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SHORT COMMUNICATION

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Allele frequency data for 16 STR loci in the Vietnamese population

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Abstract The short tandem repeat systems ACTBP2, D3S1358, TH01, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, VWA, D8S1179, TPOX and FGA were studied in a population sample from Vietnam (178 individuals, mainly from the Hanoi area). The 16 loci met Hardy-Weinberg expectations and possess a combined power of discrimination greater than 0.9999999999999999998 and a combined power of exclusion greater than 0.99999994 in this Vietnamese population.

Keywords PowerPlex16 · Vietnam · Population genetics · Multiplex PCR · ACTBP2

Introduction

The aim of this work was to establish a database of the Vietnamese population for forensic purposes including paternity testing. Therefore we have applied the recently introduced PowerPlex16 kit (Promega, Madison, Wis.) that amplifies the 7 ENFSI STR loci as well 13 CODIS STR loci in addition to the two pentameric markers Penta D and Penta E [1] and the amelogenin locus for gender identification and additionally we have typed ACTBP2 [2]. In this study we present the allele frequencies and forensic efficiency values for the 16 loci in a sample of 178 unrelated Vietnamese.

Materials and methods

DNA for PCR analysis was extracted from oral swabs of 178 unrelated individuals (56 female, 122 male; mainly from North Vietnam, Hanoi area) by the proteinase K/Chelex method [3]. PCR amplification and capillary electrophoresis on an ABI PRISM 310 (ABI, Foster City, Calif.) was performed according to the manufacturer's manual (PowerPlex16, Promega) or according to [4] using a 6-FAM labelled ACTBP2 allele ladder (Serac, Bad Homburg, Germany). Evaluation of Hardy-Weinberg expectations and other forensic statistical parameters was done with the computer programmes HWE-Analysis (version 3.2) and PowerStats (Promega), respectively. Alleles not included in the PowerPlex16 ladder were isolated by the crush-and-soak method as described elsewhere [5] and directly sequenced using the BigDye terminator cycle sequencing kit and ABI PRISM 310 (ABI) with primers for both strands.

Results and discussion

In this study two alleles not contained in the allelic ladders were identified by sequencing as the TPOX allele 14 and Penta D allele 20 (data not shown). Allele frequencies and forensic parameters for the 16 loci are given in Table 1. No significant deviation from Hardy-Weinberg equilibrium was observed. In interpopulation comparisons between Vietnam and Thailand [nine loci from 6] using the program R×C (http://bioweb.usu.edu/mpmbio/rxc.htm), no similarity could be observed (data not shown). The PowerPlex16 loci in addition to ACTBP2 have a combined power of discrimination greater than 0.9999999999999999998 and a combined power of exclusion greater than 0.99999994 in the Vietnamese population. According to these statistical parameters the combination of these 16 STR systems is a powerful tool for forensic identification and paternity testing.

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Table 1 Allele frequencies and forensic efficiency parameters of 16 STR loci in a Vietnamese population (n=178) (*HWE* exact test probability performed by running 5,000 random shuffles, *PIC* polymorphism information content, H_{obs} observed heterozygosity, H_{exp} expected heterozygosity, unbiased, *PD* power of discrimination, *PE* power of exclusion)

Allele	D3S1358	TH01	D21S11	D18S51	Penta E	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	VWA	D8S1179	TPOX	FGA	ACTBP2
5	–	–	–	–	0.048	–	–	–	–	–	–	–	–	–	–	–
6	–	0.157	–	–	–	–	–	–	–	–	–	–	–	–	–	–
7	–	0.357	–	–	0.003	0.031	0.003	0.011	–	0.006	0.031	–	–	0.008	–	–
8	–	0.059	–	–	0.006	–	0.295	0.143	0.003	–	0.076	–	0.003	0.534	–	–
9	–	0.329	–	–	0.011	0.065	0.166	0.076	0.216	0.028	0.343	–	–	0.107	–	–
9.1	–	–	–	–	–	–	–	0.003	–	–	–	–	–	–	–	–
9.3	–	0.031	–	–	–	–	–	–	–	–	–	–	–	–	–	–
10	–	0.065	–	–	0.053	0.228	0.124	0.202	0.135	0.171	0.135	–	0.171	0.037	–	–
11	–	0.003	–	0.011	0.250	0.284	0.230	0.340	0.270	0.267	0.132	–	0.124	0.292	–	–
12	0.003	–	–	0.039	0.090	0.236	0.152	0.197	0.272	0.441	0.121	–	0.138	0.020	–	–
13	–	–	–	0.157	0.051	0.149	0.028	0.025	0.073	0.079	0.110	–	0.143	–	–	–
14	0.042	–	–	0.216	0.101	0.008	0.003	0.003	0.031	0.006	0.045	0.315	0.152	0.003	–	–
15	0.303	–	–	0.202	0.067	–	–	–	–	0.003	0.006	0.034	0.171	–	–	0.011
16	0.399	–	–	0.169	0.073	–	–	–	–	–	–	0.124	0.070	–	–	0.020
17	0.202	–	–	0.059	0.056	–	–	–	–	–	–	0.233	0.022	–	0.006	0.042
18	0.048	–	–	0.042	0.065	–	–	–	–	–	–	0.154	0.006	–	0.020	0.051
19	0.003	–	–	0.045	0.034	–	–	–	–	–	–	0.126	–	–	0.098	0.084
19.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.003
20	–	–	–	0.025	0.048	–	–	–	–	–	0.003	0.011	–	–	0.065	0.042
20.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.003	0.017
21	–	–	–	0.020	0.037	–	–	–	–	–	–	0.003	–	–	0.140	0.034
21.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.017	0.022
22	–	–	–	0.003	0.003	–	–	–	–	–	–	–	–	–	0.211	0.011
22.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.006	0.031
23	–	–	–	0.003	0.006	–	–	–	–	–	–	–	–	–	0.169	0.003
23.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.011	0.045
24	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.126	–
24.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.014	0.062
25	–	–	–	0.006	–	–	–	–	–	–	–	–	–	–	0.076	–
25.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.011	0.073
26	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.020	–
26.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.110
27	–	–	–	0.003	–	–	–	–	–	–	–	–	–	–	0.008	–
27.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.09
28	–	–	0.045	–	–	–	–	–	–	–	–	–	–	–	–	–
28.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.093
29	–	–	0.303	–	–	–	–	–	–	–	–	–	–	–	–	–
29.2	–	–	0.008	–	–	–	–	–	–	–	–	–	–	–	–	0.053
30	–	–	0.219	–	–	–	–	–	–	–	–	–	–	–	–	–
30.2	–	–	0.022	–	–	–	–	–	–	–	–	–	–	–	–	0.045
31	–	–	0.065	–	–	–	–	–	–	–	–	–	–	–	–	–

Table 1 (continued)

Allele	D3S1358	TH01	D21S11	D18S51	Penta E	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	VWA	D8S1179	TPOX	FGA	ACTBP2
31.2	–	–	0.070	–	–	–	–	–	–	–	–	–	–	–	–	0.025
32	–	–	0.034	–	–	–	–	–	–	–	–	–	–	–	–	–
32.2	–	–	0.169	–	–	–	–	–	–	–	–	–	–	–	–	0.025
33	–	–	0.017	–	–	–	–	–	–	–	–	–	–	–	–	–
33.2	–	–	0.042	–	–	–	–	–	–	–	–	–	–	–	–	0.003
34	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
34.2	–	–	0.006	–	–	–	–	–	–	–	–	–	–	–	–	0.006
H_{obs}	0.758	0.68	0.781	0.882	0.871	0.764	0.803	0.832	0.798	0.730	0.809	0.820	0.860	0.612	0.854	0.966
H_{exp}	0.706	0.733	0.819	0.852	0.892	0.787	0.796	0.780	0.784	0.700	0.814	0.793	0.861	0.618	0.873	0.940
HWE	0.483	0.259	0.375	0.287	0.111	0.610	0.124	0.244	0.953	0.203	0.728	0.061	0.588	0.242	0.138	0.808
PD	0.846	0.891	0.938	0.951	0.973	0.919	0.923	0.908	0.918	0.851	0.941	0.914	0.960	0.787	0.966	0.987
PE	0.524	0.398	0.564	0.759	0.736	0.534	0.605	0.659	0.595	0.477	0.616	0.637	0.714	0.306	0.703	0.932
PIC	0.650	0.690	0.790	0.830	0.880	0.750	0.760	0.750	0.750	0.650	0.790	0.760	0.840	0.560	0.860	0.930

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