

A new model for the spread of the first farmers in Europe

Ron Pinhasi

Department of Biological Anthropology, University of Cambridge, UK
ron.pinhasi@chello.at

ABSTRACT – The appearance and dispersion of the first farmers in Europe has been the subject of heated debate among anthropologists, archaeologists, and linguists for over a century. There is no consensus regarding two main aspects: (1) the extent to which the transition to farming was an indigenous process, and (2) the historical pattern in terms of the timing and tempo of the dispersion events. Morphological variability and affinities are assessed among Mesolithic and Early Neolithic populations of the Near East, Anatolia and Europe. Statistical results reveal regional and temporal differences in the dispersion process among these populations. Based on these results, a new model is presented for the spread of farming in Europe.

IZVLEČEK – Pojav in širjenje prvih kmetovalcev v Evropi je že več kot stoletje predmet vročih razprav med antropologi, arheologi in lingvisti. Zaenkrat še ni soglasja glede dveh glavnih vidikov: (1) do kakšne mere je bil prehod v kmetovanje domoroden proces in (2) kdaj se je začelo in kako hitro se je kmetovanje razširilo. V članku ocenimo morfološko raznolikost in sorodnost mezolitskih in zgodnje neolitskih populacij Bližnjega vzhoda, Anatolije in Evrope. Statistični rezultati kažejo, da so med temi populacijami v procesu širjenja regionalne in časovne razlike. Na temelju teh rezultatov predstavimo nov model razširjanja kmetovanja v Evropi.

KEY WORDS – *craniometric analysis; biological distances; morphological variability; Mesolithic; Early Neolithic; Europe; Levant; Anatolia*

INTRODUCTION

There is a view prevailing among archaeologists, anthropologists, geneticists, and linguists that skeletal studies of population affinities are a legacy of the past. Such scholars tend to point out that past studies of this sort were associated with the study of human races and eugenics and are thus better off being put away. Another prevalent assumption is that as bone growth and development is strongly affected by various environmental factors such as climate, diet, and activity, it can tell us nothing about genetically based biological variability among populations.

These assumptions are just as outdated as the study of human races. The application of skeletal techniques to the study of human populations is a resour-

ceful and unique avenue to the study of our past. Each discipline has its drawbacks and misconceptions. Some of these are the outcome of the type of data under examination, others are the result of misconceptions and prejudiced assumptions accumulated throughout the history of a particular scientific discipline.

The field of biological anthropology has a particularly infamous history. One of the outcomes of decades of racist research is a tendency among researchers from other related disciplines to question the validity of biological anthropology as a scientific discipline. The abolition of the concept of races and present emphasis on the uniformity of the human species is, in a sense, a positive consequence. How-

ever, such an approach disregards the fact that there exist both phenotypic and genotypic differences among human populations. Emphasising the fact that past and present human populations share biological similarities undermines the notion that each of these populations possess some unique biological variability. The fact that the concept of human races should be discarded does not imply that there are no significant differences in biological variability across space and time.

There exist relatively large Neolithic skeletal collections from localities in Europe and the Near East. Most of these skeletons are from well-stratified, radiocarbon dated archaeological contexts. These contexts therefore provide the researcher with comparatively accurate spatial and temporal attributes. Archaeological data provides invaluable information about past humans' behaviour and human-environment relationships. The archaeological record of Mesolithic and Neolithic populations is particularly rich and the analysis of these data in the context of human evolution is of great potential.

Renfrew (1992) pointed out that perhaps the greatest advantage of cranial data is its time span. Thus, anthropometric analysis can be grounded on the one hand in the archaeological background which provides the relevant historical context, and modern genetics on the other, which provides a reference to both past biological variability and past population structure and affinities (e.g. maps of clinal distributions of genetic traits).

At present there is a lack of consensus regarding the following aspects:

- ① The extent to which the transition to farming was an indigenous process, involving some admixture between incoming farmers and local hunters, or a population replacement process.
- ② The historical pattern in terms of the timing and tempo of the dispersion events.

The first stage of the project involved the analysis of archaeological data from approx. 2200 sites/contexts. The data was analysed in regard to its spatial and temporal attributes (i.e., radiocarbon dates, and geographic location in longitude/latitude) as well as for archaeological culture (Pinhasi 2000). Emphasis was placed on observing the temporally based distribution of Mesolithic vs. Neolithic occupation across Europe by using Arcview GIS application. Maps of settlement patterns by chronological period are depicted in Figures 1-7.

The analysis of archaeological data yielded the following results:

- The density of Mesolithic occupation at the time of the appearance of farming varied greatly between regions.
- The timing and density of Neolithic occupation also varied between regions.
- The dynamic pattern of Mesolithic colonization will tend to obscure any clinal trends that are presently attributed to the Neolithic 'wave of advance'.
- Any arriving farmers would have met very competitive and interactive conditions with a divergent potential for gene flow.
- The variability in population densities had a genetic effect on immigrant Neolithic farmers, and this should be modelled at a regional level.

Five models for the spread of farming in Europe were developed, partially on the basis of the results obtained, and partially on the basis of other prevalent theories (Ammerman & Cavalli Sforza 1984; Zvelebil & Rowley-Conwy 1984; Zvelebil 1986; Zvelebil & Zvelebil 1988; Zvelebil & Dolukhanov 1991; Zilhão 1993; Dennell 1985). The first part of this paper will expose these models and specify the corresponding expectations of each model in regards to the 'neolithisation' process across Europe.

Three main aspects of 'Neolithisation' will be examined in this paper. The first aspect begins with the assessment of the relationships among the Mesolithic groups in order to examine whether some of these groups are similar enough (morphologically) to be regarded as a single biological population. The section proceeds to examine affinities during the Early Neolithic period. The questions being addressed are as follows. What type of morphological affinities can one detect among the Early Neolithic populations? Are some groups similar enough to be regarded as belonging to a single population? This question is therefore identical to the one for the Mesolithic. However, morphological affinities must be interpreted in the specific context of the specified models. Particularly, the question of greatest relevance is whether a pattern of morphological affinities is compatible with a demic dispersal.

The second aspect is the specification of a plausible area of origin from which the first farmers spread to Europe, and whether a linear correlation between distance from source area and morphological differentiation exists, as suggested by the findings of Menozzi & Cavalli-Sforza (1978). The two centres exa-

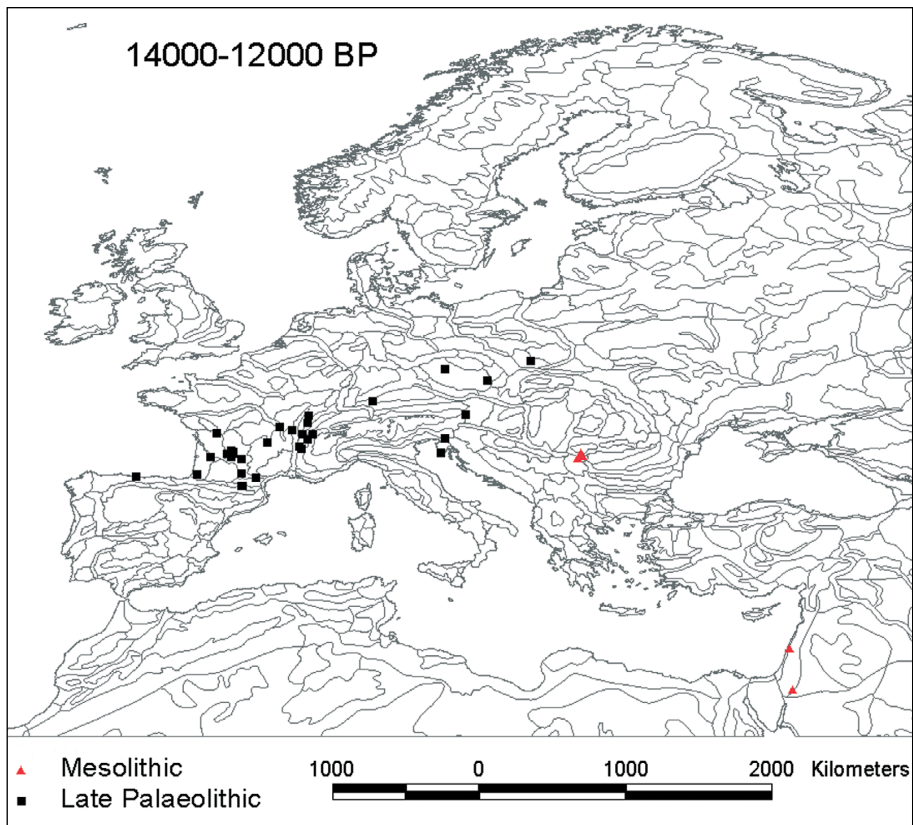


Fig. 1. Settlement pattern during the period 14 000–12 000 BP.

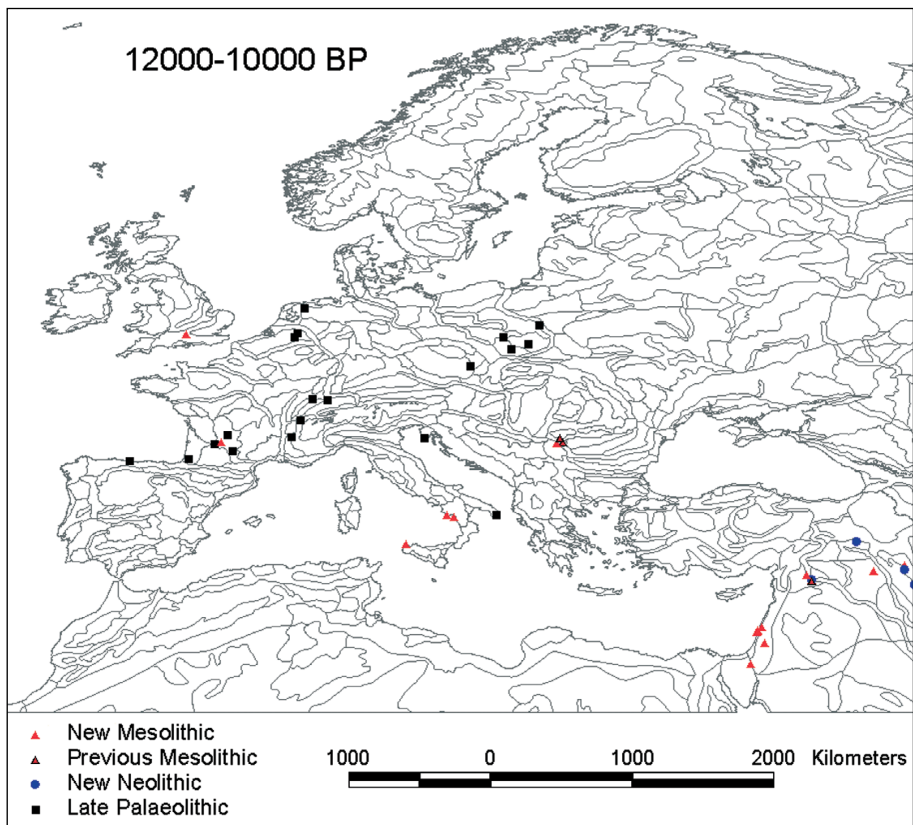


Fig. 2. Settlement pattern during the period 12 000–10 000 BP.

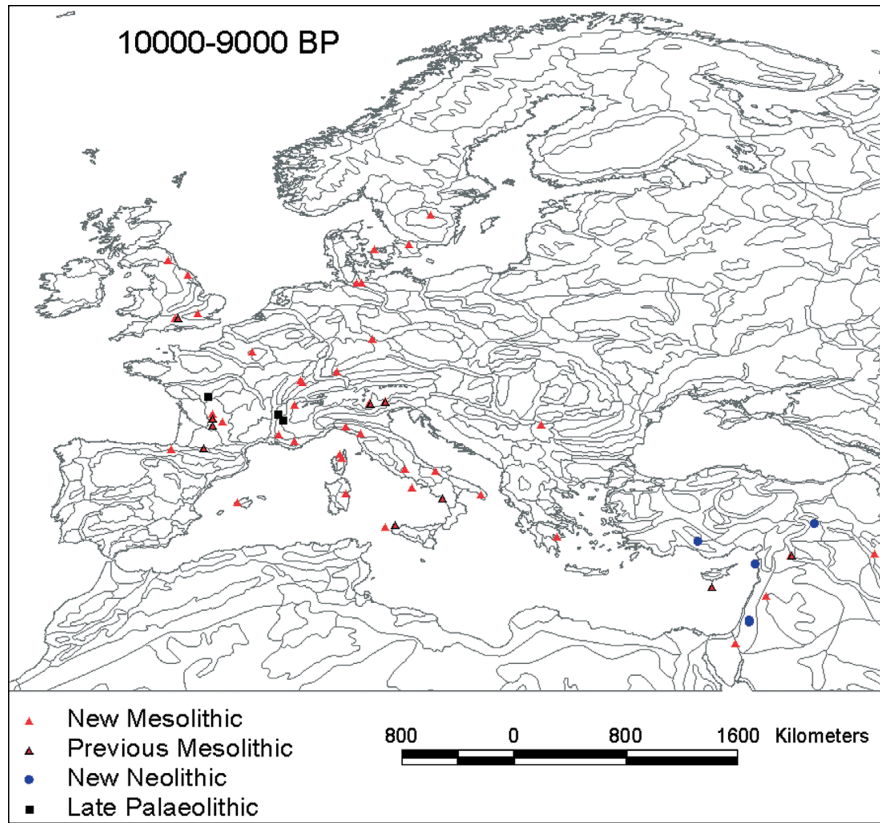


Fig. 3. Settlement pattern during the period 10 000–9000 BP.

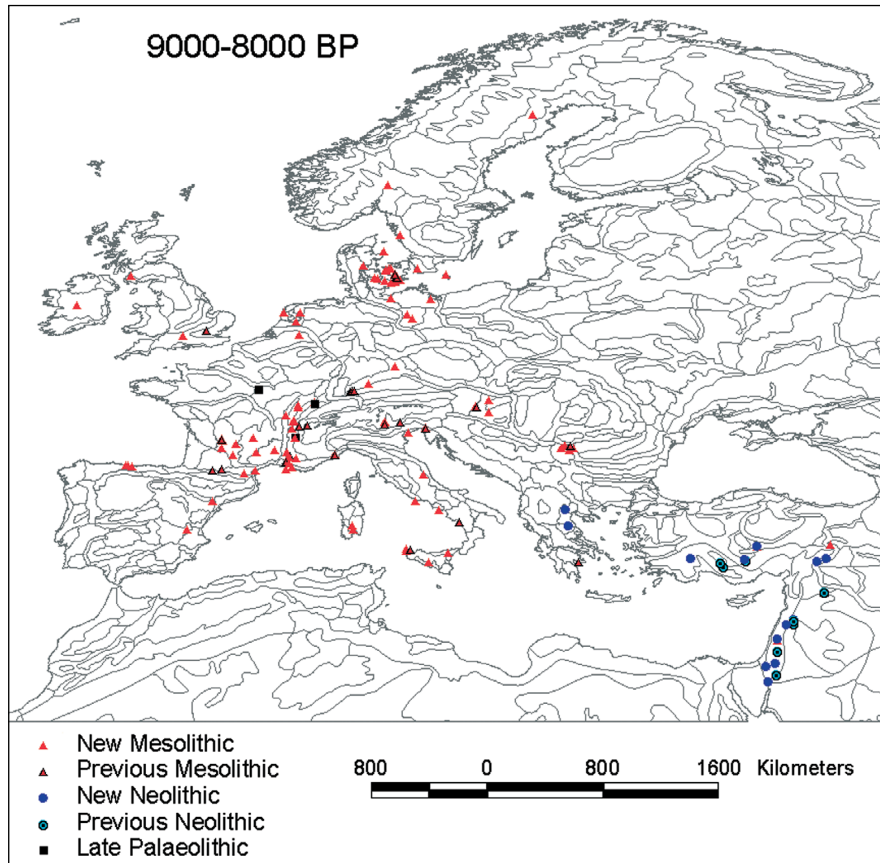


Fig. 4. Settlement pattern during the period 9000–8000 BP.

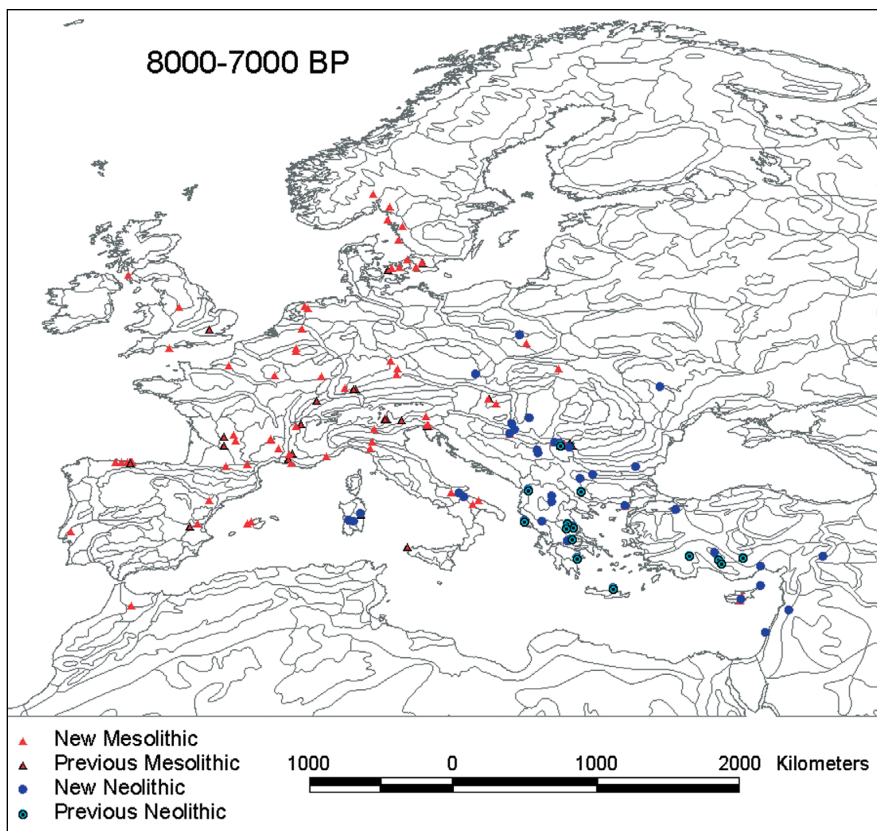


Fig. 5. Settlement pattern during the period 8000–7000 BP.

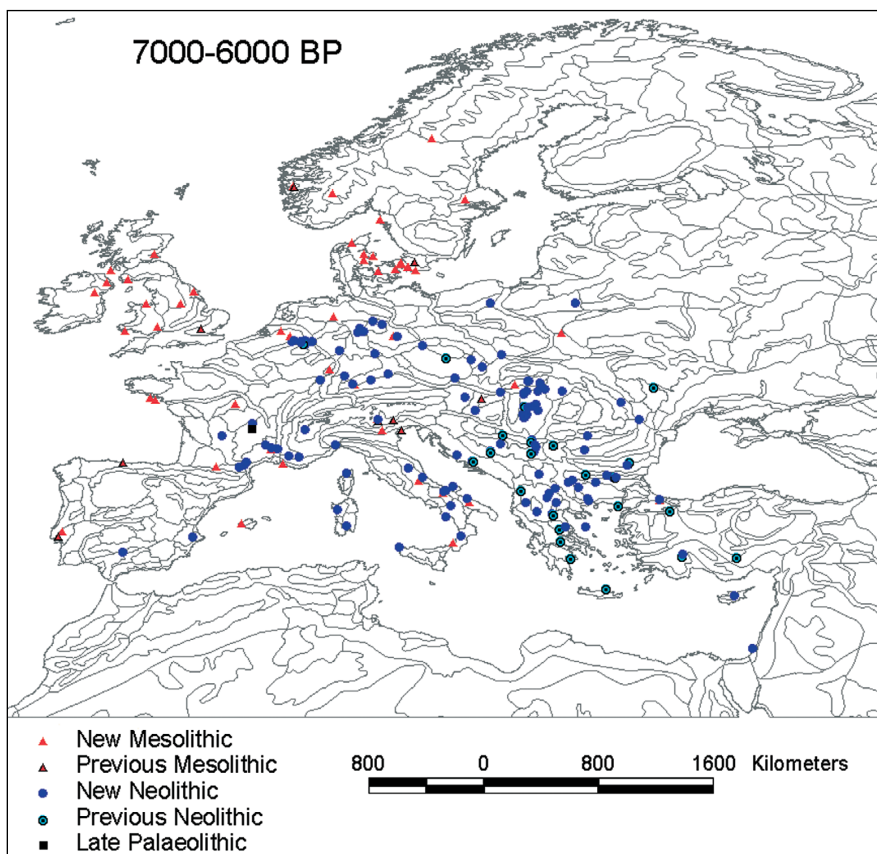


Fig. 6. Settlement pattern during the period 7000–6000 BP.

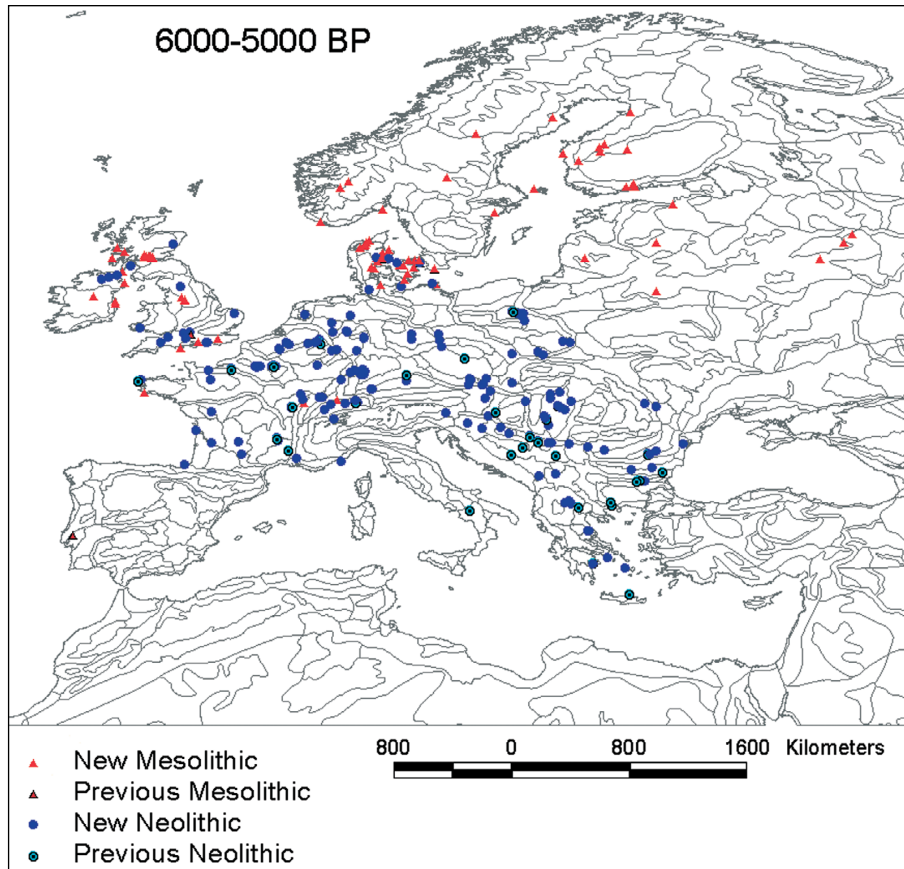


Fig. 7. Settlement pattern during the period 6000–5000 BP.

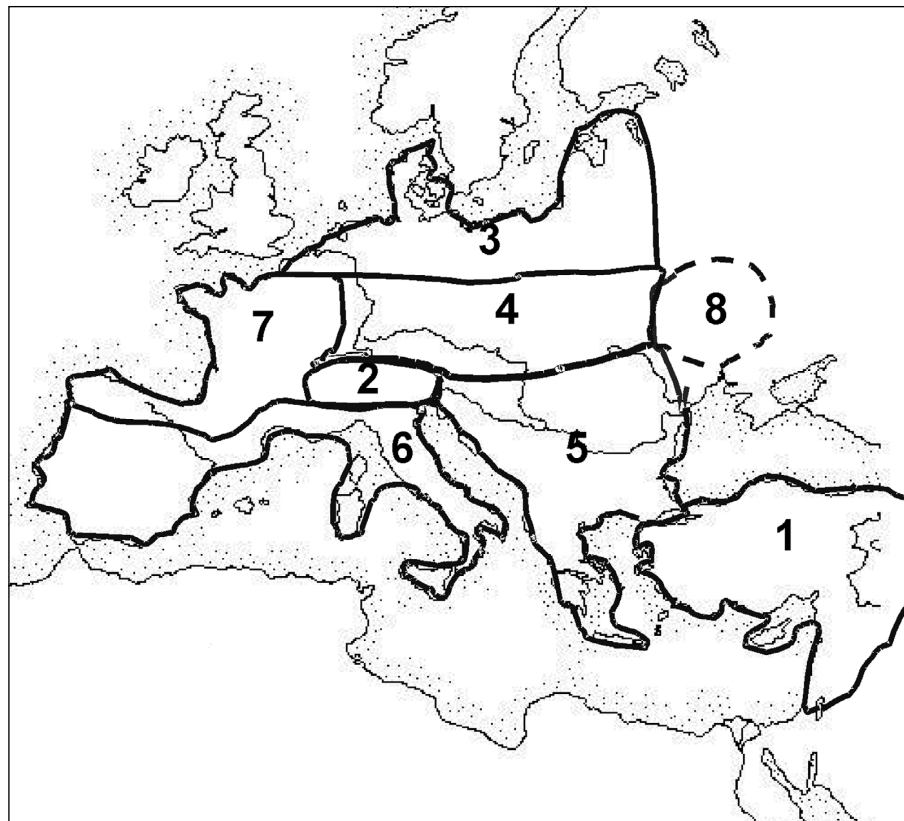


Fig. 8. The division of the studied groups according to geographic regions.

mined are SE Anatolia, represented by the population from Çayönü, and Central Anatolia, represented by the population of Çatal Höyük. The possibility of other locations (Levant, Cyprus) is rejected on the basis of the evidently large distances between the PPNB populations from these regions and the Early Neolithic European populations.

In the last part of this work a regional-based analysis of craniometric data is performed. The underlying hypothesis is that the process of neolithisation differed across space and time and thus needs to be assessed in greater depth (see *Pinhasi 2000; Lahr et al. 2000*). This is achieved by examining the degree of regional continuity between local hunters and incoming farmers in the various regions of Europe as a series of case studies. Temporal variation in spatial units is examined by modelling expected patterns of continuity (i.e., admixture) and discontinuity in various regions. The placement of a given specimen in a specific region was solely based on the geographic location of its associated site. The demarcation of the regions is depicted in Table 1 and in Figure 8.

MODELS FOR THE SPREAD OF FARMING IN EUROPE

Model 1 – Autochthonous transition across Europe

This model proposes that the transition to agriculture occurred as a series of local events that took place in different locations and time across Europe. The model is based on the idea of ‘Neolithisation’ through a process of cultural diffusion but without

any migration or expansions of farming populations. This model fits with the theory of in situ transition and cultural rather than demic diffusion of the Neolithic across Europe (see *Whittle 1996; Dennell 1985* and others). The model is represented in Figure 9.

Under this model, regionally based changes in morphological variation and changes in sexual dimorphism are the outcome of an adaptive response to environmental changes such as changes in diet, activity pattern, climate and mobility, and/or changes in mating networks. Thus, changes are not expected to be external (i.e. gene flow from migrations), but rather internal. In such a case, changes should be more pronounced at the period between stage 1 and stage 2, during which the Early Neolithic cultures appear across Europe. This is because this model places emphasis on a culturally-based transition. The archaeological record attests to the fact that in the case of most of the regions of Europe changes in lifestyle, mobility pattern and mating networks occurred during the initial transition to agriculture (i.e., during the Early Neolithic period). Less ‘functional’ morphological changes are expected among populations that were already ‘fully Neolithic’, and little would have changed during the subsequent period in terms of the above-mentioned factors.

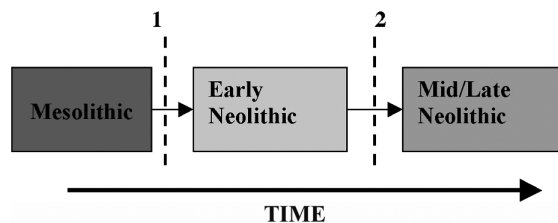


Fig. 9. A model of autochthonous transition across Europe.

Region	Description
1 Anatolia and the Levant	Consisting of modern-day Turkey, Syria, Lebanon, and Israel.
2 The Alpine region	Consisting of present-day Austria and Switzerland, and the Alpine regions of Italy and France.
3 Northern Europe	Consisting of all specimens between longitude 6°E and 26°E, and north of latitude 51°N. It includes the area of present-day northern Belgium and Holland, Northern Germany, Poland, Scandinavia, and the Baltic states.
4 Central Europe	Consisting of Slovakia and the Czech Republic, south and central Germany up to latitude 51°N, and mostly falling between 48°N and 51°N, and east of longitude 6°E.
5 South East Europe	Including mainland Greece and the Greek Islands, Bulgaria, Romania, Serbia, Macedonia, Bosnia, Croatia and Hungary.
6 Mediterranean Europe	Including the Adriatic coastal region of Albania, Bosnia and Croatia, all of Italy (with the exception of the Alpine region), Corsica, Sardinia, and Mediterranean France.
7 Atlantic Europe	Including Great Britain, all parts of France and Belgium west of longitude 6°E and north of latitude 44°N, Majorca, Spain and Portugal.
8 Dniepr Region,	Including the Mesolithic and Neolithic cultures of southern Ukraine.

Tab. 1. Description of the regions analysed.

Model 2 – Incoming farmers with differential degrees of admixture

Model 2a – Differential admixture across space

This model is in congruence with the ‘demic diffusion’ model. The underlying assumption is that the Neolithic farmers spread across the continent and ‘absorbed’ differential amounts of genes from indigenous Mesolithic populations (Fig. 10). Note that this model does not differentiate between scenarios which assume varying degrees of demic input from

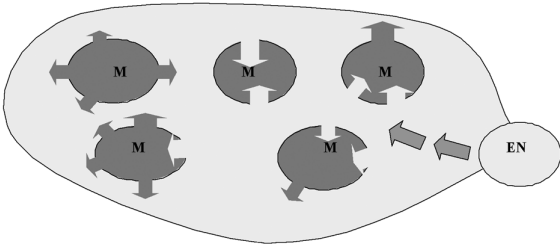
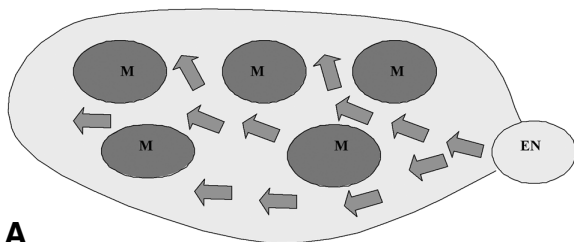


Fig. 10. A model that assumes a process of neolithisation with incoming farmers (EN) with differential degrees of admixture with local Mesolithic populations across space.

the Mesolithic populations. Thus, the degree of admixture may have been weak or extensive. Nevertheless, the underlying assumption is that the spreading farmers absorbed Mesolithic populations along their path and not a scenario in which the greatest contribution to the Neolithic gene pool came from Mesolithic populations.

Model 2b – Differential admixture across time – “Delayed Admixture”

The second variant of model 2 is one which adds the element of delayed admixture. The underlying assumption is that the Early Neolithic farmers did not admix with the Mesolithic hunters, but rather that an admixture occurred later on during the Middle/Late Neolithic period (Fig. 4). During the Early Neolithic period, the farmers would have undergone a process of ‘consolidation’, during which they expanded across the continent and intensified and diversi-



A

Fig. 11. A model that assumes a process of neolithisation with incoming farmers (EN) with differential degrees of admixture with local Mesolithic populations across time. **A:** 8000–6000 BP (Early Neolithic). **B:** 6000–4000 BP (Middle/Late Neolithic).

fied their lifestyle. Subsequently, as the settlement pattern became denser and population density increased, mating networks and acculturation between Neolithic and Mesolithic populations became more prevalent. Consequently the genetic contribution of Mesolithic groups to the Middle/Late Neolithic populations would have been significant.

Model 3 – Complete replacement without admixture

This model assumes a demic diffusion process without any admixture. In figure 12 the Mesolithic populations are represented as moving northwards. Another possibility is their extinction without any genetic contribution. Consequently, all Early Neolithic populations are regarded as being directly affiliated with the Levantine and/or Anatolian Early Neolithic

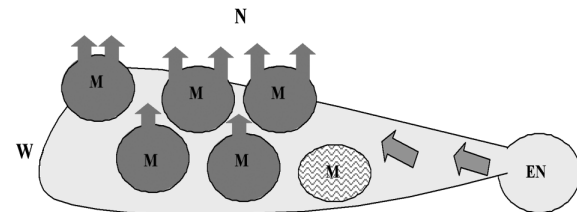
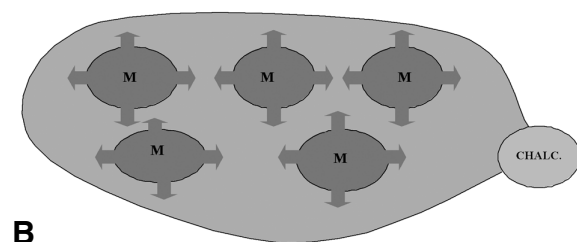


Fig. 12. A model of complete replacement, with some extinction and dispersion of Mesolithic populations northwards. Hatched lines represent extinction.

populations and share no affinities with any of the European Mesolithic populations. Changes in the genetic composition of the dispersing populations due to stochastic effects (series of founder effects, isolation, etc.) are ruled out from this model as it assumes sufficient gene flow along the dispersion path.

Model 4 – Admixture as a function of geographic region and distance from the source population

This model is a variant of model 2a (Fig. 13). However, ‘differential admixture’ is assessed as a function of the geographic region under examination and its



B

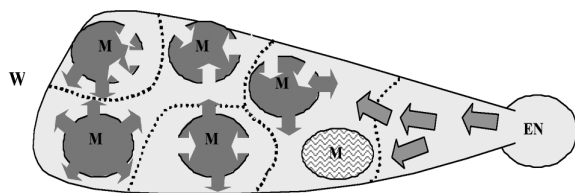


Fig. 13. Differential contribution of Mesolithic populations to incoming farmers across space and time. Contribution varies by region and with corresponding admixture levels varying in a scale between no contribution to intensive admixture.

distance from the Near East/Anatolia. The model therefore places emphasis on examining the 'Neolithisation' process according to regions rather than as a pan-European phenomenon. Therefore, any theory which proposes a complex geographically based scenario with a differential admixture due to the impact of geographic/spatial factors is congruent with this model.

MATERIALS

The skeletal material consisted of the following:

- ❶ Data collected during fieldwork. These data comprised of:
 - a. Cranial measurements.
 - b. Mandible plus lower dentition measurements.
- ❷ Data collected from the literature and from the ADAMS database, Department of Anthropology, University of Geneva, Switzerland.

Description of the data is provided in Table 2 (a = Personal data, b = ADAMS, c = published data).

METHODS

All measurements were taken from the skull, mandible and teeth of each individual. In the case of the majority of the analyses performed, only a subset of the total set of variables was utilised. The subset of measurements utilised in the following analyses is described in Table 3.

The sex of specimens studied by the author was evaluated by using three systems.

- ❶ A general assessment of sex based on the criteria outlined in the book *Standards for Data Collection from Human Skeletal Remains*, by J. E. Buikstra and D. H. Ubelaker (1994).
- ❷ An assessment of sex by means of a plasticine cast of the endocranial part of the external audi-

tory meatus (Joachim Wahl, *Landesdenkmalamt Baden-Württemberg, pers comm.*).

- ❸ An assessment of sex following the method developed by Graw and co-authors (1999).

Age estimation was based on the age assessment in the available registry books at the given institution, as well as an assessment of age based on the skull carried out by the author. The two main criteria for the assessment of age were the degree of cranial suture closure (specifically basi-occipital-sphenoid synchondrosis, as described in *Acsádi and Nemeskéri 1970*), taken together with the presence of fully erupted second molars. This 'system' is in many respects inaccurate (see discussion in *Schwartz 1995, 206–211* regarding age assessment techniques using the skull). However, it is adequate to exclude the majority of sub-adult specimens. Thus, the overwhelming majority of skulls being measured were those of adult specimens.

STATISTICAL METHODS

The following is a brief description of the statistical methods utilised in the following sections.

Univariate methods

a. Kruskal-Wallis test

The Kruskal-Wallis ANOVA by ranks test assumes that the variable under consideration is continuous and that it was measured on at least an ordinal (rank order) scale. It tests the null hypothesis that the different samples in the comparison were drawn from the same distribution or from distributions with the same median. Thus, the interpretation of the Kruskal-Wallis test is basically identical to that of parametric one-way ANOVA, except that it is based on ranks rather than means. This procedure is more robust (albeit less sensitive) as it uses a rank order scale, and therefore can be applied to small sample sizes.

b. Analysis of boxplots

The analysis of boxplots is a straightforward procedure. The common boxplots (in SPSS) compare ranks rather than means and thus depict differences in group medians. It also allows the comparison of interquartile ranges per variable.

Bivariate methods

Following the univariate procedures, part of the data was scrutinised using bivariate analyses. In each of

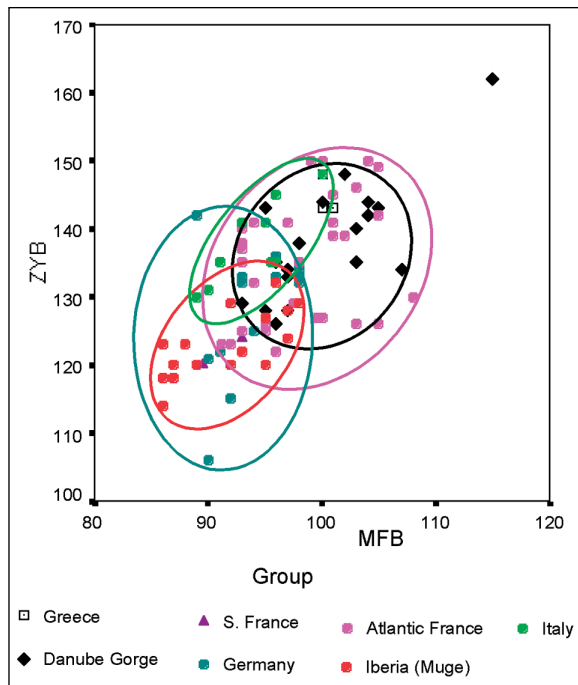


Fig. 14. Minimum Frontal Breadth vs. Zygomatic Breadth for individual Mesolithic specimens, by group.

the bivariate analyses, the individual data for a pair of variables (measurements) were plotted in a scatterplot. Using these scatterplots, the position of single finds and the variability of groups can be visually assessed. The simplicity of the scatterplot procedure is that it does not amplify between-group variability or distort the output.

Multivariate methods

a. Discriminant analysis

This statistical procedure is in fact a set of closely related procedures under one broad term (Klecka 1980). The procedure is applied when there exist two or more samples from potentially different populations and the researcher wishes to distinguish among them. Discriminant function analysis has two main applications:

- ① Interpretation of the ways in which the groups differ from each other. Is one able to discriminate between the groups on the basis of certain characteristics? How well do the groups discriminate, and which characteristics are the most powerful discriminators (Klecka 1980).
- ② Classification: to predict group membership from a set of predictors, the derived equations (canonical functions) combine the groups' characteristics in a way that will allow one to identify the group to which each case most closely approximates (in terms of the relation of the individual

case values for a set of traits and the average value of those traits for each of the groups). The case under examination may be of either a known or an unknown group (Tabachnick and Fidell 1996), thus allowing both the comparison of the accuracy with which certain traits allow identifying the group of origin of known cases, and the potential classification to known groups of ungrouped cases.

b. Principal Components Analysis

Principal components analysis (PCA) is a powerful exploratory technique in which a large number of variables are reduced to a smaller number of factors (Tabachnick and Fidell 1996). The multivariate technique of principal components analysis is usually applied for the purpose of data reduction and de-correlation of the variables. However, in this work, principal components analysis is mainly applied as an exploratory tool in the search for underlying patterns/structures of relationships between discrimination and association of past populations and corresponding specific morphological features.

c. Squared Mahalanobis Distances

The generalised distance, D_2 , developed by Mahalanobis, provides an effective measure for estimating group differences between biological populations. The Mahalanobis distance statistic is often applied in the analysis of prehistoric populations (Van Vark

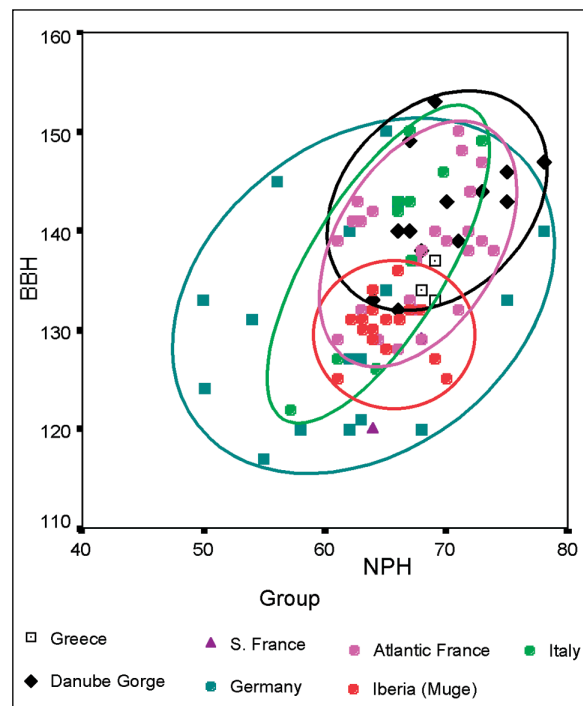


Fig. 15. Nasion-Prosthion Height vs. Begma Height for individual Mesolithic specimens, by group.

and Schaafsma 1992; Howells 1973; 1989; Keita 1990; 1992). It is regarded by many anthropologists and biologists as being the standard and most effective measure of distance between two or more populations when the observed data are quantitative (Bedrick *et al.* 2000). It has been used by various researchers in the study of affinities within and between prehistoric populations (see for example, Bräuer & Rimbach 1990; Van Vark *et al.* 1992). The Mahalanobis distance is an effective measure when variables are correlated, and it includes both variances and correlations (Campbell 1984). According to Van Vark and Schaafsma (1992), Mahalanobis distances calculated from skull measurements can be used in order to trace historical events such as population influx, admixture, and drift. Thus, while morphometric similarities among groups/individuals are not the same as genetic relatedness, there exists a significant correlation between the two. It follows that Mahalanobis distances between samples of ancient populations are to a certain extent genetically based, and their interpretation in terms of between-population genetically based affinities is valid (Van Vark and Schaafsma 1992).

PART 1 – ASSESSING POPULATION AFFINITIES BY PERIOD

Affinities between the Mesolithic populations of Europe

The bivariate graphs investigate the relationship among the European Mesolithic groups. The question in mind is whether one can detect any affinities/patterns between groups.

The bivariate graph (Fig. 14) indicates that, with the exception of one specimen, the Danube Gorge material falls within the range of variation of the French and the Italian Mesolithic. The Iberian and French/Danube/Italian samples have a relatively small overlap (the largest Iberian with the smallest French/Danube/Italian), while the German remains also show comparatively small values of min frontal breadth. The under-representation of individuals from southern France and Greece does not permit the drawing of inferences regarding the morphological variability and association of these groups.

The pattern observed in the scatterplot on Figure 15 is a much greater overlap among all groups, with the German variation encompassing almost all other variation. Individuals that belong to the Danube

Gorge group are relatively clustered as is the case for Muge and Greece. In contrast, we see that the specimens of the German Mesolithic and Italian Mesolithic groups are more scattered.

The scatterplots suggest some regionally-based discrimination between the European Mesolithic groups, with a considerable element of intra-sample variability. We therefore do not see a clear-cut morphological differentiation. Scatterplots do not apply distance algorithms that intend to maximise among-group differences while minimising the effects of intra-sample variance (such as the squared Mahalanobis distance). One, therefore, may conclude at this stage that the Mesolithic groups of Europe are morphologically diverse. No visible patterns of affinities were observed.

Affinities between the Early Neolithic populations of Anatolia, the Levant, south-east and central Europe.

In this section we examine morphological relationships among the Early Neolithic populations of Anatolia, Levant and south-east and central Europe. The main issue that we opt to tackle may be phrased as follows.

What is the relationship among the Early Neolithic groups from the Levant, Anatolia and the Early Neolithic groups from the various parts of Europe?

We are now looking for more definite answers regarding the population relationships during the period of the appearance of the first farmers in Anatolia and the Levant, and subsequently in south-east and central Europe. We expect to detect:

- ❶ Some similarities between many of the Early Neolithic European groups.
- ❷ Some of the Early Neolithic European groups are morphologically similar to one or more of the Levantine, and/or Anatolian groups (in the case of Demic Diffusion).

Univariate analysis

Table 4 shows the groups (the Natufian sample and Early Neolithic) and corresponding codes used in the analyses.

A Kruskal-Wallis Anova rank analysis was carried out in order to assess whether significant differences between the groups for the following set of variables exist: GOL, XPB, ZYB, NPH, NLH, NLB, and OBH. This non-parametric method is preferable over

Lat	Long	Location	N	Date	Arch Period	Zone	Database	Collection/Reference
35.87	38.4	Abu Hureyra	5	10 790	PPNB	1	a	1
32.76	35.36	Ain-Mallaha (Eynan)	3	11 547	Epipaleolithic	1	a	1
30.23	35.53	Basta	3		PPNB	1	a	3
34.12	35.65	Bayblos	2		Chalcolithic	1	c	<i>Kurth 1973</i>
37.1	32.13	Çatal Höyük	49	7499	Neolithic	1	c	<i>Ferembach 1981</i>
38.23	39.65	Çayönü	8	9360	PPNB	1	a	1
31.42	35.06	Erq-El-Ahmar	2	11 000	Epipaleolithic	1	a	1
32.67	35	Fallah- Nahal Oren	9	10 046	Epipaleolithic	1	a	1
32.9	35.22	Hayonim	4	12 010	Epipaleolithic	1	a	1
32.00	35.00	Jericho	9		Chalcolithic	1	c	<i>Kurth 1973</i>
32.8	35.33	Pkein	29		Chalcolithic	1	a	1
48.47	20.52	Aggtelek	1		Neolithic	5	a	7
47.30	19.03	Agostonpuszta	1		Eneolithic	5	a	7
47.00	17.00	Ajaki Kokornaki	2		Eneolithic	5	a	7
47.18	19.12	Alsónémedi	5	4500	Badeni	5	a	7
41.39	21.58	Anza	3		EGEAN	5	b	ADAMS
47.32	19	Aszód-Papífüldök	6	5669	Neolithic	5	a	7
37.99	23.73	Athens	1		Neolithic	5	c	<i>Boev 1973</i>
46.83	17.98	Balatonendried	1		Neolithic	5	a	7
46.7	21.26	Békés-Povád	4		Szakálhát	5	a	7
39.60	22.50	B'Koybeleiki	2		Neolithic	5	a	17
48.00	21.00	Bodrogkersztur	1		Eneolithic	5	a	7
47.30	19.03	Budakalász	21		Badeni	5	a	7
47.30	19.08	Budapest	1		Neolithic	5	a	7
47.30	19.06	Budapest-Andor	1		Badeni	5	a	7
44.12	26.46	Cascioarele, Locus 1	1	5598	Neolithic	5	a	5
44.18	28	Cernavoda	21		Hamangia	5	b	ADAMS
46.3	24.12	Cipa	1		Cris	5	b	ADAMS
47.25	18.95	Csepel Sziget	3		Neolithic	5	a	7
46.4	20.31	Csóka	1		Neolithic	5	a	6
46.22	20.25	Desyk-Olajkut	2	6570	Körös	5	a	6
46.12	20.15	Deszk	2		Cris	5	b	ADAMS
43.23	24.95	Deveta kata Pe tera	1		Early Neolithic	5	b	ADAMS
46.94	20.78	Endröd	1	6566	Neolithic	5	a	6
39	22.3	Franchthi Cave	3		Early Mesolithic	5	b	ADAMS
44.35	23.91	Gîrlsti	2		Neolithic	5	a	5
44.08	26.63	Gumelnita	1	5557	Gumelnita	5	a	5
46.48	23.36	Gura Bacului	1	6650	Cris	5	b	ADAMS
46.64	21.32	Gyula	1		Neolithic	5	a	7
37.42	22.18	Hageorgitika	1		Neolithic	5	b	<i>Boev 1973</i>
46.36	20.18	Hódmezővásárhely	1	6450	Körös	5	a	6
46.39	20.39	Hódmezővásárhely	3	6190	Late Neolithic	5	a	6
46.39	20.39	Hódmezővásárhely–B.	1		Körös	5	a	6
46.4	20.31	Hódmezővásárhely–G.	4	6050	Late Neolithic	5	a	6
43.00	27.00	Janka	8	5700	#NAME?	5	b	ADAMS
43	24	Jasa Tepe	1	6600	Karanovo 2	5	b	ADAMS
42.36	25.54	Karanovo	2	6600	Karanovo 1	5	b	ADAMS
42.36	25.24	Kasanlak	1	6500	Karanovo 2	5	b	ADAMS
34.54	33	Khirokitia	21	7350	PPN	5	b	ADAMS
47.5	20.5	Kisköre-Gát	7	5942	Neolithic	5	a	7
47.00	19.50	Kkotac Tanya	2		Eneolithic	5	a	6
46.41	20.31	Kotacpart	7	6450	Körös	5	a	6
46.23	18.21	Lengyel	1		Neolithic	5	a	14
44.3	22.06	Lepenski Vir	16	7300	Mesolithic	5	b	ADAMS
44.33	22.03	LepenskiVir	23		Starcevo	5	b	ADAMS
45.00	18.00	Mogyorós	1		Neolithic	5	a	6
40.65	22.3	Nea Nikomedeia	13	8180	Early Neolithic	5	c	<i>Angel 1973</i>
47.73	18.37	Neszmély	1		Neolithic	5	a	7
46.38	18.57	Paradicsompuszta	1		Lengyel	5	a	7
48.14	20.67	Paszar	1		Eneolithic	5	a	7
47.00	19.30	Puszaistvánháza	3		Eneolithic	5	a	7
43.54	26.00	Rusé	3	5200	Mound Culture	5	b	ADAMS
45.54	25.18	Sf.Gheorghe Bedehaza	1		Cris	5	b	ADAMS
42.4	23.18	Sofia	2		Early Neolithic	5	b	ADAMS
47.06	21.54	Solca	1		Cris	5	b	ADAMS
44.49	20.42	Starcevo	1		Starcevo	5	b	ADAMS
47.47	18.42	Sturovo	5		Zeliezovce	5	b	ADAMS
46.29	20.26	Szegvár-Tüzköves	1	6000	Neolithic	5	a	7
47.67	19.08	Szentendre	1		Neolithic	5	a	7
38.52	23.98	Tharounia	1		E. Neolithic	5	a	17

Lat	Long	Location	N	Date	Arch Period	Zone	Database	Collection/Reference
39.68	21.68	Theopetra	1		E. Neolithic	5	a	17
39.68	21.68	Theopetra	1		Mesolithic	5	a	17
47.17	26.33	Tirpesti	4	6240	Gumelnita	5	a	5
47.87	21.12	Tiszapolgar-Basatanya	8	5060	Eneolithic	5	a	7
47.00	18.00	Tököl	2		Bell Beaker	5	a	7
47.00	16.00	Tordékes Koponya	1		Lengyel	5	a	7
44.23	27	Varasti	43	5360	Gumelnita	5	a	5
46.94	20.23	Vészto-Mágori Halom	7	6200	Körös	5	a	6
46.52	18.26	Villánykövesd	7		Lengyel	5	b	ADAMS
44.48	20.36	Vinca	9		Starcevo	5	b	ADAMS
44.31	22.01	Vlasac	56	7700	Mesolithic	5	b	ADAMS
39.30	22.80	Volos	3		Neolithic	5	a	17
43.48	7.30	Abri de Pendimoun	1.00		Cardial	6	c	Riquet 1973
40.06	-2.48	Alcazar del Rey	3.00		Neolithic	6	a	14
41.12	1.00	Arboli	1.00		Bell Beaker	6	c	Alcobé 1973
38.33	16.12	Arene Candide	1.00		Cardial	6	c	Riquet 1973
38.33	16.12	Arene Candide	3		Early Mesolithic	6	b	ADAMS
42.37	13.37	Arma dell'Aquila	3.00		Cardial	6	c	Riquet 1973
43.06	0.24	Arudy	1.00		Late Mesolithic	6	b	ADAMS
37.9	13.48	Buffa Cave	1		Neolithic	6	b	ADAMS
43.48	7.3	Castellar	1		Cardial	6	b	ADAMS
43.24	5.12	Chateauneuf	2.00		Cardial	6	b	ADAMS
40.06	8.3	Condeixa	60		Cardial	6	b	ADAMS
44.12	8.18	Finale Ligure	3		Cardial	6	b	ADAMS
37.18	-2.06	Gerundia	1.00		Almeria	6	c	Riquet 1973
37.24	-2.54	Gorafe	2.00		Almeria	6	c	Alcobé 1973
43.18	2.54	Grotte de Bize	1.00		Middle Neolithic	6	c	Riquet 1973
43.24	5.12	Grotte Sicard	2.00		Cardial	6	c	Riquet 1973
37.18	-3.12	Gudaix	1.00		Neolithic	6	c	Alcobé 1973
43.12	2.18	Iziar	2.00		Mesolithic	6	b	ADAMS
42	13.3	La Punta	1		Early Mesolithic	6	b	ADAMS
43.24	4.46	Llanes	1.00		Mesolithic	6	b	ADAMS
43.03	13.04	Maddalena di Muccia	1		Cardial	6	b	ADAMS
40.54	17.24	Monopoli	2		Cardial	6	b	ADAMS
39.12	8.42	Muge	24	9000	Late Mesolithic	6	b	ADAMS
39.06	8.42	Mugem arruda	10		Late Mesolithic	6	b	ADAMS
38.37	8.58	Mugem moita	15		Late Mesolithic	6	b	ADAMS
47	7	Niederhergsheim	1		Campaniform	6	c	Riquet 1973
47.12	7	Oberentzheim	1		Campaniform	6	c	Riquet 1973
42	13.3	Ortucchio	3	12 500	Mesolithic	6	b	ADAMS
43.24	6.54	Peillon	1		Mesolithic	6	b	ADAMS
41.38	2.18	Sabassona	1		Cardial	6	c	Alcobé 1973
41.09	1.12	Salamno	3.00		Bell Beaker	6	c	Alcobé 1973
42.54	2.54	Salces	4		Cardial	6	b	ADAMS
38	14.36	San Fratello	4	12 000	Mesolithic	6	b	ADAMS
42	13.3	San Teodoro	4		Mesolithic	6	b	ADAMS
38.24	-9.06	Sesimbra	2.00		Almeria	6	c	Alcobé 1973
39.06	-0.12	Tabernes de Valdigno	2.00		Neolithic	6	c	Alcobé 1973
42.06	3.09	Toroella	1.00		Bell Beaker	6	c	Alcobé 1973
40.24	3.42	Urtiaga	2	11 500	Mesolithic	6	b	ADAMS
41.18	1.09	Vilavert	1.00		Neolithic	6	c	Alcobé 1973

Key to location of collections:

- 1 Department of Anatomy and Anthropology, University of Tel Aviv, Israel.
2. Department of Anthropology. Hacetepe University at Beytepe Campus, Turkey.
3. Göttingen University, Department of Anatomy, Germany.
4. British Museum, London, England.
5. Francis Rainer Institute of Anthropology, Bucharest, Romania.
6. József Attila University, Department of Anthropology.
7. Natural History Museum, Department of Anthropology, Budapest.
8. Jena University, Germany.
11. State Archaeological Institute, Munich, Germany.
12. University of Vilnius, Fac. of Medicine, Dept. Anatomy, Histology & Anthropology.
13. Institute of History, Department of Archaeology, Tallinn, Estonia.
14. Panum Institute, Copenhagen, Denmark.
15. Natural history Museum, Prague., Czech Republic.
17. Department of Animal and Human Physiology, University Athens, Greece.

Table 2. Summary table of data.

Measurement Acronym	Measurement Description	Source	Presence in ADAM
Cranial measurements			
GOL	Maximum cranial length	Howells, 1973	yes
BBH	Basio-bregma height	Howells, 1973	yes
XFB	Maximum frontal breadth	Howells, 1973	yes
XPB	Maximum parietal breadth	Howells, 1973	yes
ZYB	Bizygomatic breadth	Howells, 1973	yes
MFB	Minimum frontal breadth (WFB)	Howells, 1973	yes
NPH	Nasion-prosthion length	Howells, 1973	yes
NLH	Nasion height	Howells, 1973	yes
NLB	Nasion breadth	Howells, 1973	yes
OBH	Orbital Height	Howells, 1973	yes
OBB	Orbital breadth	Howells, 1973	no
Mandibular measurements			
RAMH	Projective height of mandibular ramus	Martin, 1957	yes
GONANG	Gonial Angle	Martin, 1957	yes
MAXL	Projective length of mandible	Martin, 1957	yes
RAMB	Minimum width of ramus	Martin, 1957	yes
GONB	Bigonial breadth	Martin, 1957	no
CONDB	Bocondylar breadth	Martin, 1957	no
ANTH	Symphysis height (id-gn)	Martin, 1957	no
ANTTHIC	Anterior thickness	Martin, 1957	no
Dental measurements			
LCMD	Lower Canine mesiodistal dimension	Hillson, 1996	no
LCBL	Lower Canine buccolingual dimension	Hillson, 1996	no
LP3MD	Lower Third Premolar mesiodistal dimension	Hillson, 1996	no
LP3BL	Lower Third Premolar buccolingual dimension	Hillson, 1996	no
LP4MD	Lower Fourth Premolar mesiodistal dimension	Hillson, 1996	no
LP4BL	Lower Fourth Premolar buccolingual dimension	Hillson, 1996	no
LM1MD	Lower First Molar mesiodistal dimension	Hillson, 1996	no
LM1BL	Lower First Molar buccolingual dimension	Hillson, 1996	no
LM2MD	Lower Second Molar mesiodistal dimension	Hillson, 1996	no
LM2BL	Lower Second Molar buccolingual dimension	Hillson, 1996	no
LM3MD	Lower Third Molar mesiodistal dimension	Hillson, 1996	no
LM3BL	Lower Third Molar buccolingual dimension	Hillson, 1996	no

Table 3 – list of cranial and mandibular variables utilised.

Anova due to the small and uneven sample sizes of the groups. Results are described in Table 5. The analysis by rank indicates that the groups are significantly different at the $p = 0.005$ level.

Figure 16 contains boxplot diagrams of the above groups by variable. The left column comprises boxplots of group medians and inter-quartile ranges, while the right column comprises means and standard deviations and standard error (the boxed area). This arrangement allows one to compare the distribution and variance of scores per measurement, and group and to detect possible ‘distortions’ due to outliers. Group 2 (Çayönü) has the largest variance for GOL, XPB, and NPH, while group 3 (Abu Hureyra) has the largest variance for ZYB, NLH, NLB and OBH. The variance of other groups is much smaller. The Levantine Natufian group has a significantly greater mean for GOL and ZYB. The European Early Neolithic groups (5–8) and Çatal Höyük display similar

means and variances for GOL, XPB, ZYB and NPH. In the case of nasal dimensions (NLH and NLB) and Orbital Height (OBH) some differences between these groups exist, as the Cardial (Impressed) Mediterranean Neolithic group has lower means. There is a significant degree of heterogeneity among the specimens of Southeast Anatolia (Çayönü) and Northeast Levant (Abu Hureyra), which is apparent from the examination of their rank and inter-quartile boxplots (left column), as well as their means and variances.

In sum, the examination of these boxplots indicates that, all in all, the European groups plus Çatal Höyük (groups 4 to 8) show similarities in means and variance, as well as in medians and interquartile ranges for the variables examined. In contrast, the first three groups (Natufian, Çayönü and Abu Hureyra) differ from this group mainly in the dispersion of the 50% range (and variance in the case of the right column), as well as from each other.

PART 2 – ASSESSING THE GEOGRAPHIC AND BIOLOGICAL DISTANCES OF EARLY NEOLITHIC EUROPEANS FROM POTENTIAL SOURCES

Underlying the demic diffusion model is the assumption of a differential admixture between dispersing farmers and local Mesolithic populations, which would explain the observed SE–NW genetic cline. Thus, the hypothesis assumes that the more distant the original farmers from their centre of origin, the more they admixed with local hunters. Ammerman and Cavalli-Sforza (1984) regarded Jericho as the area of origin for the first farmers. This observation is inaccurate. While Jericho is one of the oldest agricultural sites in the region, there exist other contemporaneous populations from the PPNB period in the Levant and Anatolia. These populations display a high degree of heterogeneity, and thus cannot be accepted as a single ancestral population. Moreover, there is a time lag of approximately 2000 years between the first appearance of Neolithic cultures in this region and the appearance of the first Neolithic sites in south-east Europe. There is no reason to assume that the farmers that dispersed to south-east Europe came from Jericho and not from another location/culture. In order to assess the demic diffusion model it is, therefore, necessary to define more accurately a possible region from which the farmers dispersed to Europe. We saw in the previous sections that among the PPNB groups only Çayönü displays some similarities to the early Neolithic European populations. Moreover, in all analyses of Early Neolithic populations, the Çatal Höyük specimens are strikingly similar to the European Early Neolithic groups.

This section examines the relationship of geographic distance from (a) Çatal Höyük, and (b) Çayönü to other European Early Neolithic sites. It does so by estimating the Mahalanobis D² distances between corresponding group centroids in order to assess the following hypothesis:

H1: Assuming that the site of Çatal Höyük represents the center of origins of the first farmers who dispersed to Europe, the further away the specimens/ site are from this centre, the further they are also in morphological distance.

The methodology applied is the analysis of squared Mahalanobis distances between groups using the following set of variables: GOL, XPB, ZYB, MFB, NPH, NLH, NLB, and OBH. Cases with missing data were excluded (no substitution). Group means and codes

Group	Code	N
Levant Mes. – Natufian	1	9
SE Anatolia – Çayönü	2	3
NE Levant – Abu Hureyra	3	3
Central Anatolia – Çatal Höyük	4	11
Greece Neolithic	5	16
Med. E. Neolithic	6	35
SE Europe – E. Neolithic	7	19
Central Europe E. Neolithic	8	27
	Total	123

Tab. 4. Groups and corresponding codes.

are described in Table 6. Geographic distances between groups were calculated using Spheric V. 1.05 software for the calculation of geographic distance between two points on Earth based on their latitude and longitude co-ordinates.

Table 7 outlines the groups and their Mahalanobis and geographic distances from Çatal Höyük. Clearly, the site with the smallest geographic distances from Çatal Höyük is Çayönü. Yet, this site has the largest Mahalanobis distance (7.42) from Çatal Höyük. The second largest squared Mahalanobis distance is of Lepenski Vir, which is 1169 km away. The smallest squared Mahalanobis distance is from Nea Nikomedeia (1.16), which is only 938 km from Çatal Höyük. However, the LBK site of Viesenhäuser Hof, which is 2253 km away from Çatal Höyük, has a squared Mahalanobis distance of 1.89. It therefore appears there is no correlation between geographic distance and morphometric distance in the case of the Early Neolithic groups. The most intriguing observation is, in fact, the LBK sites, which are more than 2000 km away from Çatal Höyük and have small squared Mahalanobis distances from this group.

We see no linear relationship between Mahalanobis and geographic distances from Çatal Höyük (Figure 17). The site of Çayönü is only 681 km from Çatal

	Code	N	Sum of Ranks
Levant Mes. – Natufian	1	9	949
SE Anatolia – Çayönü	2	3	136
NE Levant – Abu Hureyra	3	5	108
Central Anatolia – Çatal Höyük	4	18	1424
Greece Neolithic	5	16	1061.5
Med. E. Neolithic	6	35	2041
SE Europe – E. Neolithic	7	19	1386
Central Europe E. Neolithic	8	30	2074.5
Kruskal-Wallis test: $H(N = 135) = 20.29882$ $p = 0.005$			

Tab. 5. Results of the Kruskal-Wallis analysis by rank (Natufian and Early Neolithic).

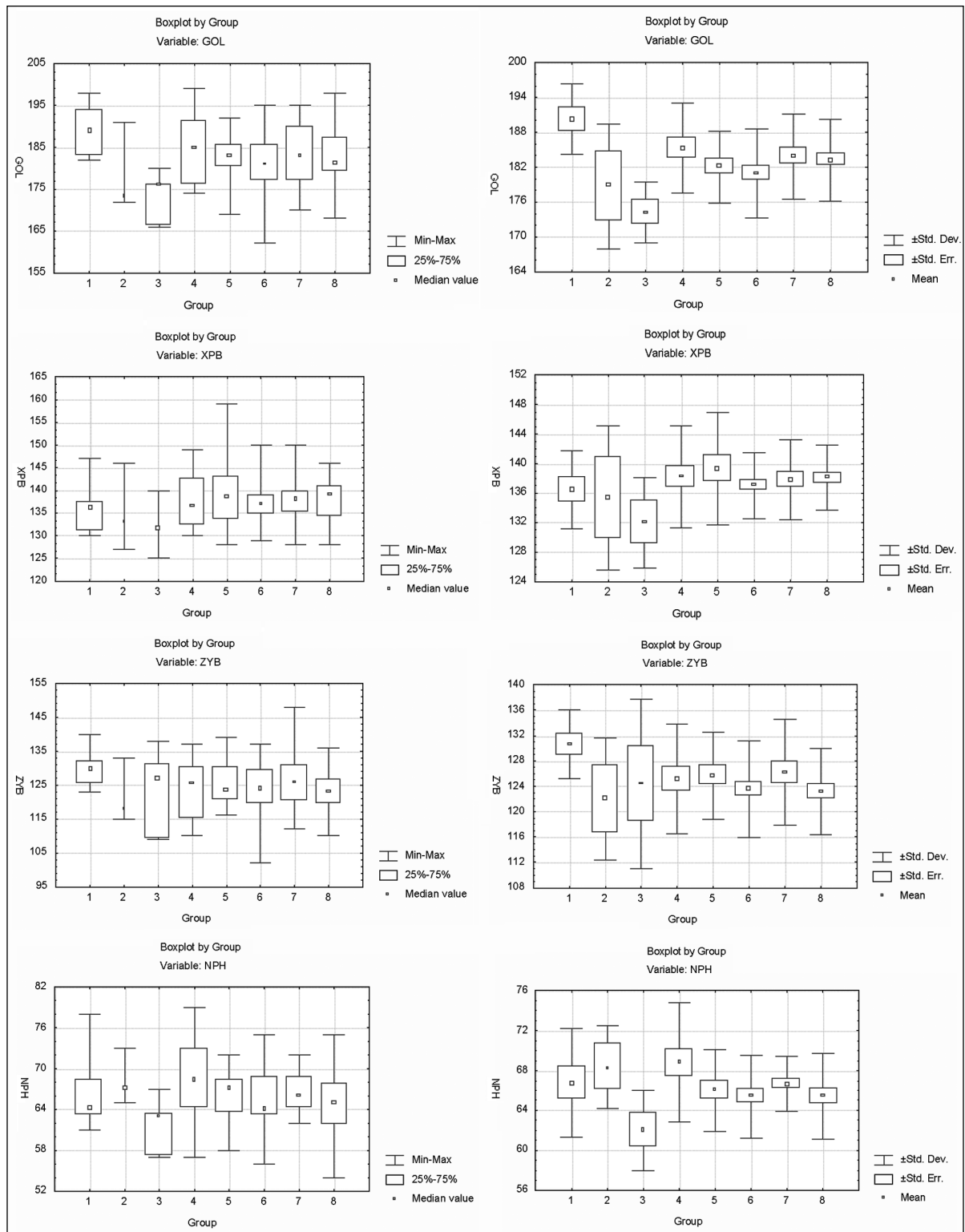


Fig. 16. Boxplots of medians and 25% quartiles (left), means and Standard Error (right) by variables.

Höyük and is geographically the closest. Yet the Mahalanobis D2 distance between Çatal Höyük and Çayönü is 7.42, by far the largest figure. We can therefore reject the above hypothesis. We will then proceed and examine the same hypothesis regarding the site of Çayönü.

H2: Assuming that the site of Çayönü represents the centre of origins of the first farmers who dispersed to Europe, the further away the specimens/site are from this centre, the further they are also in morphological distance.

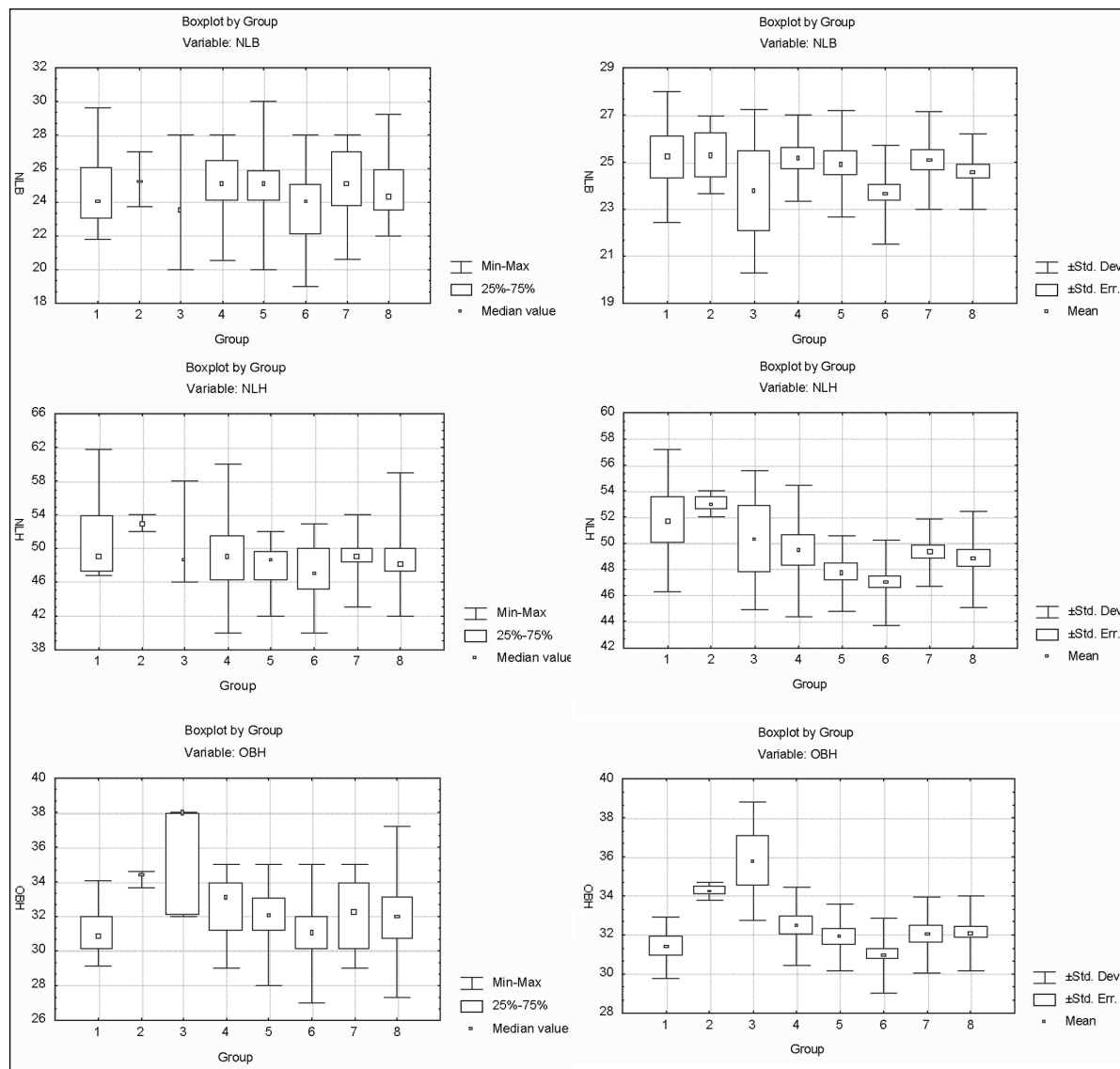


Fig. 16. Cont.

Table 8 presents the morphological (Mahalanobis D2 distances) and geographic distances of European Neolithic specimens to that of Çayönü.

The first observation is that the squared Mahalanobis distances from Çayönü to the other sites are much larger. The largest Mahalanobis distance is to Condeixa (11.5), followed by Lepinski Vir (10.81). We observe no uniformity in scale of distances, as Viesenhäuser Hof, which is 2700 km away from Çayönü, has the smallest squared Mahalanobis distances from this group (3.76). There is clearly no linear correlation between geographic and morphometric distances (Fig. 18).

These results indicate that morphological distances between the European Early Neolithic groups and either Çatal Höyük or Çayönü are not related to geo-

graphic or to chronological distances per se. This finding is relevant, keeping in mind that we are looking only at Early Neolithic groups which could be regarded as representative samples of the first European farmers. We may speculate that the lack of association with geographic distance is due to the rapidity or particular route of the dispersal, thus explaining why a German LBK group may be morphologically more similar to an Early Neolithic Anatolian group than to a Danish Group. Moreover, the distances of the Early Neolithic European sites to Çatal Höyük are much smaller than the distances to Çayönü.

PART 3 – ANALYSIS BY GEOGRAPHIC REGION

The regionally-based approach was applied successfully in the case of the archaeological site analyses

	GOL	XPB	ZYB	MFB	NPH	NLH	NLB	OBH	Valid N
Çayönü	178.67	135.33	122.00	94.33	68.33	53.00	25.30	34.23	3
Çatal Höyük	184.95	138.59	125.45	94.73	67.27	48.36	25.00	31.82	11
Lepinski Vir	186.33	142.67	138.33	99.00	70.67	51.33	26.67	32.00	3
Vészto-Mágori halom	187.00	134.17	123.00	96.17	65.33	48.58	24.78	32.15	6
Nea Nikomedeia	180.82	138.82	123.36	94.45	66.45	46.82	25.18	32.00	11
Schwetzingen	179.80	138.10	123.40	95.66	64.41	46.98	24.74	31.80	10
Sondershausen	187.40	139.20	126.60	98.40	67.52	50.46	23.90	32.82	5
Viesenhäuser Hof	183.67	138.00	122.13	95.14	65.68	49.89	24.70	32.28	12
Condeixa	179.00	137.12	122.69	95.31	65.15	46.12	23.15	30.69	26
All Groups	181.99	137.80	123.89	95.47	66.02	47.95	24.39	31.74	87

Table 6 Group means and codes utilised.

(Pinhasi et al. 2000). On the basis of these analyses, it was possible to develop a model in which different degrees of admixture and interaction were hypothesised for the various regions of Europe (Lahr et al. 2000).

The model is examined using the available skeletal samples. The statistical procedures applied are PCA and discriminant function analyses. The first technique can be used in an exploratory manner, as no dependent variables need to be specified. The lack of grouping criteria makes it possible to perform analytical runs with relatively small numbers of specimens, and thus to narrow the temporal and geographical range. The second technique is mostly used for classification purposes. Nevertheless, its second value is in the interpretation of the findings. Due to word limits, results presented below include findings from the analyses of regions 1, 5 and 6.

Region 1 – Turkey and the Levant

In the Levant, it is common to distinguish between the Epipalaeolithic period – 13 000–10 500 BP, followed by two pre-pottery Neolithic periods – PPNA and PPNB. The PPNA is the period between ca.

Group Name	Mahalanobis distance	Geographic distance (km)
Çayönü	7.42	674.748
Lepinski Vir	4.29	1169.748
Vészto-Mágori halom	1.81	1468.144
Nea Nikomedeia	1.16	938.59
Schwetzingen	1.75	2333.112
Sondershausen	2.00	2310.736
Viesenhäuser Hof	1.89	2253.615
Condeixa	2.45	2095.071

Tab. 7. A comparison of Geographic and Mahalanobis distances from Çatal Höyük to European Neolithic specimens.

10 500–9300 BP. During this time, villages are found on a rather narrow territory, extending from the Damascus Basin in the north to the Trans-Jordan in the south (Yakar 1998). The lithic industry from this period shows discontinuity with the Natufian cultures. In the PPNB period (ca. 9300–7800/7500 BP) villages are on average larger than before, some of them reaching 10–12 hectares (Yakar 1998).

The aims of the analysis are as follows:

- ❶ To check the position of the specimens from the PPNB sites of Çayönü, Basta and Abu Hureyra in relation to the Natufians, and the Chalcolithic site of Pkein.
- ❷ To assess the position of the Mesolithic and Early Neolithic specimens from Greece in relation to Khirokitia.

All analyses on specimens from this region were performed on the data set after performing a Norm NORM V. 2.03 (2000) imputation procedure for missing data. The location of specimens utilised is depicted in Figure 19.

Analysis of cranial dimensions

The following set of cranial variables was selected: GOL, XPB, ZYB, MFB, NPH, NLH, NLB, and OBH. The total sample included a set of 106 specimens. Eigenvalues, means, standard deviations, and factor loadings are given in Table 9.

Figure 20 is a scatterplot of the first two components. The facial height variables NPH and NLH, and cranial length variable (GOL) have high positive loadings on the first component. Thus, PC1 describes crania that are either long with tall faces, or short with short faces. The variables MFB, ZYB, and XPB load highly on the second component, while GOL and NPH have small negative loadings. Therefore, PC2

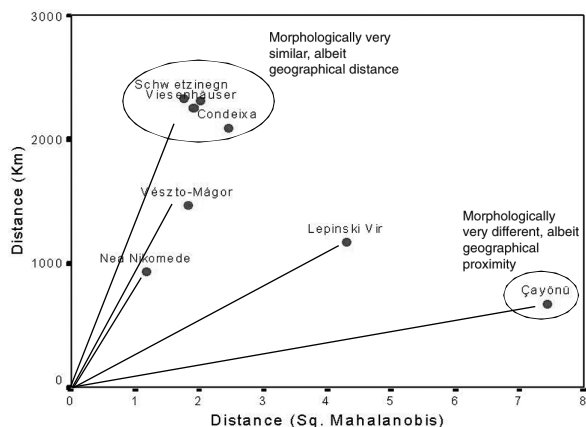


Fig. 17. A scatterplot of Square Mahalanobis distances vs. geographic distances from Çatal Höyük to European Neolithic specimens.

describes crania that are either very broad (in both vault and zygomatic dimensions), and moderately short with short faces, or the opposite shape. Orbital Height (OBH) and MFB have high positive loadings on the third component (especially OBH), while XPB and ZYB load negatively on this component. Thus, PC3 describes crania that are either very broad with short orbits and narrow frontals, or very narrow with tall orbits and broad frontals.

Mandibular variables

The Eigenvalues, means, standard deviations, and factor loadings of the PCA of mandibular dimensions are given in Table 10. The analyses extracted three components, but only the first two have Eigenvalues above 1.

Figure 21 is a scatterplot of the first and second components. The upper part of the scatterplot includes two outliers, one from Çayönü and the other from Abu Hureyra. The Jericho PPNB group have positive PC1 scores and are thus located in the right part of the graph. The largest range of variation is among

Group Name	Mahalanobis distance	Geographic distance (km)
Çatal Höyük	7.42	674.748
Lepinski Vir	10.81	1619.438
Vésztó-Mágori halom	7.85	1856.873
Nea Nikomedeia	7.26	1514.494
Schwetzinegn	6.30	2763.415
Sondershausen	6.66	2689.569
Viesenhäuser Hof	3.76	2700.287
Condeixa	11.50	2702.951

Tab. 8 A comparison of Geographic and Mahalanobis distances from Çayönü.

the Natufians. However, with the inclusion of the two outliers mentioned above, both Abu Hureyra and Çayönü have a large range of variation comparable to that observed for the Natufians. The scatterplot shows poor morphological differentiation between most groups, with the exception of Basta and Abu Hureyra, which are clearly separated. The factor loadings show that all variables load high on the first component, which may thus be interpreted as describing overall mandibular size. Ramus breadth and height have high positive loadings on the second component, while bigonial breadth and condylar breadth load negatively. Therefore, the second component describes two contrasting mandibular shapes – narrow mandibles, with broad and tall rami, and broad mandibles, with narrow and short rami.

Dental dimensions

The third morphological complex selected is one defined by the dimensions of the lower dental arcade (excluding incisors). A principal component analysis was performed on the same set, including 75 specimens. Eigenvalues, means, standard deviations and factor loadings are given in Table 11.

Figure 22 is a scatterplot of the first and second components. The component loadings indicate that all variables load positive on the first component. The mesio-distal dimensions of the two premolars have the largest positive loadings on the second component. The highest negative loadings are of the bucco-lingual dimensions of the two premolars and the canine. However, these loadings are much smaller in scale.

The specimens from Abu Hureyra are scattered in the upper left part of the scatterplot. The specimens from

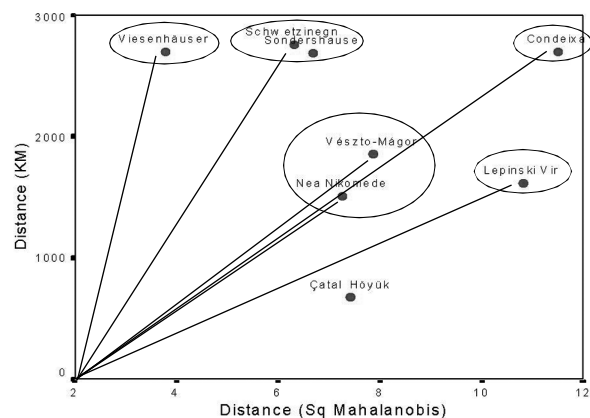


Fig. 18. A scatterplot of Square Mahalanobis distances vs. geographic distances from Çayönü to European Neolithic specimens.

Jericho form a cluster in the middle right part of the graph, next to the specimens from Basta (which, nevertheless, have comparatively smaller dental dimensions), and within the larger clusters of the Natufian and Çayönü groups. Most of the Natufian specimens show comparatively large tooth sizes. In terms of morphology, these results imply that the Abu Hureyra specimens have large mesiodistal premolar dimensions, but within an overall small dentition (negative PC1 scores).

The results of the PCA using cranial dimensions indicate a morphological differentiation between the PPNB specimens from Basta, Abu Hureyra and Khirokitia on the one hand, and the Natufians, Çatal Höyük and Çayönü on the other hand. The second and third analyses displayed no separation between groups, with the exception of the relatively distinct dental dimensions of Abu Hureyra in relation to the other PPNB groups. In all three analyses, the intra-group range of morphological variability of the Natufians overlaps with that of Çayönü, Çatal Höyük, and Jericho PPNB. We may therefore conclude that a considerable amount of intra-group and inter-group morphological variability exists among the PPNB groups.

Discriminant analysis

Following the results obtained from the PCA, we now examine the same data using discriminant analysis. The analysis expands both the temporal and geographic scope, as it includes the Greek Early Neolithic groups and two Levantine Chalcolithic groups. The Levantine Chalcolithic samples represent the populations of the Levant that succeeded the Neolithic in this region. The groups uti-

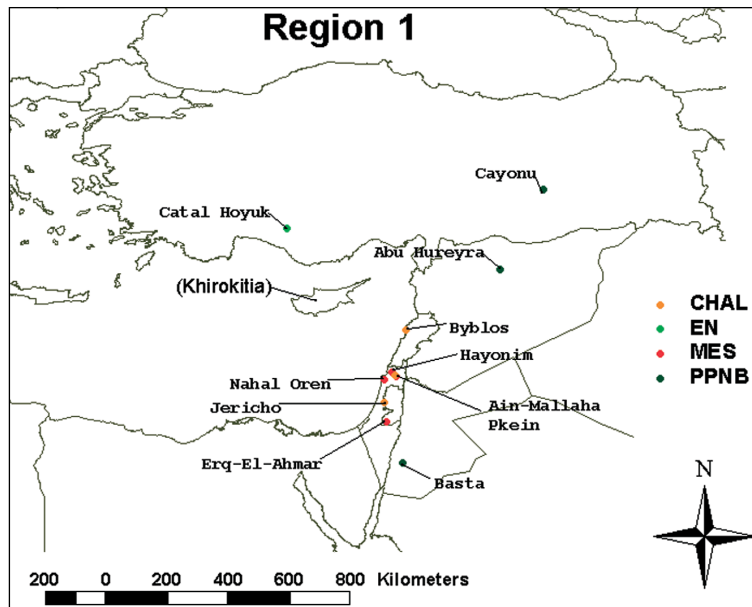


Fig. 19. Location of analysed skeletal samples from Region 1 (by site).

lised in the first analysis are outlined in the Table 12.

The variables included are GOL, XPB, ZYB, MFB, NPH, NLH, NLB, OBB, and OBH. All groups were included in the discrimination process, with the exception of half of group 3 (Çatal Höyük) and group 4 (E. Neolithic - Greece). Half of group 3 was excluded from the configuration of the canonical functions in order to evaluate the performance of the classification in the next step. Group 4 was excluded in order to determine its affinities in the classification phase.

Results are described in Table 13. Two functions, explaining 92.4% of the variance, had Eigenvalues above 1.

Results indicate that the variables mostly correlated with the first function are GOL and MFB, while OBB is highly correlated with the second function. Wilks's lambda shows that residual discrimina-

a. Means and standard deviations		
	Mean	S.D.
GOL	181.29	10.51
XPB	139.89	7.30
ZYB	127.23	8.45
MFB	99.02	12.20
NPH	66.85	5.57
NLH	49.85	4.50
NLB	25.03	2.32
OBH	31.96	2.00

lised in the first analysis are outlined in the Table 12.

b. Eigenvalues and variance				
	Eigenvalue	Total	Cumulative	Cumulative
	%	variance	Eigenvalue	%
1	2.18	27.28	2.18	27.28
2	1.51	18.89	3.69	46.16
3	1.45	18.15	5.14	64.31

Tab. 9a-c. Results of the principal component analysis of cranial dimensions.

c. Factor loadings			
	PC 1	PC 2	PC 3
GOL	0.58	-0.22	-0.15
XPB	-0.07	0.60	-0.58
ZYB	0.43	0.57	-0.49
MFB	-0.07	0.74	0.41
NPH	0.85	-0.21	0.06
NLH	0.84	0.07	0.29
NLB	0.45	0.11	-0.23
OBH	0.13	0.41	0.74

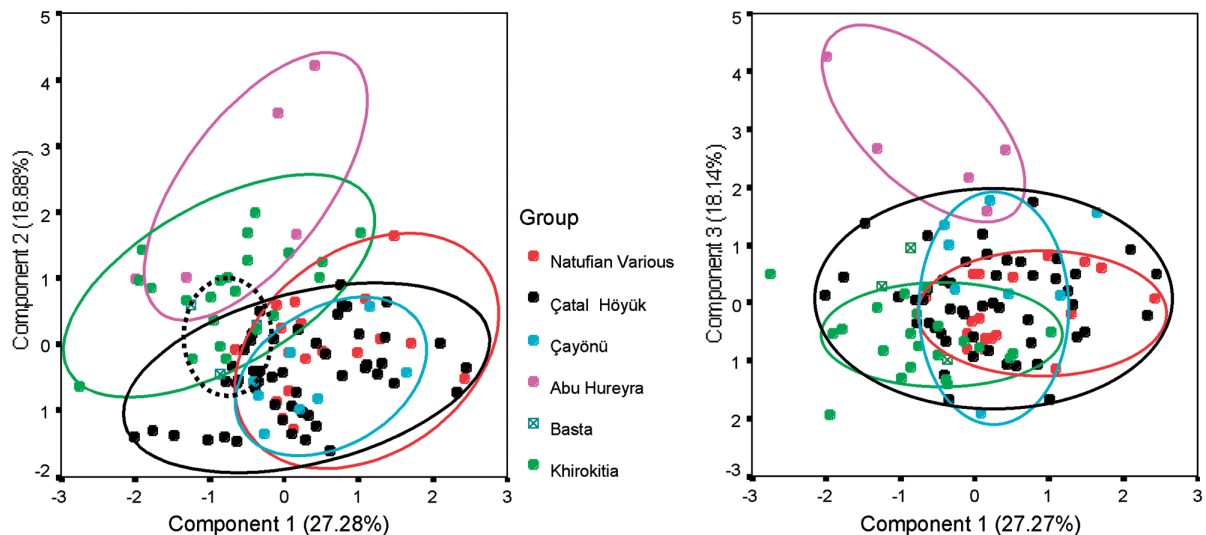


Fig. 20. Scatterplots of the 1st & 2nd and 1st & 3rd components.

tion after the derivation of the first two canonical functions is small (Wilks' Lambda = 0.755). We therefore only examine the scatterplot of the first two functions. Examination of the group centroids and scatterplot of individuals' scores (Fig. 23) indicates that the Natufian specimens (and one Greek Neolithic outlier) are very large, and thus have larger than most Fcn1 scores. Some of the Çatal Höyük specimens, as well as some of the Nea Nikomedeia sample, are particularly small. Jericho-Chalcolithic specimens are the only group with all negative values on Fcn2 (narrow orbits), and thus different from the others (albeit some overlap with remains from Nea Nikomedeia), while those from Çayönü are the only group with only positive values on Fcn2 (homogeneously wide orbits).

Classification

In total, 80.5% of the selected cases were correctly classified (Tab. 14).

Among the interesting aspects of this high classification result, we may observe that:

- ❶ Most of incorrectly classified Natufian remains (18.2%) were classified as PPNB, while a remaining 9.1% as Levantine Chalcolithic.
- ❷ All of the misclassified PPNB (Çayönü and Abu Hureyra) remains (25%) had higher probabilities of belonging to the Natufian group. Together with the observation above, this highlights that the Natufian and PPNB samples clearly have two distinct morphologies, which, nevertheless, overlap in a portion of their ranges.
- ❸ This latter inference can further be extended to the Anatolian Neolithic remains of Çatal Höyük in relation to the PPNB material. The former had 25% misclassified cases, all of which grouped with the PPNB sample.
- ❹ The material from Nea Nikomedeia is more variable, with some cases classified as PPNB, others as Anatolian Neolithic.
- ❺ Finally, the Levantine Chalcolithic remains are very distinct from the rest; 100% of them were correctly classified.

The high percentage of correct classification and the scatterplot of the first and second discriminant func-

a. Means and standard deviations		
	Mean	S.D.
MAXL	102.45	8.08
RAMB	35.19	3.02
RAMH	58.31	5.28
GONB	95.19	7.52
CONDB	115.87	8.21
ANTH	32.97	4.25

b. Eigenvalues and variance				
	Eigenvalue	% of Total variance	Cumulative eigenvalue	Cumulative %
1	2.72	45.40	2.72	45.40
2	1.08	17.93	3.80	63.33
3	0.75	12.42	4.55	75.75

c. Factor loadings		
	Factor 1	Factor 2
MAXL	0.69	0.25
RAMB	0.48	0.66
RAMH	0.62	0.37
GONB	0.65	-0.57
CONDB	0.80	-0.32
ANTH	0.76	-0.12

Tab. 10a-c. Results of the principal component analysis of mandibular dimensions.

tions indicate that discrimination between these groups was easily achieved with the given variable set. The most distinctive group is the Chalcolithic Levantine, which had all its specimens classified correctly and is comparatively homogenous. The second distinctive group is Nea Nikomedeia, with 83.3% of correct classification and a rather homogenous distribution of cases. The Natufians are variable. Although distinctive enough to have the majority of specimens correctly classified, some Natufian specimens approximate the morphology of the PPNB or the Chalcolithic.

Summary

The first two functions of the PCA of the cranial dimensions indicated the existence of three clusters: one of the Natufian, Çayönü, and Çatal Höyük; a second, of Khirokitia, and a third, of Abu Hureyra. The PCAs based on the teeth and mandibular dimensions showed little differentiation between the groups.

The first discriminant analysis indicated a successful discrimination among most groups. In particular, the Natufians and the Jericho Chalcolithic group were separated from the rest with their high positive scores on the first function. The results show a lack of discrimination between Çatal Höyük, Körös, Nea Nikomedeia and Early Neolithic Greece.

a. Means and standard deviations		
	Mean	S.D.
LCMD	6.88	.58
LCBL	7.71	.76
LP3MD	6.85	.51
LP3BL	8.00	.57
LP4MD	6.99	.52
LP4BL	8.28	.55
LM1MD	11.03	.64
LM1BL	10.99	.59
LM2MD	10.65	.66
LM2BL	10.71	.65
LM3MD	10.57	.85
LM3BL	10.23	.80

The PPNB specimens from Basta and Çayönü are in an intermediate position between the Natufians and the Early Neolithic European groups. Çatal Höyük is clearly much closer to the Early

b. Eigenvalues and variance				
	Eigenvalue	% of Total variance	Cumulative eigenvalue	Cumulative %
1	6.22	51.85	6.22	51.85
2	1.54	12.85	7.76	64.70

Tab. 11a-c. Results of the principal component analysis on dental dimensions.

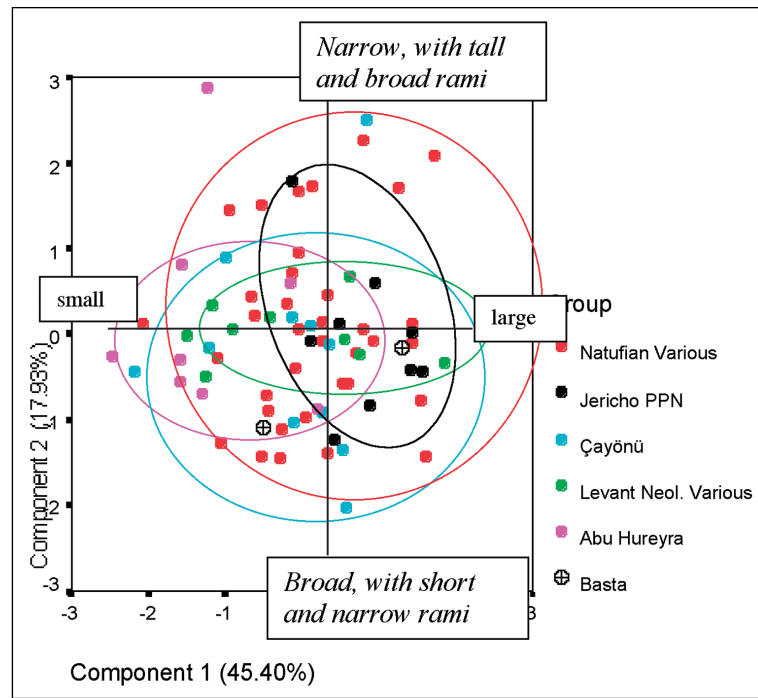


Fig. 21. A scatterplot of the first and second components (mandibular dimensions).

Neolithic specimens from Greece (see the first discriminant function analysis) than to Çayönü. We can, therefore, confidently conclude that Çatal Höyük is much closer to the European Early Neolithic groups than to any of the other Anatolian/Levantine PPNB groups. Once again, we observed extensive heterogeneity within and between Levantine PPN groups and the lack of affinities between these groups and the SE European groups.

The analyses also demonstrate a lack of continuity between the Early Neolithic of the Levant and the Chalcolithic groups. The latter could easily be discriminated from most of the PPN and south-east European Neolithic groups. The position of Khirokitia as an outlier was once again confirmed. If

c. Factor loadings		
	Factor 1	Factor 2
LCMD	0.76	-0.15
LCBL	0.73	-0.33
LP3MD	0.54	0.58
LP3BL	0.71	-0.43
LP4MD	0.46	0.75
LP4BL	0.67	-0.25
LM1MD	0.73	0.29
LM1BL	0.83	-0.16
LM2MD	0.68	0.13
LM2BL	0.89	-0.15
LM3MD	0.69	0.34
LM3BL	0.86	-0.12

this culture belonged to the PPNB cultures of the Levant, then its odd position further strengthens the hypothesis of a large degree of heterogeneity among PPNB cultures.

The PCAs cannot differentiate between the morphology of the Natufians and their PPNB successors, with the exception of the Abu Hureyra group, which is clearly an outlier. However, the first and second discriminant analyses show the discrimination between the Natufians and other populations.

Region 5 – Greece and south-east Europe

The affinities between Early Neolithic specimens from the Levant, Anatolia and south-east Europe were previously addressed. The aim of this section is to go further, and specifically examine the following questions:

- ❶ Is there any evidence for continuity between local Mesolithic and Early Neolithic populations in south-east Europe?
- ❷ What is the relation of the Early Neolithic groups from south-east Europe to the Anatolian Early Neolithic/PPNB populations?
- ❸ What degree of morphological homogeneity can we detect among the Early Neolithic specimens from south-east Europe?

The location of specimens studied is provided in Figure 24.

PCA

The PCA examines the relationship between Early Neolithic specimens from Greece and Çayönü, and

Group	Code
Mesolithic Levant – Natufian	1
PPNB – Abu Hureyra + Çayönü	2
Neolithic Anatolia – Çatal Höyük	3
E. Neolithic – Greece Various	4
EN Greece – Nea Nikomedeia	5
Chalcolithic Levant – Jericho	8

Tab. 12. Groups utilised in the discriminant function analysis.

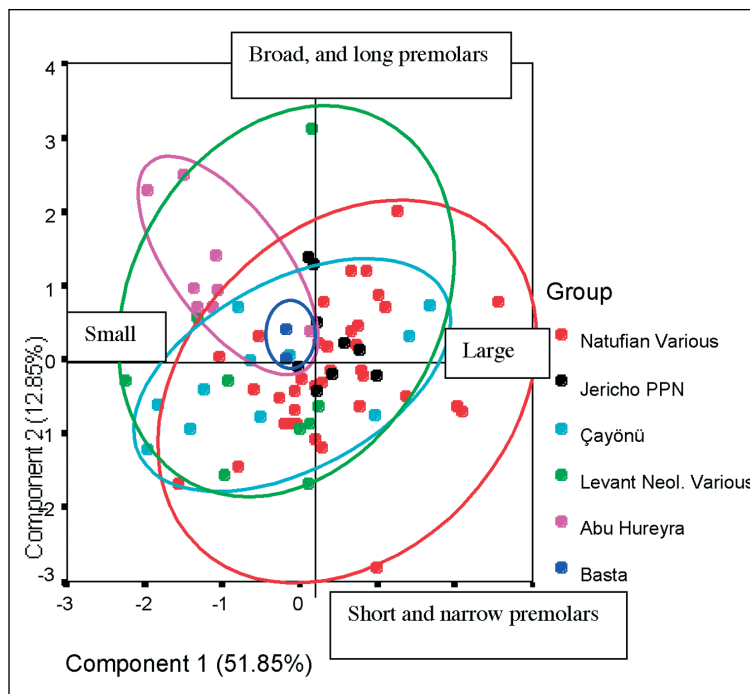


Fig. 22. A scatterplot of the first and second components.

the Mesolithic specimens from Italy and Greece (Mediterranean Mesolithic), and the Danube Gorge (Vlasac and Lepenski Vir Mesolithic). The PCA results are described in Table 15. The selected set of variables is similar to the one utilised for Zone 1. However, the nasal length and breadth dimensions were replaced by cranial height (BBH). This set was chosen in order to minimise the number of excluded cases due to missing data and yet retain the main vault and face variables utilised throughout this work.

Figure 25 depicts the scatterplot of the individual factor scores on the first and second components. All factor loadings, with the exception of OBH (which has a small negative loading on PC1), are positive on the first component. High loadings on the second component are of OBH (0.93) and NPH (0.56). The first component, therefore, differentiates mainly according to the size of the vault. The figure indicates a differentiation between the two Mesolithic groups on the one hand, and the majority of the Neolithic specimens on the other. This is achieved by the first component, with Mesolithic specimens having positive loadings, while most Neolithic specimens have negative loadings. The main exceptions are the two Mesolithic specimens from Ortuccio and some specimens from Çatal Höyük, which have, respectively, small and large sizes. The Mediterranean Mesolithic specimens have low faces and low orbits and thus have negative PC2 scores. The Mesolithic specimens from Franchthi Cave in Greece are not closely asso-

ciated with any of the Nea Nikomedeia specimens. The group of Greek Neolithic specimens from various locations shows much variability, with some specimens such as Athens-Agora, Hageorgitika, and Greek Neolithic remains from Volos positioned next to the Greek Mesolithic cluster. The specimens from the SE Europe Early Neolithic group vary in their factor scores, and thus do not form a distinct cluster.

Discriminant analysis

A discriminant analysis was performed on the same set. The variables selected were GOL, XPB, ZYB, NPH, NLH, NLB and OBH. The groups used and sample sizes are described in Table 16, and the results of the analysis in Table 15.

The first part of the discriminant analysis examines the distribution of specimens from the seven groups

Group	Arch. Period	Code	N
Levant-Natufian	Mesolithic	1	11
Çayönü	PPN	2	4
Çatal Höyük	E. Neolithic	3	8
Greece-Neol.	Neolithic	4	none
Nea Nikomedeia	E. Neolithic	5	12
Jericho	Chalcolithic	8	6
Total			41

Eigenvalues		Wilk's Lambda							
Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation	Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1	2.422	60.7	60.7	.841	1 through 4	.097	78.040	32	.000
2	1.268	31.8	92.4	.748	2 through 4	.333	36.829	21	.018

	Function			
	1	2	3	4
GOL	.540	-.178	.432	-.324
OBB	.056	.770	.301	-.459
MFB	.330	.069	.641	.153
NLH	.267	.174	-.347	.017
NLB	.012	.070	-.157	.071
NPH	-.068	.069	-.119	-.068
OBH	-.160	.052	.033	.603
XPB	.040	.195	.537	.541

Tab. 13a–c. Results of the discriminant function analysis. analysis.

in relation to each other, and the location of group centroids in the discriminant space (Fig. 26). Function 1 has a strong positive correlation with ZYB, GOL and NLH, thus describing long skulls, with broad faces and tall noses. Function 2 describes contrasting shapes defined by long (GOL: +0.418) and narrow (XPB: -0.468) skulls, with moderately tall faces, and the opposite combination.

The main observation is the disassociation of Khirokitia from all other groups analyzed. The Khirokitia centroid and associated specimens are clustered at the lower part of the graph, and are completely separated from all other groups by their high negative values on the second function (describing very short and broad skulls). The second observation is a cluster of Mediterranean Mesolithic specimens at the upper right section, and the proximity of their centroid to the centroids of the Danube Gorge Mesolithic and Danube Gorge Neolithic groups. The centroids of Çatal Höyük (code 4) and Körös (code 6) are very close to each other, while the centroid of Nea Nikomedeia is to the left. It is therefore possible to discern a cline of overall size (defined by facial breadth and height and cranial length) along Function 1, from the smaller groups (Nea Nikomedeia), to Çatal Höyük, to Körös, to the Mediterranean Mesolithic, with the Danube Gorge Mesolithic overlapping the range of variation of the latter and partially Körös. Although there is much overlap in each case, the trend in size is apparent.

CLASSIFICATION

The classification included all groups plus an additional group of early Neolithic specimens for which posterior probabilities were recorded (group 8), but were not selected for the calculation of the discriminant functions. Altogether 61.4% the cases were correctly classified into one of the seven groups. Classification is 100% in the case of Khirokitia (group 1), followed by 90.9% in the case of the Mediterranean Mesolithic (group 3). In the case of the Danube Gorge Mesolithic group, the percent of correct classification is 58.3%, with 25% of the cases being misclassified into the Mediterranean Mesolithic and an

additional 16.7% into Nea Nikomedeia. In the case of the Danube Gorge Neolithic group, classification is poor. Only 33% of the cases were correctly classified, with single cases (i.e., 16.7% each) being assigned into groups 1, 2, 3 and 7. Among the Nea Nikomedeia specimens (group 7), 72.2% are correctly classified, and misclassification occurs in groups 1, 2, 3 and 6. In the case of Çatal Höyük, four specimens are misclassified into the Nea Nikomedeia group, while single cases are misclassified into groups 2, 3, 5 and 6. Among the Körös specimens (group 6) correct classification is 50 %, with 37.5% of the cases misclassified into the Nea Nikomedeia group and a single case into the Mediterranean Mesolithic group. In the case of group 8 (Tab. 19), all cases were assigned to one of the Early Neolithic groups.

What we therefore see is a much higher degree of misclassification occurring among the Early Neolithic groups. The Danube Gorge Mesolithic and Neolithic groups have a relatively high number of cases being misclassified. These results show that discrimination between Khirokitia, the Mediterranean Mesolithic and the Early Neolithic groups is clear. However, discrimination between the Danube Gorge Mesolithic and other groups is not clearly achieved.

Summary

It is now possible to address the three questions posed in the introductory part of this section.

		Predicted Group Membership						Total
		Code	1	2	3	5	8	
Count	1	8	2	0	0	1	11	
	2		1	3	0	0	4	
	3		0	2	6	0	8	
	5		0	1	1	10	12	
	8		0	0	0	0	6	
	%	1	72.7	18.2	.0	.0	9.1	100.0
	2	25.0	75.0	.0	.0	.0	100.0	
	3	.0	25.0	75.0	.0	.0	100.0	
	5	.0	8.3	8.3	83.3	.0	100.0	
	8	.0	.0	.0	.0	100.0	100.0	

Tab. 14. Classification results.

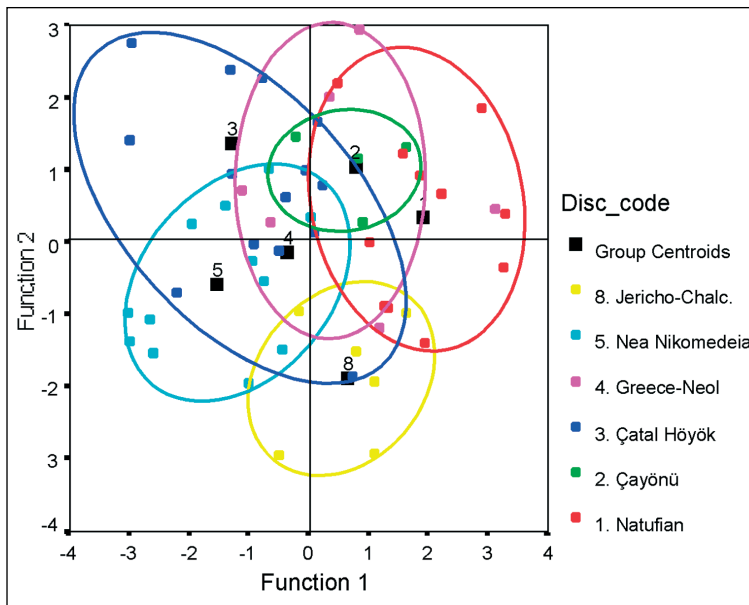


Fig. 23. A scatterplot of the first two canonical fun.

Is there any evidence for continuity between local Mesolithic and Early Neolithic populations in south-east Europe?

There is some evidence for Mesolithic/Early Neolithic continuity only in the case of the Danube Gorge. Only about 50% of the cases of the Danube Gorge Early Neolithic groups were classified into another Early Neolithic European group or to Çatal Höyük. The other 50% were assigned to the two Mesolithic groups and to Khirokitia. In the case of Çatal Höyük, only 20% of the cases were assigned to a Mesolithic group. With Körös, only 10% (a single case) were assigned to a Mesolithic group. In the case of Nea Nikomedeia, about 30% of the cases were assigned to Khirokitia, or to one of the two Mesolithic groups.

What is the relation of the Early Neolithic groups from south-east Europe to the Anatolian Early Neolithic/PPNB populations?

The Khirokitia group stands as a population distinct from other PPNB, Mesolithic and Early Neolithic populations. In the case of Çatal Höyük, about 50% of the specimens were classified into another Early Neolithic European group. However, none of the Early Neolithic European specimens was misclassified to the Çatal Höyük group. The position of the Çatal Höyük centroid is next to the Körös centroid, and in proximity to the

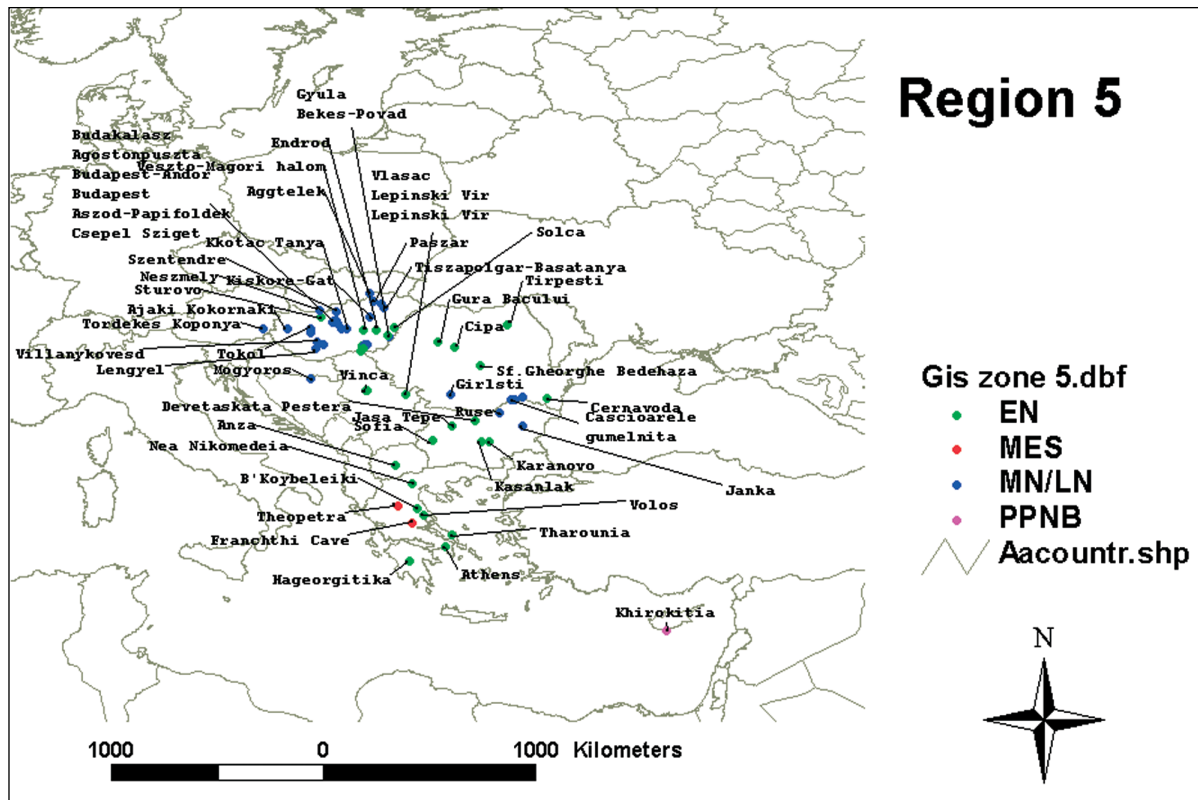


Fig. 24. Location of analysed skeletal samples from Region 5 (by site).

centroids of Nea Nikomedeia (on the left) and the Danube Gorge groups (on the right). We may therefore conclude that this group is much more similar to the Early Neolithic European populations than to any PPNB or Mesolithic groups.

What degree of morphological homogeneity can we detect among the Early Neolithic specimens from south-east Europe?

The above set of analyses was not set to particularly assess homogeneity, but rather population affinities and distances. However, the PCA gives us some idea about the range of intra-group variability. We see in Figure 22 that the Early Neolithic specimens are scattered and not clustered together as in the case of the Mediterranean Mesolithic. Nevertheless, given the existing variability of the Early Neolithic groups, most cases were still distant from the Mesolithic groups (with the exception of the Danube Gorge). This observation suggests that the apparent heterogeneity among the Early Neolithic groups is not due to their admixture with local Mesolithic populations, but rather due to other demographic, historical reasons. In addition, as this range of variability is not estimated, it is possible that it still complies with an expected range of variation in an average biological population.

Region 6 – The Mediterranean regions of France and Italy

The Mesolithic/Neolithic transition in the western Mediterranean region was a complex and diverse process (see *Pluciennik 1997*). Part of this complexity is due to the fact that this region extends over a very large area of ecologically diverse zones. The review also pointed out to a ‘delayed’ Neolithic occupation in most of the western Mediterranean region. The majority of secure dates are from the early part of the 7th millennium BP. This implies a gap of at least 1000 years between the Early Neolithic in the Balkans and northern Greece and the western Mediterranean. In addition, the review from the various localities indicated a hiatus of more than 500 radiocarbon years between the Mesolithic and Early Neolithic occupation layers at various sites.

The questions to be addressed in this section are as follows:

- ❶ Regarding the Mesolithic/Neolithic transition, is there evidence for Mesolithic-Neolithic morphological affinities? We know that the ‘Impressed Neolithic’ pottery culture extended all across this region.
- ❷ Do the ‘Impressed Neolithic’ specimens share morphological similarities with the Anatolian speci-

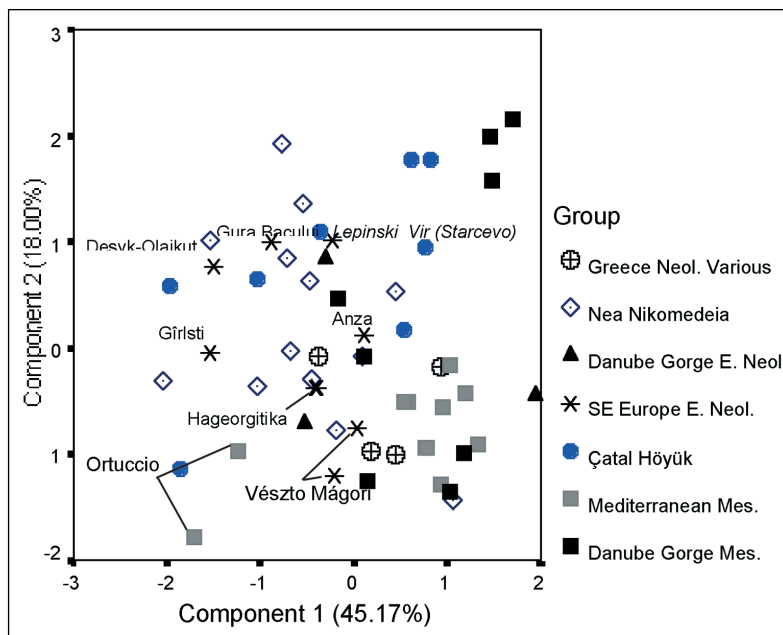


Fig. 25. A Scatterplot of the first two components.

mens from Çatal Höyük and some of the south-east European specimens?

- ③ Does the morphological analysis of western Mediterranean Early Neolithic groups support the theory of a gradual logistic dispersal, or rather suggest a more rapid movement of farmers?

The location of specimens studied is depicted in Figure 27.

PCA

Analysis 1

Table 20 depicts the groups selected. The Impressed Neolithic is represented by two groups, one containing specimens from various sites (group 2) and the second containing specimens from the site of Condeixa in Sardinia (group 4). The Nea Nikomedeia is selected, as this site securely belongs to an early Neolithic occupation (group 5). The SE Europe group

(group 7) contains various specimens from the following sites: Anza, Cipa, Deszk, Gura Bacalui, Devetačkata Peštera, Endröd, Hódmezövásárhely-Bodzáspart, Hódmezövásárhely-Kovács J. Tanya, Jása Tepe, Karanovo, Kasalnak, Kotacpart, SF. Gheorge Bedehaza, Sofia, Solca, Sturovo, and Vészto-Mágori. These are all Early Neolithic sites in the Balkans and Southern Hungary. The Mediterranean Mesolithic group includes specimens from Franchthi Cave, Arene Candide, Ortuccio, La Punta, San Fratello and San Teodoro, and several other Mesolithic sites.

The first analysis was performed on 72 specimens from the above set using the following variable set: GOL, XPB, MFB, BBH, NPH, NLB, NLH, and OBH. The results of the analysis are described in Table 21. Figure 28 displays the heterogeneity of the analysed groups. No separation is achieved between the Mesolithic and Neolithic groups. Positive PC2 scores are associated with high orbits, low vault, and high and narrow noses. The two Mesolithic specimens from Arene Candide (Fig. 18) belong to this type. Negative PC2 scores are associated with low orbits, wide and low noses and high vaults. The two SE Early Neolithic specimens from Devetačkata Peštera and Lengyel belong to this type.

Analysis 2

The second PCA was performed on averaged data. The groups were selected so that each one represents a single site (Tab. 22).

Results are provided in Table 23. Twenty-two groups were included in the analysis. The variables selected were GOL, XPB, MFB, ZYB, NPH, NLH, NLB, and

a. Descriptive statistics		
	Mean	S.D.
GOL	185.11	7.67
BBH	136.59	6.39
XPB	138.85	6.04
NPH	67.04	4.45
OBH	32.02	2.01
ZYB	128.59	9.31
MFB	95.67	4.35

b. Eigenvalues and variance				
	Eigenvalue	% of Total variance	Cumulative eigenvalue	Cumulative %
1	3.16	45.17	3.16	45.17
2	1.26	18.00	4.42	63.17
3	0.94	13.37	5.36	76.54

c. Factor loadings		
	PC1	PC2
GOL	0.78	0.02
BBH	0.78	-0.05
XPB	0.63	0.11
NPH	0.66	0.56
OBH	-0.18	0.93
ZYB	0.83	-0.25
MFB	0.63	-0.07

Tab. 15a-c. Results of the principal component analysis.

OBH. Eigenvalues and cumulative variance by factor are almost identical in magnitude to those obtained in the case of the above factor analysis. The factor loadings indicate that all variables, with the exception of NLB, load highly on the first factor. The highest positive loading on the second factor is of NLB (.940). The highest negative loading is of ZYB (-.40). The highest positive loadings on the third component are of MFB (.70) and XPB (.50), and the highest negative loadings are of OBH (-.426), and GOL (-.385). We can therefore deduce that the first component accounts for general size, while the second is positively correlated with nasal breadth and minimum frontal breadth, and negatively correlated with zygomatic breadth. The third component is for the most part a reflection of variations in frontal and parietal breadth. The Mediterranean Mesolithic specimens from San Teodoro, San Fratello, Franchthi and Arene Candide are located in the fourth quadrant of the graph and thus have generally large dimensions with narrow noses and wide zygomatics. The specimens from Ortuccio, Condeixa and the two Muge sites have generally small dimensions, but share with the above groups the morphological fea-

tures of narrow noses and wide zygomatics. The two Cardial Neolithic groups of A. Dell'Aquila and Finale Ligura and the specimens from Tirpești, have average cranial dimensions, but particularly wide noses and narrow zygomatics.

Figure 29 illustrates the positions of the groups in the two dimensional space of the first two components. Great variability is evident in the distribution of Impressed Ware Neolithic specimens. We see two of the sites at the top of the scatterplot, while Grotte Sicard is at the bottom. Variability is mostly along the second axis, and thus mainly reflects variation in nasal breadth among the Impressed Ware groups.

In contrast, the Mediterranean Mesolithic groups are mostly scattered in the bottom right part of the plot, with the exception of the site of Ortuccio, which is positioned at the left part of the plot. The Early Neolithic sites of Vésztó-Mágori and Nea Nikomedeia are clustered next to each other at the top centre part, very close to the sites of Çatal Höyük and Çayönü and in proximity to Tirpești. We see variability in the location of the Late Mesolithic sites, with Vlasac and Hoëdic at the top right (positive factor scores on both components), while the two Muge sites are towards the bottom left (negative factor scores on both components). Khirokitia is positioned in the middle of the scatterplot, and is closer to the Early Mesolithic groups and remote from the Early Neolithic Anatolian groups. The Vinča and Lepenski Vir Neolithic groups are positioned near each other at the centre-right part of the graph, near the Vlasac Mesolithic group. Thus, among the analysed Early Neolithic groups, these two groups are clearly the closest to the Danube Mesolithic and to other Mesolithic groups.

Summary

The above results point to the large heterogeneity among the Impressed Ware Neolithic groups. In the case of the cluster and PCA analyses, Arma Dell'Aquila and Finale Ligure are associated with Tirpești. Grotte Sicard is associated with Mediterranean Mesolithic groups, such as San Fratello and San Teodoro. The scatterplot of the PCA (Fig. 29) indicates that Condeixa is associated with the Muge groups and with Ortuccio, and is thus much closer to the Mesolithic groups than to the Early Neolithic groups. We can therefore deduce that in the case of the Mediterranean Zone, it is not possible to rule out admixture with local Late Mesolithic groups. The lack of a satisfactory sample size and geographic coverage

a. Site names and codes		
Site	Code	n
Khirokitia	1	4
Vlasac Mesolithic	2	12
Franchthi Cave	3	2
Ortuccio	3	2
San Fratello	3	3
San Teodoro	3	2
Theopetra	3	1
Çatal Höyük	4	11
Lepenski Vir Neolithic	5	3
Vlasac Neolithic	5	3
Vésztó-Mágori	6	6
Desyk-Olajkut	6	2
Nea Nikomedeia	7	13
Athens-Agora	7	1
B'Koybea 1	7	1
Athens-Neolithic	7	3
Tirpești*	8	1
Cascioarele*	8	1
Gîrlști*	8	2
Kasanlak*	8	1
Gura Bacului*	8	1

* Cases not included in the DA run, but only in the classification.

Tab. 16. Results of the principal component analysis.

for the Early Neolithic Mediterranean does not allow an in-depth examination of the specific areas of admixture.

The first Impressed Ware Neolithic sites appear along the Adriatic coast, and this culture only reaches the Iberian Peninsula about a millennium later. We may therefore assume a gradual spread of this culture along the Mediterranean coast, and generally along the east-west axis at the southern part of the continent. We cannot, however, based on the above results, detect whether this spread was gradual or rapid.

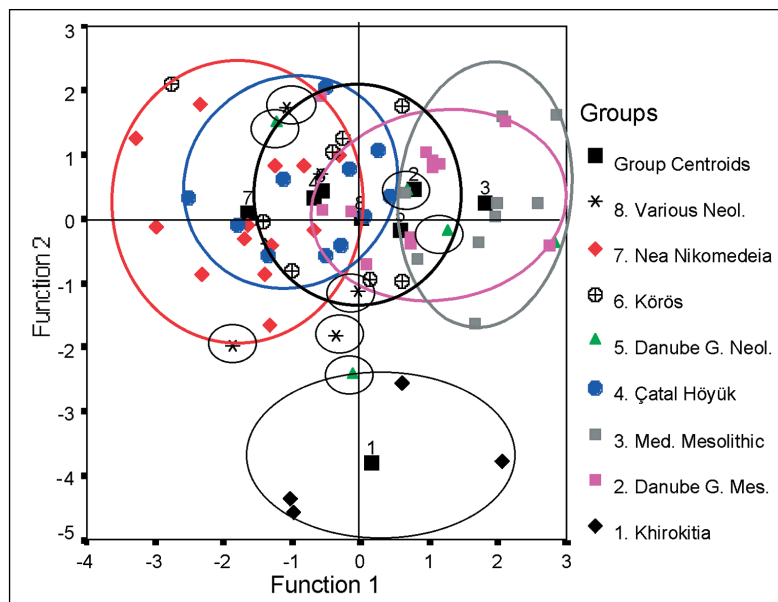


Fig. 26. A scatterplot of the first and second discriminant functions.

The Danube Gorge groups display similarities to each other and suggest local continuity. It is important to distinguish between the Balkans zone, as a whole, and the specific Danube Gorge Groups. While in the Gorge evidence for continuity may be found, the rest of the Balkan populations show clear evidence of affinities to each other, to Nea Nikomedeia, and to Çatal Höyük. These results support the hypothesis of a dispersal of farmers from central Anatolia (represented by Çatal Höyük), to the Greek Mainland and the Balkans, as well as to the southern part of Hungary.

ASSESSING THE RESULTS IN THE CONTEXT OF GENETIC STUDIES

The above discussion suggests that a general spatial analysis of genetic data may suffice to reveal general clinal patterns, but that the association of these patterns with historical events of expansion and migration is ambiguous and problematic. In general, geneticists seem to overlook the complexity of historical processes, and the fact that such processes complicate our understandings of the observed genetic patterns across space. Interpolation, coalescence,

a. Eigenvalues and Wilk's lambda									
Eigenvalues				Wilk's Lambda					
Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation	Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1	.907	43.1	43.1	.690	1 through 6	.201	99.427	42	.000
2	.785	37.3	80.5	.663	2 through 6	.384	59.406	30	.001
3	.239	11.4	91.8	.439	3 through 6	.685	23.497	20	.265

b. Structure matrix		
	Function	
	1	2
ZYB	.733	-.320
GOL	.684	.418
NPH	.246	.267
NLH	.431	-.076
OBH	-.153	.188
XPB	.014	-.468
NLB	-.084	.264

Tab. 17a–b. Results of the discriminant analysis.

and other mathematical models and methods often applied by geneticists tend to smooth out differential densities of genetic markers in specific regions, and steep genetic boundaries in favour of clinal patterns. It has also been pointed out by Barbujani (1995), Barbujani and Bertorelle (2001), and Sokal (1991), that migratory events without admixture, and gradual dispersal with admixture, can result in similar geographic distributions of gene frequencies. As Barbujani and Bertorelle (2001.22) point out: "A cline or gradient, for example, may reflect adaptation to variables environments, or a population

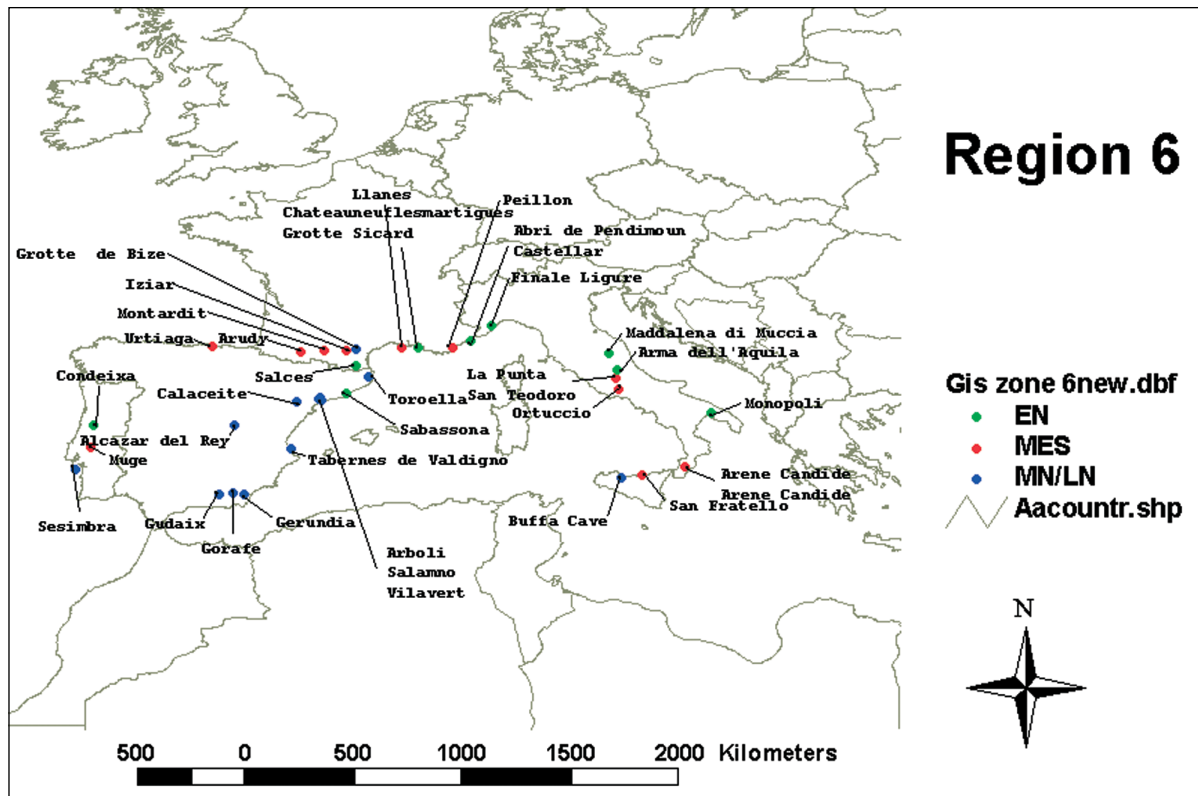


Fig. 27. Location of analysed skeletal samples from Region 6 (by site).

expansion at one moment in time, or continuous gene flow between groups that initially differed in allele frequencies". Thus, the genetic analyses cannot detect more particularistic, population-specific patterns. These specific patterns can only be revealed by the incorporation of non-genetic information. This information should include geographic data which take into account geographic barriers such as seas, lakes, mountain ranges, and possibly ecological

barriers, such as deserts, forests, and so on. Most importantly, it should include archaeological and biological (i.e., skeletal) data, the only actual evidence of past peoples in time and space.

Support for 'demic diffusion' (model 2a) comes from the study by Semino and colleagues (1996) of frequencies of two distinct Y-chromosome markers, the p12f2-8-kb and the 49a, f-Ht 15 alleles among 3000 subjects, mainly from Europe. The study revealed that the p12f2-8-kb allele is specific to western Eurasian populations. The frequencies of this allele among Near Eastern and European populations display a cline decreasing from the Near East to north-western Europe. In contrast, a map of 49a, f-Ht 15 allele frequencies displays a cline in the reverse direction, with its highest frequencies among north-western Europeans and the Basque. On the basis of these geographic patterns, these results have been interpreted as suggesting that the 49a-f-Ht 15 allele can be considered as a proto-European haplotype, while the p12f2-8-kb allele is a Near Eastern haplotype. The south-east to

	Predicted Group Membership							Total	
	Group	1	2	3	4	5	6		7
Count	1	4	0	0	0	0	0	0	4
	2	0	7	3	0	0	0	2	12
	3	0	0	10	0	0	1	0	11
	4	0	1	1	3	1	1	4	11
	5	1	1	1	0	2	0	1	6
	6	0	0	1	0	0	4	3	8
	7	1	1	2	0	0	1	13	18
%	1	100.0	.0	.0	.0	.0	.0	.0	100.0
	2	.0	58.3	25.0	.0	.0	.0	16.7	100.0
	3	.0	.0	90.9	.0	.0	9.1	.0	100.0
	4	.0	9.1	9.1	27.3	9.1	9.1	36.4	100.0
	5	16.7	16.7	16.7	.0	33.3	.0	16.7	100.0
	6	.0	.0	12.5	.0	.0	50.0	37.5	100.0
	7	5.6	5.6	11.1	.0	.0	5.6	72.2	100.0

Tab. 18. A summary of the classification results.

Location	Assigned Group
Tirpesti	5
Cascioarele	4
Gîrlsti	6
Gîrlsti	4
Kasanlak*	6
Gura Bacului*	7

Tab. 19. Classification results for unselected cases (group 8).

north-west distribution of the latter is therefore in agreement with the ‘demic diffusion’ model. However, an examination of the published table (*Semino and colleagues 1996.Tab 1*) indicates that the frequency distribution of this allele is not uniform, being high among Near Eastern, Greek, Albanian, and Italian populations ($f > 20$), and much lower ($f < 8$) among Spanish, French, Hungarian and English populations. It is therefore questionable whether such results actually support the ‘demic diffusion’ model.

Lucotte and Loirat (1999) analysed the distribution of haplotype 15 at p49 (locus DYS1) of the Y-chromosome among present-day Europeans. Their sample included 2,418 individuals originating from 28 different geographic locations in Western Europe. They found the highest frequencies of the p49 TaqI haplotype 15 among French Basques (72.2%), Spanish Basques (53.8%), and individuals from the Montpellier region in France (53.5%). Frequencies were considerably lower in south-western European regions and in central Europe, while a minor peak was detected in north-west Europe (Great Britain, Brittany, Northern France, Germany, Belgium). The spatial plotting of these results, using frequency contours, reveals that there exists a gradient from north-west Europe and the Basque area into south-eastern and peripheral countries. This pattern is opposite in direction to the cline observed for the HLA genes, but is in agreement with the clinal distribution observed in the fifth synthetic map produced by Cavalli-Sforza and his team (1994.294). This map has very wide bands, which may represent the pre-Neolithic relict populations.

Similar results were obtained by Wilkinson-Herbots and colleagues (1996) (see also Richards *et al.* 1996) in their analysis of human mtDNA at site 73 of hypervariable region II. A reduced median network of mtDNA control region sequence data for European populations (Wilkinson-Herbots 1996.Fig 1) suggests the presence of 5 groups. The diagram indica-

tes that the phylogenies of groups 1 and 4 are star-like, while those of groups 2, 3, and 5 are not. A possible explanation for the star-like structure of groups 1 and 4 is that they reflect the population expansion of the Late Glacial Maximum (20 000 BP), perhaps from one or two relict populations (Wilkinson-Herbots *et al.* 1996). The estimated age of these two groups is around 25 000 BP, using an evolutionary rate of 11.81% originally obtained by Stoneking and colleagues (1992 as cited in Wilkinson-Herbots 1996). Based on the same mutation rate, an estimate of 45 000 BP was obtained for group 5 and suggests that this population, together with parts of groups 2 and 3, represents the pre-glacial populations of Europe.

Chikhi and colleagues (1998a; 1998b) looked at nuclear DNA clinal variations across Europe. They found that out of 34 DNA alleles, 22 showed significant spatial structure. Approximately one third of the alleles were arranged in broad, statistically-significant gradients, while for some other alleles, long-distance differentiation was evident. These results indicate that (1) patterns observed by the study of molecular markers (Menozzi *et al.* 1978; Cavalli-Sforza 1994; Sokal *et al.* 1989) do not differ much from studies of non-molecular markers; and (2) there is evidence to suggest that isolation by distance has affected genetic variation at the molecular level. Chikhi and colleagues admit that more research is required in order to reveal whether these DNA markers are affected by selective forces. Nevertheless, the presence of a clinal pattern among these markers casts some doubt on the aforementioned argument of Fix (1996) for a selection-based clinal pattern. It thus remains to be investigated whether the European clinal pattern is the outcome of ‘demic diffusion’, which assumes a certain level of admixture with local Mesolithic populations, or a ‘stepping-stone’ model of founder effects, which annuls any admixture.

In a recent work, Chikhi and colleagues (2002) studied Y chromosome markers, using a genealogical

Group	Arch. Period	Code
Impressed Ware – various	Impressed Ware	1
Impressed Ware – Condeixa	Impressed Ware	2
Nea Nikomedeia	Early Neolithic	3
SE Europe – Various	Early Neolithic	4
Çatal Höyük	Early Neolithic	5
Med. Mesolithic	Mesolithic	6

Tab. 20. Groups selected and corresponding codes.

likelihood-based approach and to examine their findings in the light of the Demic Diffusion model of Ammerman and Cavalli-Sforza (1984) and the Cultural Diffusion model (i.e. indigenous transition). Their main innovation was the evaluation of genetic data from European, Anatolian and Near Eastern populations, modelling for admixture between migrating Neolithic farmers and local Mesolithic populations, as well as for the effects of drift. The data set comprised 22 binary markers from the non-recombining region of the Y chromosome (NRY) in a large number of European populations ($n = 1,007$ chromosomes from 25 samples). These markers are considered to be the result of unique mutational events and are called unique-event polymorphisms and are thought to be rare enough to have occurred only once in the recent history of human populations. In order to estimate admixture, the genetic structure of the original Neolithic population was derived from three samples from Syria, Turkey and Lebanon. The Mesolithic (or Paleolithic) population was represented by two samples of Basques.

The results of the analysis of Chikhi et al. indicate that there is a clear trend across Europe, with the proportion of Neolithic genes decreasing from modal values around 85–100% in Albania, Macedonia, or Greece, to around 15–30% in France, Germany, or Catalonia. The statistical significance of this trend was then assessed and quantified by combining information from the individual populations and their geographic distance from the Near East and by plotting the regressions. Estimated average p_1 values across Europe were compared with the values given by Semino and colleagues (2000) for the same data set. Chikhi and colleagues found an average Neolithic contribution of 50% across all samples. Furthermore, Chikhi and colleagues (2002) point out that these figures are likely to be underestimates of the true genetic contribution of the Neolithic farmers. This is since the method utilized estimates only the proportion of

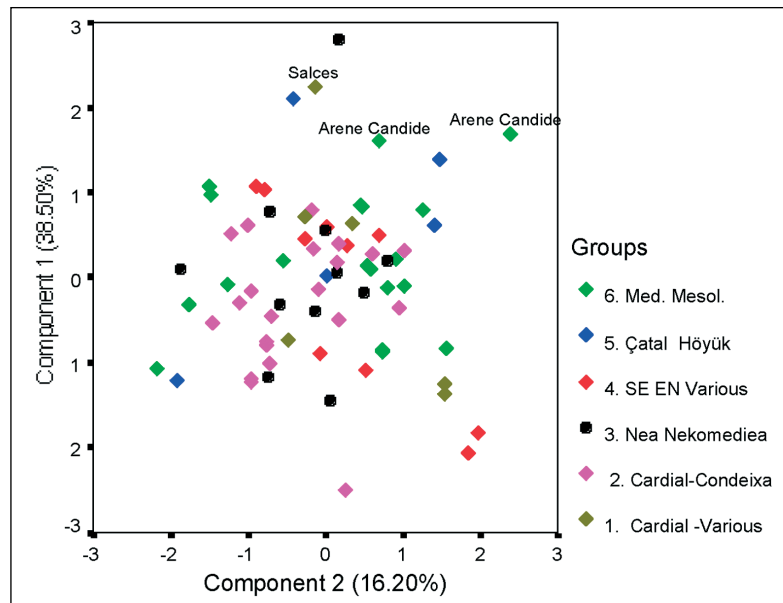


Fig. 28. A scatterplot of the 1st and 2nd components.

genes that can be traced back to ancestors in the Near East rather than the true proportions of Neolithic vs. Paleolithic genes during the initial formation of Neolithic settlements in Europe. Thus, according to Chikhi and colleagues, the contribution of Neolithic farmers to the current gene pool of the various European populations is in fact between 65 and 100%. These results provide further support for the ‘Demic Diffusion’ model. Moreover, the study reveals the importance of the incorporation of demographic parameters such as admixture rates and drift in any study of the spread of farmers in Europe.

A more geographically oriented approach was applied in a study of Simoni and colleagues (2000). They analysed more than 2600 sequences of the first hypervariable mitochondrial control region for geographic patterns in Europe. Spatial autocorrelations were used in order to examine the relationship between genetic variability in this region and geographic distances. However, only a limited geographic pattern was observed. An area of significant clinal variation was identified around

a. Eigenvalues and variance			
	Eigenvalues	% Total variance	Cumulative %
1	3.08	38.50	38.50
2	1.30	16.20	54.70
3	0.96	12.01	56.71

Tab. 21a–b. Results of the principal component analysis.

b. Factor loadings		
	PC1	PC2
GOL	0.79	–0.15
BBH	0.76	–0.39
XPB	0.42	0.16
MFB	0.55	–0.27
NPH	0.78	0.27
NLH	0.77	0.38
NLB	0.34	–0.56
OBH	0.28	0.70

the Mediterranean Sea, but not in the more northern parts of Europe. According to Simoni and colleagues (2000.275): “A simple demographic expansion from the Levant is easy to reconcile with the gradients observed at many nuclear loci, but it is not easy to link with the fact that mitochondrial variation is clinal only in southern Europe.” These findings may suggest greater gene flow (female, at least) along the southern Mediterranean region than across the northern part of the continent (Simoni et al. 2000). These findings agree with the suggested model. As the Impressed Ware people expanded westwards, they would have absorbed differential amount of genes from local foraging groups. Signs of initial admixture were observed in section 9.8 in the case of some of the initial Impressed Ware sites.

There is an apparent discrepancy between findings from mitochondrial DNA studies (Richards et al. 1996; Richards et al. 1998; Wilkinson-Herbots et al. 1996), which suggest a Palaeolithic ancestry to modern western European populations, and the findings from nuclear DNA (Chikhi et al. 1998a; 1998b) and classical markers (Menozzi et al. 1978; Cavalli-Sforza et al. 1994), which suggest a Neolithic demic

diffusion from the Levant as the main contributor to the European gene pool. This incompatibility can be explained if one is to accept that the gene pool of all modern European populations is to some extent admixed, with differential percentages of Palaeolithic and Neolithic ancestral contributions. This supposition is supported by evidence from mtDNA studies (Richards et al. 1996), which points to the mixed indigenous Palaeolithic and Neolithic (i.e., demic diffusion) ancestry of European populations. In the case of Y chromosome markers, results obtained by Semino et al. (1996; 2000) suggest that the contribution of incoming Neolithic farmers to the gene pool of the current European populations was as low as 22%. These results contrasts with results of the analysis of Y chromosome markers by Chikhi and colleagues (2002) suggesting that the genetic contribution of the incoming farmers may have been around 70%, and thus more in agreement with the demic diffusion model than with the concept of cultural diffusion without dispersal of farmers.

The analyses of variability and morphological affinities suggest that the Epipalaeolithic populations from the Levant (Natufian) differed to a fair extent from

Location	N*	Date (bp)	Lat. (N)**	Long. (E)**	Arch Period	Group Code
Arma Dell'Aquila II	3		42.37	13.37	Impressed Ware	1
Condeixa	60		40.06	8.30	Impressed Ware	1
Finale Ligure	3		44.12	8.18	Impressed Ware	1
Grotte Sicard	3		43.24	5.12	Impressed Ware	1
Arene Candide	3		38.33	16.12	Early Mesolithic	2
Franchthi Cave	3		39.00	22.30	Early Mesolithic	2
Ortuccio	3	12500	41.54	13.42	Early Mesolithic	2
San Fratello	4	12003	38.00	14.36	Early Mesolithic	2
San Teodoro	4		42.00	13.30	Early Mesolithic	2
Nea Nikomedeia	11	8180	40.65	22.30	Early Neolithic	3
Vészto-Mágori	7	6200	46.94	20.23	Körös	3
Tırpești	4	6240	47.17	26.33	Pre-Cucuteni	3
Vlasac	56	7755	44.31	22.01	Late Mesolithic	4
Hoëdic	18		47.21	2.52	Late Mesolithic	4
Muge-Arruda	10		39.06	8.42	Late Mesolithic	4
Muge –Moita	14		38.37	8.58	Late Mesolithic	4
Teviec	31	9025	47.00	3.00	Late Mesolithic	4
Çatal Höyük	50	7499	37.10	32.13	E. Neolithic	5
Çayönü	9	9360	38.23	39.65	PPN	5
Khirokitia	21	7368	34.54	33.00	PPN	5
Lepenski Vir – E. Neol.	23		44.33	22.03	Starcevo	6
Vinca-Neol	9		44.48	20.36	Starcevo	6

* Sample sizes are given prior to the casewise exclusion due to missing values
** Latitude and longitude are in the North East quadrant and in decimal notation

Table 22. Groups analysed in PCA mean data analysis.

the Mesolithic population of the Danube Gorge, western Mediterranean and central Europe. As discussed before, no close similarities were observed between Early Neolithic and Mesolithic European groups in any of the studied regions, with the possible exception of the Danube Gorge, Mediterranean Europe, and the unstudied region of Atlantic Europe. However, there were also no clear affinities observed between the Epipalaeolithic Near Eastern groups and any other Mesolithic or Neolithic groups. These results imply a third scenario: that the original Epipalaeolithic population from which the first Anatolian farmers descended is yet to be “discovered”, as there are at present no skeletons, and meagre evidence for Epipalaeolithic occupation in Anatolia (Özdoğan 1999). According to Özdoğan (1999), the late phase of the Upper Palaeolithic period is either absent or poorly represented in both central and eastern Anatolia. The absence of sites from this period seems to reflect the scant occupation of these regions, rather than any excavation bias.

The observed variability between Levantine and European Epipalaeolithic/Mesolithic groups should be studied in relation to the Upper Palaeolithic populations of Europe and the Near East. Thus, genetic studies that point to an Upper Palaeolithic ancestry of modern European populations should take into consideration population bottlenecks and segregation during the Late Glacial period, which can perhaps account for the above noted morphological variability during the Mesolithic.

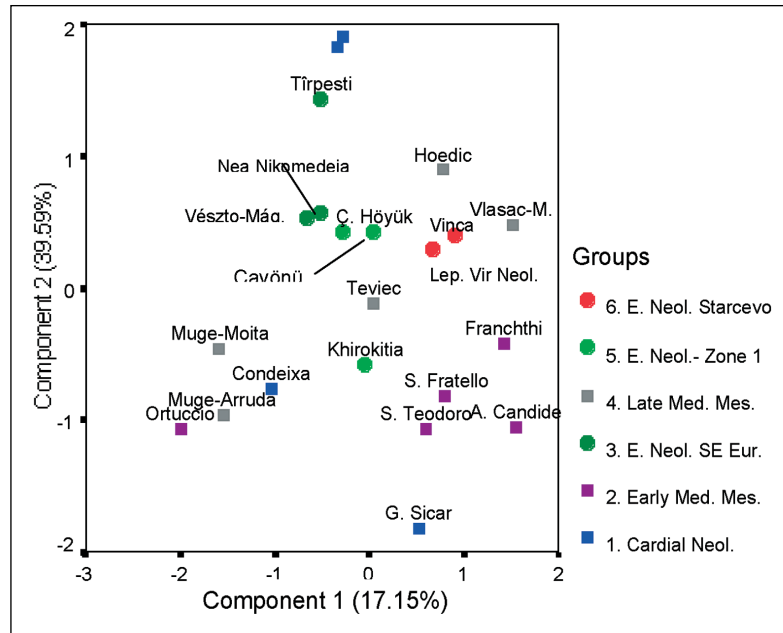


Fig. 29. A scatterplot of the 1st and 2nd components.

the first synthetic map in the study of Cavalli-Sforza and colleagues (1994). The claim that the observed genetic cline is in fact the outcome of a ‘demic diffusion’ across Europe as proposed by Ammerman and Cavalli-Sforza (1984) is only partially in agreement with the current results (genetic, archaeological and palaeobiological). An examination of the model outlined in figure 10.4 indicates that the SE-NW genetic cline is, in fact, a synthesis of a southern (Mediterranean) cline and the northern/western cline generated by the expansion northwards and westwards of the Early Neolithic cultures of SE and central Europe. In other words, the new model agrees with the demic diffusion model in respect to western (i.e., Atlantic and western Mediterranean regions) and northern Europe, but not in the case of south-east and central Europe. One possibility is that the genetic cline is partially the outcome of the subsequent expansion of the Early Farmers, and partially the outcome of gene flow during later historical periods.

The current findings question the interpretation of

a. Means and standard deviations		
	Mean	S.D.
GOL	185.65	6.39
XPB	138.53	3.75
MFB	95.55	3.21
NPH	66.32	2.98
NLH	49.56	2.13
NLB	24.66	1.20
OBH	31.43	1.32
ZYB	130.60	7.90

b. Eigenvalues and variance			
Component	Eigenvalue	% Total variance	Cumulative %
1	3.17	39.59	39.59
2	1.37	17.15	56.74
3	1.21	15.08	71.82

Tab. 23a–c. Results of the PCA analysis on group means (n = 22).sis of cranial dimensions.

c. Factor loadings			
	PC 1	PC 2	PC 3
GOL	0.62	0.30	-0.39
XPB	0.67	0.02	0.51
MFB	0.52	0.36	0.70
NPH	0.74	-0.17	-0.21
NLH	0.85	-0.15	-0.24
NLB	0.05	0.94	-0.07
OBH	0.48	0.24	-0.43
ZYB	0.75	-0.40	0.14

ASSESSING THE MODELS FOR THE SPREAD OF FARMING IN EUROPE

Model 1 – Autochthonous transition across Europe

The ‘indigenous’ model views the transition to farming as the result of cultural diffusion, without associated migrations or dispersals of human populations. Under such a model, local European hunter-gatherer populations adopted farming either as a form of independent ‘discoveries’ or consequential to the arrival of knowledge and technology from the Neolithic cultures of the Near East and Anatolia. Underlying this approach is the assumption that the transition to farming occurred at different times and in different manners in the various regions of Europe. Archaeologists that support this model provide evidence which suggests continuity in material culture, and emphasise the economic, technological and cultural complexity of many of the Mesolithic cultures, which are viewed as a sort of ‘pre-adaptive’ stage followed by the choice of an agricultural lifestyle.

The central tenet of this model is that in each region, the Early Neolithic farmers are the descendants of local Mesolithic populations. These descendants may differ in some morphological aspects from their ancestral Mesolithic predecessors due to admixture with other Neolithic groups and changes in morphology associated with their new lifestyle. Nevertheless, their morphology must display some affinities to their Mesolithic ancestors or similarities to contemporaneous neighbouring Mesolithic groups. Moreover, one should also see regional differences in morphology, as local continuity with minimal gene flow is assumed for each of the regions addressed. If this was the case, one should expect to see morphological distances across space being greater than morphological distances by period. However, the results of the analysis of the squared Mahalanobis distances between Mesolithic and Early Neolithic groups (*Pinhasi 2003*) indicate that this is not the case. The only possible case of regional continuity observed was in the case of the Danube Gorge region, where distances between these Mesolithic groups to the Early Neolithic context from Lepenski Vir are smaller than distances between the former and other Early Neolithic European groups. It is possible that, had the data set contained specimens from Atlantic Europe and the Iberian Peninsula, one would have found similar indications for local continuity in these regions.

No firm evidence for local continuity was obtained in the case of the Levant region (*Pinhasi 2003*). The analysis of Levantine groups demonstrated a possible continuity between the Natufians and the Northern Levant and Jericho PPN in terms of their mandibular and dental dimensions. However, other PPN groups showed lack of affinities to the Natufians. One of the most intriguing results was the large degree of variability among the PPNB ‘Initial Neolithic’ groups from the Levant and Anatolia. The position of Khirokitia and Abu Hureyra as outlier populations was particularly noticed in numerous analyses. Moreover, the Natufians as a group display a large degree of heterogeneity, which suggests that they either represent several biological populations, a period of morphological transition with differential expression through time and space (the Natufian samples derive from several sites spanning a few thousand years), or still a period of comparatively relaxed selective pressures (in relation to earlier Upper Palaeolithic groups) that led to increased diversity.

The regional analysis indicated lack of continuity between the Early Neolithic populations of the Levant and Chalcolithic groups. The latter could be easily discriminated from most of the PPN and south-east European Neolithic groups. The observed differences reflect populations that were isolated enough from each other to allow the development of regionally-specific morphological patterns. It is then possible that, after the initial phase of adoption of agriculture in the Levant and Anatolia, the PPN populations became isolated from each other and did not share a large mating network, as in the case of various hunting populations. The existence of biologically diverse PPNB groups in this region is likely, considering the time span of 2000 years or more during which agriculture communities existed prior to the first spread of farming into Europe. In fact, we see a similar process of diversification following the first period of the Neolithic in Europe. This diversification is evident culturally in the appearance of diverse stylistic groups in east and central Europe (*Sherratt 1983; Thorpe 1996*). What is important in this scenario of a period of differentiation of PPN populations in the Levant prior to expansion of agriculturists outside the region is that the group that contributed to the gene pool of European farmers (or originated it) need not be representative of the entire PPN Levantine population, but rather of one isolated and already somewhat differentiated group.

The other possibility is that the heterogeneity among the PPNB populations reflects differences in mor-

phology among their ancestral Epipalaeolithic populations. As there are hardly any human remains from the Epipalaeolithic period of Anatolia, we presently know very little about the late hunters from this region and cannot therefore evaluate this hypothesis.

Beyond the zone of Anatolia and the Near East we find a striking degree of morphological similarities among Early Neolithic populations. Thus, the first farmers from Nea Nikomedeia and other Greek Neolithic sites are similar to the first farmers from Çatal Höyük, as well as to specimens of the Körös and Starčevo cultures and to the first LBK groups of Central Europe. The analyses showed no similarities between Greek Neolithic specimens and the Mesolithic specimens from Franchthi Cave, and thus no evidence for local continuity in the region of mainland Greece.

Equally, there appear to be no affinities between any of the LBK groups and the German Mesolithic specimens from Ofnet, Hohlestein, Kaufertsberg, Stetten or Bottendorf (analysis of region 4 in *Pinhasi 2003*). These findings agree with Thorpe (1996:29), who asserts the following in regard to the appearance of the LBK culture of Central Europe “...there have been a few archaeologists arguing that the Mesolithic population of Central Europe as far north as the fringes of the north European plain and as far west as the Paris Basin played much part in the agricultural transition of the region, apart for some evidence for continuity in stone tool production.”

The relationship between the Mesolithic and Neolithic populations of Northern Europe was examined in the analysis of region 3 (*Pinhasi 2003*). The discriminant function analysis performed included a group of four Mesolithic specimens (group 1), one of which was the Mesolithic specimen from Spiginas, Lithuania. The other three were specimens from the Danish sites of Koelbjerg, Vedbaek and Korsør. Discrimination between this group and the rest of the (Neolithic) Danish groups was achieved along the first canonical function. Because of the small sample size of the Danish Mesolithic sample, the possibility that some affinities existed between this group and Neolithic populations of the area cannot be ruled out. Nevertheless, the lack of association (in the form of easily achieved discrimination) between the two periods is a theme which has been noticed throughout.

In sum, the review indicates that local continuity may have occurred in the Danube Gorge region and southern Scandinavia, and possibly also in the Medi-

terranean zone and Atlantic Europe, although the evidence for these latter areas is still tentative and dependent on more in-depth analyses. Therefore, in the case of the latter zones it is necessary to examine this claim with larger skeletal samples. From the point of view of the debate on the origins of agriculture in Europe, the model of an autochthonous development does not fit the current findings regarding the regions of the Levant, Anatolia, SE Europe and central Europe.

Model 2a – Demic diffusion

The ‘wave of advance’ model argues for a large-scale advancement of farmers from the Near East or Anatolia into Europe in a more or less constant expansion rate of 1.1 km/year (*Cavalli-Sforza et al. 1994*). The hypothesis was largely based on a model for the ‘wave of advance of advantageous genes’ originally proposed by Fisher (1937). This mathematical model assumes that a biological population that grows at a constant rate reaches local saturation and spreads at a constant rate of migration, randomly in all directions, tending to grow and move away from its centre of origin at a radial constant rate of advance. Ammerman and Cavalli-Sforza adopted this theoretical model and applied it, with some modifications, to their study of Neolithic demic diffusion. Ammerman and Cavalli-Sforza (1984) used Jericho as the centre of origin from which the farmers dispersed towards Europe. The main supporting evidence underlining their model was as follows:

- ❶ The expansion of farmers from the Middle East to Europe was very slow, gradual, and regular, thus more compatible with the expansion of people than of a technique.
- ❷ Knowledge from contemporary ethnographic observations regarding demographic growth and expansion allows one to predict that the diffusion of agriculture is compatible with demic expansion.
- ❸ Ethnographic observations based on African Pygmies suggest that hunter-gatherers show little tendency to acculturate when in contact with farmers.
- ❹ A study of the modern geographic distribution of genes in Europe strongly suggests diffusion from a centre of origin in the Middle East, as well as other less important migrations (*Menozzi et al. 1978*).

The results obtained do not support the wave of advance model. Firstly, the analysis of population variability during the Early Neolithic revealed a contrasting pattern of high heterogeneity within the Early Levantine and Anatolian populations as op-

posed to an apparent homogeneity among the first farming populations of Europe. We also saw that the Mahalanobis D2 distances of the Early Neolithic groups from (1) Çatal Höyük and (2) Çayönü did not reveal any correlation between the geographic distances from each of these sites and Mahalanobis distances measured from remains from other Early Neolithic sites. Moreover, both Çatal Höyük and Çayönü are much closer (morphologically), to the early Neolithic European populations than to any of the PPNB Levantine groups (i.e., Basta, Abu Hureyra, Jericho, etc.).

Secondly, the 'wave of advance' model explains the observed genetic SE-NW cline as being due to the gradual absorption of the Mesolithic populations (Ammerman and Cavalli-Sforza 1984). If this was the case, then one should clearly see some morphological similarities between Mesolithic and Early Neolithic populations due to the impact of absorbing some of the Mesolithic gene pool. Furthermore, one should observe a clinal increase in similarity between Neolithic and Mesolithic groups, as the advancing wave would progressively be composed of a greater and greater proportion of Mesolithic genes. However, the craniometric analyses showed no evidence for such a pattern. The analysis revealed very limited and not overwhelming evidence of continuity of a Mesolithic morphology into Neolithic populations. This evidence was of possible local continuity in the case of the Danube Gorge Neolithic, and in the western Mediterranean. The analysis of northern Europe (region 3) also indicated possible continuity, but this could not be further assessed due to the lack of specimens from the Early Neolithic and Mesolithic periods in this area. The Atlantic European zone was not examined due to the lack of appropriate skeletal samples. Yet in the regions in which agriculture originated and first appeared in Europe (i.e., regions 1, 4 and 5), we found no evidence for affinities between Early Neolithic populations and the preceding Mesolithic inhabitants.

Thirdly, Barbujani (1995) pointed out that a demic diffusion without any absorption of Mesolithic populations can also result in the observed SE-NW cline. This has been outlined in various models of stochastic change (i.e., non-selective) due to drift and a series of founder effects (see Wright 1921; 1933; 1951; 1969; Koningsberg 1990; Relethford 1991; 1996). Similarly, Sokal et al. (1991) pointed out that persistent long term demic diffusion originating from a single source population, and repeated migrations by different ethnic groups along established corri-

dors, will leave similar indistinguishable marks on gene frequency surfaces. The 'demic diffusion' model, therefore, does not agree with the observed findings, as no clinal pattern was observed, but rather clear morphological affinities between geographically distant Early Neolithic populations.

Model 2b

Model 2b proposes a scenario in which the admixture between Mesolithic and Neolithic farmers was delayed due to a period of consolidation, and therefore occurred in the Middle/Late Neolithic period rather than during the Early Neolithic period. The corresponding biological pattern should show some affinities between Mesolithic and Middle/Late Neolithic populations in a given region. Such a scenario must also presume similarities between Early Neolithic and Middle/Late Neolithic populations in a given region, as it would have been the former who underwent a period of population growth and consolidation which continued into the Middle/Late Neolithic.

Previous analyses of intra-population variability by period (Pinhasi 2003) show that the only similarities between Mesolithic and Middle/Late Neolithic groups was that in both periods sexual dimorphism and variability in general is more pronounced than in the case of the Early Neolithic period. However, when scrutinising specific indices and other morphological variables by period, it becomes apparent that many differences between the populations of these two periods exist.

The analysis of inter-population distances by period (Pinhasi 2003) pointed to regional differentiation during the Middle/Late Neolithic, with some Late Neolithic groups from central Europe and Hungary having large distances from each other. We know from the settlement pattern analysis (Pinhasi et al. 2000) that the evidence for Mesolithic occupation in south-east Europe is meagre. The apparent regional diversification during the Middle and Late Neolithic period cannot be associated with a delayed Mesolithic-Neolithic admixture in the case of this region. We must, therefore, conclude that a delayed admixture process is not supported by the data from the zones analysed in this work.

Model 3

The third model proposes a complete population replacement without admixture. To a fair extent, the obtained results are compatible with this scenario.

The small distances between Çatal Höyük and Early Neolithic European populations, and among the latter, do not support differentiation by distance. The small distances between Visenhäuser Hof, Schwetzingen, Kotacpart and Çatal Höyük suggest that, at least in southeast and central Europe, Early Neolithic populations are strikingly similar to each other. However, as mentioned before, we found some evidence for local continuity in the Danube Gorge, as well as possible continuity in Denmark and along the Western Mediterranean coast. The possibility of admixture between the local foragers and incoming farmers in these areas should be taken into account. Therefore, this model must be rejected, as it does not agree with the complete picture.

Model 4

The fourth model proposes that admixture was a function of the geographic region under consideration and its relevant distance from the centre of origin of the source population. Various geographic barriers exist in Europe, which more than likely affected the rate and direction of demic diffusion. These include the Mediterranean Sea, the Alps, the Pyrenees, and the Carpathians, to name but the conspicuous few. If one adds to this list an obvious preference among the dispersing farmers for fertile soils, river valleys and water sources, then the path by which the Early farmers dispersed looks much more specific and less like a radial dispersal. Moreover, the ecological preferences and geographic boundaries cannot be simply taken into account by slightly modifying existing formulas for dispersal rates, but rather requires an in-depth anthropological approach to assess past dispersal patterns.

Van Andel and Runnels (1995) brought forth a modified model for the dispersal of the first farmers into Europe. They based their model on the earliest occupation radiocarbon dates used by Ammerman and Cavalli-Sforza, plus additional dates from various sources.

Van Andel and Runnels point out that the wave of advance model assumes the following:

- ① An initially logistic population growth curve, which yields a continuous advance across a broad front.

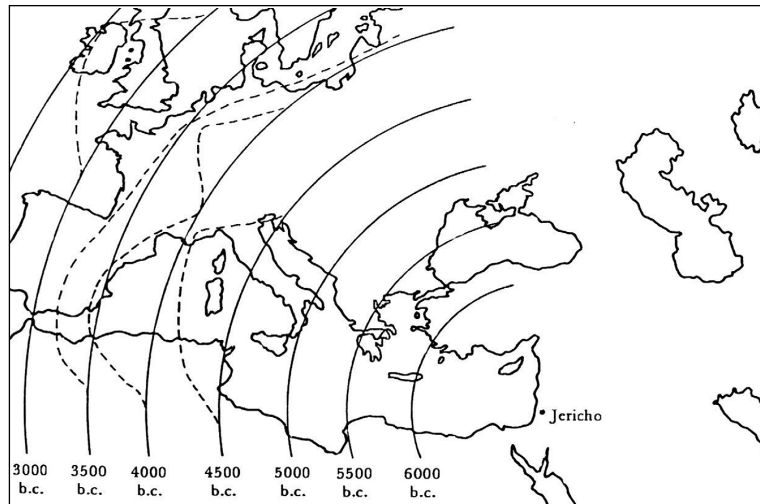


Fig. 30. The Wave of advance model. (from Ammerman and Cavalli-Sforza 1984).

- ② Local migratory activity that is, to a first approximation, continuous and random in direction (Fig. 10.2a).

This model assumes that population increase and migratory activity occurred only at the wave front, and that the rate of advance was roughly constant. Well behind the wave front, population growth slows down due to lack of room for expansion.

Van Andel and Runnels developed this model taking into account geographic barriers to dispersal. They contend that the Aegean Sea might be regarded as a geographic barrier. While sea-travel was apparently possible, it created a bottleneck that limited the number of migrants. Van Andel and Runnels (1995) suggest a two-phase colonisation model. At the initial stage, colonists from the Levant arrived early and almost simultaneously on Crete, at Franchthi Cave and in Thessaly, but probably only in small numbers (Fig. 10.2b). In the second step, migrating farmers, possibly from central Anatolia (T2 in Figure 10.2b) dispersed, reaching the northern part of Greece as well as Macedonia and Thrace. Van Andel and Runnels (1995) assert that the lengths of each step and the intervals between them were dictated by geography and by population growth in each of a slowly rising number of parent areas. However, taking a less environmentally-determined approach, one could also argue that the second wave could have been triggered by other culturally induced factors.

Van Andel and Runnels (1995) argue that the original dispersal westwards was by sea routes. They propose a dispersal from central Anatolia (Hacilar,

Can Hassan, and Çatal Höyük) to Crete (Knossos) and the southern Peloponnese (Franchthi Cave), reaching the Larissa Basin, Thessaly and Macedonia. This model is based on the chronological discrepancies between “older” radiocarbon dates from Knossos, Franchthi, Nea Nikomedeia and Sidari, and “younger” dates from Macedonia, south Bulgaria and the Sava Valley. As has been previously mentioned, Perlès (2001) proposed to differentiate between “Initial Neolithic” dates in Greece, which cluster around 8800 cal BP, and the “Early Neolithic” occupation, which clusters around 8100 cal BP. The initial phase belongs to “pre-pottery” sites, which share many similarities with the ‘pre-pottery’ sites in Anatolia and the Levant.

The first dispersal event by sea-route would have thus been part of the dispersal of a “pre-pottery” culture which prevailed in Anatolia and the Levant and reached Crete, Cyprus, and the southern Peloponnese around 9000 cal BP. The second dispersal event would have originated from central Anatolia approximately a millennium later, and Anatolian migrants would have appeared in Thessaly and rapidly spread across south-east and central Europe. This model is illustrated in Figure 32.

Although the study of Van Andel and Runnels provides a more complex and realistic model of the initial spread of farmers into Europe, involving more than one historical event, as a model it is based on the concept of demic diffusion. The results obtained in this work do not disagree with the demic diffusion model in regards to the logistic, temporal, advance of farmers across Europe. This work did not bring forth any new evidence that indisputably supports the assertion of a rapid dispersal. The analysis of longitude and latitude of Early Neolithic sites and corresponding radiocarbon dates for first occupation showed a positive correlation between date and latitude, and a negative correlation between date and longitude, which supports a SE–NW linear advance pattern of Neolithic settlements (Pinhasi *et al.* 2000). One should then expect to detect a corresponding clinal pattern from the craniometric data, similar to the one observed for the settlement pattern analysis and Cavalli-Sforza’s gene frequencies. However, the analysis of skeletal data showed no indication for such a cline. The pattern observed is of a logistic dispersal of farmers from the south-east to the north-west, without any morphological cline.

In sum, while Van Andel and Runnels’ model agrees in many aspects with the obtained results, it never-

theless works with the underlying assumption of ‘demic diffusion’, and thus that as farmers dispersed they absorbed the local Mesolithic populations. We must, therefore, reject this model because we can not accept the assumption of a gradually increasing input of Mesolithic genes into the Neolithic gene pool as the wave of advance progressed north-westward.

Model 5

Zilhão (1993; 2001) proposed a model that views the spread of a Neolithic lifestyle across Europe as a punctuated process with two main pulses. The first pulse would have begun around 6800–6400 BP, characterised by the spread of farming along (1) the Danubian route, and (2) the Mediterranean route. According to Zilhão, while the spread of farming along the Danubian route was rapid and involved the absorption of local Mesolithic groups, the spread of farming along the Mediterranean coast was slower, due to the predominance of hunter-gatherer groups in these regions. Consequently, hunter-gatherer bands and a more mobile settlement system continued to exist along the western Mediterranean shores for some time.

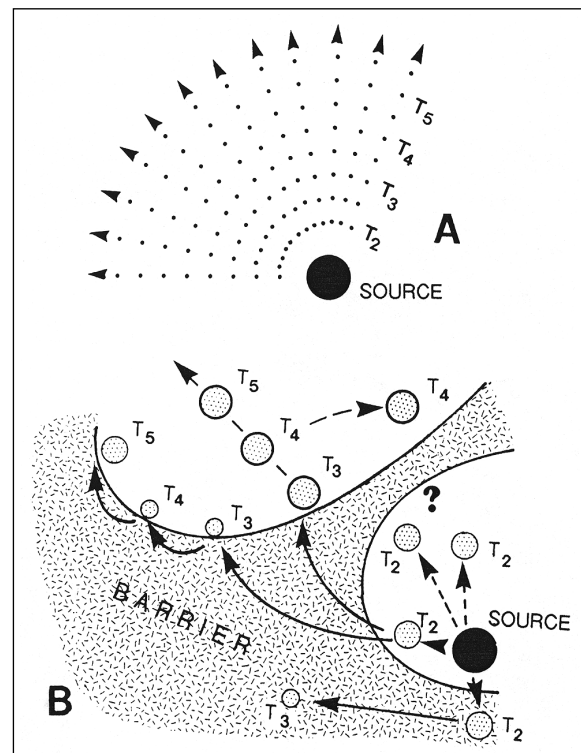


Fig. 31. The original wave-of-advance model (a), modified (b) by the addition of a barrier to gradual movement (sea, desert or mountain range), combined with strong preference for a specific but rare environment (large floodplains) from Van Andel and Runnels 1995).

A second pulse would have occurred after 6000–5500 BP, in which agricultural populations would have reached northern Iberia, western France, the Low Countries, the British Isles, and Scandinavia. Zilhão contends that in contrast with the first pulse, the spread of farming in these regions is mainly the result of the adoption of these practices by local hunter-gatherer groups, rather than being due to an incoming wave of farmers.

The results from the regional analysis agree to a fair extent with Zilhão's model. However, there are a few points that must be stressed. Firstly, this model examines the later stages of the spread of farming in Europe, and thus does not apply to the first stages of the process. Dates for the first pulse post-date the arrival of the first farmers in south-east Europe. Secondly, the results obtained did not indicate any absorption of Mesolithic populations along the Danubian route. The Danube Gorge sites of Lepenski Vir and Vlasac, in which local continuity probably occurred, are situated in the south-eastern part of the river and thus in a zone marginal to the westward direction of dispersal. Thus, the issue is the extent of genetic absorption of hunter-gatherer bands proposed in Zilhão's model. If the demographic process underlying the progression along the Danubian route involved but a negligible amount of gene flow from Mesolithic bands, then one should not expect to detect such a pattern in the craniometric analyses.

In sum, the results obtained do not contradict Zilhão's model. However, this model does not examine what happened during the preliminary stages of the process of spread of farming, and therefore does not offer a sufficiently extensive reconstruction to account for the spread of farming as a comprehensive historical event.

A NEW MODEL FOR THE SPREAD OF FARMING IN EUROPE

A new model is proposed. Its main tenets are as follows. The PPNA and PPNB were the periods in which we have truly 'transitional' agricultural communities. During these periods the Neolithic mode of life gradually developed, first with the development of domestic wheat, and later with the domestication of

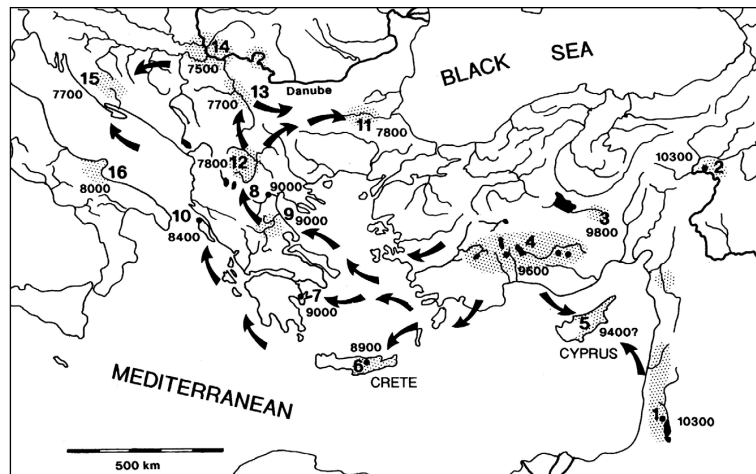


Fig. 32. Van Andel and Runnels' multi-phase colonisation model (Van Andel & Runnels 1995).

sheep, goats, cattle and, possibly, pigs. The PPNA period lasted for approximately 800 years, and was succeeded by the PPNB period, which lasted approximately 2000 years (see *Yakar 1998*). The time-span of these periods implies that the transition from a hunter-gatherer semi-sedentary lifestyle, which is best exemplified by the Natufians, to the fully sedentary agricultural Neolithic village, which is best exemplified by Çatal Höyük, was not an abrupt change, but rather a gradual development. The PPNB cultural zone consists of the Levant, Anatolia and Cyprus, and possibly extended further west to other parts of the Aegean. The boxplot analysis (Fig. 16) illustrated that PPNB populations have an extensive degree of morphological heterogeneity. The observed heterogeneity must be associated with one or more of the following aspects:

- ① Heterogeneity due to geographic/cultural isolation between some of these early agricultural populations, which occupied a very large geographical area.
- ② Heterogeneity due to morphological differences inherited from different ancestral Epipalaeolithic populations in the Levant and various Anatolian regions as the first farming practices spread throughout a "culture zone".
- ③ Heterogeneity due to differential adaptations to changes accompanying the transition to agriculture.

Özdoğan (1995) proposes a scheme in which the Early Neolithic cultures of Anatolia may be considered as two distinct entities: (1) the Neolithic of south-east Anatolia, which is related to the Mesopotamian-Levantine tradition, and (2) the indigenous Neolithic of the Anatolian plateau. These entities are also separated temporally as the south-east Anatolian cul-

ture begins about 2000 years before the Central Anatolian culture (Özdoğan 1999). The former phase is characterised by the Neolithic culture of Çayönü, while the site of Çatal Höyük belongs to the latter. Following this scheme one should expect to see more similarities between specimens from Çayönü and the Natufians than between the latter and Çatal Höyük. However, the results of the analysis performed are somewhat contradictory in this respect:

- ❶ The results of the analysis of squared Mahalanobis distances between groups (Fig. 10) indicated that the morphological distance between Çayönü and Nahal Oren is larger than the distance between the latter and Çatal Höyük (Pinhasi 2003).
- ❷ The PCA analyses of region 1 (Figs. 20, 21, 22) point to a lack of differentiation between the Natufians, Çatal Höyük and Çayönü groups.
- ❸ The discriminant analysis of region 1 indicates that the centroid of Çayönü is close to the centroid of the Natufian group, and that they are both distant from the Çatal Höyük centroid (Fig. 23).

We may therefore conclude that the analyses discussed above do not unequivocally support local continuity between Çayönü and the Natufian populations.

Nevertheless, various analyses showed that the Çatal Höyük group is similar to Early Neolithic European groups of south-east and central Europe, and that this similarity contrasts with the lack of association between the latter and Abu Hureyra, Khirokitia and Basta. Based on these results it appears that the first farmers that colonised Europe did not originate from the Near East, but rather from central Anatolia. Their best represented type population is the one from Çatal Höyük, which represents the successful culmination of the 2000 years of agricultural development in Anatolia. This suggests that these farmers first arrived in south-east Europe through western Anatolia, and not by sea travel through the Greek Islands. The remarkable homogeneity among the first farmers, taken together with the differentiation between them and Mesolithic populations from these regions, implies lack of admixture between farmers and hunter-gatherers, and supports an initial 'logistic dispersal without admixture'.

Figure 33 illustrates the proposed model. The dark area represents the zone of the first farmers. The farmers would have arrived and dispersed across this zone without any significant admixture with the local foragers. The hatched circle in the Balkans represents the Danube Gorge. In this micro-region, the Mesolithic population possibly underwent an autochthonous transition to a Neolithic lifestyle, with or without some limited admixture with the incoming farmers. The spotted grey zone is the zone of the Early Impressed Ware culture.

Around 6000 BP, the dispersal of farmers would have continued in two main directions. One group of farmers advanced westward along the Mediterranean region, eventually reaching the Iberian Peninsula. This advance would have been of the Early Impressed population. The other group represents the dispersal to northern and Atlantic Europe. This dispersal would have occurred between 6000–4000 cal BP. The dispersed populations would have been the descendants of the first farmers (dark zone) who expanded westwards and northwards. This zone (northern and Atlantic Europe) was more densely occupied by foraging populations, and therefore it is postulated that the transition to agriculture in this region took different demographic paths. In some cases, the foraging populations became Neolithic through autochthonous development; in other cases the incoming farmers absorbed some local foraging tribes.

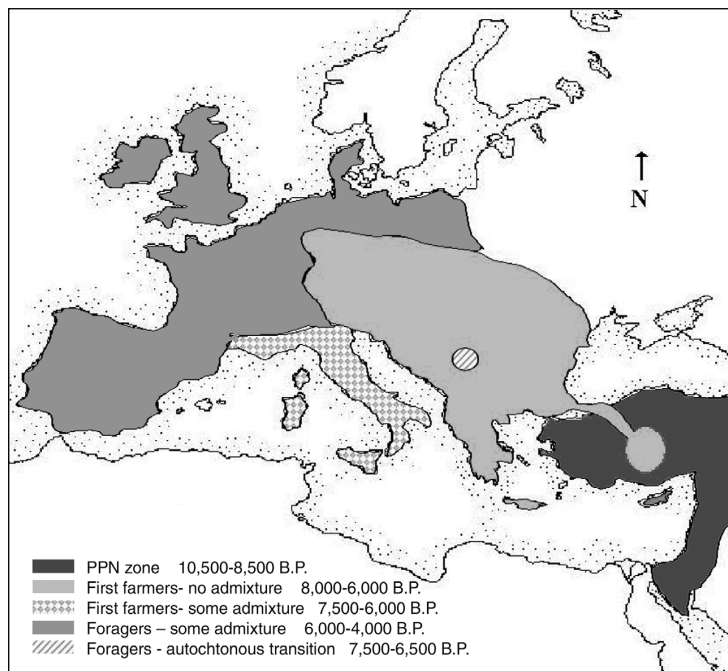


Fig. 33. A multi-stage model for the spread of farming across Europe.

SUMMARY AND CONCLUSIONS

This work elaborated upon the complex set of events that gave rise to the spread of farming across Europe. In light of the findings from the various craniometric analyses, any simplistic model that explains the prevalent pattern of population diversity across the continent as an outcome of a single evolutionary or historical process was rejected.

The review of the genetic findings suggests that the gene pool of modern European populations displays mixed contributions from 'indigenous' European Palaeolithic ancestors and from the demic diffusion of the first farmers from Anatolia. However, this statement only offers a broad generalisation at a continental level. The main point of argument, therefore, is what proportion each group contributed to each modern European population, and more importantly, the historical/demographic process that resulted in the observed genetic structure of modern European populations.

The model proposed as the outcome of this study is in broad agreement with the genetic findings, in the sense that it posits a more complex demographic process than was previously postulated by the majority of genetic studies. We saw that an original dispersal of farmers occurred during the 8th millennium BP. The source population was most probably located in central Anatolia. The dispersal of the first farmers is, therefore, in agreement with the 'Demic Diffusion' model in the temporal sense of a 'cline' in radiocarbon dates as one progresses from the south-east to the north-west of the European continent. However, the demographic aspects of this dispersal cannot be explained by a logistic pattern of absorption

of local foraging populations. The proposed model differentiates between a first expansion without admixture (in the case of most of south-east and central Europe), and a second subsequent expansion with some admixture (in the Mediterranean zone of Italy and south-east France). This two-phase model does not necessarily imply any temporal hiatus or change in the rate of dispersal across the continent. It does, however, speculate that the first expansion was more rapid than that of the subsequent phases.

Further research is required in order to illuminate the nature of the spread of farming in the Western European regions. Based on the regional approach, one expects to detect temporally based regional variations in the degree of admixture between local hunters and migrating farmers. With additional craniometric data from these regions, and the application of corresponding craniometric analyses based on the above methodology, it would become possible to bring forth a more detailed model in the near future.

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