

Research Article

The Population of the Mediterranean Basin in the First Millennium AD Migration Period

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Abstract

The peopling of the Mediterranean basin in the first millennium AD can be determined by exploring a combination of cultural, economic and biological factors that influence the structure of populations and determine particular situations of gene frequencies. Quantitative characters from 2,487 adult crania of both sexes from central and southern Europe and the Italian peninsula were analyzed using multivariate statistical analyses. Biological distances representing phenotypic variation between these populations were not found. An analysis of Mahalanobis D2 distances established a great homogeneity. This scarce morphological variability is shown also by principal component analysis. The application of cluster analysis shows the formation of two clusters: one distributed along the Adriatic coast; the other along the Tyrrhenian. This model is similar to the first millennium BC pattern. The difference is that in this case there are no significant biological divergences but only geographic ones, perhaps attributable to micro-adaptive factors. These two lines flow together in the populations of central and southern Italy. The phenomenon of the Migration of People (or Barbarian Invasions) in Italy during the first millennium AD does not seem to produce a significant variation in the Italian genetic substratum. This could be associated with the great gene flow that the Roman Empire opened, not only in the Mediterranean basin but also in Europe, following the conquest wars. Over time this produced a new general genetic model common to southern Europe and Italy that explains the low variability found in this study.

Keywords: Biological relationships; Craniometrics traits; Central and Southern Europe; Italy

Introduction

The history of the biological population in the Mediterranean basin during the first millennium AD is very complex and interesting. Today many scholars have re-evaluated the importance of this period, also in the light of the recent interpretations of old and new anthropological, genetic and archaeological data [1-10]. The fall of the Western Roman Empire produced new situations under many aspects: cultural, social, economical and biological. In the first millennium AD there was a great population movement from central and Eastern Europe to new southern settlement sites [10-12]. These human groups were able to adapt quickly, even if these areas were different in climatic, environmental and geographic configuration from the original ones [7]. From the biological point of view, there were various problems. The demographic decline at the particular moment of the massive migrations from outside [13,14], the biogenetic flow between old and new populations settled on the territory [10,12], their cultural divergence, the conservative effects of a strong gene flow [15], the change of the nutritional habits and the rise of the incidence of epidemiological diseases [3,16-18] were the principal problems of this period. Understanding the principal evolutionary events that provide an explanation for the population and the divergence of ancient human groups in the Mediterranean basin and in particular in Italy is an anthropologically relevant topic. Many studies have evaluated biological, geographic, and/or chronological distances. Such works have used information derived from very

different samples (for quality of preservation and numerosity) that belong to different regions of the Mediterranean basin [9-12,19,20]. In particular, during the first millennium BC the peninsular population in Italy was divided into two genetic patterns: Tyrrhenian and Adriatic. This model was attributable to the scarce gene flow across the mountains of the Apennine chain [9]. During the Roman period the building of roads eased the movement of people, with a consequent rise in bio-dynamic flow [20], not only in peninsular territories but also in central and southern Europe [12].

The Migration Period, also called the Barbarian Invasions or Völkerwanderung (German for “migration of the peoples”), was a period of human migration that occurred roughly between the 300 to 700 CE in Europe, marking the transition from Late Antiquity to the Early Middle Ages [21]. These movements were catalyzed by profound changes within both the Roman Empire and the so-called ‘barbarian frontier’. Migrating peoples during this period included the Lombard, Goths, Vandals, Bulgars, Avars, Alans, Sueves, Frisians, and Franks, among other Germanic and Slavic tribes [21,22]. Migrations of peoples, although not strictly part of the ‘Migration Age’, continued beyond AD 1000, marked by Viking, Magyar, Turkish and Mongol invasions, and these also had significant effects, especially in eastern Europe. The migration movement may be divided into two phases: the first phase, between AD 300 and 500, largely seen from the Mediterranean perspective of Greek and Latin historians with the aid of some archaeology, put Germanic peoples in

Table 1: Sample sizes from the central-southern Europe and Italy.

	Total number	Males	Females
Alemannics	434	227	207
Burgundies	319	189	130
LNE	159	87	72
LNO	142	91	51
LAIC	273	131	142
OIC	264	158	106
IC	46	21	25
IM	574	255	319
Swiss	276	158	118

control of most areas of the former Western Roman Empire [21]. The first to enter Roman territory formally - as refugees from the Huns - were the Visigoths in 376. Tolerated by the Romans on condition that they defend the Danube frontier, they rebelled, eventually invading Italy and sacking Rome (410). They were followed into Roman territory by the Ostrogoths, led by Theodoric the Great, who settled in Italy itself. In Gaul, the Franks, a fusion of western Germanic tribes whose leaders had been strongly aligned with Rome, entered Roman lands more gradually and peacefully during the 5th century and were generally accepted as rulers by the Roman-Gaulish population. Fending off challenges from the Alemans, Burgundians and Visigoths, the Frankish kingdom became the nucleus of the future states of France and Germany. The second phase, between 550 and 700, saw tribes settled in central and particularly in Eastern Europe gradually becoming predominant. One of these populations was the Lombards, a Germanic people settled in northern Italy in the region now known as Lombardy. The role of the Lombards in the historical and biological events of Italy is well known. The Lombard presence in central Italy was represented principally by soldiers [23]. This fact probably caused a different bio-cultural effect compared to the organic migration of a whole ethnic group [24]. During the first period of Middle Ages, the social structure of Italy was strongly Germanised, even if with a heterogeneous modality [25]. In this context, the Lombards found it easy to settle. Their presence on the Italian territory during the 6th - 7th century AD has been estimated at around 5-8% of the whole population [26]. According to some recent hypotheses, the genetic substratum of the Lombards and the autochthonous population of central Italy was very similar during the early Middle Ages [26].

Because of the continuous default of the main urban areas, two basic events took place. One was demographic decrease. This factor is due to a lesser settlement density and a greater trend of epidemic events to spread [3,9,13], caused by the decline in the socio-sanitary system imposed during the Roman period [27].

The other factor that is in some way related to demographic decrease and to the situation of hygiene and health was the continuous movement of small human groups into new territories [16]. This phenomenon can be attributed to the need to change economic subsistence patterns in order to survive, but it also produced a rise in epidemic diseases such as plague, leprosy, tuberculosis and smallpox [3,9]. The convergence of these components during the first millennium AD determined a population decrease of up to 40-45% in some areas of Italy [9,13,14].

The aim of this study is to investigate and discuss the dynamics of the human biological population in the Mediterranean basin following the Migration of Peoples during the first millennium AD.

Materials and Methods

The skeletal sample of crania consists of 2,487 adult, male and female individuals (Table 1). For the unpublished data, age at death and sex were determined following standardized methods described by Buikstra and Ubelaker [28]. The sample originates from southern and central Europe (Germany, France and Switzerland) and the Italian peninsula. The sample was divided into nine groups based on geographic and cultural identification (Figure 1): Alemans [29-32]; Burgundians [31,33,34]; Swiss [35-37]; Lombards of northeastern Italy -LNE- [23,38]; Lombards of the north western Italy -LNO- [39]; Lombards and Avars of the Central Italy -LAIC- [24,26,40,41]; Ostrogoths of the Central Italy -OIC- [42]; autochthonous of Central Italy -IC- [12,43,44]; autochthonous of southern Italy -IM- [1,45,46,47]. All the samples date between the 3rd and the 9th century AD.

On the cranium, nineteen traits were measured according to the Martin and Saller method [48]: maximum cranial length, maximum cranial breadth, basionbregma height, porionbregma height, minimum frontal breadth, maximum frontal breadth, upper facial breadth, upper facial height, bizygomatic breadth, nasal height, nasal breadth, orbit height, orbit breadth, biorbital breadth, basionprosthion length, alveolar breadth, alveolar length, palatine breadth, palatine length (Table 2).

The morphological variability between populations was evaluated with Mahalanobis D^2 [49], Principal Component Analysis and Cluster Analysis [50,51]. D^2 square is a permutation test for two multivariate groups. Principal components analysis (PCA) is a procedure for finding hypothetical variables (components) that account for as much of the variance in the multidimensional data as possible [50,51]. These new variables are linear combinations of the original variables. Cluster Analysis was used to find hierarchical groupings in multivariate data sets. The hierarchical clustering routine produces a 'dendrogram' showing how data points can be clustered. Furthermore, a dendrogram using the Neighbor-Joining method [52] was employed to demonstrate the possible kinship relationships based on inter-group distances. This method tries to minimize the total length of the tree by linking the closest or neighboring Operative Taxonomic Units.

Results

An interesting scarce morphological variability was found in the contrast between the nine samples studied. Table 3 shows that all the inter-group Mahalanobis D^2 scores are statistically nonsignificant. Furthermore, the values of D^2 are all around 0. The Principal Component Analysis confirms the results of the D^2 , showing through the first two components (with eigenvalues respectively of 47, 96 and 33) on the whole a variance percent of 63.73%. This result explains a middle-low degree of dispersion among samples. Figure 2 shows that the samples from North of the Alps (Alemans, Burgundians and Swiss) tend to be distinguished from other samples, even if this is not in significant terms. The only exception is represented by the Lombards of northwestern Italy, who show a modest presence

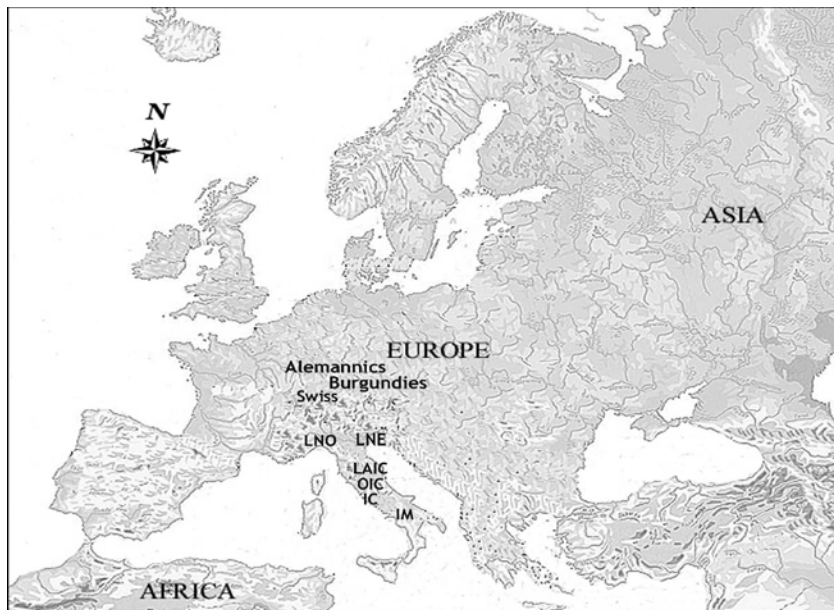


Figure 1: Geographic location of the samples.

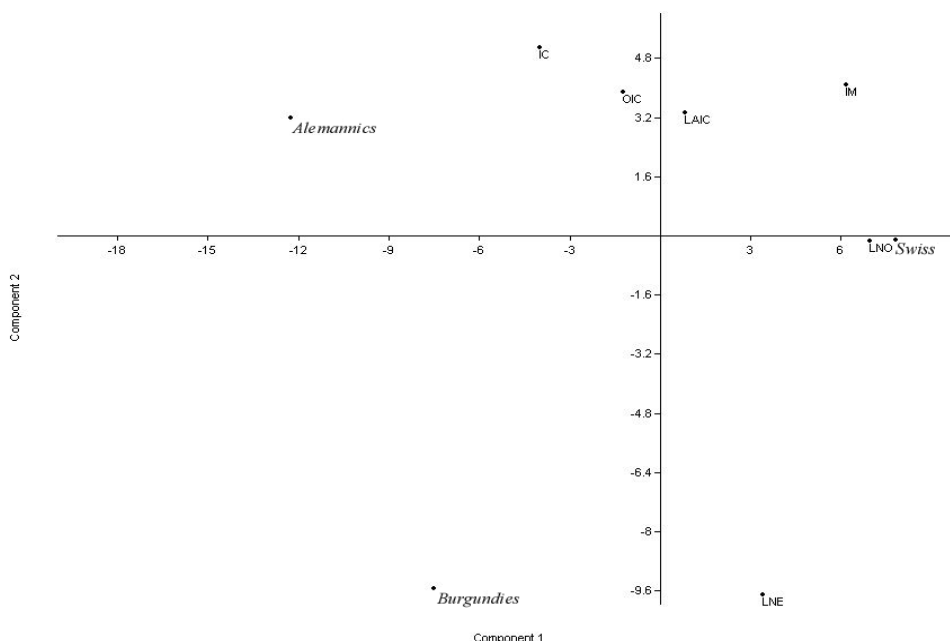


Figure 2: Analysis of the principal components (1 and 2).

around the Swiss sample. The low degree of dispersion shown by the percentage value of the variance explained is probably the result of a high morphological homogeneity between the samples investigated.

A further level of investigation is represented by the application of Cluster Analysis. It was applied to visualize the results of the comparisons through the construction of a dendrogram (Figure 3). The samples are concentrated in two large clusters, A and B, not very far apart. Both are located around -20 of similarity. Cluster A is slightly beneath this value while Cluster B is slightly above it. Cluster A shows a further division into two sub-clusters around the value of

similarity -10: a and b. In a there are the samples of the Lombards of northwestern Italy, autochthonous of southern Italy and Swiss; in b there are the Lombards and Ostrogoths of central Italy. Cluster B is also divided at a similar value of similarity into two sub-clusters: c and d. The Alemans and autochthonous of central Italy are present in c, in d the Burgundians and Lombards of northeastern Italy.

The application of the Neighbor Joining method shows a phenetic tree (obtained from the Mahalanobis D^2 distances) that corresponds with the other results obtained by the cluster analysis. The only exception is represented by the position of the Lombards

Table 2: Means of the craniometric measures used in multivariate analysis.

	Alemannics	Burgundies	LNE	LNO	LAIC	OIC	IC	IM	Swiss
1	188.6	189.2	186.8	188.9	187.5	190.2	189.4	189.1	187.4
2	141.3	144.2	133.7	138.4	140.1	144.3	141.6	142.8	139
3	136.3	138.1	135.7	133.1	140.3	139.2	131.1	134.2	136.2
4	116.7	118.7	115.6	116.3	117.2	115.8	119.2	116.7	113.4
5	100.9	97.6	95.6	94.5	99.2	97.1	98.3	98.9	97.7
6	120.7	120.3	121.1	120.9	118.7	122.3	121.9	122.6	120.6
7	120.3	113.8	114.7	118.6	119.2	120.6	120.8	119.3	117.2
8	73.7	64.2	64.9	68.8	69.2	72.3	71.4	71.1	66.2
9	129.4	130.6	124.7	117.2	119.3	125.1	124.2	116.8	115.4
10	40	42.4	41.2	36.7	38.8	38.3	39.1	37.8	39.2
11	33.5	36.4	37.8	31.9	34.2	33.5	33.6	34.2	34.8
12	28.8	25.6	23.8	23.4	27.7	30.1	29.7	26.6	27.2
13	54.3	54.7	50.8	53.2	48.7	49.3	49.6	48.8	50.1
14	63.8	62.4	60.9	62.7	62.1	59.9	59.8	60.4	61.6
15	54.1	54.6	53.7	55.5	50.2	50.3	51.4	52.8	52.7
16	38.3	37.7	40.7	42	41.8	39.7	39.2	38	38.6
17	48.3	43.5	45.5	47.7	46.4	44.2	45.8	44.9	45.1
18	111.3	103.5	99.7	100.6	105.2	98.7	106.4	98.4	100.1
19	91.3	87.6	86.8	88.2	91.2	89.1	90.4	87.6	89.8

and Ostrogoths of central Italy: the Lombards are situated with the populations of the western side, while the Ostrogoths with the populations of the eastern side (Figure 4).

Discussion

The results obtained from the comparison of the nine human groups derived from as many geographic areas of southern and central Europe show an order of morphological and genetic divergence that is very low but also very interesting in its development. Although the multivariate analysis is not statistically significant, the results show the presence in Italy of two distinct parallel biological lines that flow in central and southern Italy. One of these lines, starting from the Swiss, is present along the Tyrrhenian side (west) with the Lombards of northwestern Italy, Lombards of central Italy and autochthonous of southern Italy. The other, starting from the Burgundians and Alemans, is distributed along the Adriatic side with the Lombards of northeastern Italy and the autochthonous and Ostrogoths of central Italy (Figure 4). The Apennines divided the two lines. In some aspects, this model re-proposes the pattern of the Italian population during the first millennium BCE, before the Roman era. During this last period too, a Tyrrhenian population and another Adriatic one were present in Italy. The only difference is that the divergence between the sides in the first millennium BCE is highly significant [53,54]. In our case, the Apennines seem not to constitute a genetic barrier but only a geographic one, as has been emphasized for the Roman period [20]. This fact is demonstrated by a great bio-morphological homogeneity of the samples with a micro-differentiation of probable adaptive nature between the two sides. Surely the infrastructures built in Italy and Europe during the Roman imperial period helped to facilitate the movement of people, goods and cultures. In central Italy, above all, the construction of roads that went from the Tyrrhenian to the

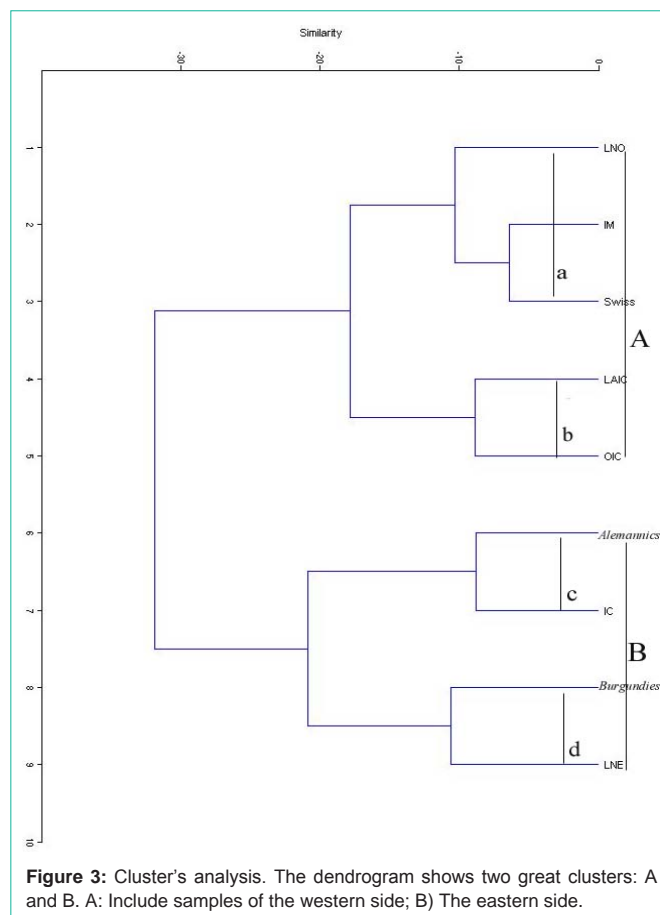


Figure 3: Cluster's analysis. The dendrogram shows two great clusters: A and B. A: Include samples of the western side; B) The eastern side.

Adriatic side (for example the “*via Salaria*”, an ancient road for the transport and trade of salt) allowed a greater and easier movement of genes which helped to mitigate the divergence present in the first millennium BCE. Despite this the migratory routes during the first millennium CE continued to be the same, the populations of Eastern Europe preferred the Adriatic route while those of Central Europe the Tyrrhenian one. This phenomenon has been present in Italy since the Mesolithic [55].

The phenomenon of the Migration Period or Barbarian Invasions, with the arrival of new populations from central and Eastern Europe in Italy, does not seem to be a disruptive event from the genetic point of view. The scarce divergence shown by the application of multivariate analysis to the samples confirms this. Furthermore, the population pattern of Italy in the first millennium CE is very similar in population distribution to the model of the first millennium BCE. From a biological point of view, the results suggest a rather homogeneous population in southern and central Europe and in particular in Italy, where a certain genetic continuity is present from ancient times.

A hypothesis to explain this phenomenon emerges from the biological history of the Roman Empire. As mentioned above the expansion of Rome opened a new gene flow, not only in Italy but also throughout the Empire. The meeting of the Roman genetic substratum with that of populations subdued or located near the limes continued over time. Furthermore, the mixture of genes was facilitated first

Table 3: Mahalanobis D² distance (in bold-face) between regions of the central-southern Europe and Italy.

	Burgundies	LNE	LNO	LAIC	OIC	IC	IM	Swiss
Alemannics	0.0874	0.1269	0.0755	0.0823	0.0836	0.1779	0.088	0.0792
	0.7625	0.5715	0.815	0.7995	0.7835	0.31	0.7605	0.794
Burgundies		0.1243	0.0789	0.0944	0.1013	0.1464	0.1036	0.0773
		0.5912	0.7975	0.724	0.1024	0.441	0.6705	0.821
LNE			0.1313	0.1688	0.1731	0.2362	0.1795	0.1216
			0.5295	0.3565	0.3392	0.1295	0.3284	0.5915
LNO				0.0886	0.0893	0.1478	0.1178	0.0795
				0.7455	0.7695	0.4515	0.5975	0.7855
LAIC					0.0721	0.1139	0.0761	0.1285
					0.8335	0.6872	0.8075	0.5328
OIC						0.1088	0.0743	0.1147
						0.6415	0.8286	0.6092
IC							0.0947	0.1715
							0.7105	0.3629
IM								0.1776
								0.3271

Under the D² there are the p values (in italic).

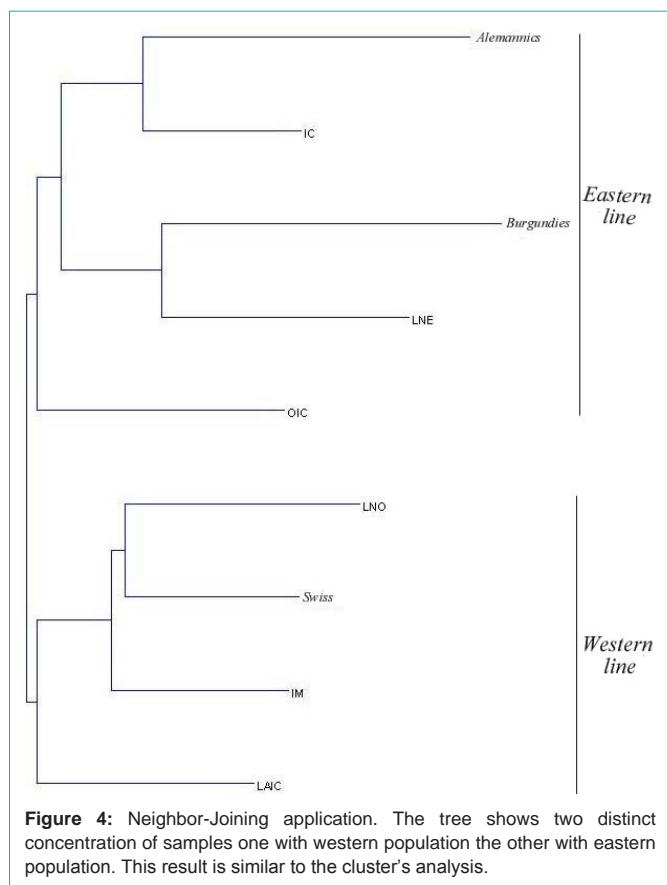


Figure 4: Neighbor-Joining application. The tree shows two distinct concentration of samples one with western population the other with eastern population. This result is similar to the cluster's analysis.

the basis for a possible first modern population. This hypothesis is confirmed by the “rebound” effect produced a few centuries later. During the first millennium CE, the migration of people brought to Italy many human groups from European territories where a new genetic substratum had been produced that tended over many generations to become homogeneous and compatible with the Italian one. The micro-differentiations attested represent the different patterns of adaptability and the normal human variability of a single population [56].

Conclusion

The results of this study were developed from a large sampling of data (more than 2,000 individuals). These samples, in turn, enabled us to include a large part of the existing genetic variability in a key region in order to understand the biological and cultural history of the Mediterranean basin.

Working under the assumption that quantitative characters are selectively neutral and have a low rate of mutation [56] the results shown in the dendrogram and on the map (Figure 4) allow us to propose an evolutionary pattern for the peopling of central and southern Europe and Italy. The pattern obtained for Italy during the first millennium CE is very similar to the archaic population of the first millennium BCE because of the close affinity that exists between them. The phenomenon of the Migration of Peoples (or Barbarian Invasions) in Italy during the first millennium CE does not seem to produce a significant variation in the Italian genetic substratum. This result could be associated with the great gene flow that the Roman Empire opened not only in the Mediterranean basin but also in Europe. This fact produced, over time, the constitution of a new general genetic model common to central and southern Europe and Italy that explains the low variability found in this study. The results obtained could suggest a model in which the modern population of central and southern Europe and Italy may begin in the first millennium CE.

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