STATISTICAL ANALYSIS USING MULTISTATE QUALITATIVE VARIABLES
APPLIED TO THE HUMAN DENTAL MORPHOLOGICAL TRAITS
IN THE BRONZE AGE (GRANADA, SPAIN, 1300-1500 B.C.)

1. INTRODUCTION

The study of genetic diversity using dental morphology is recent and constitutes an element providing a great quantity of information in anthropological investigations. The Arizona State University Dental Anthropology System uses a set of traits that allows us to measure the presence/absence dichotomy and obtain replicability of results among observers. The ASU standard obtains the maximal and the minimal trait expression, and various gradations between these points.

Although the set of traits proposed by the ASU standard is very large, in this paper we use a subset of them, due to the characteristics shown by the archaeological remains, using the following criteria (TURNER, NICHOL, SCOTT 1991):

– the selected traits are the most easily and reliably observed;
– they persist for many years even if the subject had a harsh lifestyle. This case is the most usual in archaeological samples;
– most traits have low or no sex dimorphism. This feature is very important because usually it is very difficult to obtain prehistoric archaeological remains having sexual distinction.
– those traits evolve very slowly and permit a distinct characterization of very well the populations for affinity studies.

2. THE ASU SIMPLIFIED DENTAL ANTHROPOLOGY SYSTEM

The scoring procedures in the ASU system are focused mainly on the morphological features of the crowns and roots mainly, having special features in function of the type of the root. Since the conditions in which the archaeological remains appear make it very difficult determine in a reliable way the degree of the traits, in this paper we propose to use the presence or absence of each feature to get the minimal and maximal trait representation, for greater reliability in the information obtained.

These simplified sets of morphological features of the crown and roots are obtained from the qualitative scoring proposed by TURNER, NICHOL, SCOTT (1991) and they are focused on upper teeth, mainly showing the following traits.

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2.1 *Crown characters of incisors and canines*

The traits used are winging with reference to the upper central incisors (Enoki, Dahlberg 1958; Turner 1970); Labial Convexity relative to upper incisors (Nichol, Turner, Dahlberg 1984; Scott, Turner 1997); Shoveling is relative to upper incisors, canine and lower incisors (Hardlicka 1920; Dahlberg 1956; Scott, Turner 1997); Double-Shoveling occurs in upper incisors, canine and lower incisors (Dahlberg 1956); the Interruption Groove appears in upper incisors (Scott, Turner 1997); the Tuberculum Dentale feature is present in upper incisors and canines (Nichol, Turner 1986); the Canine Mesial Ridge or Bushman canine is located in upper and lower canines (Morris 1975; Scott, Turner 1997); Canine Distal Accessory Ridge appears in upper and lower canines (Morris 1975; Scott, Turner 1997); the Peg-Shaped character occurs in the upper lateral incisors (Scott, Turner 1997); Congenital Absence character appears in the upper lateral and lower central incisors (Montague 1940; Scott, Turner 1997); the Canine Root Number is present in lower canines (Scott, Turner 1997).

2.2 *Crown characters of premolars*

The traits studied include the Double-Shoveling located in the first premolar (Dahlberg 1956); the Premolar Mesial and Distal Accessory Cusps occurs in the upper premolars (Turner 1967); Tricusped Premolars is a very rare trait located in the upper premolars (Scott, Turner 1997); the Distosagittal Ridge or "Uto-Aztecan Premolar" appears in the first upper premolar (Morris *et al*. 1978); Enamel Extensions are present in the upper premolars (Pedersen 1949); Premolar Root Number is measured in the upper premolar (Scott, Turner 1997); the presence of Odontome occurs in the upper and lower premolars (Pedersen 1949; Alexandarsen 1970; Scott, Turner 1997); Congenital Absence character appears in the upper lateral and lower second premolars (Montague 1940; Scott, Turner 1997); Tomes' Root is present in lower first premolars (Tomes 1923; Scott, Turner 1997).

2.3 *Crown characters of molars*

The traits considered are the Metacone and the Hypocone characters located in the upper molars (Dahlberg 1951; Turner 1979); Cusp 5 or Metaconule trait appears in upper molars (Harris 1977); the Carabelli's trait appears in the upper molars (Dahlberg 1956; Scott, Turner 1997); the Parastyle character is located in upper molars (Bolk 1916; Scott, Turner 1997); Enamel Extensions are present in the upper molars (Pedersen 1949); the Upper Molar Root Number is measured in the upper molars (Scott, Turner 1997); the Peg-Shaped molar character occurs in the upper third molar (Scott, Turner 1997); Premolar Lingual Cusp Variation is very sen-
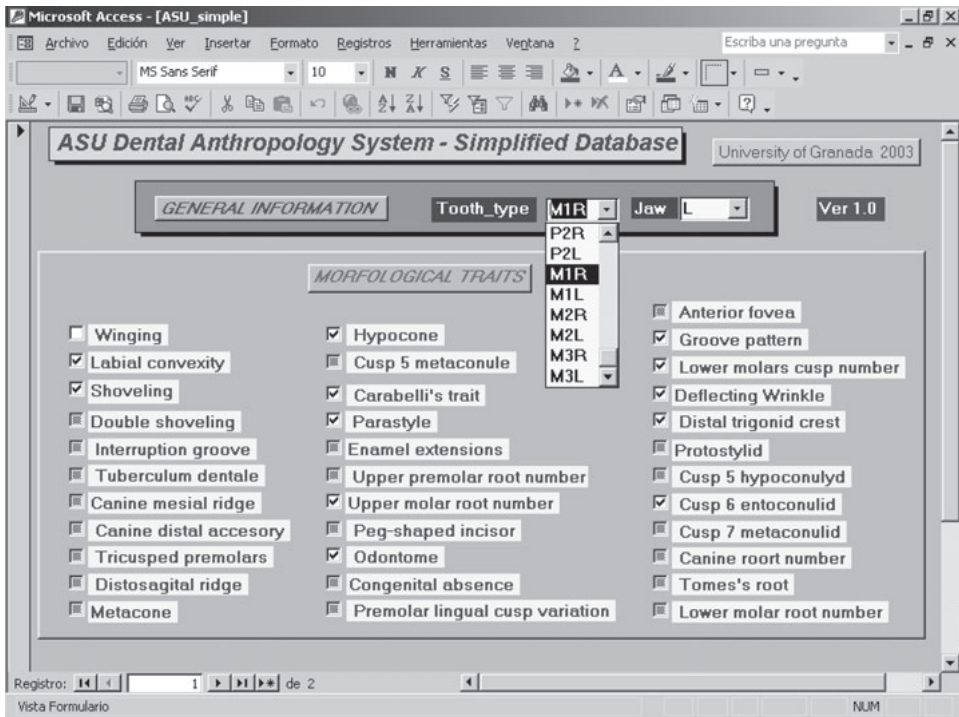
Fig. 1 – The ASU system. Simplified database.

sitive to wear and occurs in the lower premolars (PEDERSEN 1949; KRAUS, FURR 1953; SCOTT, TURNER 1997); the Congenital Absence character appears in the upper lateral and lower third molars (MONTAGUE 1940; SCOTT, TURNER 1997); the Anterior Fovea trait is located in the lower first molar (HARDLICKA 1924; SCOTT, TURNER 1997); the Groove Pattern feature appears in the lower molars with three scorings: X, Y and + (HELLMAN 1928; JORGENSEN 1955; SCOTT, TURNER 1997); the Cusp Number scores the cusp number in the lower molars (GREGORY 1916; SCOTT, TURNER 1997); Deflecting Wrinkle appears in lower first molar (SCOTT, TURNER 1997); Distal Trigonid Crest occurs in the lower molars (HARDLICKA 1924; HANIHARA 1961; SCOTT, TURNER 1997); Protostylid character is located in the lower molars (DAHLBERG 1956; SCOTT, TURNER 1997); Cusp 5, Cusp 6 and Cusp 7 are located in lower molars (SCOTT, TURNER 1997); Lower Molar Root Number is present in lower molars (TURNER 1971; SCOTT, TURNER 1997).

This set of morphological features is stored by means of a database developed in ACCESS database management using a form of data recording that includes the set of simplified morphological dental features (Fig. 1).

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This database form developed is easy to use, and includes the list of the teeth (see diagram) and the list of the jaws, and features verification fields to avoid possible mistakes. It also includes other optional information about the archaeological site: the settlement key (in Spain this codification is composed of two alphabetical characters belonging to the province, two alphabetical characters belonging to the town, and a number (with three digits) corresponding to the settlement in the town, the place-name, the chronology and the UTM coordinates of the settlement. This information is important for comparing two or more different settlements, but it is possible to save each archaeological site data set in an independent file and merge the files later.

The information recorded in the database can be exported to another software like EXCEL, SPSS, MATLAB, the interchange format ASCII, and so. This data set file can be analysed by means of standard statistical procedures, MATLAB routines, etc., or can be written using WORD or other software packages.

3. The MMD (Median Measures Divergence) method

The previous method allows us to convert the variables in dicotomized qualitative variables, and it makes the assumption that there is only a single genotype for any specific trait, and that, when asymmetry is present, the antimere exhibiting the greater degree of trait expression is the more accurate indicator of the genotype. The score used is the highest grade of expression observed between the two sides (Turner, Nichol, Scott 1991). However, the statistical MMD method is established for general qualitative multistate variables, and not presence/absence variables only.

The statistical procedure assumes that the variables are independent variables with no correlation between them, and each one follows a binomial distribution because the global population is very large. Then, for each trait the expectation of the proportion p and the variance of p is:

$$E(p) = P \qquad Var(p) = \frac{P(1-P)}{N}$$

being P the proportion of the trait in the total population (an unbiased estimator of P, that has the least variance and is a sufficient estimator) and N is the number of individuals in the sample. However, if N is small for a variable there may be great discrepancies between p y P, and all the proportions do not have equal importance. Therefore, it is essential to transform the proportion p in a new variable with no dependent variance of the population proportion P; this new quantitative variable is obtained using the inverse sine transformation, measured in radians, by means of the formula (Grewal 1962):

$$\Theta = arcsin(1 - 2p)$$

This variable has the advantage that the variance is approximately 1/N instead 820.7/N (this is the variance obtained using the more usual transformation $\Theta = \arcsin\sqrt{p}$) (BERRY, BERRY 1967; SJØVOLD 1973).

The test of differences between two populations was established by BERRY (1963) according to:

under the hypothesis that there is no genetic difference between the populations compared, the proportions p1 and p2 in two samples must be equal apart from sampling fluctuations. Then, the difference $\emptyset_1 - \emptyset_2$ is approximated by a normal distribution with variance $(1/N_1 + 1/N_2)$, and the statistic

$$\frac{\Theta_1 - \Theta_2}{\sqrt{\dfrac{1}{N_1} + \dfrac{1}{N_2}}}$$

is distributed by means of a normal distribution N(0,1). Therefore, the expression

$$\frac{(\Theta_1 - \Theta_2)^2}{\dfrac{1}{N_1} + \dfrac{1}{N_2}}$$

follows a χ_1^2 distribution, and the expression

$$X = (\Theta_1 - \Theta_2)^2 - \left(\frac{1}{N_1} + \frac{1}{N_2}\right)$$

will be approximately distributed according to $\left(\dfrac{1}{N_1} + \dfrac{1}{N_2}\right)(\chi^2 - 1)$. And it can be demonstrated (SJØVOLD 1973) that the expectation of X is E(X)=0 and the variance of X is

$$Var(X) = 2\left(\frac{1}{N_1} + \frac{1}{N_2}\right)^2$$

The Mean Measure Divergence between the samples 1 and 2 using the mean of X extended to all traits is defined by:

$$MMD_{12} = \frac{\displaystyle\sum_{i=1}^{V}\left[(\Theta_{1i} - \Theta_{2i})^2 - \left(\frac{1}{N_{1i}} + \frac{1}{N_{2i}}\right)\right]}{V}$$

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being:

θ_{1i}=angular transformation of the proportion p_1 of elements in the sample 1 for the trait i;

θ_{2i}=angular transformation of the proportion p_2 of elements in the sample 2 for the trait i;

N_{1i}=number of elements in the sample 1 having no missing the trait i;

N_{2i}=number of elements in the sample 2 having no missing the trait i;

V=number of traits that can be evaluated in the samples.

The variance of MMD is obtained by means of the expression (BERRY, BERRY 1967):

$$Var(MMD) = 4\left(\frac{1}{N_1} + \frac{1}{N_2}\right) \frac{\sum_{i=1}^{V}\left[(\Theta_{1i} - \Theta_{2i})^2 - \left(\frac{1}{N_1 i} + \frac{1}{N_2 i}\right)\right]}{V}$$

The p_{1i} and p_{2i} proportions can take extreme values distorting the angular transformation. In this case the previous values must be replaced by the following values (SJØVOLD 1973):

– if the proportions are near 0 we must take $p_{1i} = \frac{1}{4N_{1i}}$ and $p_{2i} = \frac{1}{4N_{2i}}$

– if the proportions are near 1 we must take $p_{1i} = 1 - \frac{1}{4N_{1i}}$ and $p_{2i} = 1 - \frac{1}{4N_{2i}}$

The MMD value is distributed according to $\frac{1}{n}\left(\frac{1}{N_1} + \frac{1}{N_2}\right)(\chi_V^2 - V)$, but it is usual to use the following rule proposed by BERRY, BERRY, UCKO (1967):

if $\frac{1}{N_{1i}} + \frac{1}{N_{2i}}$ is bounded for each i, the MMD is asymptotically normally distributed and is significant at the 0.05 probability level when the MMD is twice than its standard deviation (SJØVOLD 1973; SJØVOLD 1977; AL-ABBASY, SARIE 1997; BAILEY 2000).

4. THE CLUSTER ANALYSIS ALGORITHM

Cluster analysis constitutes a very important statistical method to detect grouping in a data set, and many techniques are developed to make classifications, groups of objects, etc., based on quantitative variables. However, an important part of the archaeological data is defined by means of

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qualitative variables with several states, but there are no procedures adapted for grouping these data except for presence/absence data (Sneath, Sokal 1973; Romesburg 1984; Krzanowski 1988).

The methods of analysis for qualitative variables usually codify each state of each variable as a new presence/absence variable, loosing the linkage between the states in the same variable. This problem has been approached by several scientific theories such as image recognition, string of symbols recognition, database management, archaeological pattern recognition of incomplete data, etc. (Michalski, Stepp 1983; Ben-Bassat, Zaidenberg 1984; Chiu, Wong 1986; Esquivel 1988; Fukunaga 1991).

According to the Shannon theory, in a mathematical communication model the information is determined by a statistic parameter associated with a probability scheme, and it must indicate a measure related to the uncertainty according to the occurrence of a particular message in a set of messages:

$$H(X) = \sum_{i=1}^{n} - p_i \log_2 p_i \qquad \sum_{i=1}^{n} p_i = 1$$

We propose that the information carried out by the x_{ik} state with experimental probability p_{ik} and n_i number of states, and the associated entropy to the Xi variable are defined as:

$$I(x_{ik}) = -\frac{1}{n_i} \log_2 p(x_{ik}) > 0 \;\; \Rightarrow \;\; H(X_i) = \overline{I(x_{ik})} = -\frac{1}{n_i} \sum_{k=1}^{n_i} p(x_{ik}) \log_2 p(x_{ik})$$

The entropy H(Xi) minimizes the influence of the rare cases; but this influence is very important to study the association between elements because: «the agreement in rare states is less probable that the agreement between frequent states and it must be more valued» (Sneath, Sokal 1973). The total entropy of the X_i (Esquivel 1988) is accord to the previous ideas:

$$D(X_i) = -\frac{1}{n_i} \sum_{k=1}^{n_i} \log_2 p(x_{ik})$$

The total entropy $D(X_i)$ measures the byass or distortion that produces a non regular variable in the space of elements.

Being $G = \{A_1, A_2, ... A_n\}$ the set of elements defined by the set of qualitative multistate variables $V = \{X_1, X_2, ... X_v\}$, and n_i the number of states of variable X_i. Each element has linked a mathematical object defined by the n-pla of measures (Dubois, Prade 1980) $m(A_i) = \{(m_1(A_i), m_2(A_i), ... m_v(A_i)\}$, $k = 1,...,v$ and $i = 1,...,n$, being $m_k(A_i) = x_{kj}$ if j is the index of the state of variable X_k that is in A_i. The set of mathematical objects defined by this proce-

dure is named the "pattern space" **S**, and using $p_i(A)$ as experimental frequency of the x_{ij} state, the distortion that produces an element is defined by the total uncertainty originated by that element in the pattern space and is formuled by the mathematical expression:

$$F(A) = -\sum_{i=1}^{v} \frac{1}{n_i} \log_2 p_i(A) \ \ being \ \ p_i(A) = p(x_{ij}) \ \ if \ \ m_i(A) = x_{ij} \ \ 1 \le j \le n_i$$

The interaction between elements determines the clustering by means of the similarity characteristics of each one. Using a similar terminology to the physical sciences and used by the pattern recognition theory, the information measurement of attraction between elements will decide that units can be clustered and the intensity of clustering. The attraction measure between two elements must reveal the common information in the variables shared by them, while the dissimilarity must quantify the difference between them.

These concepts need the previous definitions:

– Common information between two elements. Is defined according to the mathematical set intersection

$$F(A_i \cap A_j) = -\sum_{k=1}^{v} \frac{1}{n_k} \log_2 p_k(A_i) \ \ if \ \ m_k(A_i) = m(A_j)$$

– Joint information between two elements. Is defined according to the mathematical set union

$$F(A \cup B) = F(A) + F(B) - F(A \cap B), \forall A, B \varepsilon \Gamma$$

The information values allowed by the common and the joint information verify the basic relations established by PAL, DUTTA MAJUMDER (1985) to quantify the degree of fuzzyness of a data set.

This theorem allows us to obtain the joint information provided by the elements of the group $G_n = \{A_1, A_2, ..., A_n\}$ according to the boolean logic rules (ESQUIVEL 1988; ESQUIVEL 1999):

$$F(G_n) = F\left(\bigcup_{k=1}^{n} A_i\right) = \sum_{i=1}^{n} F(A_i) - \sum_{i<j}^{n} F(A_i \cap A_j) + ... \pm \sum_{i<j<...<h}^{n} F(A_i \cap A_j \cap ... \cap A_h) \pm F\left(\bigcap_{i=1}^{n} A_i\right)$$

In a space pattern, the study of the relations needs a parameter that quantifies the distance between groups of elements, or conversely a similarity measure because the basic relation is d(A,G)=1-S(A,G) (in this paper we use a similarity measure). In the case of similarity between two elements, the affinity measure is the common information between them. The relation between the affinity function and the information of elements is established by the following expression (ESQUIVEL 1988; ESQUIVEL 1999):

$$A_t(A, G_n) = F\left(\left(\bigcup_{i=1}^{n} A_i\right) \cap A\right) \quad \forall A \quad \forall G_n \in \Gamma \qquad A_t(G_1, G_2) = F(G_1, G_2)$$

This definition verifies the properties established by BACKER, JAIN (1981) that must verifiy each affinity measures:

1) the affinity measure element-group should not be smaller if the element is a member of the group that if it is not contained in him;
2) the affinity will be near 0 when the element is spurious to the group;
3) the affinity will be an absolute maximum if the group is constituted by an single element having the same localization that the previous element.

Two basic forms are possible to establish a similarity measure:

$$S_1(G_1, G_2) = \frac{F(G_1 \wedge G_2)}{F(G_1 \cup G_2)} \quad G_1 \wedge G_2 = \left(\bigcap_{i=1}^{n1} A_i\right) \cap \left(\bigcap_{j=1}^{n2} B_j\right) \quad \forall A_i \in G_1 \quad \forall B_j \in G_2$$

This measure verifies the conditions established by BACKER, JAIN (1981) and only quantifies the uncertainty provided by the states that appear in all and each one of the elements of the groups.

$$S_2(G_1, G_2) = \frac{A_t(G_1, G_2)}{F(G_1 \cup G_2)} \quad 0 \le S_2 \le 1$$

The S_2 measure doesn't verify the conditions imposed by Backer and Jain since it takes into account all the occurrences among the elements of the groups, and therefore the uncertainty is added to the total value increasing. Also, it is less strict than the previous measure.

5. DATA SET AND RESULTS OF ANALYSIS

The data have been obtained from the remains of burials belonging to three contemporary settlements belonging to different cultures and with great geographic proximity (about 150 km). The Castellón Alto and the Fuente Amarga settlements are prototypes of the Argaric culture and they are located in Galera and Huéscar (Granada, Spain), on the left bank of the river Galera, on a steep terraced hill. In the construction of the cottages, the inhabitants took advantage of the natural terraces. Their main cultural characteristics are the production of a special pottery, a diet based on agriculture, and the burial of the inhabitants with their trousseau under the houses or inside tiny caves in the walls of the hill.

The La Navilla settlement is a megalithic dolmen with multiple burial that contains the remains of 54 human bodies, most conserved in an incom-

plete state. It is contemporary to the other locations and it is located in the right bank of the river Cacín. Culturally it is quite different from the Castellón Alto and Fuente Amarga settlements since it belongs to the Copper Age. There are no burials under the cottages or in the little caves, and they were stock-breeders but not farmers; however the pottery found in the burials is an Argaric typology, maybe due to the geographical proximity and to contemporary acculturation phenomena that occured.

The data set is composed of the teeth of 54 individuals in the megalithic cemetery of La Navilla and of 114 individuals, generally incomplete, found in the Argaric settlements of Castellón Alto and Fuente Amarga in a good conservation state. The dental morphological variables have been studied according to the methodology of the ASU system and other pathologies have been analyzed (caries, toothloss before death and dental waste).

We carried out previous morphological studies to obtain the distribution of the different characters of the maxillary and the jaw for sides and sex, to determine that differences do not exist due to the sex or the laterally using χ^2 tests. We have distinguished males, females and undetermined (all non adults and those older than 20 years for whom it has not been possible to determine the sex are included in this category).

In all the cases the non existence of statistically significant differences with a significance level p <0.05 was determined, which is in agreement with the results obtained in previous works (TURNER, NICHOL, SCOTT 1991; HILLSON 1996; SCOTT, TURNER 1997), indicating that dental morphological characters usually exhibit a high grade of symmetry. In some studies already completed, the agreement between both sides exceeds 95% and only 7% of fellows sample some asymmetry, generally in expression grades (SCOTT, TURNER 1997).

Since many characteristics are not represented and in order to assign greater value to the possible differences than to the similarities, 36 features have been selected among those whose frequencies diverge more (see Tables 1 and 2). The values of the MAD and their standard deviation, as much for the maxillary one as for the jaw, do not reflect statistically significant differences at p<0.05 significance level. In this study we have distinguished between the maxillary and the jaw cases to obtain greater detail in the results; also most of the characteristics of the jaw do not appear in the maxillary.

The global MMD value for traits in maxillary is 0.184 with standard deviation Ã=0.059, showing no statistically significant differences between the Argaric settlements and the non-Argaric Navilla settlement, with a significance level p<0.05 because the MMD value is not twice its standard deviation. Also, the analysis of the jaw provides a global MMD value 0.125 with standard deviation Ã=0.038, showing no statistically significant differences between the Argaric settlements and the non-Argaric Navilla settle-

Traits	MMD
Canine Distal Accessory Ridge	0.290
Premolar Lingual Cusp Variation P^2	0.039
Anterior Fovea	0.170
Groove Pattern X M^2	0.232
Groove Pattern Y M^1	0.084
Groove Pattern X M^3	-0.005
Cusp Number M^1	0.084
Cusp Number M^2	-0.009
Distal Trigonid Crest M^2	0.396
Protostylid M^1	0.058
Protoslylid M^3	0.021
Protostylid M^3	-0.076
Cusp 5 M^2	-0.009
Cusp 5 M^3	0.341
Cusp 7 M^1	0.232
Canine Root Number	-0.011
Congenital Absence I^1	0.170
Congenital Absence M^3	0.238

Tab. 1 – MMD results for the present traits in the maxillary between the Navilla settlement and the Argaric settlements.

ment, with a significance level $p < 0.05$ because MMD<2 Ã (Sjøvold 1973; Sjøvold 1977; Al-Abbasy, Sarie 1997; Bailey 2000).

The analysis using the MMD test indicates that significant differences do not exist for the total of dental variables between the sample of the Navilla and that of the Argaric settlements in Galera. Although variables with more differences were selected for this analysis, the result has been negative. According to the historical data, the two population samples studied descend biologically from the populations that inhabited East Andalucia in the Copper Age and, therefore, they do not differ from each other, too very little time has passed for evolutionary phenomena to occurr. Some of these traits present significant differences and could correspond to endogamy phenomena and/or drift genetics, which demonstrates that, inside the generality, each group presents some distinctive characteristics.

In general, both populations, as well as those of the Neolithic and Copper Age in Andalucia (Gallardo 2001), although among them some small differences appear, fit the general profile that defines the populations from Europe and Western Asia for dental morphological variables.

These measures get very good results from clustering a data set defined by qualitative multistate variables. The previous cluster analysis algorithm has been applied to the data set and confirms the results provided by the MMD test, i.e., there is no separation between the Argaric and non-Argaric populations, and the teeth of both populations appear mixed in the groups and subgroups obtained in the dendrogram tree.

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Traits	MMD
Canine Distal Accessory Ridge	0.290
Premolar Lingual Cusp Variation P^2	0.039
Anterior Fovea	0.170
Groove Pattern X M^2	0.232
Groove Pattern Y M^1	0.084
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Protostylid M^3	-0.076
Cusp 5 M^2	-0.009
Cusp 5 M^3	0.341
Cusp 7 M^1	0.232
Canine Root Number	-0.011
Congenital Absence I^1	0.170
Congenital Absence M^3	0.238

Tab. 2 – MMD results for the present traits in the jaw between the Navilla settlement and the Argaric settlements.

Due to the great quantity of data available, in this paper the results described are those obtained when applying the algorithm to the teeth of the maxillary. The categories used have been the tooth type (M1, M2 and M3) and those specific variables of the maxillary ones: Metacone, Hypocone, Cusp 5, Carabelli's Trait, Parastyle, Enamel Extensions and Root Number. The teeth numbered 1-25 are the non-Argaric. The dendrogram shows the following results (Fig. 2):

– There are no isolated groups for Argaric and non-Argaric settlements using the teeth of the maxillary.
– Each group is composed of teeth belonging to both cultures, without distinction between them.
– There is not a specific typology that allows us to determine if a tooth belongs to one or another culture.

6. CONCLUSIONS

In this work we have studied the remains of maxillary and jaws belonging to 168 individuals with a total of 1313 pieces belonging to the multiple megalithic graves of La Navilla (necropolis of the Pantano de los Bermejales, Granada) and of the Argaric settlements of Castellón Alto and Fuente Amarga (near Galera, Granada), sites that are near to each other geographically. This material has been analyzed on the basis of the dental morphological characteristics using the ASU (Arizona State University) system.
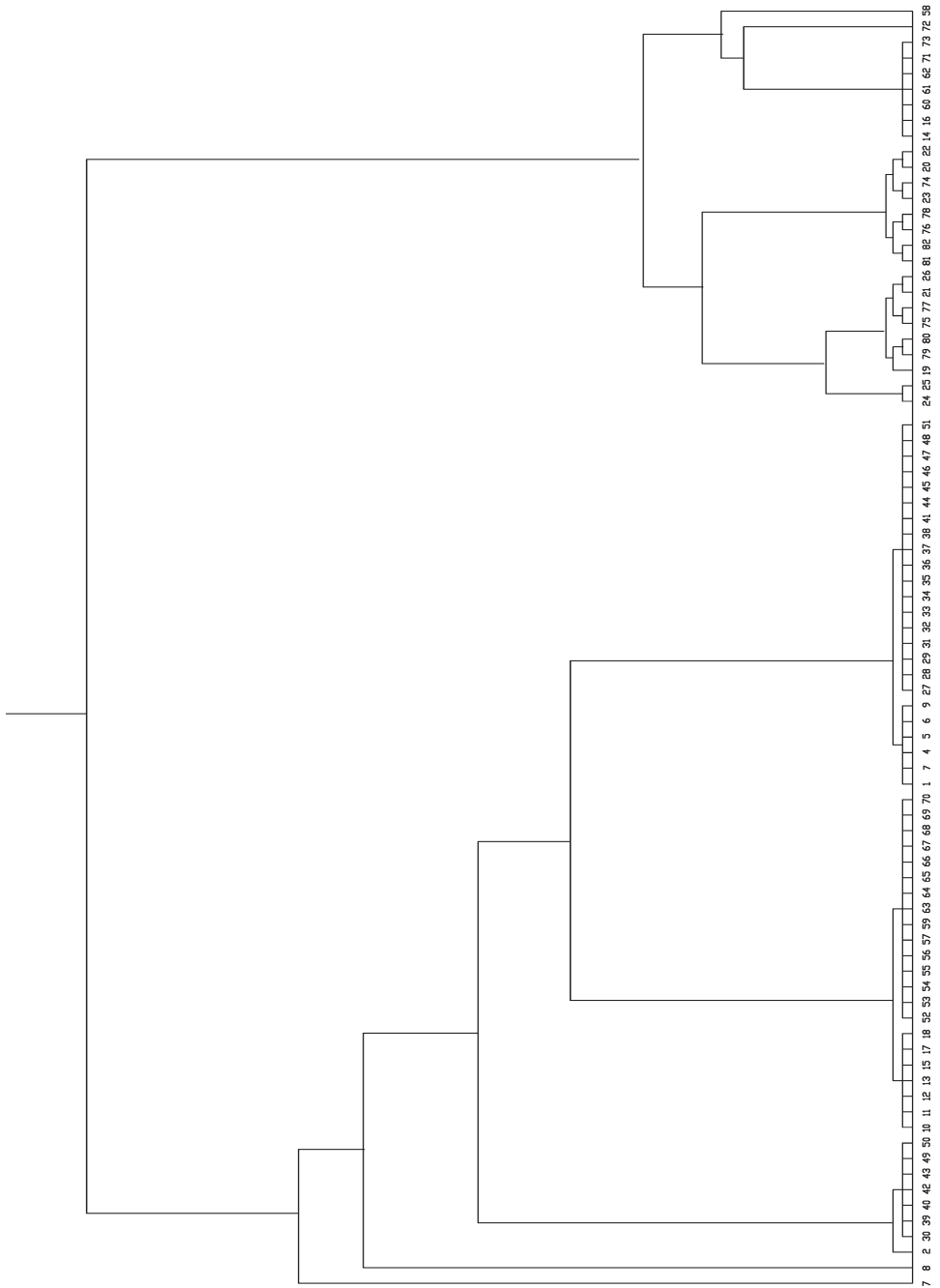
Fig. 2 – Dendrogram obtained by means of cluster analysis algorithm using qualitative multistate variables.

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Although the study was very complicated due to the high grade of deterioration of the Argaric teeth, and the mixed disposition of the material of La Navilla, satisfactory results have been obtained.

The previous analyses do not show statistically significant differences between jaw and maxillary or between sexes, which coincides with the characteristics of the phenotypic distribution of the dental morphological variables. Therefore, the morphological features of the ASU system are an excellent indicator for the comparison between biological populations that are not affected by environmental factors such as diet, disease, etc.

The application of the MMD test of differences shows that statistically significant differences do not exist among contemporary and very near geographically Argaric and non-Argaric populations in Granada, showing that the people studied belong to the same biological population. Therefore, any differences among these locations will be due to cultural factors, etc.

These results have been confirmed by means of the application of an algorithm of cluster analysis developed to use multistate qualitative variables, showing that independent groups do not exist between the Argaric and non-Argaric populations studied.

The trait frequencies of the ASU system indicate that the populations studied belong biologically to that which Scott and Turner (1997) have defined as populations from Western Eurasia. That is to say, they form part of the group of populations from Europe, North Africa and Southwest Asia.

Some characteristics present different frequencies from those of Western Europe, but we cannot determine if they are or are not characteristic features of Mediterranean populations, since the moment the number of studies of this type in the North valley is very small and therefore a biological characterization of these populations has not been made based on their dental morphological variables.

The frequencies obtained are very similar to the signal ones recorded by Gallardo (2001) for the populations of the Neolithic Age and the Copper Age in Granada. Therefore, it is possible to affirm that a biological continuity exists in the region from the Neolithic to the Bronze Age.

José Antonio Esquivel
Departamento de Prehistoria y Arqueología
Instituto Andaluz de Geofísica
Universidad de Granada

Ihab al Oumaoui
Departamento de Prehistoria y Arqueología
Universidad de Granada

Silvia Jiménez-Brobeil
Departamento de Ciencias Morfológicas
Laboratorio de Antropología Física
Universidad de Granada

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ABSTRACT

The study of dental morphological traits in prehistoric populations is a new method of analysis and allows us to determine important characteristics of different human populations. In this paper we study the dental feature traits proposed by the ASU System (developed by Turner *et al*. in Arizona State University) by means of an alphanumeric and graphic database recording the dental morphological characteristics and the possible dental diseases (caries, dental wear, etc.). These traits are easily and reliable observed, and persist many years in dentally harsh life styles, evolving very slowly or without sex dimorphism.

The multivariate data set obtained using the ASU System is defined by means of multistate qualitative variables, and the methodology of statistical analysis is the following:

–   The MMD test (Mean Measures of Divergence) was developed by SJOVOLD (1977) to observe the differences between two or more previously established and defined groups by means of multistate qualitative variables. It is also possible to test if existing differences among populations are ethnic, cultural, etc.

–   A Cluster Analysis algorithm developed by one of the authors (ESQUIVEL 1988) that enables us to build a grouping using qualitative multistate variables by means of specific developments in Information Theory established by Claude Shannon. Therefore, it is possible to determine the similarities of dental morphological traits between human groups, and compare these results with other previous information from archaeological data.

This methodology has been applied to analyze human genetic diversity using exclusively dental morphological characteristics to determine the diffusion of the culture of the Argar, a prehistoric culture which existed in 1300-1500 B.C. The analysis has been applied to the teeth of 116 subjects belonging to the Argaric culture in the neighbouring settlements of Castellón Alto and Fuente Amarga (Granada, Spain), and the teeth of 58 subjects belonging to the non-Argaric settlement of La Navilla, also 1300-1500 B.C., about 150 Kms. distant. The results show a biological continuity, endogamy phenomena and genetic drifts. Finally, the study of the maxillar pathology like cavities and dental wear tells us about dental health, food and food preparation.