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ARTICLE

MtDNA and Y chromosome polymorphisms in Hungary: inferences from the palaeolithic, neolithic and Uralic influences on the modern Hungarian gene pool

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Magyars imposed their language on Hungarians but seem not to have affected their genetic structure. To better investigate this point, we analysed some mtDNA and Y chromosome polymorphisms in a sample of the Hungarian Palóc who, for historical reasons, could have retained genetic traces of Magyars more than other groups. In addition, we examined a mixed sample from Budapest. About 100 individuals were tested for the markers defining all the European and Asian mtDNA haplogroups and about 50 individuals for some Y chromosome markers, namely the 12f2 and 49a,f/TaqI RFLPs, the YAP insertion, the microsatellites YCAIIa, YCAIIb, DYS19 and the Asian 50f2/C deletion. In the mtDNA analysis only two subjects belonged to the Asian B and M haplogroups. The Y chromosome analyses showed that the Palóc differed from the Budapest sample by the absence of YAP$^+$ allele and by the DYS19 allele distribution; that the proto-European 49a,f Ht 15 and the neolithic 12f2–8Kb were rather uncommon in both groups; that there is a high prevalence of the 49a,f Ht 11 and the YCAII a5–b1; and that the Asian 50f2/C deletion is absent. These results suggest that the influence of Magyars on the Hungarian gene pool has been very low through both females and males and the Hungarian language could be an example of cultural dominance. Alternative explanations are discussed. An expansion centred on YAP$^-$; 49a,f Ht 11 is revealed by the median network based on compound haplotypes. 49a,f Ht 11 could represent either a paleolithic marker of eastern Europe which underwent expansion after the last glacial period, or a marker of the more recent spread of the Yamnaia culture from southern Ukraine. *European Journal of Human Genetics* (2000) **8**, 339–346.

Keywords: Hungary; Palóc; mtDNA variations; Y chromosome polymorphisms

Introduction

Linguistic relationships among populations generally correlate with their genetic affinities.[1,2] In Europe, the only populations of non-Indo-European language are the Basques and the Finno-Ugric speakers (Saami, Finns, Estonians and Hungarians). The Finno-Ugric languages were brought from the Urals to eastern-Europe by migratory tribes. In Hungary, the Finno-Ugric language arrived with the Magyars who settled in the Carpathian Basin in 895 AD where other populations such as Slavs, Avars, and Bulgarians were present and subsequently assimilated. After the Magyar conquest, Hungary experienced other invasions, the most important of which was the Turkish, and also admixtures with neighbouring populations.[3] It is a matter of debate as to what extent the Finno-Ugric invaders affected the genetic structure of the local pre-existing inhabitants.

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Analyses of classical markers showed that, as for the Finns, only about 10% of Hungarian genes could be of non-European origin.[4] Subsequently, mtDNA and Y chromosome markers, which make it possible to identify separately male and female components in the genetic structure of a population, have been very helpful in revealing that the Uralic speakers, Finns and Saami, show almost exclusively mtDNA lineages of European ancestry[5–8] but a considerable Y-specific lineage which can be traced back to Siberian and Central Asian peoples.[9–11] An important Uralic male component has also been identified in Estonians.[10] These findings are in agreement with the notion that Y chromosome features parallel linguistic data more than do mtDNA and nuclear genes.[12–14] By contrast, this Uralic Y-specific lineage was not observed in a sample of Csángó of Hungary[15] and in mixed samples from Budapest.[10–15]

To increase our knowledge of the genetic structure of the Hungarian population, we analysed another ethnic group the Palóc, for some mtDNA and Y chromosome polymorphisms, as well as a control sample from Budapest. Through these studies, not only could we investigate the Magyar contribution to the Hungarian genetic structure and verify if it was mainly male mediated, but we could also search for paleolithic and neolithic components in this eastern European population.

The mtDNA markers we used were the haplotypes defined by the six classic enzymes,[16] and the restriction sites which identify all European and Asian specific haplogroups.[7,17–19] As to Y chromosome variations, the two Hungarian samples were analysed for the 50f2/C deletion, which has been considered to be a very valuable marker of the Uralic migrations;[9] for the 49a, f and 12f2/TaqI RFLPs[20,21] which allowed some paleolithic and neolithic European male lineages to be highlighted.[22] In addition, the Y Alu polymorphism (YAP) which, as the 12f2 system, is a monophyletic bi-allelic marker,[23] and the DYS19 and YCAIIa and b microsatellites[24,25] were examined. Compound haplotypes (c-Hts) were obtained by combining the single system 'alleles' for each individual, and were used to construct phylogenetic networks.

Materials and methods

The Palóc

The Palóc live in a border region of the northern Carpathian basin (Matra, Figure 1) neighbouring the Slavs in the higher mountains and speaking a specific Hungarian dialect. Their origin is yet unclear. The Palóc land, first inhabited by western Slavs, was occupied by Magyars in the second half of the 10th century. Subsequent invasions from south-eastern and central Europe experienced by Hungary from the 14th century onward did not seem to have influenced the Palóc. They are believed therefore to be direct descendants of the Hungarians of the 10th–13th centuries.[3]

The sample

The sample consisted of 102 unrelated healthy subjects who gave their informed consent. Twenty-two were 'mixed Hungarians' from Budapest, and 80 were Palóc.

Blood specimens were collected in EDTA and buffy coats were separated and frozen within 24 hours. DNA was extracted according to standard methods.

mtDNA analyses

Six classical enzymes This analysis was performed according to Passarino *et al*.[26]

Haplogroup analyses With the exception of the Asian haplogroup (Hg) F (– *Hpa*I/*Hinc*II 12406 site), G (+*Hae*II 4830 site) and T (+*Bam* HI 13366 /–*Ava* II 13367 and –*Msp*I 15925 sites) which were detectable by the six classic enzyme analyses, the Caucasoid and the remaining Asian haplogroups were identified by PCR amplification of the relevant fragments[26] and digestion with the appropriate enzymes.[7,18,27]

Y chromosome analyses

50f2/C deletion (DYS7C), and YAP insertion (DYS-287) These polymorphisms were determined as described by Jobling *et al*[9] and Hammer and Horai,[23] respectively.

TaqI 12f2 and 49a,f polymorphisms (DYS11, DYS1) The conditions of these analyses are detailed in Passarino *et al*[13]

STRs analyses DYS19 and YCAII STRs were analysed according to Roewer *et al*[24] and Mathias *et al*,[25] respectively.

Phylogenetic analyses

A median network,[28] has been drawn with the Network 1.6 program.[29] In this phylogeny the YAP$^+$ and 12f2–8 Kb alleles were considered as separate lineages, and differences among microsatellites were considered according to the stepwise model,[30] by weighting each single step as 1; similarly, each band acquisition and loss in the 49a,f system

Figure 1 Map of Hungary showing the Matra region, where the Palóc sample was collected.

was considered as a single step, by weighting the most variable A band as 1[31] and the other polymorphic fragments as 2.

Results

MtDNA analyses

The distribution of the mtDNA types defined by the 'six classic enzymes', together with that of the Caucasoid and the observed Asian specific haplogroups are reported in Table 1.

The 'six classic enzymes' analysis shows the profile of the Caucasoid populations, although with a lower frequency of types 6 and 18, and a particularly high frequency of type 1. Type 1 is the most represented type in Caucasoids, but it is very frequently also in Orientals.[16,32] In this analysis, however, typical Oriental features, as those characterised by *Hpa*I morph 1 (site loss at np 12406) or by *Hae*II Morph 5 (site loss at np 4830), which define the Asian lineages F and the M subgroup G, respectively,[33] were not observed. The frequency distribution of the continental specific haplogroups shows that 93.9% of the Hungarian mtDNAs were Caucasoid, 4.1% of unidentified origin, and only two subjects belonged to the Asian haplogroups M (Budapest) and B (Palóc). As to the European mtDNA lineages, the two Hungarian groups significantly differ from each other for the H lineage (50.6% in the Palóc *vs* 33.3% in the Budapest sample, *P* approximately 0.02). In both samples, this lineage, as in the other European populations, is the most frequent, followed by the U (17.3%). Haplogroups T, K and V occur at low frequencies (2.0%, 2.0% and 1.0%, respectively) and X and I are absent. Haplogroup J, which is considered a neolithic arrival,[19] has a frequency (12.2%) in the range of the other European populations. Since all the four subjects of unidentified origin did not show any of the Asian haplogroup markers (also including the *Alu*I site loss at np 5176 which is an indicator of the Asian *Dde*I$_{10394}$–*Alu*I$_{10397}$ [––] sub-haplogroup D[19]), these analyses indicated that at least 94% of the Hungarian mtDNAs have European characteristics. In agreement with other data (P Lahermo 1998, personal communication) these results suggest, therefore, that the female contribution of the Uralics to the Hungarian gene pool has been very low.

Y chromosome analyses

Data on Y chromosome single polymorphisms are reported in Figure 2 and Tables 2–4; the frequencies of the compound haplotypes (c-Hts) are given in Table 5.

As shown in Figure 2A, the 50f2/C deletion was not observed in the Hungarian sample, whereas it is quite common in Mongolians and especially in Siberians, Finns and Saami.[9,11] Thus, in keeping with the finding of Zerjal *et al*[10] and Lahermo *et al*,[15] a genetic male contribution of Uralics into the Hungarian genetic structure has not been detected in this analysis.

Table 1 Associations between the mtDNA continent-specific haplogroups and classic enzymes types in Hungarians. Percent frequencies of haplogroups are compared with those of some relevant populations

Haplogroups	*pre-HV*	*H*	*V*	*U*	*W*	*X*	*T*	*J*	*K*	*I*	*M*	*B*	*Others*[b]	*n.t.*	*Total*
Types[a]															
1.2 (2.1.1.1.1.2)	7	37	1	15				10			1	1	4	4	80
1.3 (2.1.1.1.1.3)		1													1
6.2 (2.1.2.1.1.2)									2						2
15.2 (2.1.1.1.8.2)		2													2
18.2 (2.3.1.4.9.2)							1								1
21.2 (2.1.1.1.2.2)					3										3
21.9 (2.1.1.1.2.9)					1										1
47.2 (2.1.1.1.3.2)								1							1
57.2 (2.3.1.4.13.2)							1								1
59.2 (2.1.1.1.20.2)				1											1
72.2 (2.1.1.1.12.2)		1													1
n.t.	1	5		1				1							8
Total	8	46	1	17	4	–	2	12	2	–	1	1	4	4	102
Hungarians (*n*=98)	**8.2**	**46.9**[c]	**1.0**	**17.3**	**4.1**	**–**	**2.0**	**12.2**	**2.0**	**–**	**1.0**	**1.0**	**4.1**		
Italians[58] (*n*=99)	n.t.	33.3	5.1	22.2	2.0	3.0	9.1	7.1	8.1	4.0	–	–	6.1		
Swedes[7] (*n*=36)	n.t.	40.5	5.4	16.2	–	–	21.6	2.7	13.5	–	–	–	–		
Finns[7] (*n*=49)	n.t.	40.8	4.1	16.3	4.1	4.1	6.1	14.3	4.1	2.0	2.0	–	2.0		
Siberians[27] (*n*=153)	n.t.	–	n.t.	n.t.	–	–	–	–	–	–	61.4	–	38.6		

n.t.=not tested; [a]In parentheses are the morphs defined by the enzymes *Hpa*I, *Bam*HI, *Hae*II, *Msp*I, *Ava*II, *Hinc*II; [b]These subjects were all *Dde*I$_{10394}$–*Alu*I$_{10397}$ (– –) and negative in the analyses for the markers of the Asian *Dde*I$_{10394}$–*Alu*I$_{10397}$ (– –) haplogroups. They were also negative when tested for the *Alu*I site loss at np 5176 which is an indicator of the Asian haplogroup D, also including the sub-haplogroup D reverted from *Dde*I$_{10394}$–*Alu*I$_{10397}$ (+ +) to *Dde*I$_{10394}$–*Alu*I$_{10397}$ (– –);[19] [c]This value refers to the whole Hungarian sample. However, the Palóc frequency (50.6%) significantly differs (*P* about 0.02) from that (33.3%) of the Budapest sample.

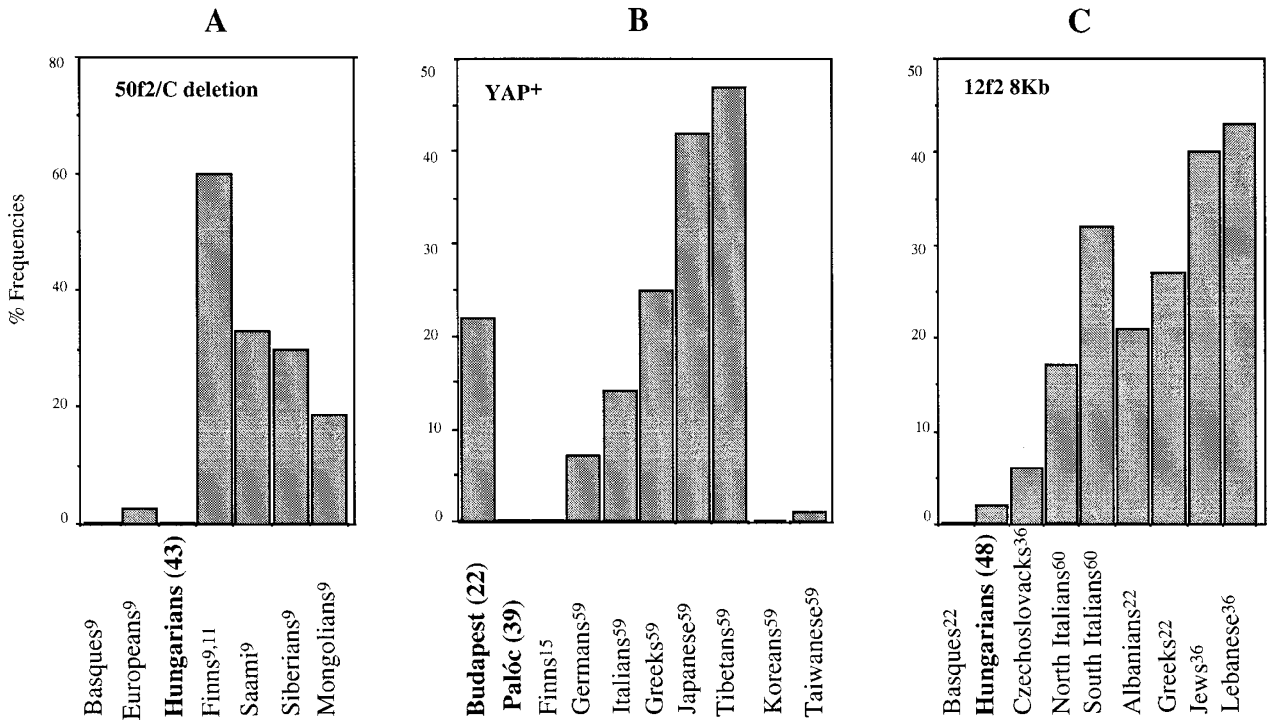

Figure 2 Distribution of 50f2/C deletion (**A**), YAP$^+$ allele (**B**), and 12f2–8 Kb allele (**C**) in Hungarians compared with some relevant populations. Populations of the present study are in bold with sample size in parentheses.

As reported in Figure 2B, all the YAP$^+$ chromosomes were observed in the mixed population of Budapest, where they account for 22.7% of the sample. This value is close to that (17.5%) found in Budapest by Lahermo *et al*.[15] Whereas in the Palóc the YAP$^+$ allele was not observed, it reaches a frequency of 37.5% in the Csángó.[15]

At the 12f2 and 49a,f RFLP analyses (Figure 2C and Table 2, respectively), Hungarians display the neolithic 12f2–8 Kb allele and the proto-European 49a,f haplotype 15, both at low frequency. By contrast, they show an incidence of the 49a,f haplotype 11 (42.5%) which is by far the highest yet observed in a European population.[34,35–38]

Data relative to DYS19 are given in Table 3. The Palóc do not display the DYS19 A allele and show one of the lowest frequencies so far encountered of the DYS19 C allele (6.7%); the DYS19 B allele has a value (53.3%) close to central-northern Europeans,[14,39–41] whereas the DYS19 D allele reaches a frequency (26.7%) similar to those of eastern European populations (31% in Trieste and Bratislava) and of a group of Mongolians (30%).[39,41,42] The 'mixed Hungarians' of Budapest significantly differ from the Palóc sample (P = 0.027, Fisher exact test). They are more heterogeneous and show a high frequency (22.7%) of the DYS19 A allele (as Romanians, 22%[39,41]), lower frequencies of alleles DYS19 B and DYS19 D (31.8% and 13.6%, respectively) and a higher frequency of the DYS19 C allele (18.2%). Both Hungarian samples show a relative high incidence of the DYS19 E allele (13–14%).

In the YCAII analysis the two Hungarian groups were very similar and were pooled (Table 4). The most important feature is the very high incidence of the YCAII a5–b1 haplotype (69.8%). This frequency is one of the highest observed in Europe,[14,25,39,41,43,44] and is close to the value (78%) displayed by the Basques.[45,46].

Table 5 shows the 22 c-Hts observed in the 46 Hungarians typed for all the systems here analysed. Fourteen c-Hts were single observations. The two stable markers (YAP and 12f2) define three main Y chromosome lineages: the YAP$^-$/ 12f2–10 Kb, the YAP$^+$/12f2–10 Kb, and the YAP$^-$/ 12f2–8 Kb, separately shown in the full median network (Figure 3). The first is the most important lineage where the most represented haplotypes carry the 49a,f Ht 11, YCAII a5–b1 and DYS19 B combination. The other two lineages account only for 10.9% (c-Hts 1–3) and 2.2% (c-Ht 22) of the sample, respectively, and do not show the preferential associations found in the first lineage. The YAP$^+$/ 12f2–10 Kb lineage shows preferential associations with 49a,f Ht 5 and DYS19 A allele, which is the most common north African combination and is also frequent in Greeks and Turks (AS Santachiara-Benerecetti, personal communication); the YAP$^-$/12f2–8 Kb lineage, here represented by only one c-haplotype, displays the association with 49a,f Ht 7 and DYS19 B allele, which is a

Table 2 Distribution of *TaqI*/49a,f haplotypes in Hungarians and in two comparison populations

Haplotypes[a]	Polymorphic fragments[b] A C D F I	Hungarians n=47	Czechoslovaks[36] n=105	Italians[34] n=125
2	0 0 1 1 1	2.1		4.0
5	2 0 0 1 1	12.8	2.9	8.0
7	2 0 1 1 0	2.1		9.6
8	2 0 1 1 1		1.9	5.6
10	3 0 0 1 0	8.5	2.9	1.6
11	3 0 0 1 1	42.5	21.0	6.4
12	3 0 1 1 0	2.1	9.5	4.8
13	3 0 1 1 1	2.1	1.9	1.6
15	3 1 2 1 1	6.4	11.4	28.0
24	2 1 1 1 1		4.8	5.6
29	2/3 1 2 1 1		3.8	7.2
31	3/4 1 2 1 1		1.0	1.6
35	3 1 0 1 1	6.4	8.6	5.6
36	3 1 2 1 0	2.1		0.8
37	3 1 2 0 1			1.6
39	3 0 0 1 0$_{\text{-BHPR}}$	4.2	1.0	0.8
51	2/3 0 0 1 1	2.1	2.9	
64	3/5 0 0 1 1	2.1	8.6	
84	5 0 0 1 1	6.4	4.8	
85	0 0 1 0 1		2.9	
Others[c]			10.5	7.2

[a]With the exception of the first nine haplotypes all the others have been renamed according to the revised nomenclature of Poloni *et al*;[12] [b]1 and 0 denote presence and absence respectively of the band, except for the A and the D fragments, for which the numbers indicate which band of the allelic set is present; solidus indicates the presence of two allelic bands in the same haplotype, in which case a locus duplication was assumed[34]; [c]Includes haplotypes found only in one subject of a single comparison group.

Table 3 Percent frequencies of the DYS19 alleles in the two Hungarian samples

bp	Alleles	Palóc n=30	Budapest n=22
186	A	–	22.7
190	B	53.3	31.8
194	C	6.7	18.2
198	D	26.7	13.6
202	E	13.3	13.6

Table 4 Percent frequencies of the YCAII haplotypes in Hungary

YCAII Haplotypes a b	No. of repeats	Frequency n=53
6/5	24/23	1.9
5/1	23/19	69.8
4/1	22/19	1.9
3/3	21/21	7.5
3/2	21/20	3.8
3/1	21/19	9.4
2/2	20/20	1.9
1/1	19/19	3.8

Table 5 Y chromosome compound (c-Hts) haplotypes obtained by combining the different alleles observed, in each individual, for 50f2/C, YAP, 12f2, 49a,f, YCAII, DYS19 polymorphisms and their frequencies in percent

c-Ht	50f2/C	YAP	12f2	Ht	49a,f fragments A C D F I	YCAII Ht a b	DYS19	n=46
1	–	+	10	5	2 0 0 1 1	3/1	A	6.5
2	–	+	10	5	2 0 0 1 1	1/1	A	2.2
3	–	+	10	11	3 0 0 1 1	3/3	A	2.2
4	–	–	10	2	0 0 1 1 1	2/2	D	2.2
5	–	–	10	5	2 0 0 1 1	5/1	E	2.2
6	–	–	10	5	2 0 0 1 1	5/1	B	2.2
7	–	–	10	10	3 0 0 1 0	3/3	D	2.2
8	–	–	10	10	3 0 0 1 0	3/2	D	4.4
9	–	–	10	10	3 0 0 1 0	3/2	C	2.2
10	–	–	10	11	3 0 0 1 1	5/1	D	10.9
11	–	–	10	11	3 0 0 1 1	5/1	C	6.5
12	–	–	10	11	3 0 0 1 1	5/1	B	23.9
13	–	–	10	12	3 0 1 1 0	3/1	B	2.2
14	–	–	10	13	3 0 1 1 1	6/5	D	2.2
15	–	–	10	15	3 1 2 1 1	5/1	C	2.2
16	–	–	10	15	3 1 2 1 1	5/1	B	4.4
17	–	–	10	35	3 1 0 1 1	5/1	B	6.5
18	–	–	10	36	3 1 2 1 0	5/1	B	2.2
19	–	–	10	39	3 0 0 1 0$_{\text{-BHPR}}$	5/1	C	2.2
20	–	–	10	64	3/5 0 0 1 1	1/1	C	2.2
21	–	–	10	84	5 0 0 1 1	5/1	E	6.5
22	–	–	8	7	2 0 1 1 0	4/1	B	2.2

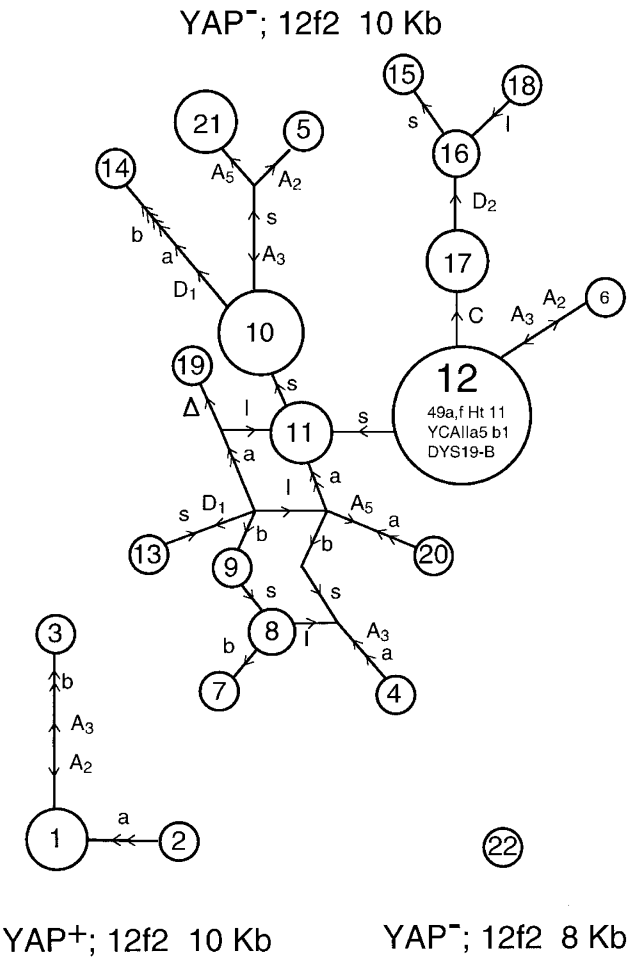

Figure 3 The full median network of the Y chromosome compound haplotypes (c-Hts) found in Hungary. Numbers in circles indicate the corresponding c-Ht (see Table 5) and the circle size is proportional to its frequency; arrows on the branches point to a repeat/fragment gain; capital letters represent fragment changes at 49a,f loci; small letters (a, b, and s) represent changes at YCAIIa, YCAIIb and DYS19 loci, respectively; Δ represents the 49a,f BHPR fragment deletion.[34]

combination very common in the Middle East (AS Santachiara-Benerecetti 1995, personal communication).

Discussion

Uralic genetic component in Hungary

Hungary is one of the few areas in Europe where a non-Indo-European language is spoken. This is due to the Magyar invasion, which at the end of the 9th century AD brought to the present Hungarian territory thousands of people (estimates vary from 50 000 to 500 000)[4] who spoke a Uralic language (the Magyar). The extent of genetic influence of the invaders on the Hungarian gene pool, which is still a puzzling problem, has been addressed by studying some mtDNA and Y chromosome polymorphisms. These sets of markers have proved to be very valuable in estimating the extent of the Uralic gene flow into the gene pool of Saami, Finns and Estonians,[6,9,10,11] who, like the Hungarians, speak a language of the Uralic family.

We have examined a Hungarian ethnic group, the Palóc, who are considered the direct descendants of the Hungarians of the Middle Ages and a control sample from the mixed population of Budapest.

The two groups are differentiated mainly by the frequencies of the mtDNA haplogroup H, and the Y chromosome DYS19 B and YAP$^+$ alleles which, in the European frame, are closer to central-northern and north-eastern Europeans in the Palóc, and to south-eastern Europeans in the Hungarians of Budapest. Both samples, however, virtually do not display Uralic characteristics. As to the mtDNA, the Asian lineages B and M were found only in one subject each; they, however, do not necessarily indicate evidence of Uralic entrance. Indeed, the 9bp deletion characterising the B Hg is a recurrent mutation.[17,47,48] As to the M Hg (in the mixed sample from Budapest) it has to be taken into account that in Hungary there are groups of Gypsies with high frequencies of Hg M (A Pandya 1998, personal communication). On the male side, Hungarian Y chromosomes lack the 50f2/C deletion that is very common among Samoyedic and Altaic Siberians (Figure 2A). Thus, unlike Finns, Estonians and Saami, where a strong Uralic male-mediated genetic influence was highlighted, Hungarians seem to have undergone a mainly Uralic cultural dominance imposed by a small number of invaders. Alternatively, a large number of Magyar speakers invaded Hungarian territory but only a few of them, from a genetic point of view, were truly Magyar. Actually, it has to be borne in mind that Magyars, after leaving the Finno-Ugric homeland about 3000 years ago, had 2000 years of nomadic life, with close contacts with other populations, especially Bulgarians and Kazars, mainly between the 4th and 9th centuries AD.[3] This second hypothesis would be consistent with the historical view that the number of newcomers (whatever it was) was not very different from the number of previous inhabitants of Hungary.[4]

Nevertheless, it cannot be excluded that, at variance with the Fenno speakers who migrated toward northern Europe, Magyars did not harbour the 50f2/C deletion right from their origins. Were this the case, the 50f2/C deletion would not be the appropriate marker to investigate the Asian Uralic male contribution to the Hungarian gene pool.

Paleolithic and neolithic genetic components in Hungary

The two Y-specific markers, the 49a,f Ht 15 and the 12f2-8 Kb allele which, as previously said, are considered European preneolithic and neolithic lineages of the modern European genetic structure, are both infrequent in Hungarians, as well as in Czechoslovaks.[36] It seems therefore, that the migrations which spread the neolithic from south-eastern to north-

western Europe affected eastern Europe only marginally, although the frequency (12%, Table 1) of the neolithic mtDNA haplogroup J,[19] is within the range of the European values. On the other hand, the low frequency of 49a,f Ht 15 indicates that also the most important pre-neolithic component of the north-western and western European populations, where it attains its maximum values (50–70%)[22,37,38] and probably rose,[49] is scarcely represented in eastern Europe.

The most frequent Hungarian compound haplotypes (Table 5) include the 49a,f Ht 11. This haplotype is rather uncommon in western Europe[35,37,38] and has a frequency of 21.0% in a sample from former Czechoslovakia,[36] and 42.5% from Hungary (Table 2). Also illustrated in the network (Figure 3), the Hungarian 49a,f Ht 11 chromosomes (c-Hts 3, 10–12) are almost exclusively YAP$^-$, as well as in other Europeans (G Passarino 2000, personal communication), and further characterised by the YCAII a5–b1 haplotype (c-Hts 10–12 in Table 5). The remarkable incidence of these c-haplotypes, particularly of the c-Ht 12, suggests that Hungarian population underwent expansion. Since the small size of the sample and the uncertainty of the mutation rate[50] do not allow this expansion to be reliably dated, the results we obtained are compatible with two not necessarily alternative hypotheses. One is of an ancient presence of YAP$^-$/49a,f Ht 11 in eastern European populations which, during the last glaciation, retreated into southern Ukraine[51] and subsequently expanded at the end of the glaciation when people returned to the abandoned territories. In this case, the YAP$^-$/49a,f Ht 11 would represent the eastern European counterpart of the western European pre-neolithic 49a,f Ht 15. The second, a more recent arrival in Hungary of this haplotype due to the spread of the Yamnaia culture from southern Ukraine, today recognised as a second development of the farming economy due mainly to the domestication of horses.[52] It characterised nomad peoples who migrated at different times, from 4300 BC to 3000 BC[53] or more recently.[54] According to Gimbutas[55] and Piazza,[56] they brought the Indo-European languages to Europe and to India.[54,57] Interesting in this regard is that, out of Europe, the YAP$^-$/49a,f Ht 11 associated with YCAII a5–b1 is frequent in the north of India (G Passarino 2000, personal communication). It would clearly be interesting to verify these hypotheses against further data on eastern European and Asian populations.

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