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SHORT COMMUNICATION

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Allele frequencies of nine STR loci of Jewish and Arab populations in Israel

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Abstract DNA typing of nine short tandem repeat (STR) loci was carried out on unrelated Israeli Jewish and Arab individuals. All loci were highly polymorphic and the distribution of the obtained genotypes did not deviate from Hardy-Weinberg equilibrium. A comparison between Jewish and Arab population data revealed statistically significant differences in allele frequency distributions for some of the loci. The results presented in this study enable the use of these nine STR loci for forensic, identification and paternity cases in the Jewish and the Arab populations of Israel.

Keywords STR · Allele frequencies · Subpopulation · Jews · Arabs

Introduction

Statistical assessment of a specific population is necessary for presenting forensic evidence. Numerous population studies for commonly used STR loci have been carried out by the forensic community (Budowle et al. 1997; Entrala et al. 1999; Marco et al. 1999; Klintschar et al. 2001). A total of nine polymorphic tetranucleotide STRs are presently employed for criminal casework and identification purposes in Israel. Hammer et al. (2000) have reported that the Jewish and Middle Eastern non-Jewish populations may have descended from a common Middle Eastern ancestral population. However, the ethnic makeup of the population in Israel suggests that a statistical evaluation of the STR allele distribution within Jewish and Arab populations is needed for forensic purposes.

In this report we present the allelic frequencies and statistical analysis of the nine STR loci TH01, TPOX, CSF1PO, vWA, FESFPS, F13A01, D13S317, D7S820, D16S539 for Jewish and Arab populations in Israel.

Materials and methods

Blood samples or buccal cells were obtained from unrelated individuals from the Arab and Jewish populations within Israel. DNA was extracted using a phenol-chloroform extraction method (Sambrook et al. 1989). The extracted DNA was amplified using the Promega GenePrint STR multiplex systems for the loci TH01, TPOX, CSF1PO, vWA, FESFPS, F13A01, D13S317, D7S820 and D16S539. The PCR products were separated on vertical, denaturing, polyacrylamide gels according to the manufacturer's manual (Promega Technical Manual 1999) and typed using silver stain detection.

The allelic frequency at each locus was calculated from the values of the genotypes recorded.

The compatibility of each of the nine STR markers with the Hardy-Weinberg (HW) equilibrium was statistically tested by a χ^2-test for goodness-of-fit, and by the heterozygosity test. Since the χ^2-tests involve some rather small expected frequencies, the χ^2-distribution cannot be a reliable approximation. The P values (i.e. the probabilities of rejecting the null hypothesis that the population is in HW equilibrium with respect to the marker under consideration) were thus estimated by computer simulations. For each marker, 1,000 simulated samples were drawn under the assumption of HW equilibrium. The proportion of samples which had a χ^2 statistic larger than the observed χ^2 was taken as an estimate of the real P value.

In order to compare the allele frequency distributions between the Jewish and the Arab populations, a χ^2-test for independence was carried out for each locus. Again, P values were estimated by computer simulations (as described above).

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Table 1 Allele frequencies of the nine STRs studied in the Jewish Israeli population

Allele	STR locus								
	TH01	TPOX	CSF1PO	vWA	FESFPS	F13A01	D13	D7	D16
3.2	–	–	–	–	–	0.1061	–	–	–
4	–	–	–	–	–	0.0474	–	–	–
5	0.0009	–	–	–	–	0.2788	–	–	–
6	0.2552	0.0009	0.0026	–	–	0.2156	–	0.0000	–
7	0.1474	0.0026	0.0009	–	0.0000	0.2968	–	0.0171	0.0031
8	0.1190	0.5268	0.0069	–	0.0203	0.0102	0.1393	0.1661	0.0433
9	0.2371	0.1321	0.0233	–	0.0011	–	0.1223	0.1118	0.1563
9.3	0.2086	–	–	–	–	–	–	–	–
10	0.0319	0.0838	0.2841	–	0.3029	–	0.0542	0.2655	0.0635
11	–	0.2314	0.3264	0.0000	0.4212	0.0045	0.3096	0.2624	0.3344
12	–	0.0225	0.2893	0.0011	0.2151	0.0023	0.2508	0.1599	0.2368
13	–	–	0.0570	0.0011	0.0372	0.0045	0.0820	0.0155	0.1316
14	–	–	0.0086	0.0809	0.0023	0.0124	0.0402	0.0016	0.0310
15	–	–	0.0009	0.1101	0.0000	0.0102	0.0015	–	0.0000
16	–	–	–	0.2169	0.0000	0.0090	–	–	–
17	–	–	–	0.3045	–	0.0023	–	–	–
18	–	–	–	0.2067	–	–	–	–	–
19	–	–	–	0.0652	–	–	–	–	–
20	–	–	–	0.0135	–	–	–	–	–
Number of alleles	1160	1158	1158	890	888	886	646	644	646
Forensic parameters									
Matching probability	0.0714	0.1733	0.1262	0.0717	0.1592	0.0863	0.0698	0.0732	0.0772
Expressed as 1 in	13.999	5.770	7.921	13.949	6.281	11.584	14.336	13.652	12.953
Power of discrimination	0.9286	0.8267	0.8738	0.9283	0.8408	0.9137	0.9302	0.9268	0.9228
Homozygosity rate	0.2259	0.3299	0.2746	0.2382	0.3063	0.2506	0.2198	0.2391	0.2167
Heterozygosity rate	0.7741	0.6701	0.7254	0.7618	0.6937	0.7494	0.7802	0.7609	0.7833
Hardy-Weinberg equilibrium									
Estimated *P* value	0.247	0.890	0.897	0.188	0.472	0.615	0.304	0.481	0.972

Results and discussion

The nine STR allelic frequencies for the Jewish and Arab Israeli populations are shown in Tables 1 and 2. Results of sample compatibility to HW equilibrium using χ^2-test for goodness of fit are presented in Tables 1 and 2.

Of the nine loci examined within the Israeli Jewish population, no significant deviations from HW expectations were observed. In the Israeli Arab population seven of the nine markers fitted the HW expectations in both tests. According to the heterozygosity test, there is a significant excess of homozygotes both in CSF1PO and D7S820. However, the goodness-of-fit test implies that there are no significant deviations from the overall HW expectations for these markers.

Of the loci examined four (TH01, FESFPS, F13A01 and D13S317) showed a significant difference in allele frequency distribution between the Israeli Jewish and the Israeli Arab populations (Table 3).

The matching probability that two unrelated individuals randomly chosen from the same population will have the same profile with respect to the nine STR loci is 6.07×10^{-10} (or 1 in 1.65×10^{9}) in the Israeli Jewish population. Within the Israeli Arab population this value is 4.99×10^{-10} (or 1 in 2.00×10^{9}). The “inter-population” matching probability, i.e. the probability that two individuals, randomly chosen each from a different population, will have the same profile is 4.23×10^{-10}, smaller (as expected) than the matching probabilities in each population, yet well within the same order of magnitude.

Although both the Israeli Jewish population and the Israeli Arab population exhibit some subpopulation structure (Amar et al. 1999), for forensic purposes, we recommend the use of the allele frequency distribution, as reported in our study, for the Jewish and the Arab populations as two homogenic groups. For those cases when the source of the DNA tested may be from an individual belonging to a distinct sub-population, a “θ correction” is implemented, as recommended by the National Research Council (1996) and by Foreman and Lambert (2000).

Forensic biology is a discipline where major technological changes occur rapidly. Although this study was undertaken using the silver staining detection technique, the results are still applicable for forensic purposes employing updated automated fluorescent systems.

Table 2 Allele frequencies of the nine STRs studied in the Arab Israeli population

Allele	STR locus								
	TH01	TPOX	CSF1PO	vWA	FESFPS	F13A01	D13	D7	D16
3.2	–	–	–	–	–	0.1459	–	–	–
4	–	–	–	–	–	0.0486	–	–	–
5	0.0000	–	–	–	–	0.2216	–	–	–
6	0.2533	0.0066	0.0000	–	–	0.2865	–	0.0000	–
7	0.1630	0.0044	0.0044	–	0.0054	0.2270	–	0.0263	0.0000
8	0.1057	0.5132	0.0154	–	0.0136	0.0189	0.1518	0.1842	0.0327
9	0.3084	0.1272	0.0219	–	0.0027	–	0.0668	0.1377	0.1347
9.3	0.1344	–	–	–	–	–	–	–	–
10	0.0352	0.0789	0.3070	–	0.2908	–	0.0405	0.2854	0.0959
11	–	0.2478	0.2982	0.0027	0.3342	0.0000	0.2611	0.1903	0.3469
12	–	0.0219	0.2807	0.0000	0.2745	0.0027	0.3441	0.1538	0.2551
13	–	–	0.0658	0.0109	0.0734	0.0162	0.1093	0.0223	0.1163
14	–	–	0.0066	0.0734	0.0027	0.0108	0.0263	0.0000	0.0143
15	–	–	0.0000	0.1087	0.0000	0.0027	0.0000	–	0.0041
16	–	–	–	0.2554	0.0027	0.0189	–	–	–
17	–	–	–	0.2880	–	0.0000	–	–	–
18	–	–	–	0.1739	–	–	–	–	–
19	–	–	–	0.0788	–	–	–	–	–
20	–	–	–	0.0082	–	–	–	–	–
Number of alleles	454	456	456	368	368	370	494	494	490
Forensic parameters									
Matching probability	0.0793	0.1684	0.1197	0.0694	0.1284	0.0739	0.085	0.0664	0.0843
Expressed as 1 in	12.618	5.939	8.356	14.410	7.791	13.540	11.769	15.071	11.864
Power of discrimination	0.9207	0.8316	0.8803	0.9306	0.8716	0.9261	0.915	0.9336	0.9157
Homozygosity rate	0.2295	0.3717	0.3098	0.2056	0.2692	0.2388	0.2271	0.2521	0.2220
Heterozygosity rate	0.7705	0.6283	0.6902	0.7944	0.7308	0.7612	0.7729	0.7479	0.7780
Hardy-Weinberg equilibrium									
Estimated *P* value	0.530	0.102	0.357	0.334	0.809	0.445	0.615	0.165	0.415

Table 3 Comparison between allele distributions in the Jewish and the Arab populations in Israel

STR locus	TH01	TPOX	CSF1PO	vWA	FESFPS	F13A01	D13	D7	D16
Estimated *P* value	0.008	0.540	0.479	0.130	< 0.001	0.003	0.002	0.111	0.088

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