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SHORT COMMUNICATION

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Human Y-chromosomal STR types in north Thailand

Abstract A north Thai Y-haplotype database consisting of the loci DYS19, DXYS156-Y, DYS390, DYS391, DYS392, DYS393, and the four subsegments of DYS389 is presented. We observed 44 Y-types in 50 unrelated Thais, and the haplotype diversity was calculated to be 97.36%. No Y-types were shared with a sample of 55 Japanese, but 3 matches were found in a sample of 61 Han Chinese, and there was one Thai-German match in a larger west German sample (*n* = 179).

Key words Y-chromosome · Short tandem repeat · STR · Microsatellite · Thailand

Introduction

Short tandem repeat (STR) polymorphisms from the male specific part of the Y- chromosome are useful for the study of male specific lineage evolution (Jobling et al. 1995, Mitchell and Hammer 1996, Forster et al. 1998) and show promise for forensic applications (Jobling et al. 1997, Kayser et al. 1997, de Knijff et al. 1997). For the forensic application of Y- linked markers knowledge of the Y-type frequencies in different populations is required. Here, we present a Y-type database derived from a Thai population sample of 50 individuals.

Materials and methods

Population samples: blood samples from 50 unrelated Thai males from the rural areas of the Chiang Mai province (Horst et al. 1997) were analysed. DNA was isolated according to standard procedures (Miller et al. 1986). PCR-protocols, primer sequences, amplification conditions, detection systems and allele nomenclature have been described elsewhere (Kayser et al. 1997) with the exception of the DYS389 locus. This was typed for its four constituent segments m, n, p, and q using the methods described in Rolf et al. (1998b). DYS389q corresponds to DYS389-I and the sum of m, n, and q corresponds to DYS389-II in the system of Kayser et al. (1997) and de Knijff et al. (1997). Furthermore, DXYS156 was scored as in Karafet et al. (1998). Simple haplotype diversity, i.e. the probability of sampling two individuals with different haplotypes, was calculated as $1-\sum_{i=1}^{n} x_i^2$, where x is the frequency of the i-th haplotype and n the total number of haplotypes (Nei 1987).

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Results and discussion

The Y-types defined by the 10 STR loci are shown in Table 1. In 50 unrelated Thais 44 haplotypes were observed. The most frequent haplotype in this study was number 27, which was found in 3 individuals. The haplotype diversity was 0,9736. For comparison, we consulted our unpublished datasets for Japanese from Shiga University (*n* = 55, 43 Y-types) and Han Chinese from Shenyang (*n* = 61, 58 Y-types). The haplotype diversities for these two samples are 0.9686 and 0.9820 respectively. No sequence matches are shared between the Thai and the Japanese, while there were 3 Thai-Chinese matches (Table 1). In addition, Thai type 29 matched one German in a set of west Germans from the Münster area (*n* = 179, 104 Y-types, haplotype diversity 0.9806). The Germans had been identified as such by their surnames (Nata et al. 1999). The match has the allele combination 12 and 5 of the ethnically informative markers DXYS156-Y and DYS389m, respectively. This combination is frequent in Caucasoids; it appears in 95% of Germans (Nata et al. 1999), whereas it is found in only 10% of the Thai, 2% of the Japanese, and 5% of the Chinese. The Thai-German match is thus not unexpected considering its Y-type class, and it is unnecessary to invoke recent migration as an explanation. 16% of the Thai display the long DYS156Y allele 14, which is characteristic of south Asians and un-

Table 1 Thai Y-STR-types consisting of DYS19, DXYS156-Y, DYS390, DYS391, DYS392, DYS393, and the four segments of DYS389

#\DYS	19	156Y	389m	389n	389p	389q	390	391	392	393	n	Han
1	14	11	5	12	3	9	24	10	11	13	1	0
2	14	11	5	13	3	9	24	10	11	13	2	0
3	14	11	5	13	3	10	24	10	11	13	1	0
4	14	12	4	11	3	11	23	10	14	13	1	0
5	14	12	4	12	3	11	23	10	14	13	1	0
6	14	12	5	11	3	9	25	11	11	12	1	0
7	14	14	4	11	3	9	25	10	14	12	1	0
8	14	14	4	12	3	9	23	10	13	12	1	0
9	14	14	4	12	3	9	24	10	14	12	1	0
10	14	14	4	12	3	9	24	10	14	13	1	0
11	14	14	4	12	3	9	25	10	14	12	1	0
12	14	14	4	12	3	9	26	10	14	12	1	0
13	14	14	4	12	3	10	23	10	14	12	1	2
14	15	11	5	11	3	9	21	10	11	12	1	0
15	15	11	5	11	3	10	23	10	11	15	1	0
16	15	11	5	11	3	11	23	11	11	14	1	0
17	15	12	4	10	3	10	25	10	13	13	1	0
18	15	12	4	12	3	10	25	9	13	14	3	0
19	15	12	4	12	3	10	25	10	13	13	1	1
20	15	12	4	12	3	10	25	10	14	13	1	0
21	15	12	4	12	3	11	23	10	13	14	1	0
22	15	12	4	12	3	11	25	10	13	13	1	0
23	15	12	4	12	3	11	25	10	13	14	1	0
24	15	12	4	13	3	10	25	10	13	13	1	0
25	15	12	4	13	3	11	23	12	13	14	1	0
26	15	12	4	13	3	11	25	10	13	14	1	0
27	15	12	4	15	3	10	23	10	14	13	3	0
28	15	12	5	12	3	10	23	10	11	13	1	0
29	15	12	5	12	3	10	24	11	11	13	1	0
30	15	12	5	12	3	11	22	10	11	12	1	0
31	15	13	4	12	3	9	23	10	12	13	1	0
32	15	13	4	13	3	9	24	10	12	12	1	1
33	15	14	4	12	3	9	24	10	13	12	1	0
34	16	12	4	11	3	10	25	10	13	15	1	0
35	16	12	4	12	3	10	24	10	13	14	1	0
36	16	12	4	12	3	10	24	11	13	14	1	0
37	16	12	4	12	3	10	25	11	13	15	1	0
38	16	12	4	13	3	10	24	11	13	14	1	0
39	16	12	5	11	3	9	22	10	11	12	1	0
40	16	13	4	11	3	9	23	10	13	13	1	0
41	16	13	4	11	3	9	24	10	14	12	1	0
42	16	13	4	11	3	10	22	10	13	12	1	0
43	17	12	4	12	3	10	24	11	13	14	1	0
44	17	13	4	11	3	9	23	10	13	13	2	0

common in north Asians (Karafet et al. 1998); this specific distribution suggests that Y polymorphisms may become useful to illuminate the evolutionary relationships between north and south Asians (Rolf et al. 1998a).

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