International Congress Series 1261 (2004) 151–153

www.ics-elsevier.com

Analysis of 12 STR loci in Antioquia (Colombia) population sample

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Abstract. In this study, the validation of 12 short tandem repeated (STRs) systems is presented in a sample of the population from Antioquia, central region of Colombia. The DNA for the analyses of PCR was obtained of 244 to 546 unrelated individuals. PCR amplification was performed according to the manufacturer's recommendations, using PowerPlex 1.2 System and FFFL Multiplex (Promega). Amplificated fragments were separated by capillary electrophoresis using the ABI Prism 310 Genetic Analyzer (PE Applied Biosystems). Allele frequencies, Hardy-Weinberg equilibrium, observed and expected heterozygosity and genetic disequilibrium were calculated using GENEPOP ver. 3.3 and GDA ver. 1.1 software. Forensic parameters were calculated using the PowerStat ver. 1.2 software (Promega). The 12 of the loci met Hardy-Weinberg expectations and they reached a combined power discrimination higher than 0.999999999999 and a combined power exclusion similar to 0.9999, showing to be a powerful tool for paternity testing, individual identification and forensic applications in Antioquia population.

Keywords: Antioquia; Population; STR; PowerPlex 1.2 System; FFFL Multiplex; Power of discrimination; Power exclusion

1. Introduction

Antioquia is a central region of Colombia, its population is predominantly Caucasian almost all Spanish descendants with some Basque component [1,2]. In this study, we present validation of 12 short tandem repeated (STR) loci for using in paternity testing and forensic analysis, PowerPlex 1.2 System and FFFL Multiplex kits (Promega). The PowerPlex 1.2 System consists of the STRs loci: CSF1PO, TH01, TPOX, vWA01, D5S818, D7S820, D13S317 and D16S539. The FFFL system consists of the loci FES/FPS, F13A1, F13B and LPL.

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0531-5131/
doi:10.1016/S0531-5131(03)01532-2

Table 1
Observed allele frequencies for PowerPlex® 1.2 System and FFFL® Multiplex loci in Antioquia (Colombia)

Alelles	CSF1PO	TPOX	TH01	vWA	D16S539	D7S820	D13S317	D5S818	F13A01	FESFPS	F13B	LPL
3.2									0.1393			
4									0.1127			
5			0.0003						0.2316			
6		0.0064	0.4042			0.0046	0.0009		0.1783		0.1176	
7	0.0079	0.0046	0.2136			0.0165		0.0211	0.2992	0.0050	0.0336	0.0017
8	0.009	0.5037	0.0938		0.0047	0.1273	0.0422	0.0105	0.0123	0.0182	0.1678	
8.3			0.0030									
9	0.0175	0.0927	0.1328		0.1183	0.0833	0.1135	0.0680	0.0021	0.0182	0.3524	0.0328
9.3			0.1148									
10	0.2408	0.0624	0.0350		0.1654	0.2876	0.0891	0.0565	0.0021	0.2475	0.3289	0.4310
11	0.2426	0.2532		0.0009	0.1904	0.2839	0.1539	0.4042		0.4455		0.2414
12	0.4188	0.0771			0.2385	0.1685	0.2974	0.2663	0.0021	0.2030		0.2345
13	0.0600			0.0093	0.1876	0.0247	0.2130	0.1590	0.0082	0.0611		0.0414
14	0.0037			0.0570	0.0804	0.0028	0.0591	0.0144	0.0041	0.0017		0.0103
15				0.1517	0.0148		0.0300		0.0041			
16				0.3245					0.0041			0.0017
17				0.2335		0.0009						0.0035
18				0.1599								0.0017
19				0.0588			0.0009					
20				0.0046								
Minimum	0.0052	0.0050	0.0059	0.0054	0.0057	0.0055	0.0056	0.0056	0.0121	0.0091	0.0094	0.0096
N	1084	1086	1002	1088	1082	1092	1066	1044	488	606	596	580
Parameters												
Ho	0.7085	0.6330	0.7629	0.7574	0.8169	0.7894	0.79412	0.7471	0.7951	0.6931	0.7215	0.7103
He	0.7043	0.6643	0.7588	0.7856	0.8254	0.7850	0.8180	0.7325	0.7943	0.6958	0.7258	0.6993
HWE-HE	0.1913	0.9967	0.4527	0.9690	0.5331	0.3223	0.6305	0.2908	0.5516	0.6972	0.7343	0.2122
Exact test	0.8565	0.1068	0.1587	0.2625	0.1316	0.4454	0.1666	0.2569	0.0527	0.3559	0.0960	0.0717
PD	0.8628	0.8435	0.9007	0.9222	0.9427	0.9213	0.9437	0.8828	0.9234	0.8510	0.8726	0.8552
PE	0.4415	0.3333	0.5209	0.5224	0.6451	0.5795	0.5882	0.5049	0.5899	0.4176	0.4623	0.4444
MP	0.1372	0.1565	0.0993	0.0778	0.0573	0.0787	0.0563	0.1172	0.0766	0.1490	0.1274	0.1448
PIC	0.6535	0.6197	0.7171	0.7538	0.7993	0.7522	0.7941	0.6923	0.7621	0.6462	0.6769	0.6478
TPI	1.72	1.37	2.05	2.06	2.85	2.37	2.43	1.98	2.44	1.63	1.80	1.73

Ho: Heterozygosity observed, He: Heterozygosity expected, HWE-HE: Hardy-Weinberg Heterozygote Excess test, PD: Power of Discrimination, PE: Power of Exclusion, MP: Matching Probability, PIC: Polymorphism information content, TPI: Typical Paternity Index.

2. Materials and methods

Blood samples were randomly taken from paternity casework of the Laboratory of Human Genetics of the University of Antioquia. DNA was isolated from all samples using a salting out extraction procedure [3]. The amplification was performed by the PowerPlex 1.2 System and FFFL Multiplex kits (Promega), following the manufacturer's recommendations. The amplified products were analyzed by capillary electrophoresis using an ABI Prism™ 310 Genetic Analyzer. The frequency of each allele for each locus tested was calculated from the number of observed genotypes in the sample using GENEPOP software ver. 3.2a [4]. Exact tests for Hardy-Weinberg equilibrium of every locus and linkage disequilibrium between loci were carried out by using GENEPOP ver. 3.2a [4] and GDA ver. 1.0 [5] software. Forensic parameters were performed using POWERSTAS ver. 12 (Promega) and GDA ver. 1.0 [5] software.

3. Results and discussion

Antioquian population data for the 12 STR loci are shown in Table 1. No deviations from Hardy-Weinberg equilibrium were observed for all markers and interclass correlation test analysis demonstrated no evidence for correlation between the alleles for any of the pair-wise comparisons of the loci. The forensic efficiency values suggest that 12 STR loci investigated in this population are highly discriminative. The combined PD of the PowerPlex 1.2 System loci is 0.9999999 and combined for all 12 loci is higher than 0.999999999999. The PE of the PowerPlex 1.2 System in Antioquian population did not provide sufficient discrimination (0.997931) for paternity testing. A combined PE with FFFL Multiplex kit was achieved and the PE value raised to 0.9999. Individuals PE values ranged from 0.3333 (TPOX) to 0.6307 (D16S539). In conclusion, the Antioquian resident population database has been established for the analyzed systems. These 12 STR loci appear to be highly discriminating, thus providing a powerful tool for paternity investigations, individual identification and forensic applications.

Acknowledgements

This work was supported by GENES. Juan José Builes has a PhD fellowship (0058/2001) from COLCIENCIAS.

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