1$ when individuals i and j have different patterns, and ij is the set of all pairwise comparisons for Y individuals, $X =$ number of individuals with $MF = 0$ or $M = 28$ (i.e., individuals without any missing or restored teeth and edentulous individuals), and $Y =$ number of individuals with $MF \geq 1$ and $M < 28$ (i.e., individuals with at least one missing or filled tooth, excluding edentulous individuals). Therefore, $X + Y = N$ of the total diversity index. The denominator used in the calculation of the conditional diversity measure accounts for the fact that all individuals with $MF = 0$ or $M = 28$ would be a mismatch to all other individuals in the dataset with $MF \geq 1$ and $M < 28$.

The random match probabilities are derived by either forming a ratio of the number of pattern matches encountered during the pairwise comparisons (as opposed to mismatches) to the total number of pairwise comparisons or by subtracting the diversity estimate from 1. The random match probability value reflects the probability that two individuals drawn at random (without replacement) from the population would share the same dental pattern.

It can be seen in Table 4 that the total diversity values (which include matches between individuals with perfect teeth and matches between edentulous individuals) are high for all of the datasets, greater than or equal to 0.98 in all instances. The random match probability values are low, generally less than 2%. It is equally important to notice that there is very little difference in either the total diversity or random match probability values based on the generic or detailed formats of the data. This shows that even dental patterns formed with only basic dental codes can be very diagnostic.

The total diversity values for dental patterns were compared to diversity values for mtDNA sequences. It was found that, when the total sample was considered, mtDNA sequences show slightly more diversity than dental patterns. Melton et al. (18) report a pooled diversity of 0.998 for mtDNA sequences derived from contemporary North American populations. (This diversity measure is based on variation as detected by sequence-specific oligonucleotide, SSO, probes. This manner of typing only captures a small portion of the total sequence variation in the hypervariable control region. This is not representative of the diversity that would be seen in the entire hypervariable region, which would result in a higher figure.) This would correspond to a random match probability of 0.002. Holland and Parsons (16) performed pairwise comparisons of all the sequences in their database of 604 Caucasian individuals and found that there were 669 instances of a match out of the 182 106 separate pairwise comparisons. They report an empirically determined random match probability of 0.0037 (i.e., two randomly selected individuals from the population will match once in approximately 270 times), which would correspond with a diversity estimate of 0.9963. Most of the values presented in Table 4 indicate that the total diversity observed in dental patterns is slightly less than the values re-

TABLE 4—*Total diversity of dental patterns based on pairwise comparisons.*

Dataset	N	Pairwise Comparisons $N*(N-1)/2$	Matches	Random Match Probability	Total Diversity Estimate
Detailed TSCOHS	19 422	188 597 331	2 906 151	0.01541	0.9846
Generic TSCOHS	19 422	188 597 331	3 246 590	0.01721	0.9828
Detailed NHANES III	9730	47 331 585	898 859	0.01899	0.9810
Generic NHANES III	9730	47 331 585	925 489	0.01955	0.9804
Pooled Detailed	29 152	424 904 976	7 002 960	0.0165	0.9835
Pooled Generic	29 152	424 904 976	7 559 116	0.0178	0.9822

ported for mtDNA, but they are comparable and indicate overall high diversity.

By removing the matches formed by edentulous individuals and individuals with perfect teeth, the diversity values become quite substantial. The conditional diversity values in Table 5 show dental patterns to be even more diverse than mtDNA. (It should be noted that a similar improvement would be accomplished with mtDNA if the most common sequence was removed from consideration.) When the detailed formats of the datasets were used (34 possible codes for each tooth), conditional diversity was always greater than 0.999 in both of the datasets (Table 5). When the generic datasets were analyzed (only four possible codes), conditional diversity was usually very similar and never dropped below 0.998 (Table 5). As stated previously, mtDNA diversity for North American populations has been calculated to be 0.998 (18), indicating that in most instances the conditional diversity estimates for dental patterns are superior to the reported mtDNA diversity. Similarly, the random match probability values are very close to zero, indicating that the chance of randomly selecting two individuals with the same dental pattern is almost nonexistent when edentulous individuals and individuals with perfect teeth are removed from consideration. These findings indicate that the lower values expressed by the total diversity (Table 4) are primarily a result of individuals with $MF = 0$. When at least one dental characteristic is present, the overall diversity of dental patterns is very high. The values presented in Table 4 for the total diversity can be considered to be a conservative estimate, while the values presented in Table 5 for the conditional diversity reflect the strong effect of individuals with perfect teeth on the overall diversity of dental patterns. Clearly dental patterns provide an excellent comparative tool for assisting in personal identification on a scale that is very similar to mtDNA.

Detailed Versus Generic Restoration Designations

This research has shown that detailed documentation of surface location for restorations does not significantly add to the discriminating power of an antemortem-postmortem comparison when sufficient dental remains are present. Patterns formed by consideration of only generic designations (i.e., filled) are nearly as individualistic as those formed by detailed criteria (i.e., mesial, distal, occlusal, facial, and/or lingual). With a complete set of dentition and several characteristics (i.e., missing or filled teeth), dental patterns are formed that are very infrequently encountered in the population. In situations when postmortem loss is extensive, the detailed data format will prove to be much more effective for forensic comparison.

As the degree of detail provided within antemortem dental records is variable, this discovery will greatly facilitate many dental comparisons. Certainly it is desirable to have thoroughly documented antemortem treatment records, but even the most basic information can be extremely useful for establishing a match to a missing individual. For example, it does not matter if a tooth is generically listed as "filled" or whether the specific surfaces are documented, as either will provide very valuable information. While in the past the generic documentation may have been considered to lack sufficient information to be used in an identification, this research has shown that patterns formed by even very simple criteria still create extremely individualistic dental patterns. The critical factor is that antemortem records need to be available for comparison and that the records are accurate.

In their study of the selectivity of dental records from a large sample of military individuals, Friedman et al. considered detailed surface information for the location of fillings during the sorting because ". . . earlier studies have showed that the only dental characteristics that significantly affected computer sorted matches lists were restored surfaces, missing, or unrestored teeth . . ." (Ref 20, p. 1359). While it is unlikely that Friedman and colleagues tested this statement by performing the same experiment with generic codes for fillings, the results of this research indicate that the use of generic restoration codes does not, in fact, hinder the identification process. Quite the contrary, very little discriminating power is lost by simplifying the codes, and it is hypothesized that the use of generic codes could actually assist investigators during the identification of individuals from a mass disaster.

An obvious challenge for odontologists working on a mass disaster is to compile all of the antemortem data and postmortem data into a format that facilitates comparison. Often the data are transcribed to a computer program (e.g., CAPMI or WinID), and sorts are performed mechanically to provide best-match scenarios. It is essential that all the antemortem and postmortem data are accurately transcribed (21). Based on this initial records sort, the odontologists can take a more detailed look at the overall correspondence between the antemortem records and dental remains to determine if an identification is warranted. As the documentation of surface locations for restorations can be ambiguous, subjective, and time-consuming, these types of initial sorts may best be handled with only generic codes when postmortem loss is not extreme.

A study performed in Sweden (22) tested the charting ability of 12 fourth-year dental students using five macerated maxillae and

TABLE 5—Conditional diversity ($MF \geq 1$ and $M < 28$) of dental patterns based on pairwise comparisons.

Dataset	X*	Y†	Pairwise Comparisons $[Y*(Y - 1)/2] + XY$	Matches	Random Match Probability	Conditional Diversity Estimate
Detailed TSCOHS	2399	17 023	185 720 930	34 544	0.00019	0.99981
Generic TSCOHS	2399	17 023	185 720 930	374 983	0.00202	0.99798
Detailed NHANES III	1486	8244	46 228 230	10 617	0.00023	0.99977
Generic NHANES III	1486	8244	46 228 230	37 247	0.00081	0.99919
Pooled Detailed	3885	25 267	417 360 306	66 788	0.00016	0.99984
Pooled Generic	3885	25 267	417 360 306	622 944	0.00149	0.99851

* X = number of individuals with $MF = 0$ or $M = 28$ (i.e., individuals without any missing or restored teeth, and edentulous individuals).
† Y = number of individuals with $MF \geq 1$ and $M < 28$ (i.e., individuals with at least one missing or filled tooth, excluding edentulous individuals).

five macerated mandibles without the aid of radiographs. They found that the most common error was the incorrect registration of restorations, followed by confusion between the identification of molars and premolars. Many of the errors regarding restorations stemmed from confusion about the extension of a filling from the occlusal surface onto either a facial or lingual surface (22). It is quite likely that the number of errors would drop substantially if the teeth had been simply designated as missing, restored, or virgin.

Antemortem records can be quickly converted into a generic format since it is usually clear whether a tooth has been restored or not; the difficulty may concern the specific location of the restoration on the tooth. Furthermore, a postmortem examination can be rapidly completed by stating simply whether a tooth is unrestored, filled, or missing. As long as the antemortem dental records are accurate, the dental patterns created by simply using the generic codes should be sufficient to easily differentiate several hundred adults. The benefit of this recommendation is that initial comparisons can be performed rapidly, after which the odontologist will be able to take a more detailed look at all of the available evidence.

Summary and Conclusions

The overall diversity of dental patterns formed by missing, filled, and unrestored teeth was explored for each of the datasets. The diversity of dental patterns was compared in both *detailed* and *generic* formats regarding the documentation of restorations. The results of this research show that the diversity of dental patterns, regardless of the data format, is very high and that the patterns formed by missing, filled, and unrestored teeth are an excellent means of personal identification. Furthermore, the dental pattern diversity values were compared to the diversity found in mtDNA sequences. It was determined that they are on a scale that is very comparable to mtDNA. Dental patterns were validated as an excellent means of forensic identification, especially when antemortem radiographic evidence is unavailable.

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