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SHORT COMMUNICATION

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Allele frequency data for the FGA locus in eight populations

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Abstract Allele frequency data of the FGA locus were determined in eight population samples. No significant deviations from the Hardy Weinberg equilibrium were observed. The heterozygosity and mean exclusion chance ranged from 82 to 93% and 70 to 75% respectively.

Key words STR · FGA · Allele frequencies

Introduction

HumFGA is a highly polymorphic STR locus (Mills et al. 1992; Barber et al. 1996) increasingly used for forensic identification and paternity testing. Here we report the allele frequencies of this locus from eight populations.

Materials and methods

The population samples were Germans, Japanese, Chinese, Ovambos, Turks, Moroccans, Australian aborigines and Papuans, they have been described in detail elsewhere (Brinkmann et al. 1997). DNA was isolated according to standard procedures, the PCR reaction conditions and primer sequences were according to Barber et al. (1996). PCR products were resolved by high resolution polyacrylamide gel electrophoresis according to Allen et al. (1989) and visualised by silver staining (Budowle et al. 1991). Alleles were identified by side-to-side comparison with a sequenced allelic ladder. The evaluation of the Hardy-Weinberg equilibrium was performed using the exact test (Guo and Thompson 1992).

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Results and discussion

Allele frequency distribution determined in eight population samples consisting of 78 to 453 individuals were similar (Table 1) and comparable to those determined previously earlier for Italians (Betti et al. 1997) and British Caucasians, Afro-Caribbeans and Indian Asians (Evett et al. 1997). The extraordinary long alleles found in this study in the Ovambo population have also been described by Evett et al. (1997) for the British Afro-Caribbean population sample and seem to be specific for sub-Saharan Africans. Data for the German population sample have been published earlier (Rolf et al. 1997) and are included for comparison. No deviations from the Hardy Weinberg equilibrium were observed. The heterozygosity and mean exclusion chance (Krüger et al. 1968) ranged from 82 to 93% and 70 to 75%, respectively (Table 1). Compared to other common STR loci, HumFGA exhibits a high mean exclusion chance and will therefore become a powerful tool for forensic identification as well as for paternity testing.

Table 1 Allele frequency data of the FGA locus from eight populations

Allele	Germans	Moroccans	Turks	Ovambos	Papuans	Australian aboriginies	Japanese	Chinese
# / *n*	453	145	202	189	104	78	136	95
16	0	0	0	0	0.96	0.64	0	0
17	0.11	0	0	0	0.96	0	0	0
18	2.32	0	0.74	0	1.44	3.85	3.31	0.53
18.2	0	0	0	0.79	0	0	0	0
19	7	7.24	6.68	8.73	13.46	6.41	5.51	4.74
19.2	0	0	0	0.26	0	0	0	0
20	16	9.66	6.19	4.5	4.33	3.85	8.09	5.26
20.2	0	0	0.25	0	0	0	0	0
21	16.34	16.65	20.05	10.58	8.17	15.38	15.07	13.68
21.2	0	0	0.99	0	0	0	0	1.05
22	16.78	16.9	18.07	18.78	12.98	19.23	20.22	15.26
22.2	1.32	0.69	0.25	0.53	0	1.28	0.37	0.53
23	14.46	20.34	18.56	15.61	7.21	18.59	23.16	22.63
23.2	0.44	0.34	0.25	0	0	0.64	0	1.05
24	13.8	13.46	16.09	17.72	18.27	10.26	13.60	14.74
24.2	0	0	0.25	0	0	1.28	0.74	0.53
25	9.16	8.28	7.67	11.38	22.61	12.81	5.51	15.78
26	1.43	4.83	2.48	1.59	4.81	3.21	3.31	3.16
27	0.22	1.03	0.99	2.91	4.81	1.92	0.37	1.05
28	0.22	0.34	0.50	1.32	0	1.28	0.37	0
29	0	0.34	0	0.79	0	0	0.37	0
29.2	0	0	0	0.26	0	0	0	0
30.2	0	0	0	1.85	0	0	0	0
31.2	0	0	0	0.79	0	0	0	0
> 31.2	0	0	0	0.79	0	0	0	0
P	0.38	0.69	0.65	0.11	0.91	0.12	0.49	0.17
Het	0.84	0.85	0.84	0.85	0.88	0.83	0.93	0.82
MEC	0.72	0.72	0.70	0.75	0.72	0.75	0.70	0.70

n is the number of individuals investigated, *p* the exact test *p*-value, Het the observed heterozygosity and MEC the mean exclusion chance

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