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Journal:	*International Journal of Osteoarchaeology*
Manuscript ID	OA-16-0026.R1
Wiley - Manuscript type:	Short Report
Date Submitted by the Author:	n/a

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Ancestry estimation based on morphoscopic traits in a sample of African slaves from Lagos, Portugal (15th-17th centuries)

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Running Title: Ancestry estimation in a slave sample from Portugal

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Abstract

In 2009, a skeletal collection of 158 individuals was excavated in Valle da Gafaria, Lagos, Portugal. These individuals were buried in an unusual way, having been discarded in an urban dump located outside the medieval city walls, dated from the 15th-17th centuries. Lagos was, at the time, an important slave trade harbour, and during the excavation, the morphological appearance of the skulls and the presence of intentionally modified teeth in some individuals raised suspicion that they were African slaves. Despite the extensive historical information about the Atlantic slave trade, so far skeletal remains identified as slaves were scarce, especially in Europe. The aim of the present study is to estimate the ancestry of a sample of 33 adult individuals (28 females and 5 males) recovered in the Valle da Gafaria applying the eleven morphological characteristics recommended by Hefner (2009) using the naïve Bayes classifier. When comparing the individuals with four groups of classification (European, African, American Indian, and Asian), 24 (72.7%) specimens were classified as Africans with a posterior probability greater than 0.90. When only two groups were considered (the African and the European), 31 (93.9%) individuals were classified as Africans with a posterior probability greater than 0.90. These results are in accordance with the historical record and previous genetic studies suggesting that this sample represents a rare archaeological sample of great interest to the history of the Atlantic slave trade, i.e., the Lagos individuals were probably of African ancestry. Although the ancestry is a parameter of the biological profile mainly estimated in forensic Anthropology, this study confirms the importance of its investigation in past populations.

Key words: Ancestry; Morphoscopic traits; Enslaved Africans; 15th-17th centuries; Bioarchaeology.

1. Introduction

Due to the construction of an underground car park in Valle da Gafaria (Lagos, Portugal), an archaeological excavation allowed the identification of two burial places: one related with a leprosarium (Ferreira et al., 2013) and another associated with a deposit of urban waste (Wasterlain et al., 2015). From this deposit of urban waste, dated from the 15th-17th centuries, the skeletons of 158 individuals were recovered.

The radiocarbon dating of one skeleton (individual 169) revealed a date of 450 +/- 40BP (2 sigma: Cal AD 1420 - 1480; cal BP 540 - 470; Beta - 276508). During that period, the 15th century, Lagos was the harbour where slaves arrived from Africa and from which they were redistributed to the Kingdom of Portugal, the Mediterranean Sea and Northern Europe (Fonseca, 2010; Caldeira, 2013). Additionally, several archaeological findings support the hypothesis that the 158 individuals recovered from the deposit waste were African slaves: the fact that their bodies were dropped mixed with waste in a large pit, disregarding the burial traditions; the recovery of several African ornaments associated with the skeletons; the apparent African facial morphology (Figure 1) (Coelho, 2012); and the presence of intentionally modified teeth in 63 individuals. For a more comprehensive contextualization of this collection please see Wasterlain et al. (2015).

The aim of the present study is to estimate the ancestry of a sample of individuals recovered in the Valle da Gafaria by applying the eleven morphological characteristics recommended by Hefner (2009) using the naïve Bayes classifier.

The ability to identify potential slaves will lead to several pertinent questions about the slave trade, such as: Were both sexes equally likely to be victims in the slave trade? What was the health status of these individuals? Is there any evidence of patterned degenerative lesions that indicate that the slaves were used for heavy manual labour? Is there any evidence of traumatic injuries that may suggest that these individuals were subjected to physical abuse? After confirming that these individuals were African slaves future research on this collection could help address this kind of questions of wider anthropological interest.

2. Material and Methods

The morphological analysis is based on two different types of nonmetric traits, the anthroposcopic traits, and the binary nonmetric traits (Hughes et al., 2011). While the anthroposcopic traits evaluate the different degrees of expression or shape of the trait (e.g. the malar tubercle), the binary nonmetric traits are recorded as “present” or “absent” (e.g. the nasal overgrowth) (Hughes et al., 2011). In the present study, the anthroposcopic traits recommended by Hefner (2009) were applied using the naïve Bayes classifier to estimate ancestry of the individuals recovered in Valle da Gafaria (Lagos, Portugal).

Of the 158 individuals of the Valle da Gafaria collection, only 33 were sufficiently preserved to allow morphological analysis. The state of preservation and completeness of the selected skeletons are presented in Table 1. Sex and age-at-death estimation, relied on metric and morphological analyses of the coxal bone and the skull (Uytterschaut, 1986; Ferembach et al., 1990; Buikstra and Ubelaker, 1994; Bruzek, 2002; Ozle et al., 2007; Shirley and Jantz, 2011). The ages are comprised between 15 and 40 years. In all, the sample is composed of 28 females and 5 males (Table 1). In the present study the sexes were combined together because the reference data provided by Hefner (2009) also pool the sexes. Besides, there are no issues with the unequal samples in the current study.

Eleven morphological characteristics were observed to estimate ancestry: anterior nasal spine (ANS), inferior nasal aperture (INA), interorbital breadth (IOB), malar tubercle (MT), nasal aperture width (NAW), nasal bone contour (NBC), nasal overgrowth (NO), postbregmatic depression (PBD), supranasal suture (SPS), transverse palatine suture (TPS Shape), zygomaticomaxillary suture (ZS Shape). All characteristics were evaluated following the descriptions of Hefner (2009) and the images of Osteoware (Smithsonian Institution, 2011).

The first step of this investigation was to ascertain if there was agreement between two observations performed by the same observer (intra-observer error) and by two different observers (inter-observer error). To assess intra-observer error, observations were collected with one week interval between each observation by the first author (CC). To investigate the inter-observer error 17 skulls were analysed by another author (MTF). Both errors were calculated through the Cohen's Kappa coefficient, measured on a -1 to 1 scale (Viera and Garrett, 2005).

Ancestry estimation can be formulated and addressed from a mathematical point of view as a statistical classification problem, that is, to allocate an object into predefined classes based on its observed features. Statistical classification and pattern recognition tools are common in anthropology because biological profiling from skeletal remains is in its essence an exercise of statistical prediction and estimation. To be able to estimate sex, age-at-death, ancestry, and stature, statistical information must be first extracted from identified reference samples. Such information can be later used to reconstruct any biological parameter from unidentified skeletal remains based on the characteristics of the osteological material. The accuracy and precision of such reconstruction depends on the quality of the methods of osteological observation and the techniques underlying statistical prediction and estimation.

Hefner and Ousley (2014) provided a significant contribution to statistical ancestry estimation by morphoscopic analysis. The authors evaluated the utility of several statistical algorithms in ancestry prediction, demonstrating that morphoscopic ancestry estimation can also be framed within a robust mathematical approach. Their work, however, is incomplete in the sense that the statistical models created and tested by the authors lack a practical and easy-to-use implementation. In fact, some of the techniques employed are impossible to use without specialized software (i.e., neural network, random forest, and support vector machine models).

Among the techniques used is the naïve Bayes algorithm. The naïve Bayes classifier is a simple, yet effective, probabilistic model that makes use of Bayesian theory with strong independence assumption (Fielding, 2007). It assumes that the presence or absence of a characteristic is not related to the presence or absence of another trait given the class variable, that is, it takes no account for partial correlations. Such assumption is called conditional independence. This modelling assumption offers a dramatic simplification of model induction: individual class-conditional marginal density of features can be estimated separately using a one-dimensional kernel density estimator or any distribution model appropriate for the continuous data. For discrete predictor class-conditional probability tables can be obtained using a histogram estimator (Hastie et al., 2009).

It is important to note that unless the data is projected into a subspace with forced orthogonality (i.e., PCA scores), it is common to observe some degree of dependency among predictors, which normally occurs in real data. However, even when there are deviations from this underlying independence assumption, this technique works well often outperforming more sophisticated algorithms that explicitly model dependencies. This occurs because model predictions will be accurate as long as probability for the true class (i.e., ancestry) is greater than the probability of any other class. To obtain correct predictions only an approximate solution is required to rank order class probabilities. Marginal class-conditional densities may be biased but that has little effect on the final posterior probabilities, especially in the decision regions (Fielding, 2007; Hastie et al., 2009).

Under the naïve Bayes classifier ancestry estimation is expressed as:

$$P(A_k|X_i) = \frac{P(A_K)\prod_{i=1}^{p} P(X_i|A_k)}{P(X_i)} = \frac{P(A_K)\prod_{i=1}^{p} P(X_i|A_k)}{\sum_{i=1}^{r} P(A_K)\prod_{i=1}^{p} P(X_i|A_k)}$$

Where A stands for ancestral group, X for the morphoscopic traits, r is the number of ancestral groups involved in the analysis, and p the number of morphoscopic traits used to compute the posterior probability.

To assess ancestry using this statistical approach, the posterior probability that a skull is from a specific ancestry, given p observed traits, is computed for each ancestral group considered in the analysis. The ancestral group that maximizes the posterior probability is considered as the most likely. In this study, the prior probability for each ancestral group, $P(A_k)$, was assumed to be uniform.

The main advantage of the naïve Bayes classifier is that it only requires knowledge of probabilities to obtain ancestry estimates. In this case the most important one is $P(X_i|A_k)$, the probability of observing a specific stage/state of a morphological trait given that ancestry is known. Bayes' theorem is then used to invert these probabilities and obtain $P(A_k|X_i)$, i.e. the probability of a skull being of a certain ancestry given the observed morphological trait(s). The required probabilities $P(X_i|A_k)$ are available from Hefner (2009), and allowed us to construct a naïve Bayes classifier. Also, detailed information regarding the reference samples, namely their size, composition, chronology, and geographic origin, can be obtained from Hefner (2009). A web application that implements the naïve Bayes classifier for morphoscopic ancestry estimation is available at www.apps.osteomics.com/hefneR.

Two predictive analyses were conducted based on the number of biogeographic ancestral groups. The first analysis included four ancestral groups (European, African, American Indian, and Asian). The second analysis was restricted to European and African ancestral groups. As previously mentioned, statistical classification was performed based on the maximization of posterior probability principle, the ancestral group with the highest posterior probability was assigned to the individual. It means that under a uniform prior, the assigned ancestral group is the one with a posterior probability greater than the (prior) random allocation probability.

3. Results

Intra- and inter-observer errors

The results of the Cohen's Kappa coefficient for the intra- and inter-observer errors are presented in Table 2. Following the interpretation of Kappa by Viera and Garrett (2005), the overall results showed substantial agreement. More specifically, in the intra-observer analysis, the zygomaticomaxillary suture (K= 0.459) showed a moderate agreement. The inferior nasal aperture (K= 0.629), the malar tubercle (K= 0.718) the supranasal suture (K= 0.770), and the anterior nasal spine (K=0.798) demonstrated a substantial agreement. The other five traits – nasal bone contour (K= 0.812), transverse palatine suture (K= 0.816), nasal aperture width (K= 0.829), postbregmatic depression (K= 0.927), interorbital breadth (K= 0.933) – showed an almost perfect agreement. The nasal overgrowth (K= 1) presented a perfect agreement between the two observations.

Regarding the inter-observer error, the malar tubercle (K= 0.186) showed a slight agreement. The zygomaticomaxillary suture (K= 0.214) and the supranasal suture (K= 0.393) showed a fair agreement. Four traits – anterior nasal spine (K= 0.500), inferior nasal aperture (K=0.553), nasal bone contour (K= 0.553), and the interorbital breadth (K= 0.589) – presented moderate agreement. The transverse palatine suture (K= 0.827) had an almost perfect agreement. The nasal aperture width (K= 1), the nasal overgrowth (K= 1), and the postbregmatic depression (K= 1) showed a perfect agreement among the two observers.

Four groups classification

The results obtained by using the naïve Bayes classifier on the first analysis are presented in Table 3. Twenty-four specimens (72.7%) were classified as Africans with posterior probability greater than 0.90. Two individuals (6.1%) were assigned to the African group with posterior probability greater than 0.80. Three specimens (9.1%) were classified as Africans with posterior probability greater than 0.70. Two skulls (6.1%) were classified in the African group with posterior probability greater than 0.50. One individual (3.0%) was classified as African with a 0.44 posterior probability. Finally, one cranium (3.0%), from the individual 63, had posterior probability greater than 0.60 to belong to the American Indian group (Figure 2).

Two groups classifications

The results of the second analysis using only two groups, European and African, are presented in Table 4. Thirty-one individuals (93.9%) were classified as Africans with posterior probability greater than 0.90. Only two specimens (6.1%) were classified as Africans with posterior probability greater than 0.80.

4. Discussion

Generally, the estimation of ancestry is considered more relevant for Forensic Anthropology than for past population studies, since it is one of the big four generic factors of a biological profile that help to establish identity and strong contextual information is usually associated with bioarchaeological investigations (i.e., artefacts, chronology, location) making ancestry estimation and the bio-geographic origin of a particular population implicit. However, there are several situations where it is worth investigating ancestry in archaeological samples, namely when the history of colonization of a given region is being investigated, in studies of endogamy vs. exogamy, when different facial morphologies inside a close group suggests the presence of newcomer individuals, and to confirm the identity when investigating historical characters. Finally, ancestry is a crucial factor in the study of the history of slavery.

As a parameter of paramount importance, the estimation of ancestry has attracted the attention of researchers in order to find more accurate methods of evaluation (Gill, 2009, Hefner, 2009; DiGangi and Hefner, 2013). The estimation of ancestry is preferably accomplished through analysis of the skull, particularly from the delicate bones of the mid-face, because this region is the most discriminant part of the skeleton (Gill, 2009). However, the most discriminative features are commonly reported only for three major population groups - the European, the African, and the Asian (Byers, 2011) - which makes it difficult to identify small-scale migrations in the past.

Morphological analysis to estimate ancestry has been largely criticized for being highly subjective and dependent on the experience of the observer. However, it has some advantages over metric analysis. For instance, the morphological traits are easily observed, not being required instruments (Hefner and Ousley, 2014). Moreover, along with adequate statistical approaches, the morphoscopic traits can be used to accurately assess the ancestry, without relying only on the experience of the observer (Iscan and Steyn, 2013; Hefner and Ousley, 2014).

The skeletal collection recovered in the Valle da Gafaria (Lagos, Portugal) is a unique sample composed of the remains of 158 individuals who lived in the 15th-17th centuries, and who were dropped in a dump after death, disregarding the canonical burial traditions. The Lagos's historical context and the presence of many individuals with intentionally modified teeth (for more details, please see Wasterlain et al., 2015) are among the facts that led the authors to suspect that these skeletons were the remains of African slaves who arrived to the Lagos's harbour during that time period. Therefore, this study aimed to estimate the ancestry of 33 adult individuals (28 females and 5 males), applying the eleven morphological characteristics recommended by Hefner (2009) using the naïve Bayes classifier.

Overall, the results obtained in the present study confirmed the African ancestry of the Lagos's individuals. More specifically, the comparison of the 33 skulls with the four major ancestral groups (European, African, American Indian, and Asian) assigned 24 (72.7%) to an

African ancestry with a posterior probability greater than 0.90. Surprisingly, one individual (number 63) was assigned to the American Indian group. As it can be observed in Figure 2, the cranium 63 presents some traits that are shared by Africans and American Indians, such as the inferior nasal aperture, and the interorbital breadth. It should not be ignored, however, that this skull was incomplete, fragmented, and it was necessary to proceed to its reconstruction, which certainly contributed and increased its post-mortem deformation. In fact, the nasal overgrowth and the postbregamatic depression are two characteristics that are important to distinguish these two ancestries and that were not possible to observe in this individual. These circumstances may have biased the obtained result. On the other hand, the likelihood of encountering an America Indian within this sample is quite low.

The results obtained when only two groups were considered (the African and the European) were even more consistent with an African origin, since 31 (93.9%) individuals were classified as Africans with a posterior probability greater than 0.90.

In 2014, Martiniano et al. obtained random short autosomal sequence reads from two individuals (125 and 166) recovered in the discard deposit burials from Valle da Gafaria, from which only one was also included in the present analysis. Interestingly, the next generation sequencing (NGS) of historical DNA sampled from the metatarsal bone of the individual 125 showed affinity with Bantu-speaking groups and Western African Mandenka and Yoruba populations, which is also consistent with African origins for these individuals.

Given the results obtained in the present study, which are consistent with historical records and are in accordance with the genetic analysis performed previously in this osteological collection, we can now state that the Lagos's individuals were probably of African ancestry. Moreover, this study confirms the importance of investigating the ancestry in past populations. Future research on this collection will help address many questions of wider anthropological interest, namely regarding their overall health status, their labour conditions, and if they were subjected to physical abuse, among others.

Acknowledgments

The authors thank Centro de Investigação em Antropologia e Saúde, Centro de Ecologia Funcional, Dryas Arqueologia Lda., and Styx, Estudos de Antropologia Lda. The co-author Catarina Coelho was financed by University of Coimbra. The co-author David Navega was financed by national funds by FCT- Fundação para a Ciência e Tecnologia with the reference SFRH/BD/99676/2014. The co-author Maria Teresa Ferreira was financed by Gerda Henkel Foundation (AZ 09/F/15). The co-author Sofia N. Wasterlain was financed by national funds by FCT – Fundação para a Ciência e Tecnologia, under the project with the reference UID/ANT/00283/2013. The authors also acknowledge the anonymous reviewers whose valuable comments and suggestions allowed us to improve the manuscript.

The authors state that they do not have any conflict of interest to declare.

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Table 1. Sex diagnosis, age-at-death, preservation and completeness of the skeletal individuals analysed in the present study.

Individual no.	Age-at-death	Sex	Preservation	Completeness
20	20-30 years	Female	Fair	Almost complete
21	20-30 years	Female	Good	Almost complete
25	15-25 years	Male	Good	Almost complete
38	20-30 years	Female	Good	Almost complete
39	20-30 years	Female	Good	Almost complete
41	30-40 years	Female	Good	Almost complete
57	15-25 years	Female	Good	Almost complete
63	30-40 years	Male	Poor	Very incomplete
65	25-35 years	Male	Fair	Almost complete
66	30-40 years	Male	Good	Almost complete
67	30-40 years	Female	Good	Almost complete
68	30-40 years	Female	Good	Almost complete
69	15-25 years	Female	Fair	Relatively complete
75	30-40 years	Female	Fair	Almost complete
77	30-40 years	Male	Good	Almost complete
78	30-40 years	Female	Good	Almost complete
81	15-25 years	Female	Good	Almost complete
82	25-35 years	Female	Good	Almost complete
93	20-30 years	Female	Good	Almost complete
95	20-30 years	Female	Good	Almost complete
96	30-40 years	Female	Good	Almost complete
110	20-30 years	Female	Fair	Almost complete

114	20-30 years	Female	Good	Almost complete
123	20-30 years	Female	Poor	Relatively complete
125	20-30 years	Female	Good	Almost complete
133	15-25 years	Female	Good	Almost complete
136	25-35 years	Female	Fair	Relatively complete
150	30-40 years	Female	Fair	Almost complete
153	25-35 years	Female	Fair	Almost complete
162	20-30 years	Female	Good	Almost complete
163	20-30 years	Female	Fair	Almost complete
169	20-30 years	Female	Fair	Almost complete
170	20-30 years	Female	Fair	Relatively complete

Poor – Severe bone damage, metaphyseal loss with long bones and cancellous exposure of the vertebrae.

Fair – Slight bone damage, erosion of bone surface and/or bone fragmentation.

Good – No significant damage of the bone surface or bone fragmentation.

Very incomplete – More than 50% of the skeleton is absent.

Relatively complete – 25-50% of the skeleton is absent.

Almost complete – Less than 25% of the skeleton is absent.

Table 2. Intra- and inter-observer error analysis using the Cohen's Kappa coefficient.

Trait	**Intra-observer Cohen's Kappa coefficient**	**Inter-observer Cohen's Kappa coefficient**
Anterior nasal spine (ANS)	0.798	0.500
Inferior nasal aperture (INA)	0.629	0.553
Interorbital breadth (IOB)	0.933	0.589
Malar tubercle (MT)	0.718	0.186
Nasal aperture width (NAW)	0.829	1
Nasal bone contour (NBC)	0.812	0.553
Nasal overgrowth (NO)	1	1
Postbregmatic depression (PBD)	0.927	1
Supranasal suture (SPS)	0.770	0.393
Transverse palatine suture (TPS Shape)	0.816	0.827
Zygomaticomaxillary suture (ZS Shape)	0.459	0.214
Mean	0.790	0.620

Table 3. Summary of the results obtained by comparing the individuals from Valle da Gafaria to four groups of ancestry classification.

Individual no.	African	American Indian	Asian	European
20	0.550517	0.281084	0.155829	0.012571
21	0.885845	0.064897	0.045798	0.003459
25	0.993707	0.003025	0.002854	0.000414
38	0.437627	0.296149	0.172366	0.093858
39	0.754649	0.125582	0.073866	0.045902
41	0.970815	0.003785	0.023625	0.001775
57	0.994896	0.001698	0.003187	0.000219
63	0.145385	0.635085	0.201174	0.018356
65	0.998003	0.000274	0.001612	0.000110
66	0.995642	0.002308	0.001885	0.000165
67	0.993695	0.000229	0.005946	0.000130
68	0.997024	0.001694	0.001156	0.000127
69	0.998380	0.000000	0.001599	0.000000
75	0.969394	0.004984	0.025250	0.000371
77	0.982793	0.004169	0.011894	0.001144
78	0.911316	0.005408	0.082632	0.000644
81	0.995617	0.001484	0.001265	0.001635
82	0.980205	0.004061	0.014015	0.001719
93	0.956052	0.013309	0.025234	0.005406
95	0.785586	0.083371	0.094501	0.036542

96	0.976501	0.005867	0.016825	0.000808
110	0.995931	0.001214	0.002762	0.000000
114	0.998301	0.000181	0.001425	0.000000
123	0.979222	0.005324	0.015074	0.000380
125	0.579405	0.196752	0.213658	0.010185
133	0.997265	0.000722	0.001931	0.000000
136	0.999610	0.000000	0.000262	0.000000
150	0.983811	0.010960	0.002163	0.003066
153	0.981274	0.005890	0.009274	0.003562
162	0.708830	0.224055	0.056727	0.010388
163	0.886734	0.065532	0.042485	0.005249
169	0.989513	0.004909	0.00526	0.000318
170	0.995931	0.001214	0.002762	0.000000

Table 4. Summary of the results obtained by comparing the individuals from Valle da Gafaria to two groups of ancestry classification.

Individual no.	African	European
20	0.977675	0.022325
21	0.996110	0.003890
25	0.999583	0.000417
38	0.823404	0.176596
39	0.942662	0.057338
41	0.998175	0.001825
57	0.999780	0.000220
63	0.887895	0.112105
65	0.999889	0.000111
66	0.999835	0.000165
67	0.999869	0.000131
68	0.999873	0.000127
69	0.999993	0.000000
75	0.999617	0.000383
77	0.998838	0.001162
78	0.999293	0.000707
81	0.998361	0.001639
82	0.998249	0.001751
93	0.994378	0.005622
95	0.955552	0.044448

96	0.999173	0.000827
110	0.999906	0.000000
114	0.999906	0.000000
123	0.999612	0.000388
125	0.982725	0.017275
133	0.999918	0.000000
136	0.999957	0.000000
150	0.996893	0.003107
153	0.996383	0.003617
162	0.985556	0.014444
163	0.994116	0.005884
169	0.999678	0.000322
170	0.999906	0.000000

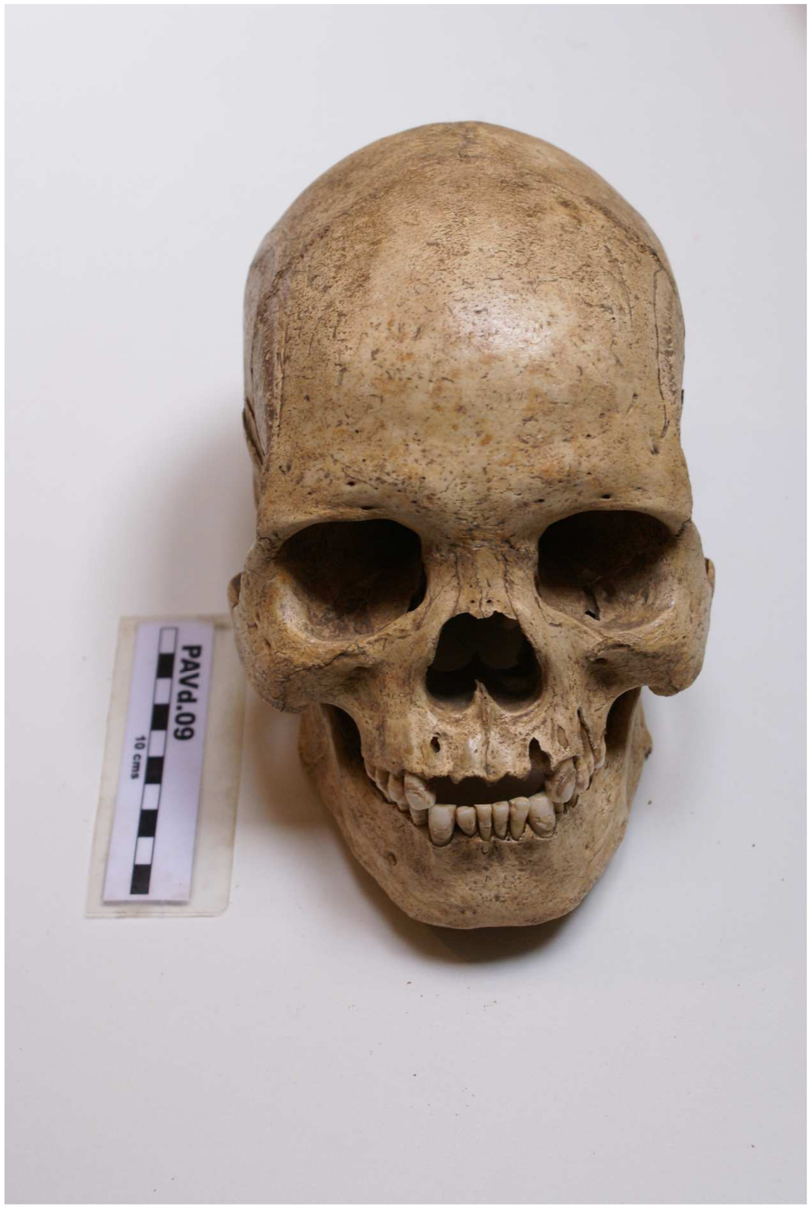

Figure 1. Cranium of individual 65 from Valle da Gafaria sample in anterior view, with an apparent African facial morphology.
914x1365mm (72 x 72 DPI)

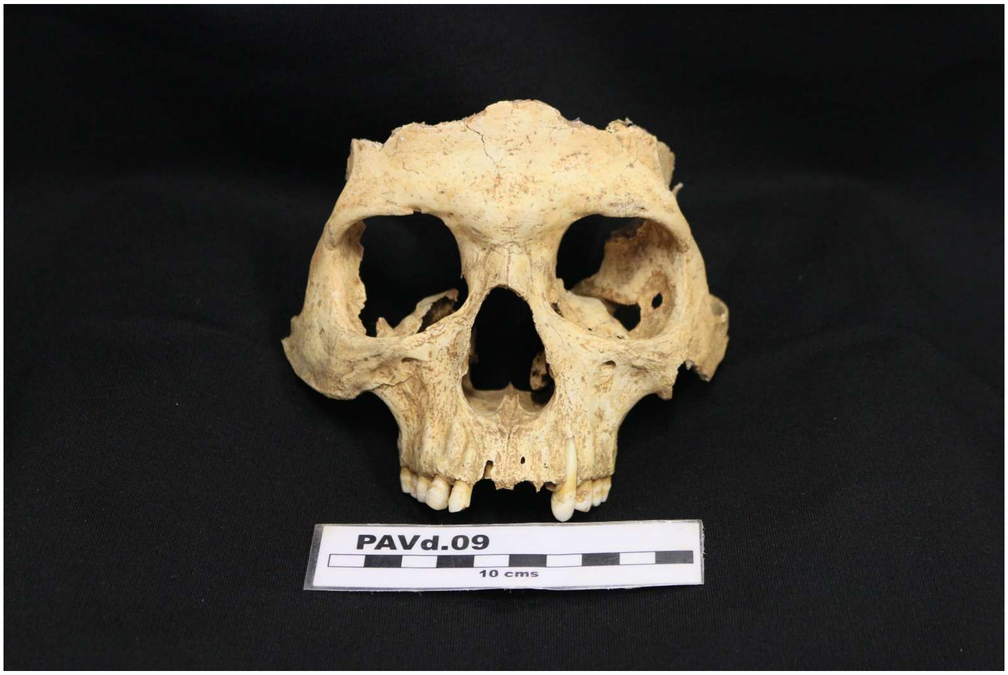

Figure 2. Cranium of individual 63 from Valle da Gafaria sample in anterior view, which was assigned to the American Indian group when applying the four major ancestral groups (European, African, American Indian and Asian).
1930x1286mm (72 x 72 DPI)