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Allele frequencies for X-chromosomal microsatellites in different populations

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Abstract. We investigated the allele distribution of several X-chromosomal (ChrX) markers in population samples from Peru, Ireland, Germany and Ethiopia. We found no homogeneity between the populations. This could be confirmed by χ^2-test. The most impressive differences were seen between the Peruvian and European population samples.

Keywords: X-chromosome; Allele distribution; Population data

1. Introduction

ChrX markers represent an efficient supplementation of autosomal and Y-chromosomal STR analyses and ChrX haplotyping can elucidate complicated kinship situations [1]. This procedure requires a broad spectrum of well established ChrX markers of well known localisation. Some of them are forensically characterised for few European and Asian population samples [2–4].

2. Materials and methods

We investigated population samples from Peru (118 alleles), Ireland (110 alleles), Germany (900 alleles) and Ethiopia (123 alleles). It has been made sure as possible, that each sample represents the indigenous population. PCR amplifications were performed with a pentaplex reaction for GATA172D05, DXS101, DXS7424, DXS6800, DXS6807, a triplex reaction for DXS6809, DXS6801, DXS6789 and a single PCR for DXS8377. Resulting PCR products were resolved and detected by capillary electrophoresis in the ABI 310 sequencer.

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Table 1
Allele frequencies [%] of the population samples: Peru (P), Ireland (I), Germany (G) and Ethiopia (E)

DXS101	P	I	G	E
12	0.0	0.0	0.2	0.8
15	1.7	5.2	4.4	0.8
16	0.0	0.0	0.5	2.4
17	0.0	0.0	0.2	0.8
18	0.8	7.3	8.5	9.8
19	1.7	5.2	4.7	2.4
20	2.5	2.1	1.2	2.4
21	0.0	6.2	3.2	4.9
22	0.8	1.0	2.2	7.3
23	6.8	8.3	6.6	6.5
24	30.5	11.5	21.2	12.2
25	20.3	20.8	15.6	11.4
26	22.0	14.6	11.4	17.1
27	8.5	6.2	7.9	8.9
28	2.5	6.2	7.0	8.1
29	0.8	4.2	2.7	3.2
30	0.8	1.0	2.4	0.8
DXS7424	P	I	G	E
10	1.7	0.0	0.3	2.4
11	0.0	1.0	0.4	3.2
12	0.8	5.1	3.5	4.1
13	4.2	3.1	6.9	2.4
14	22.9	14.3	22.0	26.8
15	29.7	38.8	29.1	25.2
16	29.7	25.5	24.0	29.3
17	8.5	8.2	10.4	4.9
18	1.7	4.1	2.1	1.6
19	0.8	0.0	1.1	0.0
172D05	P	I	G	E
6	14.4	13.4	14.8	33.3
7	0.0	0.0	0.2	2.4
8	6.8	23.7	16.7	15.4
9	3.4	2.1	5.5	5.7
10	35.6	30.9	27.2	24.4
11	24.6	13.4	24.1	8.9
12	15.2	16.5	11.2	9.8
13	0.0	0.0	0.2	0.0
DXS6807	P	I	G	E
10	0.0	0.0	0.0	1.6
11	36.4	57.1	49.2	65.8
12	3.4	1.0	2.1	4.1
13	22.0	1.0	1.1	4.9
14	25.4	26.5	23.5	14.6
15	12.7	13.3	20.2	4.1
16	0.0	1.0	2.9	3.2
17	0.0	0.0	1.0	1.6
DXS6800	P	I	G	E
16	84.0	40.8	36.7	32.5
17	2.5	2.0	5.2	4.9
18	6.8	13.3	8.2	26.0
19	5.1	31.6	33.5	30.1
20	0.8	6.1	4.6	4.1
21	0.0	6.1	9.4	2.4
22	0.8	0.0	2.3	0.0

DXS6809	P	I	G	E
27	0.0	0.0	1.5	1.6
28	0.8	0.0	3.7	2.4
29	0.0	1.0	1.3	8.9
30	2.5	0.0	4.1	5.7
31	16.9	17.0	15.4	14.6
32	23.7	15.0	14.6	16.3
33	32.2	36.0	27.9	26.8
34	15.2	17.0	19.1	17.1
35	5.9	7.0	7.7	5.7
36	2.5	5.0	3.4	0.0
37	0.0	1.0	0.8	0.0
38	0.0	1.0	0.4	0.8
DXS6789	P	I	G	E
15	2.5	7.0	3.6	16.3
16	16.1	1.0	1.4	4.1
17	0.0	1.0	0.1	0.8
18	1.7	0.0	0.2	1.6
19	5.1	0.0	2.9	1.6
20	48.3	31.0	37.9	31.7
21	13.6	34.0	28.6	21.1
22	8.5	19.0	17.3	14.6
23	2.5	7.0	6.3	6.5
24	1.7	0.0	1.6	1.6
DXS6801	P	I	G	E
6	0.0	0.0	0.0	0.8
8	0.0	2.0	1.0	0.0
10	22.0	6.0	3.1	5.7
11	62.7	57.0	55.7	42.3
12	10.2	26.0	26.8	31.7
13	4.2	6.0	11.3	17.1
14	0.8	3.0	2.1	2.4
15	0.0	0.0	0.0	0.0
DXS8377	P	I	G	E
39	0.0	0.0	0.7	0.0
40	0.0	0.0	1.0	0.0
41	0.0	3.3	2.4	0.8
42	0.0	2.2	3.1	1.6
43	9.7	8.8	4.4	3.2
44	19.3	5.5	4.3	8.1
45	15.0	2.2	5.0	5.7
46	0.0	5.5	6.9	8.1
47	16.1	17.6	9.2	7.3
48	8.6	14.3	11.0	10.6
49	14.0	13.2	11.3	16.3
50	3.2	7.7	12.7	7.3
51	5.4	4.4	8.2	7.3
52	3.2	3.3	6.3	10.6
53	2.1	2.2	6.0	7.3
54	2.1	5.5	4.0	3.2
55	0.0	2.2	1.4	0.8
56	0.0	2.2	1.4	0.0
57	1.1	0.0	0.5	0.8
58	0.0	0.0	0.1	0.0
59	0.0	0.0	0.1	0.0
60	0.0	0.0	0.0	0.8

4. Results

Allele frequencies of the population samples are shown in Table 1.

There were significant higher and significant lower observed alleles compared to expected allele numbers after assumption of homogeneity between populations. Detailed data are available by the authors.

4. Discussion

The differences between allele frequencies (Table 1) are indicating that there is no homogeneity between the investigated populations. This could be confirmed by testing homogeneity of allele distribution by χ^2-test. The most impressive differences were seen between the Peruvian and European population samples. In the German population significant linkage disequilibrium was observed between the markers DXS7424 and DXS101 [5]. Hence, for this linkage group haplotype frequencies must be estimated directly from population data. With this study we collected the first haplotype data for other populations, but to check for linkage disequilibrium the number of individuals is insufficient. Apart from the forensic significance of allele distribution and linkage disequilibrium, these results give some interesting information on human world migration history.

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