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SHORT COMMUNICATION

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Kurdish population data for 11 STR loci (ACTBP2, CSF1PO, FGA, TH01, TPOX, vWA, D3S1358, D5S818, D7S820, D13S317 and D21S11)

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Abstract In a Kurdish population sample composed of 950 unrelated individuals from Northern Iraq, 11 tetrameric short tandem repeat (STR) loci from 10 different chromosomes (i.e., ACTBP2, CSF1PO, FGA, TH01, TPOX, vWA, D3S1358, D5S818, D7S820, D13S317 and D21S11) were typed to establish a database for immigration cases. The combined power of discrimination (PD) and the combined power of exclusion (PE) of all 11 loci were 0.99999999999994 and 0.99996, respectively.

Keywords Population genetics · Short tandem repeat polymorphism · DNA database · Kurdish population

Introduction

After publication of our 1997 study on various subpopulations living in Turkey [1] it now arises that an ethnic assignment of the Kurdish samples obtained from Turkey is uncertain (S. Atasoy, personal communication). Due to the large and ever increasing number of immigration cases involving Kurds, STR frequencies for this population group are currently of great interest. We therefore typed a population sample of Kurds from outside Turkey, namely Iraqi Kurds from our current immigration casework, at 11 autosomal STR loci (ACTBP2, CSF1PO, FGA, TH01, TPOX, vWA, D3S1358, D5S818, D7S820, D13S317 and D21S11) and compared them with the earlier data on Kurds [1] and with the Turkish data from the Adana region [2, 3].

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Materials and methods

Sample preparation

Genomic DNA from oral cottonwool swab samples, obtained from routine immigration cases originating from Northern Iraq (i.e. north of latitude 36° N), were extracted by the proteinase K/Chelex method [e.g., 4, 5].

STR amplification and analysis

The AmpFlSTR Profiler PCR amplification kit (Applied Biosystems, Foster City, Calif.) was used according to the manufacturer's instructions [see, e.g., 6]. The self-constructed duplex PCR consisting of the STRs ACTBP2 and D21S11 was carried out using published primer sequences [3, 7] in a Perkin-Elmer GeneAmp PCR System 9600 thermal cycler. Amplification was performed in a final volume of 12.5 µl containing 1 µl of Chelex extract, 1.5 mM of $MgCl_2$, 0.4 mg/ml of BSA, 0.2 mM of each dNTP, 0.25 µM of each primer and 2.5 U of Gold Taq DNA polymerase (Eurogentec, Seraing, Belgium). The cycling protocol was: 94°C for 1 min followed by 29 cycles of 94°C for 30 s, 61°C for 30 s, 72°C for 1 min, followed by the final cycle of 94°C for 30 s, 61°C for 30 s and elongation at 72°C for 30 min. Typing was performed using denaturing capillary gel electrophoresis on an ABI PRISM 310 Genetic Analyzer with laser-induced fluorescence detection.

Statistical analysis

Evaluation of forensic statistical parameters was performed using the software packages PowerStats (Promega, Madison, Wis.) and HWE-Analysis 3.2 (C. Puers, Münster). The frequency profile comparisons between different populations were carried out using the program R×C (Mark P. Miller, http://www.public.asu.edu/~mmille8).

Results and discussion

Since the combined power of exclusion (PE) of the Profiler kit in the Kurdish population did not provide sufficient discrimination (0.9991) for paternity testing in immigration cases, a duplex PCR composed of the polymorphic loci ACTBP2 and D21S11 was set up and subsequently a combined PE of 0.99996 was achieved. Individ-

Table 1 Observed allele frequencies and statistical data for 11 STR loci in an Iraqi Kurdish population (*n* number of unrelated individuals, H_{obs} observed heterozygosity, H_{exp} expected heterozygosity, *P-value* HWE exact test probability, *PD* power of discrimination, *PE* power of exclusion)

Allele	ACTBP2	CSF1PO	FGA	TH01	TPOX	vWA	D3S1358	D5S818	D7S820	D13S317	D21S11
6	–	–	–	0.271	0.001	–	–	–	0.001	–	–
7	–	–	–	0.192	0.007	–	–	0.002	0.025	0.001	–
7.3	0.001	–	–	–	–	–	–	–	–	–	–
8	0.003	0.001	–	0.131	0.512	–	–	0.005	0.165	0.142	–
9	–	0.028	–	0.24	0.103	–	–	0.054	0.094	0.055	–
9.3	–	–	–	0.142	–	–	–	–	–	–	–
10	–	0.274	–	0.024	0.087	–	–	0.095	0.247	0.066	–
11	0.012	0.337	–	–	0.26	–	–	0.314	0.269	0.291	–
12	0.007	0.303	–	–	0.03	0.001	0.001	0.333	0.17	0.336	–
12.2	0.001	–	–	–	–	–	–	–	–	–	–
12.3	0.003	–	–	–	–	–	–	–	–	–	–
13	0.02	0.05	–	–	–	0.004	0.004	0.183	0.028	0.085	–
13.3	0.001	–	–	–	–	–	–	–	–	–	–
14	0.02	0.006	–	–	–	0.097	0.049	0.012	0.002	0.023	–
14.2	0.001	–	–	–	–	–	–	–	–	–	–
14.3	0.002	–	–	–	–	–	–	–	–	–	–
15	0.032	0.001	–	–	–	0.095	0.262	0.003	–	0.001	–
15.2	0.001	–	–	–	–	–	–	–	–	–	–
16	0.059	–	–	–	–	0.228	0.288	–	–	–	–
16.2	0.003	–	–	–	–	–	–	–	–	–	–
16.3	0.002	–	–	–	–	–	–	–	–	–	–
17	0.08	–	–	–	–	0.286	0.249	–	–	–	–
18	0.095	–	0.007	–	–	0.184	0.137	–	–	–	–
18.2	0.001	–	0.001	–	–	–	–	–	–	–	–
19	0.073	–	0.056	–	–	0.085	0.009	–	–	–	–
19.2	0.001	–	0.001	–	–	–	–	–	–	–	–
20	0.057	–	0.086	–	–	0.018	0.002	–	–	–	–
20.2	0.005	–	–	–	–	–	–	–	–	–	–
21	0.026	–	0.169	–	–	0.001	–	–	–	–	–
21.2	0.021	–	0.007	–	–	–	–	–	–	–	–
22	0.005	–	0.169	–	–	–	–	–	–	–	–
22.2	0.033	–	0.007	–	–	–	–	–	–	–	–
23	–	–	0.201	–	–	–	–	–	–	–	–
23.2	0.034	–	0.007	–	–	–	–	–	–	–	–
24	0.001	–	0.145	–	–	–	–	–	–	–	–
24.2	0.042	–	0.002	–	–	–	–	–	–	–	–
25	–	–	0.089	–	–	–	–	–	–	–	–
25.2	0.024	–	0.001	–	–	–	–	–	–	–	–
26	0.001	–	0.044	–	–	–	–	–	–	–	0.002
26.2	0.026	–	–	–	–	–	–	–	–	–	–
27	0.001	–	0.004	–	–	–	–	–	–	–	0.011
27.2	0.059	–	–	–	–	–	–	–	–	–	–
28	–	–	0.002	–	–	–	–	–	–	–	0.13
28.2	0.048	–	–	–	–	–	–	–	–	–	–
29	–	–	0.001	–	–	–	–	–	–	–	0.224
29.2	0.062	–	–	–	–	–	–	–	–	–	–
30	–	–	–	–	–	–	–	–	–	–	0.199
30.2	0.053	–	–	–	–	–	–	–	–	–	0.026
31	–	–	–	–	–	–	–	–	–	–	0.044
31.2	0.043	–	–	–	–	–	–	–	–	–	0.118
32	0.004	–	–	–	–	–	–	–	–	–	0.012
32.2	0.02	–	–	–	–	–	–	–	–	–	0.159
33	0.003	–	–	–	–	–	–	–	–	–	0.003
33.2	0.007	–	–	–	–	–	–	–	–	–	0.061
34	0.003	–	–	–	–	–	–	–	–	–	0.001

Table 1 (continued)

Allele	ACTBP2	CSF1PO	FGA	TH01	TPOX	vWA	D3S1358	D5S818	D7S820	D13S317	D21S11
34.2	0.002	–	–	–	–	–	–	–	–	–	0.005
35	0.002	–	–	–	–	–	–	–	–	–	0.005
35.2	0.001	–	–	–	–	–	–	–	–	–	–
n	488	932	949	936	934	950	949	934	930	934	485
H_{obs}	0.941	0.686	0.859	0.791	0.636	0.804	0.743	0.727	0.775	0.754	0.847
H_{exp}	0.950	0.716	0.861	0.795	0.651	0.806	0.766	0.745	0.801	0.767	0.849
P-value	0.424	0.371	0.367	0.298	0.357	0.116	0.202	0.355	0.065	0.723	0.197
PD	0.993	0.870	0.964	0.926	0.829	0.936	0.907	0.895	0.93	0.912	0.957
PE	0.879	0.406	0.712	0.582	0.336	0.607	0.498	0.471	0.554	0.516	0.690

Table 2 Interpopulation comparison between the Kurdish and the Turkish populations

Locus	*P*-value
ACTBP2	0.02±0.01
D21S11	0.01±0.01
FGA	0.24±0.02
TH01	0.45±0.03
vWA	0.89±0.01

Data for the Turkish population from the Adana region are from [2, 3] or B. Brinkmann (unpublished results).

ual PE values ranged from 0.336 (TPOX) to 0.879 (ACTBP2).

The observed heterozygosities ranged from 0.636 (TPOX) to 0.941 (ACTBP2, Table 1). No significant deviation from Hardy-Weinberg equilibrium could be observed at any of the 11 loci. An interpopulation comparison between the Kurds and the geographically closely located Turkish population from the Adana region [2, 3] revealed significant differences at the ACTBP2 and D21S11 loci (p=0.02 and 0.01, respectively) (Table 2). The Iraqi Kurds reported here showed significant differences to the subpopulation originally described as Turkish Kurds [1] at the vWA and TH01 loci (p=0.00 for both), which throws doubt on the ethnicity of the individuals in the population originally described as Turkish Kurds.

The power of discrimination (PD) was >0.7 for all 11 loci tested. The investigated loci cover 6 of the 8 systems from the German DNA database stored at the Bundeskriminalamt (BKA). These loci possess a combined PD of 0.999999996 in the Kurdish population, while the combined PD of all 11 STR loci is 0.99999999999994.

The combination of these 11 STRs is a powerful tool for individual identification as well as paternity investigations in the Kurdish population.

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