

A Y-Chromosomal Comparison of the Madjars (Kazakhstan) and the Magyars (Hungary)

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ABSTRACT The Madjars are a previously unstudied population from Kazakhstan who practice a form of local exogamy in which wives are brought in from neighboring tribes, but husbands are not, so the paternal lineages remain genetically isolated within the population. Their name bears a striking resemblance to the Magyars who have inhabited Hungary for over a millennium, but whose previous history is poorly understood. We have now carried out a genetic analysis of the population structure and relationships of the Madjars, and in particular have sought to test whether or not they show a genetic link with the Magyars. We concentrated on paternal lineages because of their isolation within the Madjars and sampled males representing all extant male lineages unrelated for more than eight generations ($n =$

45) in the Torgay area of Kazakhstan. The Madjars show evidence of extensive genetic drift, with 24/45 carrying the same 12-STR haplotype within haplogroup G. Genetic distances based on haplogroup frequencies were used to compare the Madjars with 37 other populations and showed that they were closest to the Hungarian population rather than their geographical neighbors. Although this finding could result from chance, it is striking and suggests that there could have been genetic contact between the ancestors of the Madjars and Magyars, and thus that modern Hungarians may trace their ancestry to Central Asia, instead of the Eastern Uralic region as previously thought. *Am J Phys Anthropol* 000:000–000, 2009. © 2009 Wiley-Liss, Inc.

The Madjar people live in the Torgay area of Kazakhstan. According to their limited written and oral history, they settled around Lake Sarikopa ~300–400 years ago, most probably arriving from the Karatau region to the south-east, which now lies in Zhambul county of South Kazakhstan (Bíró, 2007). The word “Madjar” as a designation of an ethnic group appeared in the 16th and 17th century in Central Asian chronicles when the group was mentioned in connection with military events in the Aral-Caspian region as participants on the side of Abulhair Khan (Yugin et al., 1969).

The Madjars lived in yurts and maintained a nomadic-pastoral style of life until the 1960s, when the former Soviet Union began to build kolkhoz systems and the tribes were forced to settle down in fixed “barrack-habitations.” Now they mostly live in relative isolation far from any city zones. They came to academic attention for the first time in 1964 when Seitbek Nurhanov, a Kazakh linguist, informed Tibor Tóth at a scientific conference in Alma-Ata of their existence. A year later, Tóth traveled to Kazakhstan and looked up the place where the Madjar tribe was expected (manuscript, the archive of the Hungarian National History Museum, Budapest). However, the government of the former Soviet Union did not permit the scientific work and ended the project.

The Madjars live in a tribal confederation with the Argün tribe and they both belong to the middle “zhuz” (Orta zhuz). The number of Madjars has been affected mainly by emigration away from the Torgay region in the past few decades. People belong to the tribe on the basis of their paternal lineage. Because of their marriage customs, the Madjars live in “local exogamy” meaning that it is prohibited for a Madjar man to marry a Madjar

woman. He is permitted to look for a wife only in other local tribes of the Orta zhuz (mainly in the Argün, Kipchak, Kerei, and Najman tribes); such a strict marriage custom is common in the Torgay area and was also common among the nomadic people of Central Asia aiming to avoid inbreeding (Bíró, 2007). As a consequence, like the other local tribes, the wife of a Madjar man often has Madjar ancestry on the maternal side and thus the local tribes live in a “regional endogamy.” The number of members of the Madjar tribe, including the migrants, is only about 2,000.

The settlement of the Hungarians (Magyars) in their present geographical location ~1,000 years ago has been studied extensively by ethnographers, linguists, and archeologists (e.g., Németh, 1930; Németh and Ligeti, 1943). The Hungarian language differs substantially from the Indo-European languages spoken in most of Europe and, together with Finnish, Saami (Lappish),

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Fig. 1. Eurasian populations that were compared in the study. 1. Madjar, 2. Hungarian, 3. Kazakh, 4. Uzbek, 5. Turkmenian, 6. Kyrgyz, 7. Tajik, 8. Uygur, 9. Uygur-Ürümqi, 10. Uygur-Yili, 11. Turkish, 12. Ossetian, 13. Azeri, 14. Georgian, 15. Kurdish, 16. Armenian, 17. Outer Mongolian, 18. Daur, 19. Inner Mongolian, 20. Oroqen, 21. Manchu, 22. Ewenki, 23. Tibetan, 24. Bulgarian, 25. Mari, 26. Ukrainian, 27. Russian, 28. Estonian, 29. Finnish, 30. Saami, 31. Greek, 32. Italian, 33. Spanish, 34. Polish, 35. German, 36. French, 37. Japan, 38. Han-Harbin.

Mari, and Estonian, belongs to the Uralic language family. It is thus likely to have an origin further east. In bones from cemeteries of the Hungarian-Conquest period (10th century), anthropological analysis showed characteristics of Central Asian origin (Tóth, 1965; Éry, 1978; Liptak, 1979). Based on the craniological analysis of the conquering Hungarians and comparisons of the data with other Eastern European populations, the Caucasus and Ural region, Central Asian and Siberian populations, Tóth suggested a contribution to the Hungarian people from the Aral-Caspian region (Tóth, 1965). Archeological remains from these cemeteries (weapons, haversacks, belt mountings, ornaments on clothing, etc.) also showed similarities to Central and Inner Asian ones (Fodor, 1973, 1995, 2006; Erdélyi, 2004). Hungarian archaeologists and ethnographies could show a series of similarities in the traditions (burial, belief, figurative arts) of the conquering Hungarians with different Central and Inner Asian cultures as the Scythian, Iranian, Turk, and several Siberian cultures (Dienes, 1975; László, 1997; Fodor, 1982). Thus an origin of the Hungarian language and early culture in a region from West Asia to Siberia is suggested, but a specific origin has been difficult to identify. Genetic studies have shown similarities of modern Hungarians to neighboring European populations and have not revealed links to speakers of other Uralic languages or Asian populations (Semino et al., 2000).

The shared name of the Madjar and Magyar populations raises the question of whether or not the present Hungarian (Magyar) and Madjar population in Kazakhstan have any direct link or genetic relationship. To investigate this possibility, a comparative genetic investigation of the two populations, and additional populations from across Europe and Asia, was performed. Because of the marriage habits of the Madjar men, who “bring” their spouses from other tribes, but from the same “zhuz”, only male specific lineages (Y-chromosomal markers, Y-STRs and Y-SNPs) would be useful in such a study. The Magyar and some Kazakh populations have been studied previously for Y-STR and Y-SNP markers,

although the Madjars have not been investigated yet (Zerjal et al., 2002; Völgyi et al., 2008). In addition to its male specificity, two features of the Y chromosome make it particularly well suited for such investigations. First, it is passed from parent to offspring (father to son) without the “shuffling” effect of recombination, which scrambles the information carried by autosomal haplotypes. This effect allows the evolution, human history, migration, and retention of wide variety of stable haplotypes/haplogroups with varying ages, related through a clear, stepwise mutational process. The second feature is the highly specific geographic pattern of Y-chromosomal variation: its diversity within populations is often lower than that of other markers, but variation among populations is higher (Seielstad et al., 1998). Thus, the Y chromosome provides geneticists and anthropologists with a powerful tool for historical and demographic studies.

This study aims to investigate the possible genetic relationships between the Madjars from the Torgay area and other Eurasian populations (Fig. 1), since the question whether the Hungarian Conquerors had traveled through Central Asia, instead of beginning their route in the Eastern part of Ural has long been the debate of historians, linguists, and anthropologists.

MATERIALS AND METHODS

Sample collection

The sample donors were asked about their male lineages, and saliva samples were collected from 45 unrelated Madjar males. The number of individuals was limited to 45 because only 45 unrelated paternal lineages survive. The samples were collected from the villages Saga, Koezbel, Kumshiq, Bidayik, Taush, Ashutasti, Aythuar settlement, and Altinsarin, and from towns close to the Torgay area, Amangeldi, Arkaliq, and Oktyabrsk, where recent emigrant Madjars live.

TABLE 1. Haplotype and haplogroup analysis of the Madjar population

No	DYS391	DYS389I	DYS439	DYS389II	DYS438	DYS437	DYS19	DYS392	DYS393	DYS390	DYS385	n	Haplogroup
1	10	12	12	29	11	15	15	12	12	23	12/12	1	F/-M89
2	11	13	12	28	10	16	13	12	13	23	13/17	24	G1/-P20
3	11	14	12	29	10	16	13	12	13	23	14/17	2	G1/-P20
4	11	14	12	29	10	16	13	13	13	23	13/17	4	G1/-P20
5	11	14	12	29	10	16	13	13	13	23	13/18	1	G1/-P20
6	11	14	13	29	10	16	13	12	13	23	13/17	3	G1/-P20
7	11	15	12	30	10	16	13	12	13	23	13/17	1	G1/-P20
8	12	14	12	29	10	16	13	12	13	23	13/17	4	G1/-P20
9	10	13	12	29	9	15	14	11	12	23	14/17	1	J2*/-M172
10	11	12	13	28	9	16	15	11	12	24	13/17	2	J2*/-M172
11	10	13	11	30	11	14	16	11	13	25	10/14	1	K (xK1,K2)/-M9
12	11	14	10	30	10	14	14	14	14	23	11/13	1	N/-M231

DNA isolation

DNA was isolated using organic extraction methods as described (Comey, 1994). DNA samples were purified with Microcon 100 and quantified using the ABI 7500 Real-time PCR System (Applied Biosystems, Foster City, CA).

Testing of Y-STR loci

DNA was amplified with the PowerPlex Y (Promega) amplification kit according to the manufacturers' instructions. It includes 12 Y-specific STR loci (DYS391, DYS389 I, DYS439, DYS389 II, DYS438, DYS437, DYS19, DYS392, DYS393, DYS390, and DYS385a/b).

PCR products were analyzed by capillary electrophoresis using an ABI Prism 310 Genetic Analyzer (Applied Biosystems). Fragment sizes were determined using the GeneScan 3.1.2 software, and allele designations were performed using the Genotyper 2.5.2 software (Applied Biosystems).

Testing of biallelic markers

When testing Y-SNP markers, amplifications of 3–5 ng genomic DNA were performed in an ABI 7500 and in GeneAmp 9700 thermal cyclers with TaqMan probes (Applied Biosystems) using the programs designed by the manufacturer (Applied Biosystems). The relative fluorescence of the PCR products were analyzed on an ABI 7500 with its SDS software as described in the manufacturers' manual (Applied Biosystems). The haplogroups tested and the markers used in the study were as follows: C-R/-M168, C/-M216, C1/-M105, C2/-M38, C3/-M217, C4/-M210, D/-M174, E/-SRY4064, E3b/-M35, E3b1/-M78, E3b2/-M81, E3b3/-M123, F-R/-M89, G/-M201, G1/-P20, G2/-P15, H/-M52, H1/-M82, I/-M170, I1a/-M253, I1b/-P37, I1c/-M223, J/-M304, J1/-M62, J2/-M172, J2a/-M47, J2b/-M68, J2c/-M137, J2d/-M158, J2e/-M12, J2e1/-M102, J2f/-M67, K-R/-M9, K1/-SRY9138, K2/-M70, L/-M11, M/-M106, N/-M231, O/-M175, O1/-M119, O3/-M122, P-R/-M45, Q/-P36, R/-M207, R1/-M173, R1a/-SRY10831b, R1a1/-M198, R1b/-P25 and R2/-M124 (Hammer et al., 1998; Underhill et al., 2000, 2001; Hammer et al., 2001; Karafet et al., 2001; Y Chromosome Consortium, 2002; Cinnioglu et al., 2004; Athey and Nordtvedt, 2005). The nomenclature of the haplogroups followed Jobling and Tyler-Smith (2003).

Statistical analysis

Haplotype and haplogroup frequencies, and haplotype and haplogroup diversity values were calculated as before (Nei, 1973). For most purposes, haplogroups were combined into the groups Y*(xA,C,D,E,F1,J,K), D, E, J, K*(xL,N,O1,O3c,P), N, P*(xR1a) and R1a so that published sources could be used for comparison (Rosser et al., 2000; Zerjal et al., 2002; Xue et al., 2006). AMOVA analysis was done using Arlequin 2.0 software (Schneider et al., 2000). Population pairwise genetic distances were calculated from all detected haplogroup frequencies of the Madjar, Hungarian, and compared populations with Arlequin 2.0. Based on the distances, a tree was constructed with the neighbor-joining method using Phylip 3.66. Phylogeographic analysis was carried out with the genetic distances and the measured geographical distances (<http://earth.google.de/>).

RESULTS

Y-STR and Y-SNP analysis

Haplotypes and haplogroups of the Madjar population are shown in Table 1. The haplotype and haplogroup diversity values were 0.7040 and 0.2485, respectively. These are substantially lower than the corresponding values for the Hungarian population, 0.9934 and 0.8668. When searching against Y Haplotype Reference Database (YHRD), four matches out of the 12 Madjar haplotypes were found. No matches could be detected with haplotypes 2–8 (haplogroup G). Haplotype 1 belonging to haplogroup F/-M89 identified two matches in the Bhutan and Nepal populations; haplotype 10 belonging to haplogroup J2*/-M172 gave two matches with the Mexican (Chihuahua) and Peru (Mestizo) populations; haplotype 11 belonging to K*(xK1,K2)/-M9 haplogroup showed two matches with two Polish populations (Novy Targ and Southeast Poland), and haplotype 12 belonging to haplogroup N/-M231 appeared to be frequent worldwide (40 matches in 26,556 haplotypes, 235 populations, YHRD Release "23"). The frequently observed haplotype 12 could be found in Finnish and Swedish populations and in the European part of Russia. Two matches out of the 40 were found in the Székely population (Hungarian ethnic group in Romania) and one in Hungary, Austria, and Belarus. Only five different haplogroups could be identified in 45 males, which were G1/-P20 (86.7%), J2*/-M172 (6.7%), K/-M9 (xK1, K2) (2.2%), and F/-M89 (2.2%). Among the 39 persons falling into the G1 haplogroup, 24 haplotypes were identical.

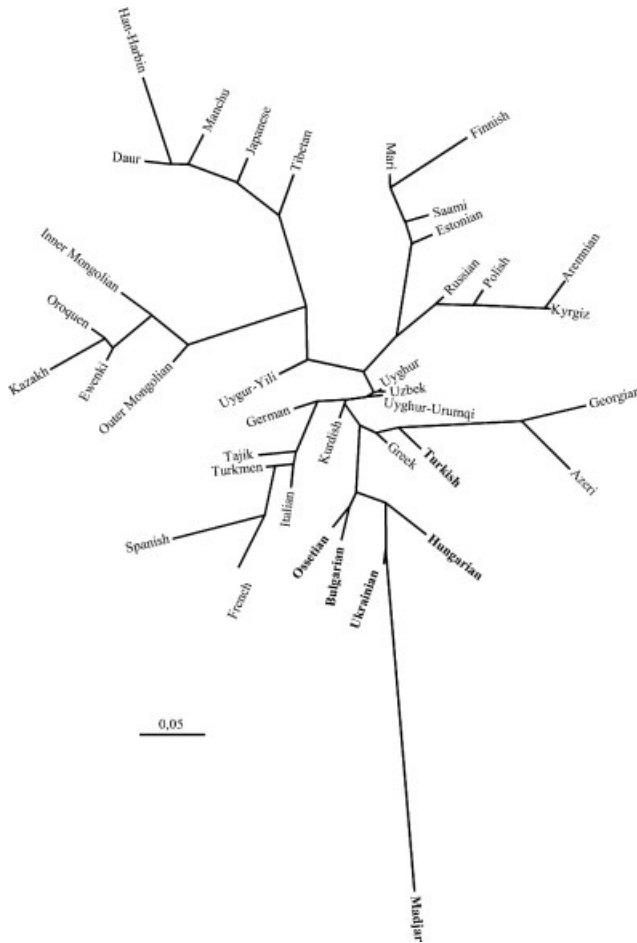


Fig. 2. Unrooted phylogenetic tree of 38 populations.

Genetic distances and Fst values

A comparison of 38 populations based on genetic distances was performed and the results are presented as a Phylogenetic tree (see Fig. 2), in which the five populations genetically closest to the Madjar population are highlighted. The Madjar-Magyar genetic distance was the shortest among the distances to the Madjar population (0.21469) and the distances of the Madjar population to the Ossetian (0.23307), Ukrainian (0.24876), Bulgarian (0.25328), and Turkish (0.28240) populations were also lower than the rest of the populations. The Han (Harbin, China) population with the value 0.70199 appeared to be the furthest from the Madjar populations. The next largest genetic distances to the Madjar population were the Kazakh (0.67966), the Ewenki (0.65354), and the Oroqen (0.64615) populations.

Affinities between populations may result from their common origin or from their recent admixture resulting from geographic proximity. In particular, genetic distances between populations can be related to geographic distances, according to a model of isolation by distance (Cavalli-Sforza and Bodmer, 1971). The genetic distances were therefore plotted against geographic distances (see Fig. 3). The points which were the closest to the Madjar population were highlighted by triangles. The point labeling the Madjar-Hungarian population distance rela-

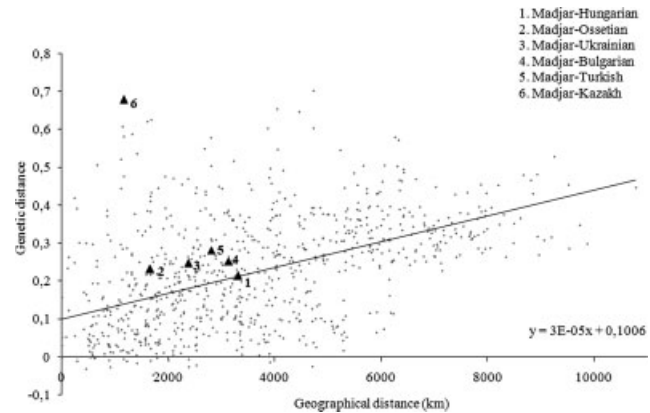


Fig. 3. Phylogeographic analysis of 38 populations. The Madjar population to the Hungarian, Ossetian, Ukrainian, Bulgarian, Turkish and Kazakh population pair data points are highlighted by triangles.

tive to the geographical distance was right on the curve, while that of the Kazakh-Madjar appeared further.

Most of the populations (84%) were significantly different from each other at 99% confidence interval ($P = 0.01$). The examined Madjar population was significantly different from all populations (see Supp. Info. Table S1). The Kazakh population was not significantly different from the Ewenki, Oroqen, and Outer Mongolian populations. Based on the genetic distances, the Ossetian population was not significantly different from the Hungarian, Bulgarian, Turkish, Kurdish, Tajik, Greek, Ukrainian, German, and French populations, although the geographical distances are large (see Supporting Information Table S1).

DISCUSSION

We set out to analyze the genetic history of the Madjar paternal lineages and investigate the intriguing similarity between their name and that of the Magyars: was this a coincidence, or did it derive from a shared history that could still be detected in the Y chromosomes of the modern populations? Clear conclusions are possible about their genetic history and, we argue, some plausible speculations about historical links between the two populations and thus can be made.

The Madjars are a small population containing only around 1,000 males, living in a social system with marriage customs that reduce Y-chromosomal gene flow into the population to very low or zero levels. Thus the male effective population size is expected to be small, of the order of a few hundred or less, and genetic drift to be high. These expectations are fulfilled by the data, with 87% of Y lineages falling into a single haplogroup and 53% into a single 12-STR haplotype: one of the lowest population diversities so far reported and evidence of extreme genetic drift. The most frequent haplotype is unknown elsewhere, as are its one-step neighbors; some of the additional haplotypes find matches in other populations and could represent founding Madjar haplotypes that have drifted to low frequency or rare examples of gene flow into the Madjars. The major haplogroup, G, occurs at ~30% in Georgia and the North Caucasus (Nasidze et al., 2003) and at 50–75% in North Ossetia (Nasidze et al., 2004). This haplogroup has been observed throughout the Middle East and is present at



Fig. 4. Hypothetical route of the ancestors of the Magyars. 1. Altay-Balhash-Alatau area, 2. Aral area, 3. western foreground of South Urals, 4. foreground of Northern Caucasus, 5. steppe between the confluence of rivers Don and Dneper, 6. northwestern foreground of the Black Sea (Bug-Dnester area), 7. Carpathian Basin. [Color figure can be viewed in the online issue, which is available at www.interscience.wiley.com.]

about 9% in Turkey (Hammer et al., 2000). It is not frequent in the Kazakh population (Zerjal et al., 2002), but in the present Hungarian population, its frequency is 4.2% (Völgyi et al., 2008), and its frequencies in Bulgaria and Ukraine are similar (Semino et al., 2000). This contrast with the Madjar frequency explains why the genetic distance from the Madjar population to all other populations was so large, and to some extent, which populations form its closest neighbors (see Fig. 2). An origin of haplogroup G has been proposed in the Middle East, 9,500 years ago by Cinniöglu et al. (2004) or 17,000 years ago by Semino et al. (2000), in either case much earlier than the events considered here. Overall, there is excellent agreement between the expectation of a small isolated male population and the genetic findings, but the extreme drift does complicate comparisons with other populations and reduce the reliability of insights into past demographic events.

Despite these limitations, our second striking observation was that the population genetically closest to the Madjars was the Magyars. Since this “closest” genetic distance is still large, is this finding meaningful? We set out to test a single hypothesis, that the Madjars and Magyars have a historical relationship and included 37 populations in the analysis, so the probability of obtaining this result by chance is 0.027 and it meets the general standard for statistical significance. It is also striking that despite the general correlation of genetic variation with geographical proximity, the Madjars are closer to the geographically distant Magyars than to their geographical neighbors. On the basis of these observations, we now consider the possible implications of a Madjar-Magyar link for the history of these populations.

A hypothetical migration map of the Magyars (see Fig. 4) was constructed based on the majority view of archeologists and linguists (Fodor, 1996), starting at the Eastern region of the Urals (Aral area) and leading to the Carpathian Basin (region 7, Fig. 4). The migration route goes from the west of the South Urals, through the

Northern Caucasus, the steppe between the rivers Don and Dneper, and northwest of the Black Sea (see Fig. 4). The Altay-Balhash-Alatau region (see Fig. 4) is also displayed on the map, South-East of the Aral area in Central Asia. Starting from this basis, and the information that the Magyars arrived in Hungary ~1,100 years ago and the Madjars in the Torgay region of Kazakhstan (located near position 2 on the map) about 300–400 years ago, we suggest that they might have come into contact, or dispersed from a common origin in Central Asia around region 1 at some time before 1,100 years ago. If so, this would place the origin of the Hungarians further to the south and east than previously supposed. Such a conclusion could be tested by additional genome wide analyses of haplotype sharing between the Madjars and Magyars, and more historical and archeological investigations of this new area. In these ways, new insights into the poorly understood early history of the Madjar and Hungarian people may be established.

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