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Comparison of two isolated "Hungarian" population to population of Budapest (mixed Hungarian) by Y-chromosomes

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Abstract

Four Y-chromosome (*DYS19*, *DYS389/I*, *DYS390*, *DYS393*) short tandem repeat (STR) polymorph systems were typed in two isolated "Hungarian" (Székely) populations. Székelys are known as Hungarian people but the origin of Székely population is still unknown. It was aimed to determine the degree of relationship between the investigated and a mixed Hungarian population. Y-chromosome STR profiles of today Székelys to the STR profiles of today mixed Hungarian population published by Furedi et al. [Int. J. Legal 113 (1999) 38] were compared. The determination of the Y-STR allele types was performed using horizontal and capillary electrophoresis. Two hundred eighteen men gave 111 different haplotypes for those four STR systems. Inter-population variance analyses were computed in a pairwise method using software ARLEQUIN version 2.000 [S. Schneider, D. Roessli, L. Excoffier, Arlequin ver. 2.000: A Software for Population Genetics Data Analysis, Genetics and Biometry Laboratory, University of Geneva, Switzerland, 2000.]. Significant differences were found between all three populations. Based on the results, it is suggested that Hungarians and Székelys should have been separated from each other more than 1000 years ago. We also suggest that the two Székely groups should have been separated from each other a long time ago.

Keywords: Y-chromosome; Short tandem repeats (STRs); Population; Hungarian; Székely

1. Introduction

The origin of different populations is an important question all over the world. It is most difficult to answer this question especially in the case of migrating people, like

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Hungarians, Mongolians and Székelys, which met some thousands years ago other populations and mixed with each other. The early home of ancient Hungarians was in West-Siberia. In the fourth century before Christ, they started to move towards Southwest direction. After decades of migration, they settled down in the Karpathian-basin in 896 A.D. It is generally admitted that the Székely people had been migrated together with ancient Hungarians but they might arrive several hundreds years before into the Karpathian-basin. Nowadays, Székelys are known as a Hungarian people but the origin of this population is still unknown.

We aimed to compare the STR profiles of today Székelys to the STR profiles of today mixed Hungarian population.

Four Y-chromosome (*DYS19*, *DYS389*/*I*, *DYS390*, *DYS393*) short tandem repeat (STR) polymorph systems were typed in two isolated "Hungarian"(Székely) populations. One of them is from Õrség (southwest of Hungary populated by Székelys) and the other population is from Corund (a Romanian town populated by Székelys) in county Hargita. We compared the allele frequencies of Y-STR systems presented in the two Székely and mixed Hungarian (Budapest) populations. We aimed to determine the degree of their relationship.

2. Materials and methods

2.1. Samples

Bloodstain samples were collected in Örség (town Öriszentpéter) and in Corund, from unrelated males (36 from Orseg, 66 from Corund). Both places are known as isolated Székely towns. Appropriate informed consent was obtained from these males and information about geographic origin and mother tongue was recorded. The results of Füredi et al. [1] for mixed Hungarian (Budapest) population (116 unrelated male) were used for comparison.

Table 1
Sequence of primers used for examinations

DYS19	nested primer 1	5′-CTACTGAGTTTCTGTTATAG-3′
	nested primer 2	5′-ATGGCATGTAGTGAGGACA-3′
	primer 1	same like nested primer 1
	primer 2	5′-CTGGGTTAAGGAGAGTGTCAC-3′
DYS389	semi nested primer 2	5′-CCAGACATTGCCAAGTGTTAC-3′
	primer 1	5′-CCAACTCTCATCTGTATTATCTAT-3′
	primer 2	5′-TCTTATCTCCACCCAGA-3′
DYS390	nested primer 1	5′-TATATTTTACACATTTTTGGGCC-3′
	nested primer 2	5′-TGACAGTAAAATGAACACATTGC-3′
	primer 1	same like nested primer 1
	primer 2	5′-GACAGTAAAATGAACACATTGC-3′
DYS393	semi-nested primer 2	5′-GGTCTTCTACTTGTGTCAATAC-3′
	primer 1	5′-GTGGTCTTCTACTTGTGTCAATAC-3′
	primer 2	5′-AACTCAAGTCCAAAAAATGAGG-3′

Table 2
One hundred eleven different haplotypes found in the populations

No.	DYS19	DYS389/I	DYS390	DYS393	Budapest	Orseg	Corund
1	12	10	24	13	1		
2	13	9	22	14	1		
3	13	9	24	13	3		1
4	13	10	22	13	1		
5	13	10	24	13	3		
6	13	11	22	13	2		
7	13	11	23	12			1
8	13	11	24	12			2
9	13	11	24	13	2	1	
10	13	11	25	13	1		
11	13	12	24	13			1
12	13	14	23	13		1	
13	13	14	24	13			1
14	14	9	22	13	4		
15	14	9	22	14	2		
16	14	9	23	12	2		
17	14	9	23	13	3	1	
18	14	9	24	12	2		
19	14	9	24	13	1		
20	14	9	25	13	1		
21	14	10	21	13		1	
22	14	10	22	12	1		
23	14	10	22	13	1	1	1
24	14	10	22	14			1
25	14	10	23	12	5		2
26	14	10	23	13	3	1	1
27	14	10	24	12	4	1	
28	14	10	24	13	1		
29	14	10	24	13	1		
30	14	10	24	13	2		
31	14	10	25	12			1
32	14	10	25	13	3		1
33	14	10	25	14			1
34	14	11	22	12			1
35	14	11	23	12	2		
36	14	11	23	13		1	3
37	14	11	23	14	1	2	
38	14	11	23	16			1
39	14	11	24	12	1		2
40	14	11	24	13	1		1
41	14	11	24	14			2
42	14	11	25	13			3
43	14	11	28	12	1		
44	14	12	23	12			1
45	14	12	23	13		2	
46	14	12	23	14			1
47	14	12	24	13		1	
48	14	13	23	13			1

(continued on next page)

Table 2 (*continued*)

No.	DYS19	DYS389/I	DYS390	DYS393	Budapest	Orseg	Corund
49	14	13	24	12		2	
50	15	9	21	15	1		
51	15	9	22	13	3		
52	15	9	23	12	1		
53	15	9	23	13	1		
54	15	9	23	13	2		
55	15	9	24	12	3		
56	15	10	22	12	1		
57	15	10	22	13		2	
58	15	10	24	13	3		
59	15	10	25	12		1	3
60	15	10	25	13	6		
61	15	10	26	13			1
62	15	10	28	13	1		
63	15	11	21	12	1		
64	15	11	22	12	1		
65	15	11	22	13		1	1
66	15	11	23	14	1		2
67	15	11	24	11			1
68	15	11	24	12		1	
69	15	11	24	13	1	1	1
70	15	11	24	14			1
71	15	11	25	11			1
72	15	11	25	12			5
73	15	11	25	13		1	
74	15	11	23	13			1
75	15	12	23	13		1	
76	15	12	24	13		2	
77	15	12	25	13		2	
78	16	7	23	13			1
79	16	9	24	12	1		
80	16	9	24	14	1		
81	16	10	22	12	1		
82	16	10	22	13		1	
83	16	10	24	12		1	
84	16	10	24	13	8		
85	16	10	24	14			1
86	16	10	25	13	2		
87	16	11	23	12			1
88	16	11	23	13	1		1
89	16	11	23	14		1	
90	16	11	24	13	2	1	1
91	16	11	25	13	1		3
92	16	11	25	14			1
93	16	11	26	13	1		1
94	16	12	22	13			1
95	16	12	23	13			2
96	16	12	24	13			1
97	16	12	25	13		1	1
98	16	12	26	13			2

Table 2 (*continued*)

No.	DYS19	DYS389/I	DYS390	DYS393	Budapest	Orseg	Corund
99	16	13	22	13		1	
100	17	9	26	14	1		
101	17	10	23	15	1		
102	17	10	24	13	3		
103	17	10	25	13	4		
104	17	10	26	13	1		
105	17	11	25	13	2		
106	17	11	25	14			1
107	17	12	24	13		1	
108	17	12	25	13		1	
109	18	10	24	13	1		
110	18	10	25	13	1		
111	18	11	25	13			1
				Total	116	36	66

2.2. DNA extraction and PCR amplification conditions

DNA was extracted from bloodstains by chelex-method. Concentration of DNA was measured by DyNA Quant200 Fluorometer (Hoefer). Quantity of DNA was higher than 100 pg in all of the cases. Every STR system was amplified using singleplex mode with the following conditions: 250 μM dNTP, 0.2 μM each primer and 1 U Taq DNA polymerase (Promega, Zenon), 2 ng DNA in 25 μl reaction volume. Cycling conditions for DYS19 were 1 min 92 °C, 1 min 56 °C, 1 min 72 °C, 30 PCR cycles; for DYS390 were 1 min 94 °C, 1 min 55 °C, 1 min 30 s 72 °C, 30 PCR cycles [3,4]; for DYS393 were 1 min denaturation 94 °C, 45 s 94 °C, 30 s 55 °C, 30 s 72 °C, 30 PCR cycles; for DYS389 were 3 min denaturation 94 °C, 15 s 94 °C, 20 s 58 °C, 20 s 72 °C, 5 PCR cycles then 15 s 94 °C, 20 s 54 °C, 20 s 72 °C, 30 PCR cycles, 10 min final extension 72 °C [5]. Short tandem repeat (STR) fragments were amplified by nested-PCR. Primer sequences are shown in Table 1.

2.3. Electrophoretic methods and software

The alleles of DYS19, DYS390, DYS393 STR systems were detected by poliacrylamide gel electrophoresis described by Wiegand et al. [6], after which silver nitrate staining was applied [7]. The allele types of DYS389/I STR system was analyzed by capillary electrophoresis in the denaturing polymer POP-4 on an ABI310 Genetic Analyzer (PE). Standard electrophoretic conditions using the run module GS STR POP4 A (1 ml) were applied in 47 cm, 50 μm ID uncoated capillary. For allele sizing of individual samples, the fluorescent ladder GeneScan-500 (ROX) (PE) was used as internal size marker. Data from ABI Prism 310 instrument were analyzed with GeneScan 2.1 software.

Table 3
Allele frequencies observed in the examined populations

		Budapest	Orseg	Corund
DYS19	12	0.008		
	13	0.103	0.055	0.090
	14	0.362	0.388	0.363
	15	0.224	0.333	0.252
	16	0.181	0.194	0.252
	17	0.103	0.055	0.015
	18	0.017		0.015
DYS389/I	7			0.015
	9	0.275	0.027	0.015
	10	0.534	0.25	0.212
	11	0.189	0.333	0.606
	12		0.305	0.151
	13		0.083	
	14			
DYS390	21	0.017	0.027	
	22	0.155	0.166	0.075
	23	0.198	0.305	0.272
	24	0.379	0.333	0.242
	25	0.206	0.166	0.348
	26			0.060
	27	0.017		
	28			
DYS393	11			0.030
	12	0.232	0.166	0.287
	13	0.689	0.750	0.500
	14	0.060	0.080	0.166
	15	0.017		0.015

2.4. Statistical analyses

Inter-population variance analyses was computed in a pairwise method using software ARLEQUIN version 2.000 [2]. We have calculated the allele frequencies, genetic distances and significance shown in Tables 3–5.

3. Results and discussion

It was found there were some similar haplotype between mixed Hungarian and Székely populations and between the two Székely populations (Table 2).

Table 4
Genetic distances calculated by software ARLEQUIN version 2.000

	Budapest	Orseg	Corund
Budapest	0		
Orseg	0.03747	0	
Corund	0.07361	0.02586	0

Table 5
Significance values calculated by software ARLEQUIN version 2.000

	Budapest	Orseg	Corund
Budapest	*		
Orseg	10^{-3}	*	
Corund	10^{-5}	0.0155	*

Table 3 shows allele frequencies found in the examined populations. The most frequent allele in STR system DYS19 and DYS393 was the same (14 and 13) in all the three populations. In case of DYS389/I the most frequent allele in the mixed population was allele 10 but in Orseg and Corund was allele 11. In case of DYS390 the most frequent allele in Budapest and in Orseg was the allele 24 but in Corund, allele 25.

Genetic distances were calculated between Budapest and Orseg, between Budapest and Corund and between Orseg and Corund (Table 4). The values of genetic distances seem to be a bit high compared the values of genetic distance in European peoples by somatic STR markers published by Budowle [8]. Little differentiation among European populations for somatic markers can be explained with the high degree of mixing and more frequent recombination events of somatic markers.

Based on the results presented in Table 5, it is suggested that there is significant difference between all the three populations. There is closer relationship between the two Székely populations than between Székely and Hungarian populations. The population living in Orseg is genetically closer to the mixed Hungarian (Budapest) population than the population living in Corund. The low number of samples from Orseg and Corund could lead to some mistakes. More samples were collected from Corund and more Y-chromosome STR systems will be examined to get pointed results. Nested PCR had to be used because of low DNA concentration. Nested PCR is not recommended under 100 pg of DNA because it should present artifacts but the quantity of DNA was higher than 100 pg in all of the cases.

Our results are in good correlation with the fact that ancient Hungarians and Székelys separated from each other more than 1000 years ago and the two Székely groups separated centuries before too. Theory of double conquest of Hungary should be supported with these results. According to this theory, a part of Székely people settled down into the Karpathian-basin before Hungarians. More samples from Székely population are being examined in order to prove the reality of this theory.

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