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SHORT COMMUNICATION

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Y-Chromosomal STR haplotypes in a population from north west Germany

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Abstract We present a German Y-chromosome short tandem repeat (STR)-haplotype database consisting of the loci DYS19, DXYS156-Y, subtypes of DYS389, DYS390, DYS391, DYS392 and as well as DYS393. 104 haplotypes were observed in 179 unrelated Germans, the haplotype diversity is 98.06%. This database is a prerequisite for the forensic application of these new markers.

Introduction

Short tandem repeat (STR) polymorphism from the male specific part of the Y-chromosome (Kayser et al. 1997; de Knijff et al. 1997; Rolf et al. 1998; Rossi et al. 1997) are increasingly being used for the study of male specific lineage evolution as well as for forensic applications (Jobling et al. 1997). Since the first Y-User Workshop (Berlin, 1996), world-wide population data have been collected, and protocols and allele frequency data have been reported. However, the forensic application of these linked markers requires knowledge of the haplotype frequencies. In this work, we present a Y-haplotype database derived from a German population sample of 179 individuals.

Materials and methods

Population samples: 179 unrelated German males from the Münster area having German surnames were analysed. DNA was extracted according to standard procedures. (Miller et al. 1986; Walsh et al. 1991). PCR-protocols, primer sequences, amplification conditions, nomenclature and detection systems have been described elsewhere (Rossi et al. 1998; de Knijff et al. 1997; Kayser et al. 1997; Rolf et al. 1998; Karafet et al. 1998). The haplotype diversity was calculated according to Nei (1987).

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Results and discussion

Variation at different Y-STR loci should be combined to haplotypes, because the Y-chromosome does not recombine. Y haplotypes of DYS19, DXYS156-Y, subtypes of DYS389, DYS390, DYS391, DYS392 and DYS393 are shown in Table 1. 104 haplotypes were observed in 179 unrelated Germans. The most frequent haplotype in this study was number 5,57, which was found in 13 individuals. The haplotype diversity obtained in our study was 0.9806. The haplotype diversity of the Yh1 haplotype format (like ours but without DXYS156-Y and with the alternative 389-I/II typing) in 4 different European populations was between 0.983 and 0.996 (Kayser et al. 1997; de Knijff et al. 1997). The further inclusion of DXYS156-Y and 389-subtypes does not increase the haplotype diversity significantly, thus these markers are not the forensic scientist's first choice. However, these two markers exhibit variations between major ethnic groups (Rolf et al. 1998; Karafet et al. 1998) thus our haplotype format may allow ethnic estimations when more databases become available. Nevertheless, the comparison of haplotypes in the Yh1-format with our database is possible. The subtypes m, n and q of the DYS389 locus are the number of repeats in the three variable repetitive stretches of the locus: $(TCTG)_m(TCTA)_n(48\ bp)(TCTG)_p(TCTA)_q$, p is always 3 in our sample. Thus, DYS389-I is q and DYS389-II is the sum of m, n and q. For example the 125 Italian males published by Caglià et al. (1998) exhibit 103 haplotypes in the Yh1 format, our sample of 179 males has 104 haplotypes of the (modified) Yh1 format. Seventeen haplotypes are shared by both samples. The reason for the smaller number of haplotypes in our sample might be the more restricted area of our sample compared to south and central Italy in the Caglià et al sample.

Table 1 Y-STR-haplotypes

Nr./DYS	19	156Y	389m	389n	389q	390	391	392	393	n
1	13	11	6	12	9	23	11	11	13	1
2	13	11	6	13	9	23	11	11	13	1
3	13	12	5	11	10	24	11	13	13	2
4	13	12	5	12	10	24	10	11	14	1
5	13	12	6	11	10	24	10	11	13	1
6	13	12	6	12	11	25	10	11	11	1
7	14	11	5	11	10	23	9	13	13	1
8	14	12	5	9	10	22	11	11	13	1
9	14	12	5	9	10	24	11	13	13	1
10	14	12	5	10	10	23	11	14	13	1
11	14	12	5	10	11	24	11	13	14	1
12	14	12	5	11	8	24	10	13	13	1
13	13	12	5	11	9	22	10	11	13	1
14	14	12	5	11	9	22	11	11	12	1
15	14	12	5	11	9	22	11	11	13	12
16	14	12	5	11	9	23	9	13	13	1
17	14	12	5	11	9	23	10	11	13	1
18	14	12	5	11	9	23	11	13	13	1
19	14	12	5	11	10	22	10	13	13	1
20	14	12	5	11	10	22	11	11	13	3
21	14	12	5	11	10	23	9	13	13	1
22	14	12	5	11	10	23	10	11	13	1
23	14	12	5	11	10	23	10	13	13	4
24	14	12	5	11	10	23	11	13	13	10
25	14	12	5	11	10	23	11	13	14	1
26	14	12	5	11	10	23	12	13	13	1
27	14	12	5	11	10	24	9	13	13	2
28	14	12	5	11	10	24	10	10	13	1
29	14	12	5	11	10	24	10	13	12	2
30	14	12	5	11	10	24	10	13	13	11
31	14	12	5	11	10	24	10	13	14	1
32	14	12	5	11	10	24	11	13	13	8
33	14	12	5	11	10	24	11	13	14	1
34	14	12	5	11	10	24	11	13	15	1
35	14	12	5	11	10	24	12	13	12	1
36	14	12	5	11	10	25	9	14	13	1
37	14	12	5	11	10	25	10	11	13	1
38	14	12	5	11	10	25	10	13	13	2
39	14	12	5	11	10	25	11	13	13	1
40	14	12	5	11	11	23	11	13	13	2
41	14	12	5	11	11	24	10	13	13	1
42	14	12	5	11	11	24	11	13	13	2
43	14	12	5	12	9	22	11	11	13	4
44	14	12	5	12	9	22	11	11	14	1
45	14	12	5	12	9	22	11	14	11	1
46	14	12	5	12	9	23	10	11	13	1
47	14	12	5	12	10	22	11	11	12	1
48	14	12	5	12	10	23	11	11	12	1
49	14	12	5	12	10	24	9	15	13	1
50	14	12	5	12	10	24	10	13	13	1
51	14	12	5	12	10	24	11	13	13	2
52	14	12	5	13	10	23	10	13	12	1
53	14	12	5	13	10	24	9	13	13	1
54	15	11	5	11	11	23	11	13	13	1
55	15	12	4	12	11	23	10	14	14	1
56	15	12	5	11	9	22	10	11	13	2
57	15	12	5	11	9	22	11	11	13	1
58	15	12	5	11	9	24	9	11	12	1
59	15	12	5	11	10	23	10	13	13	1
60	15	12	5	11	10	23	11	13	13	1
61	15	12	5	11	10	24	10	12	14	1
62	15	12	5	11	10	24	10	13	13	3
63	15	12	5	11	10	24	11	13	13	1
64	15	12	5	11	10	25	10	11	13	2
65	15	12	5	11	10	25	10	14	13	1
66	15	12	5	11	11	24	11	13	13	1
67	15	12	5	12	9	22	11	11	14	2
68	15	12	5	12	9	22	12	11	13	1
69	15	12	5	12	10	24	10	11	13	1
70	15	12	5	12	10	24	11	11	13	1
71	15	12	5	12	10	25	10	11	13	1
72	15	12	5	12	10	25	11	11	13	3
73	15	12	5	12	10	26	10	11	13	1
74	15	12	5	12	11	23	10	12	15	1
75	15	12	5	12	11	25	11	13	13	1
76	15	12	5	13	10	25	9	11	13	1
77	15	12	5	13	10	25	10	11	13	1
78	15	12	5	13	10	25	11	11	13	1
79	15	12	5	13	11	23	11	12	15	1
80	16	12	5	10	10	25	10	11	13	1
81	16	12	5	11	9	21	10	11	14	1
82	16	12	5	11	9	22	11	11	13	1
83	16	12	5	11	10	22	11	11	14	1
84	16	12	5	11	10	25	9	11	13	1
85	16	12	5	11	10	25	10	11	13	2
86	16	12	5	11	10	25	10	11	14	2
87	16	12	5	11	10	25	11	11	13	1
88	16	12	5	11	11	26	11	11	13	1
89	16	12	5	12	10	25	10	11	13	5
90	16	12	5	12	10	25	10	12	13	1
91	16	12	5	12	10	25	11	11	13	1
92	16	12	5	12	11	25	10	11	13	1
93	16	12	5	13	9	25	11	11	13	1
94	16	12	5	13	10	23	10	11	13	1
95	16	12	5	13	10	23	11	9	13	1
96	16	12	5	13	10	24	10	11	13	1
97	16	12	5	13	10	24	11	11	13	1
98	16	12	5	13	10	25	10	11	13	2
99	16	12	5	13	10	25	11	11	13	1
100	17	12	5	11	10	25	11	11	13	1
101	17	12	5	12	10	24	10	11	13	1
102	17	12	5	12	11	25	10	11	13	1
103	17	12	5	12	11	26	11	11	13	1
104	17	12	5	13	10	24	10	11	13	1

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