

Discussion and Criticism¹

On Physical Anthropological Aspects of the Mesolithic-Neolithic Transition in the Iberian Peninsula²

MARY JACKES, DAVID LUBELL, AND CHRISTOPHER MEIKLEJOHN

Department of Anthropology, University of Alberta, Edmonton, Alberta, Canada T6G 2H4 (Jackes and Lubell) Department of Anthropology, University of Winnipeg, Winnipeg, Manitoba, Canada R3B 2E9 (Meiklejohn). I IV 97

Lalueza Fox (CA 37:689–95) examines two propositions: (1) that the Iberian physical anthropological data “support the hypothesis of population replacement in the Neolithic as postulated by Ammerman and Cavalli-Sforza” and (2) “that the Neolithic period effectively homogenized the Iberian populations” (p. 690). He argues that osteological and dental data from Portuguese Mesolithic and post-Mesolithic samples support the demic-diffusion model of Neolithic origins (Ammerman and Cavalli-Sforza 1973, 1984) in Iberia. He states that there was “an important replacement of the population, even in the areas densely populated by Mesolithic groups” (p. 694), followed by demographic expansion and homogenization of the population. Further analysis does not support this point of view.

First, despite his expertise in the extraction and analysis of ancient mtDNA (e.g., Lalueza Fox 1996b), Lalueza Fox refers to only two published papers by geneticists on the application of the demic-diffusion model to Iberia: Bertranpetit and Cavalli-Sforza (1991) and Calafell and Bertranpetit (1994a). More recent papers suggest that additional data may not support the demic-diffusion model.

Secondly, we question the appropriateness of the osteological and dental data used by Lalueza Fox and in particular the use of incomplete data for the Portuguese

Mesolithic and Neolithic. This is critical, because his thesis is dependent on the Portuguese Mesolithic data set.

THE DEMIC-DIFFUSION MODEL

The demic-diffusion model is founded on the demonstration by Clark (1965), amplified by Renfrew (1973), that there is a patterning of radiocarbon dates for European sites with early agriculture. The model was expanded by Ammerman and Cavalli-Sforza (1973, 1984), who argued that a fit between the radiocarbon chronology and the results of a principal-component analysis of the distribution of a series of polymorphic alleles of the blood in modern European populations demonstrated that European agriculture originated with the displacement of (Mesolithic) hunters and gatherers by incoming (Neolithic) farmers. This model has been incorporated into the synthesis of Cavalli-Sforza, Menozzi, and Piazza (1994) and the work of Sokal and colleagues (Sokal, Harding, and Oden 1989, Sokal, Oden, and Wilson 1991, Sokal, Oden, and Thomson 1992, Sokal, Jacquez et al. 1993, Sokal, Oden et al. 1996).

The coastal distribution of cardial impressed pottery in West Mediterranean Europe (see, e.g., Lewthwaite 1986) as well as across the Maghreb (Gilman 1992, Lubell, Sheppard, and Gilman 1992) provides good evidence of circum-Mediterranean contacts by sea. The diffusion of ideas and technologies is hardly to be questioned and provides a means for the appearance of new elements in the economy. The discussion here, however, is on “demic diffusion,” and the possibility of a Neolithic replacement population must be appraised. This necessitates examination of the evidence provided by research into population genetics.

Research supporting the model. Cavalli-Sforza, Menozzi, and Piazza (1994:291) state that their first synthetic map of European gene frequencies reflects the spread of agriculture from the Middle East and list the genes which have high correlations with the first principal component (for all Europe) of those gene frequencies.

Sokal, Oden, and Wilson (1991) state that only six gene systems need be considered with reference to the spread of farmers. They determine that five alleles (100 A10; 101 B8; 101 B13; 102 BW35; 200 Gm1-2) demonstrate the cline that might be explained in terms of the spread of agriculture (Sokal, Harding, and Oden 1989). Cavalli-Sforza, Menozzi, and Piazza (1994), in contrast, find many genes to be highly correlated with their first principal component. HLAB*8 (101 B8) is the only allele common to the two lists. Since elevated frequencies of HLAB*8 are believed to be associated with intol-

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erance of gluten, especially of wheat but also of rye, barley, and oats, there is certainly reason to hypothesize that low frequencies of this gene may indicate a long period of using as staples plants which are high in gluten.

Separate studies of Iberian Peninsula genetics give discrepant information and results. In two papers, the Iberian second principal component is said to illustrate the spread of agriculture, although no HLA data are included (Bertranpetit and Cavalli-Sforza 1991, Calafell and Bertranpetit 1993, reiterated in Cavalli-Sforza, Menozzi, and Piazza 1994). An expanded data set has given more details on alleles contributing to the first principal component, expressing the divergence between Basques and other Europeans: Calafell and Bertranpetit (1994a, b) give varying and apparently contradictory lists, with positive and negative correlations reversing, HLA included in one analysis but ABO in the other. However, details on the Iberian second principal component have been published only in Bertranpetit and Cavalli-Sforza (1991). The Iberian second principal component of Bertranpetit and Cavalli-Sforza (1991) is echoed by Sokal, Harding, and Oden (1989: fig. 11 illustrating 4.1 D) and, for example, by the distribution for P1*1 illustrated by Cavalli-Sforza, Menozzi, and Piazza (1994: 422, 424). It raises the possibility of gene flow across the Straits of Gibraltar.

Cavalli-Sforza, Menozzi, and Piazza (1994:286) state that gene flow from North Africa does not explain the Iberian second principal component. However, while we have little basis for assessing the demographic impact of North African immigration, gene flow undoubtedly occurred when, from A.D. 755 to A.D. 1492, Berbers and Arabs lived in southern Spain and Portugal.

In order to explore the possibility that Berber genes are expressed in Spain, we analyzed the data in appendix 2 of Cavalli-Sforza, Menozzi, and Piazza (1994:470–71 and 476–77 for sources of data) for seven populations: Europe 4 (Basques), 20 (French), 40 (Portuguese), 44 (Spanish), and Africa 1 (Algeria), 26 (Berber), and 46 (Morocco). The only clear result from our analyses is the stable grouping of Portugal with France rather than with Spain.³ Such pooled data do not provide fine-grained information, and there is a lack of data for North Africa (see also Moore 1995).

Two genes have the highest positive correlation on the first European principal component of Cavalli-Sforza, Menozzi, and Piazza (1994), ACP1* C and HLAB* 21. Contrary to the expectation of the demic-diffusion hypothesis, Portugal appears to have the highest frequencies for ACP1* C in the entire world data set (followed by the Lapps). The North African samples have no data for this gene, so we simply cannot assess its importance. Highest incidences of HLAB* 21 centre on Mecca and the area from Port Sudan to Mesawa.

Mecca being the focus of the yearly pilgrimage, its importance in any discussion of gene flow is obvious. The Tigre area (Cavalli-Sforza, Menozzi, and Piazza 1994: sample Africa 59) encompasses the end points of major trade routes across Africa (Ade Ajayi and Crowder 1985) from the pre-Axumite "Southern Arabian period" but especially from the Axumite period. This is well demonstrated at the port of Adulis, which exported African goods and where excavated Mediterranean goods attest to long-distance Axumite trade (Connah 1987).

None of the next nine alleles most highly correlated with the first European principal component is well documented for the Iberian Peninsula south of the Basque region. Limited samples from Barcelona, Madrid, Porto, Coimbra, or Lisbon may perhaps explain the discontinuous pattern of the Iberian second principal component as illustrated in Calafell and Bertranpetit (1993). In the case of some of the genes this seems to be the full extent of the available data, while in others there is either one or no sample available for Iberia. There are also cases in which the Iberian data set represents an outlier.

Cavalli-Sforza, Menozzi, and Piazza (1994) have put forward an interesting hypothesis, but more data and stringent multidisciplinary examination are required before it can be accepted.

Recent research not supporting the model. The large contribution of A, B, and O alleles to the first principal component of Bertranpetit and Cavalli-Sforza (1991) must be evaluated in terms of known differential susceptibility of alleles of the ABO system to cholera, smallpox, influenza, and plague (e.g., Berger, Young, and Edberg 1989). Emphasis on the importance of human leucocyte antigens (HLA) must acknowledge the associations between HLA alleles and disease susceptibility (Thompson 1995). Fix (1996:641) has argued for selection rather than population movement: "The results of . . . simulation experiments show that clinal patterns similar to those observed in European populations can be produced by temporal gradients in natural selection."

Recent research links both Basques and Spaniards with Berbers on HLA allele and haplotype frequencies (Arnaiz-Villena et al. 1995, Martinez-Laso et al. 1995) and proposes a pre-Neolithic common ancestry for all three. Identification of genetic markers for later population movements may clarify the timing of periods of gene flow between North Africa and the Iberian Peninsula (e.g., Loirat, Hazout, and Lucotte 1997).

A number of papers discuss Iberian mtDNA with special reference to Basques (e.g., Bertranpetit et al. 1995). Overall, the interpretation of the work on mtDNA is of a European gene pool established not at the beginning of the Neolithic (Richards et al. 1996) but much earlier. Wilkinson-Herbots et al. (1996) discuss the evidence that the majority of European mtDNA originated 25,000 to 45,000 years ago.

With regard to Iberia specifically, the conclusion is of "a common origin of all Iberian populations in the Upper Palaeolithic" (Côte-Real et al. 1996:343). Cataloni-

3. Moral et al. (1997) have shown by principal-components analysis of blood groups, red cell enzymes, and serum protein polymorphisms that when ungrouped Spanish data are used, France and Portugal cluster more closely than do the Spanish samples.

ans are differentiated from other groups in Iberia as well as from other Europeans. Andalusians are diverse, and there is some evidence of North African genetic input (10% in Spain, 7% in Portugal, 0% in Basques). There is evidence for gene flow from the east which could be associated with the spread of agriculture (7% in Spain, 6% in Portugal, and under 3% in Basques). Thus, gene flow from North Africa appears to be as important as gene flow from the rest of Europe⁴ and undermines any assumption that the modern Iberian population must be solely the result of a Neolithic population replacement: Richards et al. (1996:196) suggest that ca. 5% of the present population of Iberia would be derived from Neolithic colonization.

The homogeneity of the Iberian population is also questioned on the basis of mtDNA, as mentioned above, echoing Reyment (1983), who noted that the Djerban Wahabites of Tunisia (Berbers) group with populations from southern and southeastern Iberia while northwestern Iberia, Basque, and Catalonian blood samples cluster. Given that mtDNA is passed only through maternal inheritance, any discontinuity needs checking from Y-chromosome-specific markers. An initial attempt to evaluate the contribution of Palaeolithic males versus that of Neolithic farmers in the present-day population of Europe proposes the use of the "Palaeolithic" 49a,f-Ht 15 allele marking populations less affected by a "Neolithic" Y-chromosome marker, P12fl-8-kb (Semino et al. 1996). While a certain trend may be apparent, much more work is required. Using the likelihood ratio, we checked the significance of the differences between members of a few key population pairs and found none. One would certainly expect Berber input to be greater in terms of Y-chromosome markers than in terms of mtDNA, but whether proponents of Neolithic population replacement assume a minimum of female migrants is not clear.

Further discussion of fertility levels and population increase in the Neolithic with regard to the hypothesis of replacement of the Mesolithic population will be found in Jackes, Lubell, and Meiklejohn (1997).

THE SKELETAL DATA

Lalueza Fox analyzes the agricultural transition through the use of skeletal and dental variables. A series of 15 skeletal samples is central to the analysis. However, only 2 of these are directly applicable to the central question of replacement at the Mesolithic-Neolithic boundary. The Mesolithic is largely represented

by data from Ferembach's monograph on the Portuguese sample from Moita do Sebastião and the Neolithic by Lalueza Fox's data from Upper Andalusia, apparently in a context lacking absolute dates.

Appropriate data for both the Mesolithic and the Neolithic are, however, considerably more numerous than suggested by Lalueza Fox. The primary Iberian Mesolithic sample is from Moita do Sebastião and Cabeço da Arruda, located about 300 m apart near Muge on a tributary to the Tagus estuary. Other large Portuguese samples exist but are currently unavailable for study and unpublished (see Morais Arnaud 1989). Ferembach's data for Moita represent only a small subset of the total sample, concentrating on complete cranial remains, and therefore extreme care should be taken in their use. Between 1984 and 1989, we restudied the Muge collections preserved in Lisbon (the materials in Porto, about one-third of the total, are still largely uncleaned and have therefore not yet been studied). The majority of the material in Lisbon also required cleaning before accurate observations could be taken. Some of the "complete" crania in Ferembach's analysis, which come from the 19th-century excavations, had been incorrectly reconstructed and required extensive alteration, in some cases resulting in changes of as much as 10% in measurements such as cranial length and breadth. We also studied a series of Neolithic human skeletal samples (Jackes 1988; Jackes and Lubell 1995; Lubell and Jackes 1985, 1988; Lubell et al. 1994; Meiklejohn and Schentag 1988; Meiklejohn, Wyman, and Schentag 1992).

Which Neolithic samples are most germane to the analysis of continuity (or its lack) is crucial. Lalueza Fox compares Portuguese Mesolithic data with Neolithic data from three widely dispersed areas of Spain, and an analysis of the transition that uses these geographically separated areas requires analysis of the variability within and between them. Given the relatively small number of samples, we see this as an intractable problem. We therefore concentrate mainly on the Neolithic samples from central and southern Portugal: Casa da Moura, Melides (Cêrca do Zambujal and Gruta do Lagar), Gruta da Feteira, Gruta da Fontainhas, and Samouqueira (Jackes 1988; Jackes and Lubell 1992; Lubell and Jackes 1985, 1988; Lubell et al. 1994).

Lalueza Fox begins with a craniometric analysis of his 15 primary samples. Ferembach's Mesolithic data clearly cluster away from all other materials, indicating that there is a clustering within Spanish post-Mesolithic samples. Historic Muslim, Jewish, and, to a lesser extent, Basque samples also separate from the general Iberian clustering. Lalueza Fox explains the separation of the Mesolithic and Basque samples as perhaps "related to a pre-Neolithic differentiation" (p. 691), thus accepting the possibility of Mesolithic heterogeneity (see also Jackes and Lubell n.d.). Given this possibility, samples used in any attempt to identify biological continuity or discontinuity at the Mesolithic-Neolithic transition must be derived from the same general area.

We have examined the craniometric relationship of the two Mesolithic samples from Moita and Arruda to

4. Bosch et al. (1997) have provided the first analysis of North African genetic history and support the view that there does not appear to have been a large infusion of North African genes into Iberia brought by Maghrebian Berber males at the time of the Islamic incursions. It is impossible to examine Maghreb-Iberian relationships in more detail because they use pooled data in their discussion of this question. The values provided in the matrix of Reynolds genetic distances can be used to produce a variety of dendrograms suggesting alternative interpretations.

the Neolithic sample from Cêrca do Zambujal at Melides, using cluster analysis, Ward's method, and 31 variables (Meiklejohn and Schentag n.d.). Moita and Arruda have average ^{14}C dates only 300 years apart (ca. 7,900 cal B.P. and ca. 7,600 cal B.P. respectively), while the Melides sample is dated to ca. 5,000 cal B.P. (see Lubell et al. 1994 for the complete list of dates). Despite this, the Melides material is as close to the two Mesolithic samples as they are to each other: in terms of craniometry there is no separation between them, even though the sites are located in ecologically different areas and separated in both space and time.

To explore this relationship further, we reanalyzed data from Lalueza Fox, González Martin, and Vives Civit (1996) with Moita and Arruda included as separate samples.⁵ Moita, Arruda, and Melides skulls were all measured in 1984 and 1985 by Meiklejohn, while Feteira, Fontainhas, Furninha, and Casa da Moura were all measured by Jackes between 1985 and 1989. Differences of technique between researchers and shifts in technique over time may be relevant, but at the very least the sites containing more complete skulls were all measured by Meiklejohn and those with the more incomplete skulls by Jackes. We can demonstrate a scattering among these sites unrelated to researcher. In order to test this, we analyzed available craniometric data employing both average linkage between groups with squared Euclidean distance (as used by Lalueza Fox) and Ward's method. We do not regard our analyses as definitive; one technique is not more appropriate than the other. We tested the robusticity of the data using multiple techniques; some groupings are completely stable, others are not. Furthermore, many sample sizes are inadequate; even when ten skulls are present, very few will be sufficiently complete to provide all measurements or even reasonable estimates.

We analyzed the cranial metrical data available to us using nine measurements from Martin (1957–66): M1 (glabella-occipital length), M5 (basion-nasion length), M8 (maximum cranial breadth), M9 (minimum frontal breadth), M40 (basion-prosthion length), M45 (bizygomatic breadth), M48 (nasion-prosthion height), M52 (orbital height), and M54 (nasal breadth). We limited the analysis to these measurements because we can be reasonably sure that they were taken in a comparable fashion by all researchers. Multivariate analyses must not use intercorrelated variables, and we have chosen measurements with this in mind. We initially used pooled male and female data to (1) increase sample sizes, (2) avoid the problems of sexing fragmentary material, (3) ensure that different sexing stratagems did not skew our samples, and (4) make sure that we were getting close to the sample mean rather than to the mean of the larger or smaller individuals in the population.

Burial patterns introduce taphonomic differences which influence analysis. Portuguese Mesolithic sites contain articulated skeletons with complete skulls,

while in Neolithic sites generally incomplete skulls are separated from the postcranials which could validate gender assignment. Thus, the quality of the data provided by Mesolithic and Neolithic sites will be different. We have already shown that sexual dimorphism did not alter considerably across the Mesolithic-Neolithic boundary (Jackes and Lubell n.d., Jackes, Lubell, and Meiklejohn 1997), and therefore we are not adding the bias of differential dimorphism to the bias introduced by differential taphonomy.

Having previously determined that the discrimination is basically spread over all variables (indicating that we were using total conformation of the skull rather than crude size as indicated by length and breadth; cf. Lalueza Fox, p. 691, who specifies that it is the small size of the Muge crania which differentiates them from later Iberian skulls), we checked the stability of cluster assignments by iterated discriminant function analysis, using the direct method rather than the stepwise discriminant function. Having conducted a very large number of analyses of this type, we find that certain pairings are invariable. For example, the Basque samples group; 19th-century Lisbon (Olivier and Almeida 1972)⁶ and Granada Muslims form a group and fall between our Neolithic Portuguese samples, plus Escoural, and the Bronze Age samples used by Lalueza Fox, plus Eira Pedrinha. However, Moita and Arruda separate completely in many analyses (around 50%). Moita has a strong tendency to group with Fontainhas, then with the other Portuguese samples (western and southern samples), while Arruda and Feteira may group with El Collado (Oliva) and northern samples.

While we can demonstrate that Moita and Arruda do not always group, figure 1 illustrates a method which forces them to cluster, this being in accord with their proximity in time and space. Figure 1 uses a six-cluster solution predicted from hierarchical cluster analysis on eight cranial variables (M48 is excluded because of missing data). Ward's method with the squared Euclidean distance measure is used, since average linkage (between groups) separates Moita and Arruda on both five- and six-cluster solutions. Here we used only *male* skulls to conform with Lalueza Fox, González Martin, and Vives Civit (1996), and the list of samples is given in table 1. The very poor Neolithic samples from Casa da Moura, Fontainhas (both requiring that missing data be replaced by the means of the Neolithic Portuguese crania), and Feteira were excluded from the analysis, as was El Collado (Oliva). Escoural and Eira Pedrinha were also excluded initially because each required the use of multiple regression to provide one missing variable. After membership in six clusters was assigned, we included Escoural and Eira Pedrinha males as unknown samples. Discriminant function analysis (direct method) was run and cluster membership stabilized immediately.

Figure 1 illustrates the first three of five functions cal-

5. For all statistical tests we have used the programs available in version 6.1.3 of SPSS for Windows.

6. Only individuals aged 30–39 years who did not die of pulmonary tuberculosis; missing data derived from multiple regression.

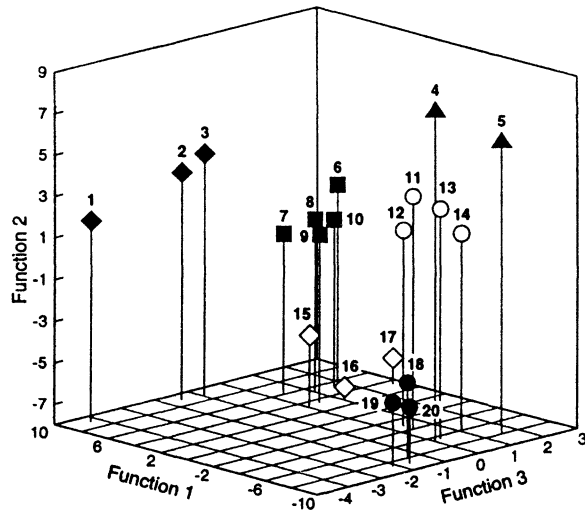


FIG. 1. Scatter plot of eight craniometric variables for male skulls only (M_1 , glabello-occipital length; M_5 , basion-nasion length; M_8 , maximum cranial breadth; M_9 , minimum frontal breadth; M_{40} , basion-prosthion length; M_{45} , bizygomatic breadth; M_{52} , orbital height; M_{54} , nasal breadth) using the first three discriminant functions, calculated by direct method, with clusters predicted from hierarchical cluster analysis. Ward's method, with the squared Euclidean distance measure. For identification of samples see table 1.

culated. Function 1 explains 67.81% of the variance and is significant at the .0000 level; function 2 explains 27.1% of the variance (significance = .0000) and function 3 explains 3.01% of the variance (significance = .04). The other functions are non-significant. The eight variables are most highly correlated with functions 2–5 in a quite random fashion. None of the variables used contributes most to function 1, M_8 is most highly correlated with function 2, and M_{52} and M_{54} are most highly correlated with function 3. On the basis of figure 1, the contention of Lalueza Fox that cranial morphology changed “dramatically” (p. 693) from the Mesolithic to the Neolithic “as a reflection of a genetic discontinuity probably associated with migration” is not upheld when more appropriate samples are used. Furthermore, there is no reason to consider post-Mesolithic Iberia homogenized by the rapid growth of a migrant population.

We have undertaken cluster analyses of Lalueza Fox's cranial data for all skulls and for males alone, together with data collected by Meiklejohn from Arruda, Moita, and Melides, Iberomaurusian and Capsian samples from the Maghreb, and the Breton Mesolithic samples from Tévéc and Hoëdic. To these we have added data from Angel (1971) on Greek skulls and a further sample of male Basques from Morant (1929) in order to test the validity of clustering techniques by ensuring that the Basque samples fall together. Irrespective of the technique used, the available measurements employed, or the samples included, one relationship is constant: Moita and Melides never separate.

We agree with Lalueza Fox that the data for stature

TABLE 1
Samples Used for Analyses

No.	Sample	Source
1	Talayotic Majorca	Lalueza Fox, González Martín, and Vives Civit (1996) (MAL2)
2	Talayotic Majorca	Lalueza Fox, González Martín, and Vives Civit (1996) (MAL1)
3	Tarragona	Lalueza Fox, González Martín, and Vives Civit (1996) (TAR)
4	Basques	Morant (1929)
5	Basques	de la Rúa (1992) (BAS)
6	Medieval Christian Cantabria	Lalueza Fox, González Martín, and Vives Civit (1996) (CAN)
7	Medieval Central Catalonia	Lalueza Fox, González Martín, and Vives Civit (1996) (CAT2)
8	Medieval Barcelona Jews	Lalueza Fox, González Martín, and Vives Civit (1996) (JEW)
9	Medieval Christian Burgos	Lalueza Fox, González Martín, and Vives Civit (1996) (BUR1)
10	Visigothic North Meseta	Lalueza Fox, González Martín, and Vives Civit (1996) (VIS)
11	Bronze Age Central Catalonia	Lalueza Fox, González Martín, and Vives Civit (1996) (CAT1)
12	Bronze Age Upper Andalusia	Lalueza Fox, González Martín, and Vives Civit (1996) (GRA)
13	Medieval Christian Burgos	Lalueza Fox, González Martín, and Vives Civit (1996) (BUR2)
14	Eira Pedrinha	Mendes Corrêa and Teixeira (1949)
15	Medieval Granada Muslims	Lalueza Fox, González Martín, and Vives Civit (1996) (MUS)
16	Escoural	Isidoro (1981)
17	Visigothic Portuguese	Cunha and Neto (1953)
18	Melides	Meiklejohn and Schentag (n.d.)
19	Cabeço da Arruda	Meiklejohn unpublished
20	Moita do Sebastião	Meiklejohn and Schentag (n.d.)

do not suggest a disruption. They are consistent with other reported data that show a gradual decrease in stature in European populations from the Upper Palaeolithic through the Neolithic, with subsequent stature increase in the post-Neolithic (Meiklejohn et al. 1984).

The caries data are also said not to show discontinuity. We agree but think the available data show a much more complex pattern than that suggested by Lalueza Fox. Lalueza Fox used Frayer's (1987) data, but we have published a larger sample (Meiklejohn and Schentag 1988; see also Meiklejohn, Wyman, and Schentag 1992, Lubell et al. 1994 for a discussion of subsets of those data). Lubell et al. (1994) have also published appropriate Neolithic data. Frayer's sample of ca. 1,000 teeth was partial (cf. Moita, $n = 918$, and Arruda, $n = 1,147$, for which the total caries rates are 11.3% and 7.7% respectively (Meiklejohn and Schentag 1988), and many specimens he examined had not been cleaned. Our data (Lubell et al. 1994: table 2 and fig. 9) generally show a pattern of reduction in the frequency of caries (occlusal and approximal) from the Portuguese Mesolithic to the Neolithic. However, variation in the expression of dental pathology and taphonomic factors cannot be ignored in any consideration of caries rates (see Jackes and Lubell 1996). We interpret the caries rates as related to complex dietary changes that were already under way during the Mesolithic and continued into the Neolithic (Lubell et al. 1994).

Our data on stable isotopes (Lubell et al. 1994) show quite complex dietary differences between sites labelled as Mesolithic and Neolithic. Thus the skeletal material recovered in "Neolithic" context at Samouqueira (ca. 7,200 cal B.P.), had a "Mesolithic" isotopic signature. We suggest, therefore, that Lalueza Fox's comment (p. 693) that "it is unreasonable to attribute all the observed changes to the Neolithic change in the diet, given that precisely the markers most dependent on diet do not reflect any remarkable disruption," is clear recognition of the absence of change that would reflect demic diffusion.

The demic-diffusion model requires that new populations with a fundamentally new diet replaced a population that had steadily and successfully maintained a hunting and gathering economy. It thus requires a massive advantage for the incoming Neolithic population, one that would permit the newcomers an extremely high fertility rate. Our analyses suggest that the Mesolithic population of Iberia was stable demographically and that Neolithic population increase was modest (Jackes, Lubell, and Meiklejohn 1997), indicating no revolutionary change in the way of life. The data that we presented in Lubell et al. (1994) led to our conclusion that "a change of diet was established by 7000 [cal] BP, but . . . the trend had been initiated soon after 8000 [cal] BP" (p. 201). The Mesolithic-Neolithic transition period shows a shift in diet and related patterns of dental pathology, but it is neither sudden nor at the boundary, as would be predicted by Lalueza Fox. Instead, it is gradual and continuous across the boundary.

CONCLUSION

We have argued that the suggested congruency of craniometric data to a demic-diffusion model is illusory. The genetic data alleged to support the model of demic diffusion for Neolithic origins in the Iberian Peninsula are far too incomplete to exclude other models. We question the applicability of the osteological data that are supposedly congruent with the genetic data. There is no evidence for local discontinuity, and we suggest that data from central Portugal, the source of the core Mesolithic data, show clear continuity. Lalueza Fox himself concludes that only in craniometry can discontinuity be discerned. We have shown that more complete data remove any evidence of discontinuity.

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