



Population genetics of 10 Y-chromosomal STR loci in Japanese using multiplexed PCR amplification kits, Y-PLEX™ 6 and Y-PLEX™ 5

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Abstract. Allele and haplotype frequencies of 10 Y-STR loci DYS19, DYS385, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS438 and DYS439 were determined in 115 unrelated Japanese males using the Y-PLEX™ 6 and Y-PLEX™ 5 PCR amplification kits. A total of 105 different haplotypes was observed, 96 of them being unique. The haplotype diversity was 0.9960 and the discrimination capacity was 0.9130. © 2003 Elsevier B.V. All rights reserved.

Keywords: Y-chromosome; Short tandem repeat (STR); Population data; Japanese

1. Introduction

We analyzed allele and haplotype frequencies of 10 Y-chromosomal short tandem repeat (Y-STR) loci DYS19, DYS385, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS438 and DYS439 in a Japanese population using the Y-PLEX™ 6 and Y-PLEX™ 5 PCR amplification kits.

2. Materials and methods

Semen or blood samples were obtained from 115 unrelated Japanese males. DNA was extracted by the phenol-chloroform method. PCR amplification of six loci DYS19, DYS385, DYS389II, DYS390, DYS391 and DYS393 was performed using the Y-PLEX™ 6 kit (ReliaGene Technologies) and the amplification of five loci DYS389I, DYS389II, DYS392, DYS438 and DYS439 was performed using the Y-PLEX™ 5 kit (ReliaGene Technologies) according to the instruction manual. DYS389II was common to the both kits. The amplified products were detected using an ABI PRISM 310 Genetic Analyzer (Applied Biosystems). The results were analyzed using GeneScan Analysis v3.1 software (Applied Biosystems) and the alleles were typed using Genotyper v2.5 software (Applied Biosystems).

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Table 1
Y-STR haplotypes detected in Japanese

H	DYS19	DYS385	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS438	DYS439	N
1	13	10–14	13	29	24	10	11	14	10	14	1
2	13	11–12	14	31	22	10	14	13	11	11	1
3	13	13–15	13	29	24	10	11	14	10	14	1
4	14	11–12	14	30	23	10	14	13	11	11	1
5	14	11–18	13	29	23	10	14	13	10	11	1
6	14	12–13	13	29	23	10	15	13	10	11	1
7	14	12–19	13	30	25	10	15	12	11	11	1
8	14	13–17	14	32	23	10	12	12	11	12	1
9	14	13–18	12	27	24	10	14	13	11	11	1
10	14	13–18	12	28	24	10	14	12	11	13	1
11	14	13–18	12	28	25	10	14	12	11	11	1
12	14	13–19	12	27	24	10	14	12	11	11	1
13	14	13–19	12	28	23	10	14	12	11	12	1
14	14	13–19	12	28	24	10	14	12	11	11	1
15	15	10–17	12	28	23	10	14	14	10	12	1
16	15	10–18	14	31	22	10	13	13	13	13	1
17	15	10–19	13	28	22	10	13	13	13	12	1
18	15	10–19	13	28	23	10	14	13	13	12	1
19	15	10–19	13	29	23	10	13	13	13	13	1
20	15	10–19	13	30	22	10	11	13	10	12	1
21	15	10–19	14	29	23	10	13	13	13	12	1
22	15	10–19	14	30	22	10	13	13	12	12	1
23	15	10–19	14	30	22	10	13	13	13	12	2
24	15	10–20	13	28	22	10	13	13	14	12	1
25	15	10–20	13	29	21	10	14	13	13	13	1
26	15	10–20	13	29	22	10	13	13	13	11	1
27	15	10–20	13	29	22	10	13	13	13	12	2
28	15	10–20	14	29	22	10	12	13	13	13	1
29	15	10–20	14	29	22	10	13	13	13	12	1
30	15	10–20	14	29	22	10	13	13	13	13	1
31	15	10–20	14	29	22	10	13	14	13	12	1
32	15	10–20	14	30	22	10	13	13	13	11	2
33	15	10–20	15	31	22	10	13	13	13	12	1
34	15	10–21	14	30	22	10	13	13	13	12	1
35	15	10–21	14	30	22	10	13	13	13	12	2
36	15	10–21	14	30	22	10	14	13	13	12	1
37	15	10–22	14	30	23	10	13	13	13	13	1
38	15	11–12	12	29	23	10	12	12	10	14	1
39	15	11–12	13	28	22	10	11	13	10	11	1
40	15	11–12	14	30	22	10	13	13	13	12	1
41	15	11–18	12	28	23	10	12	12	10	11	1
42	15	11–18	13	31	23	10	11	14	10	11	1
43	15	11–19	12	29	23	10	12	12	10	11	1
44	15	12–13	12	29	23	11	14	13	10	12	1
45	15	12–14	14	30	24	11	11	13	10	11	1
46	15	12–16	12	26	24	10	13	13	10	11	1
47	15	12–17	12	29	25	8	11	13	10	13	1
48	15	12–17	13	29	24	11	13	12	10	11	1
49	15	12–17	13	30	23	10	11	14	10	11	1
50	15	12–18	13	31	23	10	11	14	10	11	1
51	15	13–13	12	28	23	10	14	13	10	12	1
52	15	13–17	14	31	24	11	11	13	11	12	1
53	15	13–17	14	31	25	10	11	13	11	13	1
54	15	13–17	14	31	25	11	11	13	11	13	1
55	15	13–17	14	32	23	10	12	12	11	12	1
56	15	14–16	13	30	25	10	11	13	10	11	1
57	15	14–17	13	29	25	10	11	13	10	13	1
58	15	14–17	13	30	24	10	11	13	10	12	1
59	15	14–17	13	30	24	10	11	14	10	12	1
60	15	14–17	13	30	25	10	11	13	10	11	1
61	15	14–17	13	30	25	10	11	13	10	12	1
62	15	14–17	13	30	25	10	11	13	10	13	1
63	15	14–17	14	30	25	10	13	13	13	12	1

Table 1 (continued)

H	DYS19	DYS385	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS438	DYS439	N
64	15	15–17	13	30	25	10	11	13	10	12	1
65	15	15–17	14	31	25	10	11	13	10	12	2
66	16	10–12	13	30	25	10	12	13	10	11	1
67	16	10–12	14	29	25	10	11	13	10	12	1
68	16	10–17	13	28	23	10	13	13	13	12	2
69	16	10–19	14	29	23	10	13	12	13	12	1
70	16	10–19	14	29	23	10	13	13	13	13	2
71	16	10–19	14	30	22	10	13	13	13	12	1
72	16	10–20	14	29	23	10	13	13	13	12	1
73	16	10–22	13	29	22	10	13	13	15	13	1
74	16	11–19	14	30	21	10	11	15	10	11	1
75	16	11–21	14	29	23	10	11	15	10	12	1
76	16	12–16	12	29	23	9	12	12	10	12	1
77	16	12–18	12	28	23	10	12	12	10	11	1
78	16	12–18	12	29	25	10	13	12	10	13	1
79	16	12–18	12	31	24	10	13	12	10	11	1
80	16	12–19	12	28	24	10	13	12	10	11	1
81	16	12–19	13	28	25	11	13	12	10	11	1
82	16	13–14	12	28	23	10	13	14	11	11	1
83	16	13–17	14	31	25	10	11	13	10	11	1
84	16	13–17	14	31	25	10	11	13	10	13	2
85	16	13–17	14	31	25	11	11	13	10	12	1
86	16	13–18	13	31	25	11	11	13	10	12	1
87	16	13–18	14	31	26	11	11	13	10	13	1
88	16	14–16	13	30	25	10	11	13	10	12	1
89	16	14–17	14	31	25	11	11	13	10	12	1
90	16	14–17	14	32	23	10	11	13	10	13	1
91	16	16–17	13	30	25	11	11	13	10	12	1
92	17	12–16	11	27	23	11	12	12	10	13	1
93	17	12–17	14	32	24	11	11	13	10	13	1
94	17	12–19	12	28	25	10	13	12	10	12	1
95	17	12–20	12	28	25	10	13	12	10	13	1
96	17	13–13	14	31	24	10	11	13	10	12	1
97	17	13–17	14	31	25	10	11	13	10	12	3
98	17	13–17	14	31	25	12	11	13	10	12	1
99	17	13–17	14	32	25	10	11	13	10	12	1
100	17	13–18	14	31	25	11	11	13	10	13	1
101	17	14–17	11	27	27	10	13	12	10	11	1
102	17	14–17	14	31	25	10	11	13	10	13	1
103	17	14–22	12	28	24	11	13	12	10	11	1
104	17	15–17	12	27	25	11	13	12	10	11	1
105	17	16–20	12	29	25	10	13	12	10	12	1

H: haplotype number.

N: individuals observed for each haplotype.

3. Results and discussion

Gene diversity values of the 10 Y-STR loci in the Japanese population ranged from 0.286 at DYS391 to 0.944 at DYS385. Haplotypes constructed from the 10 Y-STR loci are shown in Table 1. A total of 115 unrelated individuals produced 105 haplotypes, of which, 96 haplotypes were unique, eight were found in two individuals and one was found in three individuals. The haplotype diversity [1] calculated from the 10 Y-STR loci was 0.9960 and the discrimination capacity was 0.9130.

Reference

- [1] M. Nei, Molecular Evolutionary Genetic, Columbia University Press, New York, 1987.