

13 *Basque dental morphology and the “Eurodont” dental pattern*

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13.1 Introduction

The Basque peoples of northern Spain and southern France have long held the interest of anthropologists and linguists. Linguistically, they are considered an isolate with no close ties to any surrounding Indo-European-speaking group. This linguistic peculiarity raised expectations that a similar situation would be found at the biological level. In the early twentieth century, studies of Basque cranial morphology were mostly typological in nature, as researchers made every effort to identify a distinctive Basque type (MacClancy 1993; de la Rúa et al. 2005/2006 for a review). In the 1930s, the discovery of remains at the site of Urutiaga (Gipuzkoa), which presumably dated to the Upper Paleolithic, pushed the origins of the Basque population further back in time. This led to a popular hypothesis that the “Basque type” reflected an indigenous and local evolution of the Cro-Magnon race (Aranzadi and Barandiaran 1948). Later radiometric dating of these skulls unequivocally placed the Urutiaga remains in the more recent Bronze Age, a finding that challenged the Cro-Magnon hypothesis of Basque origins (Altuna and de la Rúa 1989).

In the mid-twentieth century, blood antigen typing replaced cranial typology in addressing questions of population origins. Cumulative information on more than a single locus seemed to confirm the idea that Basques were a locally evolved population that had descended from Upper Paleolithic Europeans. Seemingly, Basques survived the impact of genetic admixture with later migrants (Near East Neolithic farmers) to a greater extent than other European populations

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(Calafell and Bertranpetit 1994a, b; Cavalli-Sforza 1988; Bertranpetit and Cavalli-Sforza 1991; Mourant 1947).

Research on a broad array of “classic genetic polymorphisms” (blood groups, serum proteins, and enzymes) pointed to the idea that the genetic distinctions of the Basque population had not been completely erased despite substantial gene flow from neighboring populations (Calafell and Bertranpetit 1994a). In a detailed synthesis of worldwide genetic data in *The History and Geography of Human Genes*, Cavalli-Sforza et al. (1994) analyzed European gene frequency variation and found Indo-European-speaking populations clustered closely with one another. The most notable European outliers were Sardinians and three non-Indo-European groups – Lapps, Finns, and Basques. Synthetic maps also suggested the Basques were distinct, especially the map based on the fifth principal component of European gene frequencies (Cavalli-Sforza et al. 1994:294). Some authors, however, contend that the methodology employed for multiple genetic data analyses (mainly synthetic maps derived from principal components analysis) may lead to spurious results (Sokal et al. 1991).

While there are numerous publications on the genetics of Basque populations, the metrics of skeletal remains have received much less attention. In contrast to the earlier typological studies of Basque skulls in the 1930s and 1940s, recent studies adopt a statistically driven craniometric approach to the issue of Basque origins and relationships (cf. de la Rúa 1992; Janzen 2011; Lalueza Fox et al. 1996). Assessing Basque cranial morphology, de la Rúa (1992) concluded that complex morphometric and multivariate analyses revealed some differentiation of Basques from Iberic populations.

Recent debate has focused on ascertaining whether Basques are the best representative population of Paleolithic Europe. Some authors contend that demic diffusion during the Neolithic had a profound impact on the genetic profile of modern Europeans (Ammerman and Cavalli-Sforza 1984; Barbujani et al. 1994, 1995; Bellwood 2001). Others suggest the genetic impact of Neolithic farmers on Europeans is evident but is not as pronounced as the demic diffusion model suggests (Richards 2003; Zvelebil 1998, 2000). A recent study on the mtDNA diversity of hunter-gatherers and first farmers in northern Spain proposed a random dispersion model for Neolithic farmers in Europe, contradicting the total acculturation and replacement models developed to explain Neolithization (Hervella et al. 2012).

Recently, genetic studies of Basque populations have focused on DNA polymorphisms, including mtDNA and nuclear markers on both autosomal and sex chromosomes (Alonso et al. 2005; Bertranpetit et al. 1995; Brion et al. 2003; Izagirre and de la Rúa 2001; Izagirre et al. 2001). The extensive literature on Basque genetics focuses on several themes (Alonso 2008): (1) internal relationships, or population structure; (2) external relationships, to neighboring or

distant groups; and (3) distinctive or unique markers in the Basque population that suggest the ancestry of Basques can be traced back to pre-Neolithic populations in Western Europe.

The isolation of Basques has resulted in some genetic heterogeneity among Basque subpopulations with respect to non-Basques in Y-chromosome but not in mtDNA lineages (Martínez-Cruz et al. 2012). These discordant results in paternal and maternal lineages explain, at least partially, the contradictory findings that support (Alfonso-Sanchez et al. 2008; Calderon et al. 2000; Iriondo et al. 2003; Manzano et al. 1996, 2002) and reject (Comas et al. 1998; Rodriguez-Ezpeleta et al. 2010) genetic heterogeneity in Basques. Still, some intrinsic level of genetic structure is present among Basque populations that may be a consequence of different cultural, geographic, and historic factors.

Regarding the relationship of Basques to other European populations, recent data on uniparental Y-chromosome lineages indicate Basques are similar to other Western European populations, although they show slight frequency differences. It has been suggested that some other Western European populations might exhibit the genetic distinctiveness of the populations inhabiting the Basque region, but that this peculiarity is not linked to having a Basque culture (language) (Martínez-Cruz et al. 2012). Finally, on the topic of distinctive or unique genetic markers in the Basque population, several lines of evidence indicate at least some (DNA) lineages (alleles) have evolved *in situ*, probably since pre-Neolithic times (Alonso and Armour 1998). This supports the idea that the ancestry of Basques can be traced back to pre-Neolithic populations in Western Europe.

Given the widespread interest in the question of Basque origins, it is not surprising there are dozens of publications on genetic and cranial diversity. Surprisingly, we know almost nothing about the Basque dentition. Worldwide surveys of tooth crown size (Kieser 1991) and dental morphology (Scott and Turner 1997) make no mention of Basque dental variation. Our aim is to use an entirely new set of biological characteristics to determine whether Basques from northern Spain exhibit a unique dental morphological profile, that is, one that distinguishes them from Indo-Europeans to the north and east, and Afro-Asiatic neighbors to the south.

13.2 Materials and methods

Morphological observations were made on living Basques, Spanish, and mixed Basque/Spanish individuals, as well as historic remains from the Cathedral of Santa Maria, Vitoria (Alava province); the latter date from the eleventh to nineteenth centuries. In 2005, crown traits were scored on 145 dental casts (36 Basque, 61 Spanish, 48 Basque-Spanish) collected by Alberto Anta at the Dental

department of the University of the Basque Country (UPV/EHU). Although data were collected in Bilbao, individuals could have come from any of the Basque provinces. In 2006 and 2008, crown and root traits were scored on 460 skeletons disinterred from the Cathedral of Santa Maria, Vitoria, Spain, under the direction of Agustin Azkarate Garai-Olaun and his associates; burial records are not exact, but it is estimated that more than 75 percent of the individuals were of Basque heritage. Vitoria attracted merchants and travelers from other countries so there are non-Basque elements in the sample, but these would be in a decided minority (Jaione Agirre-Garcia, personal communication). Although we can provide an initial characterization of Basque tooth crown and root morphology, we are not in a position to address such issues as Basque population structure. Dental variation among Basque subpopulations in Spain and France is likely, but this issue will have to be addressed when more regional samples have been studied.

Following the Arizona State University Dental Anthropology System (ASUDAS; Turner et al. 1991), 16 crown traits were scored on 29 teeth for presence and degree of expression in each dental cast. Two crown traits (Bushman canine, enamel extensions) were not scored on casts but were recorded for skulls. Eighteen crown traits, six root traits, and missing/pegged/reduced UM3 were scored on teeth of the historic remains. As crown and root traits are not sexually dimorphic, data for males and females were combined (Scott and Turner 1997). Regarding issues of left and right sides, the individual count method was followed whereby an individual was classified according to the antimer that exhibited the greatest degree of trait expression (Scott 1980).

Crown frequencies for the four samples from northern Spain were compared to 25 worldwide composite groups from Scott and Turner (1997). Given the limitation of casts, analysis involved nine crown traits: UI1 shoveling, three-cusped UM2, UM1 Carabelli's trait, four-cusped LM1 and LM2, Y-groove pattern on LM2, and cusp 6, cusp 7, and the deflecting wrinkle on LM1. To include root traits and focus specifically on Western Eurasian populations, 15 traits (11 crown, four root) were compared between the historic Vitoria sample and 16 geographic groups from Europe, North Africa, the Middle East, and India. Distance values were derived through Nei's genetic distance program in NTSYS; cluster analysis of these intersample values based on UPGMA and the neighbor-joining method yielded congruent trees; as such, only the UPGMA results are shown.

13.3 Results

In compiling comparative data on Western Eurasian and other world groups, a recurrent hindrance is the use of different traits and breakpoints.

Table 13.1. *Total crown and root trait frequencies for key teeth by breakpoint*

Trait	Tooth	Breakpoint	Spanish	Living Spanish-Basque	Basque	Cathedral of Santa Maria	Compared to World
Winging	UI1	1-3/0-3	0.017	0.000	0.000	0.096	Low
Shoveling	UI1	3-6/0-7	0.034	0.043	0.083	0.044	Low
Double shoveling	UI1	2-6/0-6	0.017	0.021	0.000	0.030	Low
Tuberculum dentale	UI2	2-6/0-6	0.258	0.392	0.200	0.226	Low
Interruption grooves	UI2	1/0-1	0.196	0.044	0.200	0.295	Intermediate
Bushman canine	UC	1-3/0-3				0.022	Low
Distal accessory ridge	LC	1-5/0-5	0.281	0.282	0.229	0.130	Low
Multiple lingual cusps	LP2	2-7/0-7	0.557	0.673	0.778	0.514	High
3-Cusped (-hypocone)	UM2	0-1/0-5	0.184	0.303	0.285	0.320	High
Carabelli's cusp	UM1	5-7/0-7	0.033	0.063	0.112	0.209	High
Carabelli's cusp	UM1	2-7/0-7	0.567	0.624	0.778	0.659	High
Cusp 5	UM1	1-5/0-5	0.228	0.244	0.193	0.225	Low
Enamel extensions	UM1	2-3/0-3				0.032	Low
Pegged/missing	UM3	1/0-1				0.116	Intermediate
4-Cusped (-hypoconulid)	LM1	0/0-5	0.086	0.174	0.114	0.076	High
4-Cusped	LM2	0/0-5	0.850	0.933	0.886	0.868	High
Y-Pattern	LM2	Y/Y-X+	0.220	0.235	0.190	0.148	Low
Cusp 6	LM1	1-5/0-5	0.125	0.178	0.182	0.079	Low
Cusp 7	LM1	2-4/0-4	0.036	0.088	0.086	0.070	Low
Protostylid	LM1	2-7/0-7	0.018	0.023	0.000	0.000	Low
Deflecting wrinkle	LM1	3/0-3	0.128	0.174	0.435	0.202	Low
2-Rooted	UP1	2-rooted/total				0.516	Intermediate
3-Rooted	UM2	3-rooted/total				0.609	Intermediate
2-Rooted	LC	2-rooted/total				0.092	High
Tome's root	LP1	4-7/0-7				0.138	Low
3-Rooted	LM1	3-rooted/total				0.013	Low
1-Rooted	LM2	2-rooted/total				0.763	Intermediate

Source: Defined in Scott and Turner (1997).

For that reason, full trait frequency distributions are presented in the Appendix for 18 crown traits (31 teeth), six root traits (six teeth), and pegged/missing/reduced UM3 for the Spanish, Basque, Spanish-Basque, and historic samples. The focus in the analysis and discussion is on trait frequencies for key teeth using the most common breakpoints (Scott and Turner 1997).

13.3.1 *Characterization of Basque tooth crown and root morphology*

Data for 18 crown traits, six root traits, and UM3 agenesis for the four samples from northern Spain are presented in Table 13.1. In the far right column, the

array of frequencies are noted as low, intermediate, or high relative to other world populations (Scott and Turner 1997).

Europeans are more often characterized by the absence or rarity of traits rather than by their presence (Mayhall et al. 1982; Lee and Scott 2011); Basques are no exception to this generalization. Traits that are absent or relatively infrequent in the Spanish/Basque samples include UI1 winging, shoveling, and double shoveling and UI2 *tuberculum dentale*, UC Bushman canine, LC distal accessory ridge, UM1 cusp 5 and enamel extensions, LM2 Y-groove pattern, and LM1 cusp 6, cusp 7, protostylid, and deflecting wrinkle. Tome's roots of LP1 and three-rooted lower first molars are also rare or in low frequency. Five traits show intermediate frequencies: UI2 interruption grooves, UM3 agenesis, two-rooted UP1, three-rooted UM2, and two-rooted LM2. Five traits found in high frequencies relative to other world populations include LP2 multiple lingual cusps, UM1 Carabelli's cusp, three-cusped UM2, and four-cusped LM1 and LM2. For roots, the most distinctive variant is the two-rooted lower canine; the Basque frequency is high even by European standards (Alexandersen 1962, 1963; Lee and Scott 2011). For high frequency traits, two involve crown simplification (hypocone loss on UM2 and hypoconulid loss on LM1 and LM2) rather than elaboration.

13.3.2 Distance analysis: Basques versus world samples based on nine crown traits

Phenetic distances, computed between the four samples from northern Spain and 25 world populations (composite samples in Scott and Turner 1997), serve as the basis for the UPGMA cluster diagram in Figure 13.1. Three fundamental divisions are evident in the dendrogram: the deepest break is for sub-Saharan Africans, followed by a division between Asian/Pacific populations on one hand, and Western Eurasians on the other. Focusing on Basques, the historic sample is the most highly differentiated group within the Western Eurasian cluster. Remarkably, there is no single variable among the nine crown traits that sets the historic Basque sample apart. The differences are minor yet act in concert to separate the Santa Maria sample from all remaining groups in the cluster. The next sample to split off is the living Basque and, in this case, an unusually high frequency of deflecting wrinkle may contribute to the result. The Basque and Spanish-Basque samples cluster closely together, as part of the third split in this grouping. All remaining Western Eurasian populations are tightly clustered. Compared to African and Asian/Pacific populations, Western Eurasians are the most coherent and least differentiated group from a dental morphological standpoint.

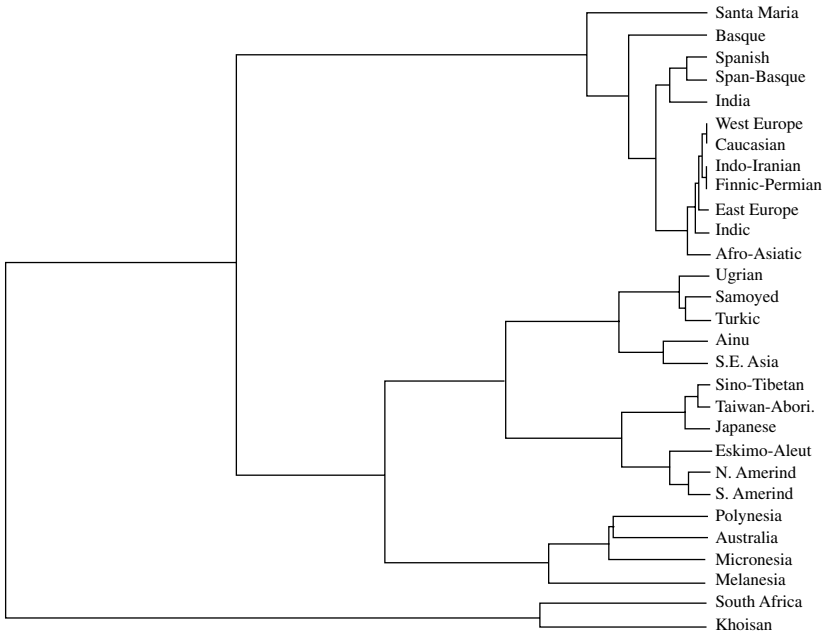


Figure 13.1. UPGMA dendrogram showing relationship of historic and modern Basques to world populations.

13.3.3 *Basques compared to Western Eurasian populations*

Table 13.2 presents data for 11 crown and four root traits in 16 samples from Europe, North Africa, the Middle East, and South Asia. The mean trait frequency, standard deviation, and coefficient of variation for each trait are listed at the bottom of the table, along with frequencies for living Basques and the historic sample from Santa Maria.

Dental trait frequency variation among Western Eurasian groups has two primary sources: (1) between group differentiation brought about by founder effect/genetic drift during colonization events that occurred mostly during the Holocene, and (2) sampling error. Prior to the wide adoption of the ASUDAS, a third source of variation would be inter-observer error. This error is much less of a problem than it was before 1980. Data in the table were obtained mostly by researchers trained at Arizona State University and/or who used ASUDAS standards (Turner et al. 1991).

Overall, dental variation among Western Eurasians is minor, corroborating results from the first analysis. Linguistically, groups in the sample are mostly

Indo-European and Afro-Asiatic. The two exceptions, in addition to Basques, are Finland (Finnic-Permian, Uralic language family) and early South Asia, where language attribution is problematic (Elamo-Dravidian?). The Finnish sample shows the highest frequency of shoveling, the lowest frequency of 2-rooted UP1, and no 2-rooted lower canines – all of which align them with North Asian populations. However, no other trait stands out in a Western Eurasian context; this pattern is also evident for Finns in genetic markers of the blood (Nei and Roychoudhury 1988). Early South Asia but not Late South Asia is distinctive for the absence of 2-rooted canines, low frequency of 2-rooted UP1, high frequency of UM1 cusp 5, high frequency of 3-rooted UM2, and high frequency of LM1 cusp 6. These five traits fall in the direction of Southeast Asian dental variation, yet the remaining nine traits are more consistent with Western Eurasia. The issue cannot be resolved here, but these data suggest a residual effect from aboriginal Indian populations who were biologically allied with Southeast Asians, compounded by late Holocene invasions from the Middle East (see Hemphill, this volume).

The two Basque samples at the bottom of Table 13.2 share more similarities with Western Eurasians than either the Finns or early South Asians. UI2 *tuberculum dentale* is at the low end of the frequency range while 2-rooted lower canines are at the high end viz. Western Eurasians. For the most part, however, Basques do not exhibit any trait that sets them apart from neighboring Indo-European or Afro-Asiatic populations in North Africa and the Levant.

13.3.4 Distance analysis of Western Eurasian populations based on dental traits

The dendrogram based on a distance analysis of 15 traits among 17 Western Eurasian groups is shown in Figure 13.2. Two groups stand out while the others fail to reveal natural geographic groupings. Finland, with several traits aligning it with North Asia, breaks out first as the most highly differentiated group in the dendrogram. Finns are followed by early South Asians with a number of frequencies that align them with Southeast Asia rather than Western Eurasia. The historic Basque sample does not separate out from the cluster as shown in Figure 13.2; it instead clusters with England and the Levant. Northwest Africa clusters with the Nile Valley, as expected, but they also group with Denmark, a finding less expected. Overall, this analysis shows that Basques are not distinct enough from other Western Eurasian groups to indicate they are a clear-cut outlier.

Table 13.2. *Basque crown and root trait variation in the context of Western Eurasian populations*

Trait:	SHOV	T.D.	Root#	MLC	Root#	HYP	C5	EnExt	Root#	C Abs	4-Cusp	Y Gr	C6	C7	Root#
Tooth:	UH1	UH2	LC	LP2	UP1	UM2	UM1	UM1	UM2	UM3	LM2	LM2	LM1	LM1	LM2
Italy (1)	0.074	0.538	0.027	0.561	0.527	0.195	0.196	0.090	0.712	0.114	0.829	0.238	0.018	0.061	0.850
NW Africa (2)	0.106	0.339	0.057	0.689	0.523	0.326	0.104	0.035	0.758	0.184	0.675	0.395	0.116	0.061	0.895
Nile Valley (3)	0.262	0.407	0.018	0.696	0.631	0.162	0.141	0.193	0.722	0.127	0.750	0.271	0.103	0.025	0.830
Denmark (4)	0.053	0.256	0.057	0.596	0.576	0.145	0.429	0.017	0.654	0.086	0.884	0.274	0.162	0.089	0.859
England (4)	0.028	0.255	0.053	0.593	0.310	0.274	0.101	0.008	0.597	0.114	0.731	0.208	0.092	0.038	0.767
Holland (4)	0.000	0.405	0.083	0.537	0.361	0.333	0.125	0.030	0.460	0.172	0.892	0.205	0.040	0.063	0.659
Ireland (4)	0.111	0.667	0.033	0.790	0.386	0.109	0.186	0.038	0.603	0.106	0.711	0.287	0.067	0.034	0.659
Scotland (4)	0.068	0.301	0.112	0.653	0.394	0.179	0.309	0.072	0.711	0.085	0.718	0.232	0.167	0.048	0.785
Greenland (5)	0.000	0.455	0.092	0.603	0.363	0.182	0.340	0.035	0.636	0.125	0.766	0.342	0.233	0.065	0.750
Norway (5)	0.000	0.535	0.043	0.457	0.600	0.241	0.204	0.011	0.641	0.160	0.910	0.194	0.105	0.032	0.762
Finland (6)	0.437	0.437	0.000	0.469	0.083	0.208	0.125	0.139	0.500	0.145	0.791	0.220	0.091	0.084	0.767
Levant (7)	0.075	0.160	0.040	0.785	0.480	0.245	0.050	0.019	0.935		0.925	0.265	0.015	0.030	1.000
Mallorca (8)		0.193		0.725		0.324	0.283				0.739	0.142	0.050	0.000	
France (9)		0.667	0.016	0.619	0.450	0.195	0.225				0.847				
Early SA (10)	0.128	0.280	0.000	0.581	0.139	0.312	0.361	0.042	0.905	0.154	0.704	0.300	0.376	0.051	0.833
Later SA (10)	0.112	0.384	0.037	0.457	0.430	0.268	0.105	0.129	0.528	0.210	0.815	0.330	0.099	0.110	0.876
Mean	0.104	0.392	0.045	0.613	0.417	0.231	0.205	0.061	0.669	0.137	0.793	0.260	0.116	0.053	0.804
S.D.	0.1178	0.1536	0.0324	0.1057	0.1561	0.0700	0.1103	0.0564	0.1372	0.0379	0.0806	0.0651	0.0926	0.0281	0.0890
C.V.	1.13	0.39	0.72	0.17	0.37	0.30	0.54	0.92	0.21	0.27	0.10	0.25	0.80	0.53	0.10
Basque (L)	0.083	0.200		0.777		0.286	0.228				0.886	0.190	0.182	0.036	
Basque (SM)	0.044	0.258	0.092	0.513	0.516	0.320	0.224	0.032	0.609	0.116	0.868	0.148	0.079	0.070	0.763

Sources: (1) Coppa et al., 1998, 2007; Vargiu et al., 2009; (2) Irish, 2000; (3) Irish, 1993; (4) Adler, 2005; (5) Scott and Alexandersen, 1992; (6) Salo, 2005; (7) Ullinger et al., 2005; (8) Garcia Savoli, 2009; (9) Laforest et al., 2011; (10) Hawkey, 2002.

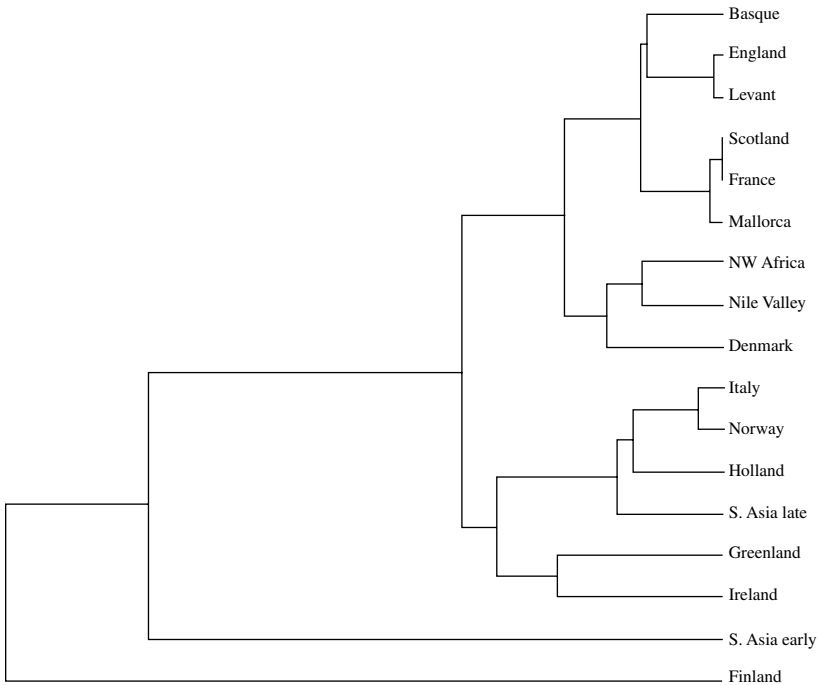


Figure 13.2. UPGMA dendrogram showing relationship of historic Basque sample from Cathedral of Santa Maria (Vitoria, Spain) to Western Eurasian populations.

13.4 Discussion

Although Basques show a general Western Eurasian dentition, the first cluster analysis indicates they are somewhat distinct in the context of world populations, yet still align with Europeans. This result parallels findings from genetics that Basques fall within the European sphere but as something of an outlier. Using gene frequency data from Roychoudhury and Nei (1988), we analyzed European samples for 12 serum protein and red cell enzyme systems (14 alleles) and eight blood group systems (nine alleles). The number of European samples for any given system ranged from 13 to 36, with most falling in the twenties. We calculated a European mean, the 95 percent confidence limits, and range for each allele. Although Basque gene frequencies usually fall within the range of Europeans, they fell outside the 95 percent confidence limit for 19 of 23 alleles. In seven of twenty-three cases, the Basque frequency was outside the range of European frequencies. This finding was especially marked for properdin factor B, where allele BF S was markedly lower (0.562) than the European

mean (0.773); conversely, allele BF F11 was considerably higher in Basques (0.145) relative to the European mean (0.014). A single Portuguese sample precluded Basques from being outside the range of Europeans for RH*r, but they were well above the 95 percent confidence limits for the allele that has long set Basques apart from other Europeans. ABO*B also falls outside the range of all other Europeans, with the exceptionally low frequency of 0.032 (viz. range of 0.044–0.222).

For crown and root traits, Basques show a similar pattern when analyzed in the context of Western Eurasians. For extant Basques, seven of nine crown trait frequencies fall outside the 95 percent confidence limits of Western Eurasian samples. For the historic sample, eight of fifteen traits are outside the Western Eurasian 95 percent confidence limits. UI2 *tuberculum dentale* and LM2 Y-groove pattern are less frequent in the Basques, while two-rooted lower canines, two-rooted UP1, and four-cusped LM2 are notably higher in one or both samples. As with genetic markers, Basques show dental differences from European, North African, and Middle Eastern groups, but there is no single feature that sets them apart.

13.4.1 “Caucasoid” dental complex

On the basis of the analysis of American white dental cast collections, Mayhall et al. (1982) defined the “Caucasoid dental complex of the permanent dentition,” which included (1) absent or trace shoveling; (2) no bilateral winging; (3) no premolar occlusal tubercles, or odontomes; (3) Carabelli’s trait often expressed as a cusp or bulge; (4) LM1 protostylid rare or absent; (5) LM1 cusp 6 rare or absent; and (6) cusp 7 rare or absent. They reported three-cusped UM2 frequencies of about 30 percent, but they did not include this trait in the dental complex.

Our analysis of Basque dental morphology, along with numerous other studies on European, Middle Eastern, North African, and Indian populations undertaken in the past 50 years (Adler 2005; Aksianova 1979; Aksianova et al. 1977, 1979; Alexandersen 1962, 1963; Bailey 2006; Brabant and Ketelbant 1975; Coppa et al. 1998, 2007; Cucina et al. 1999; Desideri and Besse 2010; Du Souich 2002; Gadzhiev 1979; García Savoli 2009; Gauta et al. 2010; Guatelli-Steinberg et al. 2001; Hawkey 1998, 2002; Irish 1993, 2000, 2006; Ismagulov and Sikhimbaeva 1989; Johnson and Lovell 1994; Kaczmarek 1992; Kaul and Prakash 1981; Khaldeeva 1979; Kirveskari 1974; Kochiev 1979; Laforest et al. 2011; Lipschultz 1997; Lukacs 1987; Pilloud 2009; Roler 1992; Rosenzweig and Zilberman 1967, 1969; Salo 2005; Scott and Alexandersen 1992; Senyurek 1952; Sofaer et al. 1986; Ullinger et al. 2005; Vargiu et al. 2009; Weets 2004;

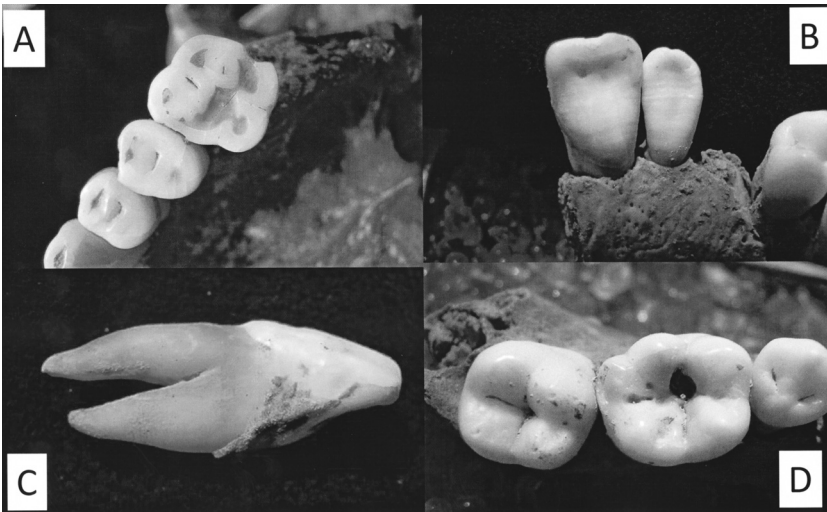


Figure 13.3. Characteristic “Eurodont” traits: (A) Carabelli’s cusp on UM1 so large that it shows exposed dentine, (B) typical spatulate and mostly featureless upper incisors, (C) two-rooted lower canine, (E) five-cusped LM1 and four-cusped LM2. (Please see color plate section.)

Zubov 1968), extends the Caucasoid dental complex to include a number of additional traits. In keeping with Turner’s dental distinction between North (Sinodonts) and Southeast (Sundadonts) Asians and Irish’s designation of an Afridont pattern for sub-Saharan Africans (this volume), we propose “Eurodont” as a shorthand term for Western Eurasian dental morphological variation. Characteristic crown and root expression includes:

1. Low frequency traits (traits uncommon/infrequent in Western Eurasians): UI1 winging, UI1 shoveling, UI1 double shoveling; Bushman canine; UM1 enamel extensions; LM2 Y pattern; LM1 cusp 6; LM1 cusp 7; LM1 proto-stylid; LM1 deflecting wrinkle; three-rooted lower first molars.
2. High frequency traits (traits most common in Western Eurasians): high frequency of UM1 Carabelli’s cusp/tubercle forms; two or more lingual cusps LP2; three-cusped UM2; four-cusped LM1 and LM2; two-rooted lower canines (Figure 13.3).

13.4.2 *Primitive and derived*

As a follow-up to extensive studies of dental morphological variation in recent African populations, Irish (1998; Irish and Guatteli-Steinberg 2003) extended

observations to the hominin fossil record to evaluate the degree to which various geographic populations exhibited primitive or derived dentitions. On the basis of a large number of trait comparisons, he found sub-Saharan Africans showed the fewest derived traits of all world populations, in accord with the recent “out of Africa” model for the origins of anatomically modern humans.

To determine how primitive or derived the Basque dentition is on a world scale, we adopted an approach that does not require comparisons to earlier hominin fossils. On the basis of monomorphic characteristics of hominoid and early fossil hominin dentitions, we utilized eleven traits that were either 0 percent or 100 percent in the ancestral population. Twelve world populations and the Basques were then compared to this standard. Traits assumed to be 0 percent in the ancestral condition include three-cusped UM2, premolar odontomes, two-rooted lower canines, four-cusped LM1, four-cusped LM2, three-rooted LM1, and pegged/missing/reduced UM3. Traits assumed to be 100 percent include two-rooted UP1, three-rooted UM2, two-rooted LM2, and Y-pattern LM2.

When trait frequencies of regional groups were compared to “ancestral standards” to estimate relative distance, a distinct pattern emerged. First, the least derived world populations are sub-Saharan Africans (0.058) and Bushmen (0.073) – a finding in accord with Irish (1998; Irish and Guatelli-Steinberg 2003). Groups from Southeast Asia and the Pacific exhibit a uniform and intermediate level of derived traits: Southeast Asia Early (0.137), Australia (0.140), Polynesia (0.155), Melanesia (0.157), and Southeast Asia Late (0.163). Groups that exhibit the most derived dentitions in the world are about equally distant from the presumed ancestral condition but for entirely different reasons. Primarily on the basis of root number reduction, the distance values for North Asian and derivative populations are American Indian (0.287), China-Mongolia (0.310), and Eskimo-Aleut (0.373). Distance values for Western Eurasians are very similar to North Asian/New World values (i.e., Western Europe [0.287], Basque [0.359]), but this finding is attributable to crown simplification (e.g., hypocone and hypoconulid reduction) rather than root reduction. Western Eurasians in general and Basques in particular have dentitions that are highly derived from the standpoint of tooth crown and root morphology.

13.5 Conclusions

Observations of tooth morphology in living Basque and Spanish populations show the former differs slightly from the latter, as well as from other

modern Europeans. This finding may be a function of conservative dental morphological differentiation through time or gene flow with neighboring non-Basque populations. More likely, it is a combination of the two processes. The Basque dentition shows the typical Eurodont dental pattern of minimal incisor shoveling, doubleshoveling, and winging, and a moderate frequency of UI2 interruption grooves. Lower molars are characterized by relatively high frequencies of four-cusped LM1 and LM2 and low frequencies of LM1 cusps 6 and 7. The deflecting wrinkle frequency is unusually high in the living Basque sample, but this may be a function of small sample size.

Cavalli-Sforza and other geneticists have adopted the view that the present day populations of Europe were strongly influenced by actual migrations of farming populations from Anatolia; however, many archaeologists take issue with this conclusion. Zvelebil (1998, 2000; Zvelebil and Zvelebil 1988) contends there is no archaeological evidence to support a major migration into Europe at the onset of the Neolithic. Richards (2003:157) notes that "Near Eastern farmers played their part, but the majority of European genetic lineages have their roots in the European Palaeolithic." Recent research suggests that modern European mitochondrial DNA diversity had a predominantly Paleolithic origin, with a Neolithic contribution of 23 percent (Richard et al. 1996; Richard 2003). Although Basques do not exhibit a heretofore unrecognized dental morphological pattern, the possibility that they are living descendants of late Paleolithic populations in Western Europe is not precluded. However, on the basis of their similarities to other Western Eurasian populations, they may not be alone in that regard.

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Appendix 13.1. *Crown and root traits for living Basque, Spanish, Basque-Spanish, and medieval/postmedieval skeletons from the Cathedral of Santa Maria, Vitoria, Spain*

Trait	Tooth	Sample	Grade									
			n	0	1	2	3	4	5	6	7	
Winging	UII	Spanish	60	98.3	1.7							
		Basque	35	100.0	0.0							
		Spanish-Basque	47	100.0	0.0							
		Santa Maria	136	90.4	5.9	2.2	1.5					
Shoveling	UII	Spanish	59	37.3	45.8	13.6	3.4	0.0	0.0	0.0	0.0	
		Basque	36	19.4	55.6	16.7	8.3	0.0	0.0	0.0	0.0	
		Spanish-Basque	46	39.1	37.0	19.6	4.3	0.0	0.0	0.0	0.0	
		Santa Maria	135	67.4	20.0	8.1	4.4	0.0	0.0	0.0	0.0	
	UI2	Spanish	60	41.7	43.3	13.3	1.7	0.0	0.0	0.0	0.0	
		Basque	36	27.8	52.8	13.9	5.6	0.0	0.0	0.0	0.0	
		Spanish-Basque	46	43.5	41.3	15.2	0.0	0.0	0.0	0.0	0.0	
		Santa Maria	128	56.3	30.5	9.4	3.9	0.0	0.0	0.0	0.0	
Double-shoveling	UII	Spanish	60	93.3	5.0	1.7	0.0					
		Basque	35	100.0	0.0	0.0	0.0					
		Spanish-Basque	47	93.6	4.3	2.1	0.0					
		Santa Maria	133	97.0	1.5	0.8	0.8					
Interruption grooves	UII	Spanish	58	100.0	0.0							
		Basque	35	97.1	2.9							
		Spanish-Basque	45	100.0	0.0							
		Santa Maria	149	95.3	4.7							
	UI2	Spanish	56	80.4	19.6							
		Basque	35	80.0	20.0							
		Spanish-Basque	45	95.6	4.4							
		Santa Maria	139	70.5	29.5							
Tuberculum dentale	UII	Spanish	58	24.1	44.8	22.4	8.6					
		Basque	36	22.2	38.9	27.8	11.1					
		Spanish-Basque	45	37.8	28.9	26.7	6.7					
		Santa Maria	134	62.7	14.9	13.4	9.6					
	UI2	Spanish	59	41.4	32.8	17.2	6.9	1.7	0.0			
		Basque	35	20.0	60.0	8.6	11.4	0.0	0.0			
		Spanish-Basque	46	28.3	32.6	28.3	10.9	0.0	0.0			
		Santa Maria	129	54.3	24.8	13.2	4.7	3.1	1.6			
	UC	Spanish	61	39.3	23.0	23.0	13.1	1.6	0.0			
		Basque	34	29.4	38.2	11.8	17.6	2.9	0.0			
		Spanish-Basque	46	41.3	23.9	23.9	10.9	0.0	0.0			
		Santa Maria	118	61.0	18.6	13.6	2.5	4.2	3.4			
Distal accessory ridge	UC	Spanish	55	16.4	30.9	29.1	20.0	1.8	1.8			
		Basque	35	28.6	25.7	28.6	17.1	0.0	0.0			
		Spanish-Basque	47	25.5	10.6	44.7	14.9	2.1	2.1			
		Santa Maria	82	56.1	3.7	11.0	25.6	3.7	0.0			

Appendix 13.1. (cont.)

Trait	Tooth	Sample	Grade								
			n	0	1	2	3	4	5	6	7
	LC	Spanish	57	71.9	22.8	3.5	1.8	0.0	0.0		
		Basque	35	77.1	20.0	2.9	0.0	0.0	0.0		
		Spanish-Basque	39	71.8	23.1	5.1	0.0	0.0	0.0		
		Santa Maria	153	86.9	3.9	5.2	3.9	0.0	0.0		
Bushmen canine	UC	Santa Maria	92	97.8	2.2	0.0					
Root number	LC	Santa Maria	295		91.5	8.8	0.4				
Multiple lingual cusps	LP1	Spanish	56	64.3	8.9	1.8	14.3	8.9	1.8		
		Basque	35	60.0	11.4	5.7	11.4	8.6	2.9		
		Spanish-Basque	48	52.1	12.5	10.4	14.6	6.3	4.2		
		Santa Maria	226	88.9	0.9	7.5	0.9	0.0	1.3		
	LP2	Spanish	61	37.8	6.6	21.3	19.7	4.9	9.8		
		Basque	35	19.4	2.8	33.3	25.0	13.9	5.6		
		Spanish-Basque	46	23.9	8.7	21.7	21.7	10.9	13.0		
		Santa Maria	181	48.1	0.6	22.1	16.0	10.5	2.8		
Root number	UP1	Santa Maria	169		48.4	51.6					
Tome's root	LP1	Santa Maria	234	60.7	4.0	13.8	7.6	9.8	4.0		
Hypocone	UM1	Spanish	60	0.0	1.7	0.0	0.0	61.7	36.7		
		Basque	36	0.0	0.0	0.0	11.1	61.1	27.8		
		Spanish-Basque	47	0.0	0.0	0.0	0.0	59.6	40.4		
		Santa Maria	235	0.4	0.4	0.0	3.4	34.5	61.7		
	UM2	Spanish	60	11.7	6.7	3.3	43.3	35.0	0.0		
		Basque	35	11.4	17.1	5.7	54.3	11.4	0.0		
		Spanish-Basque	43	7.0	23.3	0.0	48.8	20.9	0.0		
		Santa Maria	200	26.5	5.5	3.0	42.5	21.5	1.0		
UM3	Santa Maria	100	66.0	9.0	9.0	12.0	4.0	0.0			
Carabelli's trait	UM1	Spanish	60	25.0	18.3	21.7	20.0	11.7	0.0	3.3	0.0
		Basque	36	13.9	8.3	25.0	25.0	16.7	2.8	5.6	2.8
		Spanish-Basque	48	18.8	18.8	27.1	14.6	14.6	2.1	2.1	2.1
		Santa Maria	144	28.5	5.6	9.7	16.0	19.4	12.5	6.3	2.1
Cusp 5	UM1	Spanish	57	77.2	17.5	5.3	0.0	0.0			
		Basque	31	80.6	16.1	0.0	3.2	0.0			
		Spanish-Basque	41	75.6	19.5	4.9	0.0	0.0			
		Santa Maria	138	77.5	9.4	11.6	0.7	0.7			
Enamel extensions	UM1	Santa Maria	156	96.8	1.3	1.9					
Root number	UM2	Santa Maria	169		17.2	21.9	60.9				
Pegged/missing/red	UM3	Santa Maria	86	88.4	11.6						

(continued)

Appendix 13.1. (cont.)

Trait	Tooth	Sample	Grade								
			n	0	1	2	3	4	5	6	7
Cusp number	LM1	Spanish	58	8.6	0.0	8.6	24.1	50.0	8.6		
		Basque	35	11.4	0.0	2.9	40.0	40.0	5.7		
		Spanish-Basque	46	17.4	0.0	10.9	39.1	30.4	2.2		
	LM2	Santa Maria	198	7.6	0.5	1.5	17.7	42.9	29.8		
		Spanish	60	85.0	6.7	5.0	3.3	0.0	0.0		
		Basque	35	88.6	2.9	5.7	2.9	0.0	0.0		
	LM3	Spanish-Basque	45	93.3	2.2	2.2	0.0	2.2	0.0		
		Santa Maria	189	86.8	2.1	4.2	6.3	0.5	0.0		
		Santa Maria	112	56.3	6.3	1.8	8.0	13.4	14.3		
Groove pattern	LM1	Spanish	30		96.7	0.0	3.3				
		Basque	19		89.5	0.0	10.5				
		Spanish-Basque	24		79.2	0.0	20.8				
	LM2	Santa Maria	186		90.3	8.6	1.1				
		Spanish	41		22.0	7.3	70.7				
		Basque	21		19.0	0.0	81.0				
	LM3	Spanish-Basque	34		23.5	2.9	73.5				
		Santa Maria	149		14.8	4.0	81.2				
		Santa Maria	76		14.5	2.6	81.6				
Cusp 6	LM1	Spanish	56	87.5	12.5	0.0	0.0	0.0	0.0		
		Basque	33	81.8	9.1	9.1	0.0	0.0	0.0		
		Spanish-Basque	45	82.2	11.1	6.7	0.0	0.0	0.0		
		Santa Maria	139	92.1	2.9	5.0	0.0	0.0	0.0		
Cusp 7	LM1	Spanish	57	80.7	15.8	1.8	1.8	0.0	0.0		
		Basque	35	77.1	14.3	5.7	2.9	0.0	0.0		
		Spanish-Basque	45	75.6	15.6	2.2	2.2	4.4	0.0		
		Santa Maria	185	93.0	0.0	2.7	2.7	0.5	1.1		
Protostylid	LM1	Spanish	57	98.2	0.0	1.8	0.0	0.0	0.0		
		Basque	34	100.0	0.0	0.0	0.0	0.0	0.0		
		Spanish-Basque	44	97.7	0.0	2.3	0.0	0.0	0.0		
		Santa Maria	147	100.0	0.0	0.0	0.0	0.0	0.0		
	LM2	Spanish	60	96.7	1.7	1.7	0.0	0.0	0.0		
		Basque	35	97.1	0.0	2.9	0.0	0.0	0.0		
		Spanish-Basque	44	97.7	0.0	0.0	0.0	0.0	2.3		
		Santa Maria	99	96.0	0.0	0.0	3.0	0.0	1.0		
Deflecting wrinkle	LM1	Spanish	39	87.2	12.8						
		Basque	23	56.5	43.5						
		Spanish-Basque	23	82.6	17.4						
		Santa Maria	89	79.8	20.2						
3RM1	LM1	Santa Maria	152	98.7	1.3						
Root number	LM2	Santa Maria	198		23.7	76.3					

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