

No Signature of Y Chromosomal Resemblance Between Possible Descendants of the Cimbri in Denmark and Northern Italy

Anders D. Børglum,^{1*} Cristiano Vernesi,² Peter K.A. Jensen,³ Bo Madsen,⁴ Annette Haagerup,¹ and Guido Barbujani⁵

¹*Institute of Human Genetics, University of Aarhus, Denmark*

²*Centro di Ecologia Alpina, Viote del Monte Bondone, Trento, Italy*

³*Department of Clinical Genetics, University Hospital of Aarhus, Denmark*

⁴*Museum of Vesthimmerland, Aars, Denmark*

⁵*Department of Biology, University of Ferrara, Italy*

KEY WORDS Cimbri; population genetics; Y chromosome

ABSTRACT Two European populations are believed to be related to the ancient Germanic tribe Cimbri: one living in Northern Italy, the other living in Jutland, Denmark. The people called Cimbri are documented in the ancient Roman historical record. Arriving from the far north their movements can be tracked from successive battles with the Romans. The Cimbri finally entered Italy from the northeast and were defeated at Vercellae (present day Vercelli) in 101 BC by Gaius Marius and his professional legions. Classical sources from the first centuries AD relate the homeland of the Cimbri to the coasts around the Elb estuary (northern Germany) or specifically towards the north (Himmerland in northern Jutland). In the alpine parts of Veneto, northeast of the historical battlefield, local traditions dating back to late medieval time, identify a

local population as *Cimbri* living in *Terra dei Cimbri*. They are considered the descendants of the Germanic combatants that fled the battlefield at Vercelli. As the defeated Cimbri that possibly fled to the mountains of Northern Italy most likely would have been male (warriors), the present study investigated the possible Y chromosomal diversity of the two present populations using microsatellite markers and single nucleotide polymorphisms. While *Cimbri* from Himmerland resembled their geographical neighbors from Denmark for the Y-chromosome markers, *Cimbri* from Italy were significantly differentiated both from *Cimbri* from Himmerland and from Danes. Therefore, we were not able to show any biological relationship for uniparentally transmitted markers. *Am J Phys Anthropol* 132:278–284, 2007. ©2006 Wiley-Liss, Inc.

The ancient Germanic tribe called Cimbri is documented in the Roman historical record. According to Roman sources, the Cimbri arrived from Northern Europe, reaching the Danube area and the fringes of the expanding Roman Empire. In 115 BC, the Cimbri and their allies defeated consul Carbo's Roman army at Noreia, situated at what is today the Italian–Austrian border. Their movements can thereafter be tracked from successive battles with the Romans (see Fig. 1) until they were finally defeated by Gaius Marius on the 29th of July 101 BC at Vercelli in the Po Valley. In Northern Italy, in the mountain area around the town of Asiago, the local tradition claims that the inhabitants called *I Cimbri* are descendants of Nordic people (Bonato, 1863). No archaeological evidence has yet been found to document that current Cimbri are really descended from the ancient Cimbri. However, that is not surprising, because it is difficult to discriminate migrations and cultural exchange from the ethnological, historical, or archaeological records. However, recent DNA-based techniques now allow one to test hypotheses on the consequences of ancient gene flow, by studying the genes of contemporary individuals.

According to late Roman sources, the Cimbri came from regions adjoining the North Sea coast, the Elb Estuary (northern Germany), or from other areas farther to the north. On Monumentum Ancyranum in Ankara an inscription in Greek and in Latin is preserved, “The Achievements of the divine to Augustus.” The Cimbri are mentioned as follows: “My fleet sailed through the Ocean eastwards from

the mouth of the Rhine to the territory of the Cimbri, a country which no Roman had visited before either by land or sea, and the Cimbri, Charydes, Semnonnes and other Germanic peoples of that region sent ambassadors and sought my friendship and that of the Roman people” (Brunt and Moore, 1967). Later sources, including Strabon and a map made by Klaudios Ptolemaios of Alexandria (see Fig. 2) also suggest a Northern homeland of the Cimbri, either near the Elb estuary, or on the top of the present Jutland, Denmark, in the area that might correspond to today's Himmerland. The landscape of Himmerland—in medieval time called “Himber Syssel” (Syssel: Shire or District)—has by a popular etymology been connected to a hypothetical Cimber Syssel and to Cimbri (Kimbri) on the Ptolemaean map. The phonetic development from H to K is common and well-known in the Nordic language areas during Viking Age and Medieval time (Broholm, 1960).

Although both the written sources and the archaeological findings must be evaluated with sound scepticism, the

*Correspondence to: Anders D. Børglum, Institute of Human Genetics, The Bartholin Building, Aarhus University, 8000 Aarhus C, Denmark. E-mail: anders@humgen.au.dk

Received 22 March 2006; accepted 9 August 2006

DOI 10.1002/ajpa.20509

Published online 28 November 2006 in Wiley InterScience (www.interscience.wiley.com).

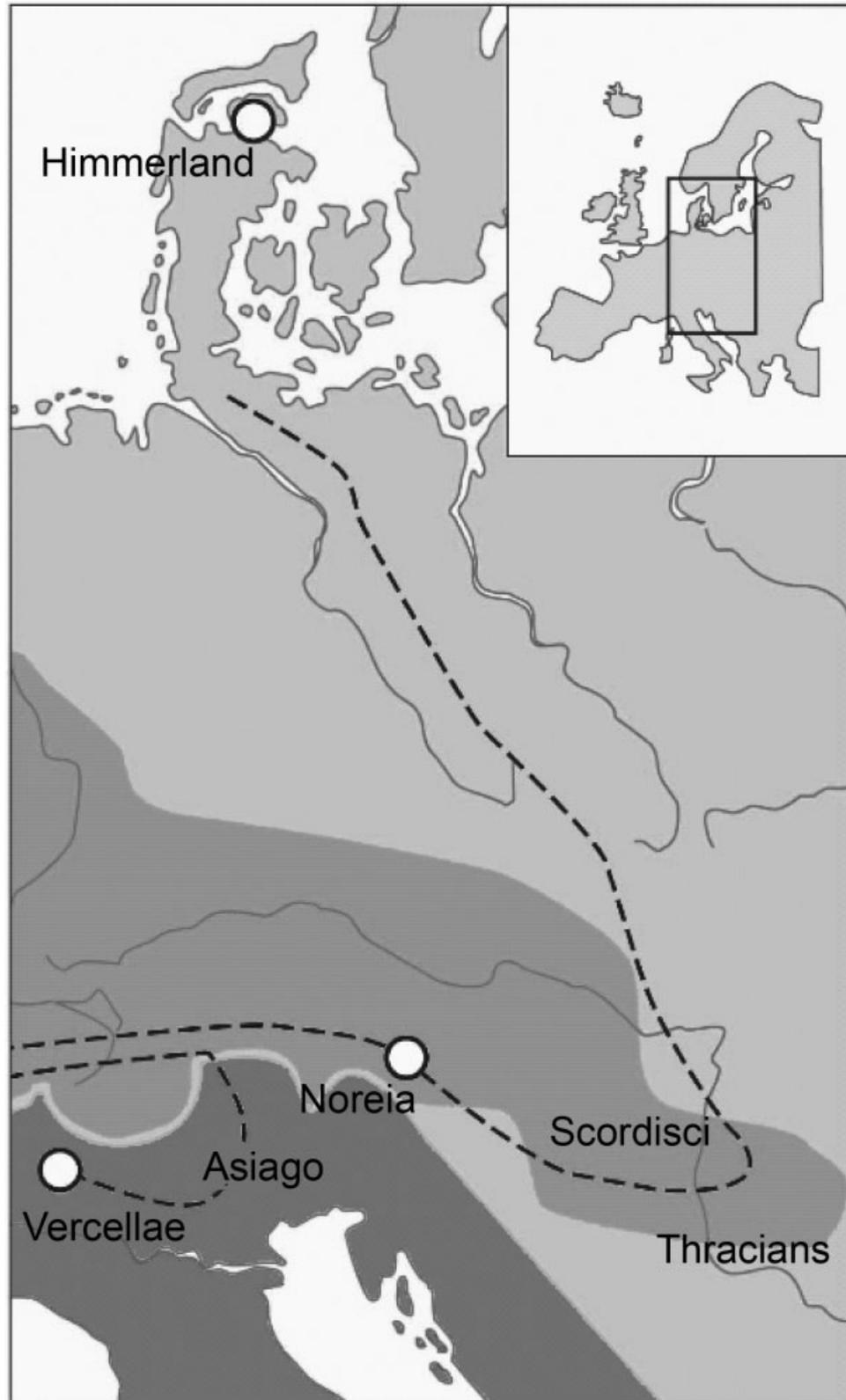


Fig. 1. The eastern route of the Cimbri ~ 116 to 101 BC in relation to Roman (lower shaded area) and Celtic areas (Kaul, 1995). Territories of Thracian and Keltic Scordisci tribes are indicated as are the homelands of the assumed “Cimbri” populations.

possibility now exists to test the hypothesis of a biological relationship between Italian and Danish populations, potentially related with the ancient Cimbri. Population genetics is revealing aspects of population history that previously proved hard to reconstruct, by integrating and

complementing the information provided by archaeological, linguistic, and historical sources. Examples are in Sokal et al. (1996), von Haeseler et al. (1996), and Cavalli-Sforza (1998). In Europe, the analysis of genetic variation has led to identification of the demographic conse-



Fig. 2. The northernmost Germanic areas. From the Ptolemaean map of the world, copied in Ulm 1482. Redrawn from photo (Broholm, 1960).

quences of prehistoric population expansions, and of successive population contacts, which often resulted in a higher-than-expected level of genetic relatedness between populations (Sokal 1991; Sokal et al., 1996).

To investigate whether the present Italian “Cimbri” population and the Danish population of Himmerland have some common ancestors, whom one would be tempted to identify with the historical Cimbri, we have engaged in a study describing the genetic diversity in the two populations and comparing them with other European groups. In particular, we tested the hypothesis that levels of genetic resemblance between the present “Cimbri” communities exceed what would be expected between populations separated by that geographic distance. Previously, we have reported population comparisons based on sequence variation of mitochondrial (mt) DNA that did not support any special relationship between the Danish and Italian groups (Børglum et al., 2002). However, a maternally-transmitted marker such as mtDNA may not be optimal to keep trace of migration phenomena that are closely related with military history (see e.g. Renfrew, 1992; Stumpf and Goldstein, 2001). If the historical Cimbri are indeed common ancestors to both the Danish and Italian groups, this hypothetical relationship might very well be male biased and mainly—or only—reflected in genetic resemblance at the Y chromosome level. Therefore, the present study reports on population comparisons based on analyses of Y chromosomal binary markers and microsatellite loci.

SUBJECTS AND METHODS

Subjects

Sixty-one unrelated males from Denmark were included in the study, all belonging to families who have been living in Himmerland for at least four generations, and several for more than 10 generations. The families were all well-known by the local genealogical associations. In addition, 50 unrelated males from unspecified regions of Jutland were also included. From Italy we sampled 49 unrelated males from three localities belonging to the Cimbri communities of Giazza, Luserna, and Roana, where a dialect related with German is still spoken. All individuals belong to families who report to have

TABLE 1. Absolute frequencies of SNP haplogroups based on eleven binary markers

	Cimbri/Denmark	Cimbri/Italy	Denmark
Hg1	0.36	0.54	0.46
Hg2	0.46	0.08	0.42
Hg3	0.06		0.06
Hg9	0.06	0.21	
Hg16			0.02
Hg21	0.06	0.04	
Hg26		0.13	0.04

The name of each haplogroup, Hg, is based on Rosser's et al. (2000) nomenclature.

been living there for at least two generations, and whose surnames are recognized as typical of the communities. All samples were collected with appropriate ethical approval and informed consent.

Binary markers

The following 11 binary markers were typed as described elsewhere: SRY-1532 originally called SRY_{10,831} (Whitfield et al., 1995) was typed according to Kwok et al. (1996), SRY-8299 originally called SRY_{4,064} (Whitfield et al., 1995) according to Santos et al. (1999), SRY-2627 according to Veitia et al. (1997), LLY22g according to Righetti and Tyler-Smith (unpublished), M9 (Underhill et al., 1997) according to Hurles et al. (1998), DYS257 according to Hammer et al. (1998), 92R7 (Mathias et al., 1994) according to Hurles et al. (1999), Tat according to Zerjal et al. (1997), YAP according to Hammer and Horai (1995), sY81 according to Seielstad et al. (1994), and 12f2 according to Rosser et al. (2000). The phylogenetic relationship of the haplogroups defined by these markers has been defined by the Y Chromosome Consortium (2002).

Microsatellite markers

Typing of five Y specific microsatellites (DYS19, DYS390, DYS391, DYS392, and DYS393) was carried out as described by Cooper et al. (1996) and De Knijff et al. (1997) using fluorescent primers, standard PCR conditions, and an ABI310 Genetic Analyzer for separation and detection.

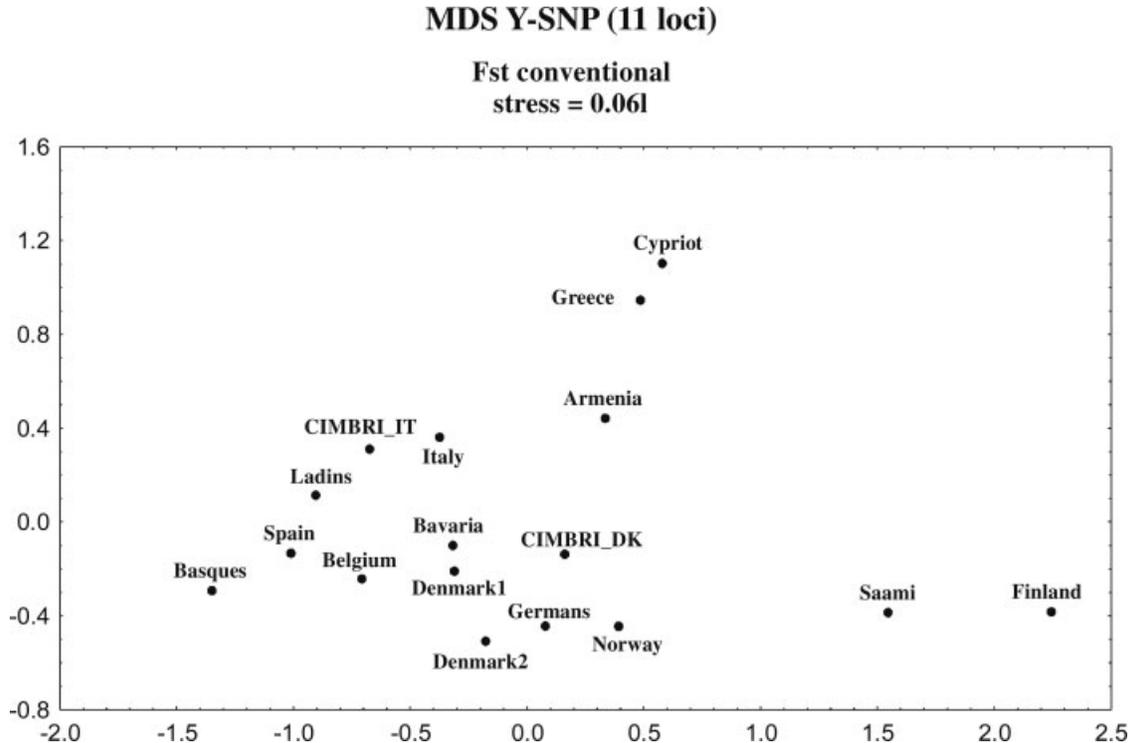


Fig. 3. Multidimensional-scaling graph of the genetic distances (measured as conventional pairwise F_{st}) among European and Mediterranean populations based on eleven binary Y-chromosome markers (SNPs). The stress value is an index of goodness of fit. When stress values are below 0.2, it is considered that the n -dimensional representation of the genetic distances matrix is satisfactory good.

Datasets used for comparisons

Data from Rosser et al. (2000) were used for comparison in Y-SNP polymorphism analyses. To ensure a better resolution, data for the Y-STR have been collected as individual haplotypes (constructed joining in a single allele combination the data from the five loci) instead of mere frequencies of individual alleles at different loci. More than 1,800 haplotypes have been retrieved from the following populations: Warsaw, Moscow, Lithuania, Estonia, Budapest, Berlin, Rome from Ploski et al. (2002), Ireland, Norway, Scotland from Helgason et al. (2000), Basques, Swiss from Kayser et al. (2001), Bedouin, Palestinian Arabs from Nebel et al. (2001), and Turkish from Di Benedetto et al. (2001).

Data analysis

Matrices of genetic distances between populations were constructed using conventional F_{st} (Wright, 1951), based only on allele frequencies, as a measure of genetic differentiation. Two-dimensional graphic representations of such distances were obtained by means of multidimensional scaling (Kruskal, 1964) and evolutionary trees were constructed using the neighbor joining (Saitou and Nei, 1987) algorithm. These methods are implemented in the following software packages, which were used throughout the analyses: Arlequin ver 2.00 (Schneider et al., 2000), Statistica 5.0, and Phylip (Felsenstein, 1995).

RESULTS

Table 1 shows the frequencies of the haplotypes defined by 11 binary markers (Rosser et al., 2000) in specimens

from Denmark ($n = 50$) and Northern Italy ($n = 49$). A multidimensional scaling comparing those samples with 14 other European populations shows no special relationship between the two groups (see Fig. 3). The Cimabri from Italy are closer to the other Italians, and the Danish Himmerland sample is close to two independent samples from Denmark. Therefore, the Y-SNPs, apart from confirming the well known pattern of geographic structuring in Europe, with an apparent E-W cline (Rosser et al., 2000; Semino et al., 2000), do not point to any particular resemblance between the two Cimabri samples.

The same pattern is evident from the multi-dimensional scaling relative to the conventional F_{st} distance values obtained by the analysis of the combined haplotypes from five microsatellites loci, namely DYS 389, 390, 391, 392, and 393 (Fig. 4). A clear geographic differentiation is also evident in the STR variation, even if the sampled populations are much fewer than those analyzed for SNPs. While the Cimabri from Denmark and the Danish reference population are very close, the Cimabri from northern Italy occupy an eccentric position in the graph, not unusual for language minorities of that area (Vernesi et al., 2002) and previously interpreted as a result of both geographic and linguistic isolation (Stenico et al., 1998; Vernesi et al., 2002). That pattern does not suggest any special relationship between Danish and Italian Cimabri. Furthermore, the Cimabri from Italy are well differentiated also from the only Italian population present in the comparison.

Both at the SNP and at the STR level, the degree of divergence between Cimabri from Italy and Cimabri from Denmark, evaluated by conventional F_{st} , is substantial and statistically significant at the 0.05 level (0.126 and 0.037 for SNPs and STRs, respectively) as well as that between Italian Cimabri and the Danes (0.0977 and 0.056

MDS Y-STR (5 loci)

Fst conventional

stress 0.13

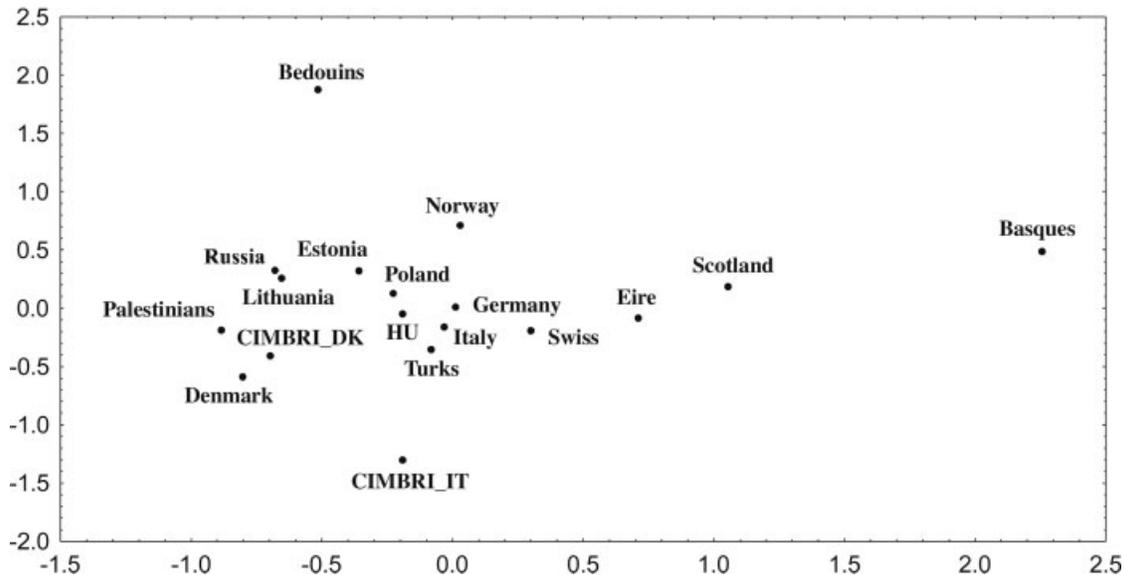


Fig. 4. Multidimensional-scaling graph of the genetic distances (conventional F_{st}) based on five Y-chromosome microsatellites (STR). As in the case of SNPs the stress value (below 0.2) shows that the two-dimensional representation is in good agreement with the matrix of genetic distances from which the graph is reconstructed. HU, Hungary.

for SNPs and STRs, respectively). On the other hand, Cimbri from Himmerland and Danes are undifferentiated with F_{st} values not different from zero.

DISCUSSION

Historical sources suggest that a Northern European population known as Cimbri might have left descendants both in Denmark and Italy. Twenty centuries later, these descendants may be part of the Danish and Italian communities living in the Himmerland and Asiago regions, respectively. There is reason to believe that, if anything, hypothetical genealogical relationship might have left a clearer sign in the male-transmitted parts of the genome, as is the case when migration events are associated with military campaigns. Therefore, evidence for common ancestry between Cimbri from Denmark and Italy is to be sought preferentially on the Y-chromosome markers. In fact, our previous analysis of sequence variation at the HVR-I mtDNA (Børglum et al., 2002) failed to identify any relationship between the Cimbri communities of Denmark and Italy; at the mitochondrial level, these communities appear as differentiated as two randomly chosen European populations. However, it should be noted that there is little geographic structuring of mtDNA variation in Europe (Simoni et al., 2000), which makes it more difficult to recognize past relationships between populations using mitochondrial polymorphisms. Therefore, by itself the lack of mitochondrial similarities does not imply the two communities had no evolutionary relationships.

To test the hypothesis that Italian and Danish Cimbri could be paternally related, we analyzed polymorphism at eleven binary markers and five microsatellites on the Y chromosome in 61 unrelated and healthy individuals from Himmerland, 49 from the Asiago area (where the Italian

Cimbri community lives), and 50 specimens from mainland Denmark. Although belonging to the non-recombining region of the Y chromosome, the SNPs and STRs should be treated as two distinct classes of markers. While the former possess a low mutation rate, and therefore each nucleotide substitution represents a unique historical event, the latter are characterized by relatively high mutation rates and therefore evolve rapidly (de Knijff, 2000). This marked difference in the mutation pattern has important consequences for the reconstruction of population history. Differences in the frequency distributions of haplogroups reconstructed from SNP variation tend to be due to relatively ancient demographic processes. Conversely, STR variation accumulates faster, and therefore it is likely to keep record of more recent events, as shown in three paradigmatic studies by Hurles et al. (1999), Helgason et al. (2000), and Wilson et al. (2001), in which the consequences of relatively recent historical events could be documented at the DNA level.

With these concepts in mind, the observed differences in SNP frequencies come as no surprise. Indeed, what is considered the most ancient stratification of Y-chromosome lineages clearly follows a South-East to North-West direction across much of Europe. Even though no clear consensus has been reached to date on the timing of the gene flow processes that generated the observed cline, whether during the initial, Paleolithic colonization of Europe (Semino et al., 2000), or at the beginning of the Neolithic period (Rosser et al., 2000; Chikhi et al., 2002), any process likely to generate a genetic gradient encompassing much of Europe occurred much earlier (at least 7,000–8,000 years; see Barbujani and Bertorelle, 2001) than the historical events that might have determined genetic affinities between the two Cimbri groups. To this respect the information retrieved from the STR analysis appears more adequate and promising, although the confounding effects

of the mutation may play an important role (Kayser et al., 2000).

The genetic distances at the STR level do not indicate any special relationship between the two Cimbri samples and between them and a Danish sample either. For a more detailed analysis, we retrieved information from several populations across Europe and Middle East not just as allele frequencies but in the form of combined individual haplotypes (de Knijff, 2000). The results of this analysis fully agree with the inferences from both Y-specific SNPs and mitochondrial DNA sequence variation.

While "Cimbri" from Himmerland resemble their geographical neighbors from Denmark for the Y-chromosome markers, "Cimbri" from Italy are significantly differentiated both from Cimbri from Himmerland and from Danes. Therefore, despite some historical evidence of a possible connection between Cimbri from Northern Italy and Cimbri from Himmerland, we were not able to show any biological relationship for uniparentally transmitted markers. In principle, one cannot completely dismiss the hypothesis of a possible limited influence between the two "Cimbri" communities. Anyway, as far as the genetic information is concerned, such influence should be regarded as quantitatively very limited and, in any case, not large enough to be identified at the sample sizes available for this study.

CONCLUSIONS

Historical sources suggest that a Northern European population known as Cimbri might have left descendants both in Denmark and Italy. Twenty centuries later, these descendants may be part of the Danish and Italian communities living in the Himmerland and Asiago regions, respectively. As the defeated Cimbri that possibly fled to the mountains of Northern Italy most likely would have been male (warriors), the present study investigated the possible Y chromosomal diversity of the two present populations using microsatellite markers and single nucleotide polymorphisms. While "Cimbri" from Himmerland resembled their geographical neighbors from Denmark for the Y-chromosome markers, "Cimbri" from Italy were significantly differentiated both from "Cimbri" from Himmerland and from Danes. Therefore we were not able to show any biological relationship for uniparentally transmitted markers.

Electronic sources: The data of this study are available at the website <http://web.unife.it/progetti/genetica/pdata.htm>, along with other data of the FHG Base (Ferrara Human Genetics Database).

ACKNOWLEDGMENTS

We thank the donors of DNA samples. We would also like to thank Annette Dahlerup, and the "Curatorium Cimbricum Veronese" for initiative and inspiring discussions, Fausto Sartori for his precious help in the collection of the Italian samples, Helle Binderup, Birgit Mølhave, Michele Aufiero, and Sara Marcolin for excellent laboratory work, and Sisse Degner for assisting with the graphical work. Finally, we would like to acknowledge the assistance of the genealogical associations of Himmerland.

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