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Data analysis of 10 STR loci in a population in the province of Neuquen, Argentina

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Abstract

Ten Short Tandem Repeat (STR) loci, CSF1PO, TPOX, THO1, D12S1090, D3S1744, D18S849, FGA, D7S820, D1S533 and D9S304, were analyzed in a population geographically located at the foot of the Andes Range in the province of Neuquen, southwestern Argentina. Allele frequencies and paternity and forensic parameters (power of exclusion, matching probability, and power of discrimination) were calculated for all 10 STR loci. The population was analyzed for Hardy-Weinberg equilibrium (HWE) and allelic and gene frequencies were compared to those observed in the Buenos Aires population. Results indicate that the population was in HWE for these 10 STR loci. Significant differences between allele and genotype frequencies were found for the D7S820 locus (gene and genotypic differentiation test) when compared with data of the Buenos Aires population. These data indicate that the allele frequency estimations can be used to reliably calculate likelihood ratios for paternity and forensic DNA casework.
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1. Introduction

The population analyzed is geographically located at the foot of the Andes Range, in the province of Neuquen, southwestern Argentina. The most important feature of this population is that it is mainly made up by the mixture of people migrating from the north and center of the country and by aboriginal natives (Mapuche people). The aim of this study was to demonstrate whether this population is in Hardy-Weinberg equilibrium

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(HWE) for 10 Short Tandem Repeats (STR) loci and to determine if there exist significant differences in allele and genotype frequencies between the population studied and that living in Buenos Aires.

2. Materials and methods

DNA was extracted by a non-organic procedure from EDTA blood [1]. STR loci were amplified in multiplex polymerase chain reactions (PCRs): one triplex reaction for CTT [2] ($N = 114$); one triplex reaction for Multiplex-I [3] ($N = 164$); one tetraplex reaction for Multiplex-II [3] ($N = 154$). Amplified products were electrophoresed in 4% polyacrylamide gels and detection was carried out by silver staining. Alleles were assigned by directly comparing with the allelic ladders provided with each typing kit [2,3].

Table 1
Allele frequencies

Allele	D12S1090	D3S1744	D18S849	CSF1PO	TPOX	TH01	FGA	D7S820	D1S533	D9S304
3.2										
4										0.0519
5										
6						0.3246				0.0130
7						0.2193		0.0065		0.0195
8				0.0088	0.4825	0.0702		0.1039	0.0844	0.3377
9	0.0671			0.0351	0.0439	0.1316		0.0779	0.0779	0.0779
9.3						0.2544				
10	0.0244			0.2719	0.0439			0.1883	0.0260	0.0325
11	0.0427			0.2719	0.3246			0.3961	0.0779	0.0974
12	0.0305		0.0061	0.3158	0.1053			0.1818	0.1948	0.2532
13	0.0122		0.0061	0.0877				0.0390	0.2532	0.1104
14	0.0366		0.0488	0.0088				0.0065	0.2273	
15	0.0061	0.0793	0.2927						0.0390	0.0065
16		0.1524	0.3537						0.0195	
17		0.1585	0.2134							
18	0.0305	0.3476	0.0549				0.0065			
19	0.0488	0.1220	0.0244				0.1234			
20	0.0671	0.0793					0.1169			
21	0.0854	0.0549					0.1299			
22	0.1463	0.0061					0.1104			
23	0.1098						0.0909			
24	0.0793						0.1299			
25	0.1037						0.1688			
26	0.0366						0.0909			
27	0.0366						0.0325			
28	0.0122									
29										
29.2										
30	0.0061									
31	0.0183									

Table 2
Neuquen population and Buenos Aires population differentiation test

Locus	Genic differentiation test		Genotypic differentiation test	
	P-val	S.E.	*P*-val	S.E.
CSF1PO	0.53363	0.01103	0.6720	0.0069
TPOX	0.09240	0.00544	0.1094	0.0067
TH01	0.32531	0.01058	0.3157	0.0101
D12S1090	0.10801	0.00935	0.0733	0.0068
D3S1744	0.38600	0.01231	0.4083	0.0123
D18S849	0.17058	0.01121	0.2012	0.0091
FGA	0.28946	0.01087	0.3711	0.0117
D7S820	0.00078	0.00049	0.0023	0.0006
D1S533	0.27483	0.01188	0.2883	0.0117
D9S304	0.14692	0.01013	0.1993	0.0088

Allele frequencies and paternity and forensic parameters (power of exclusion, matching probability and power of discrimination) were calculated for all 10 STR loci using the PowerStat software (Promega). Exact tests (heterozygote deficit and excess, and probability test) for HWE equilibrium and gene and genotypic differentiation tests were performed using Genepop Software (Raymond M. & Rousset F., Version 3.3, March 2001).

3. Results

Allelic frequencies are shown in Table 1. When compared to data of the Buenos Aires population, significant differences were found in allele and genotype proportions for the D7S820 locus (Table 2).

The population was found to be in HWE. Table 3 shows *P*-values (*P*-val) and standard error (S.E.) for heterozygote deficit and excess tests, and probability test for all 10 STR loci.

Table 3
HWE exact tests

Locus	Heterozygote deficit		Heterozygote excess		Probability test	
	P-val	S.E.	*P*-val	S.E.	*P*-val	S.E.
CSF1PO	0.1860	0.0143	0.8063	0.0162	0.2716	0.0171
TPOX	0.1266	0.0065	0.8813	0.0063	0.2193	0.0081
TH01	0.9215	0.0056	0.0698	0.0047	0.6990	0.0079
D12S1090	0.3929	0.0333	0.5209	0.0370	0.4632	0.0355
D3S1744	0.6392	0.0164	0.3796	0.0186	0.4005	0.0149
D18S849	0.0365	0.0061	0.9658	0.0075	0.1813	0.0157
FGA	0.1204	0.0123	0.8378	0.0142	0.1740	0.0125
D7S820	0.4826	0.0220	0.4625	0.0217	0.3980	0.0190
D1S533	0.3199	0.0196	0.6531	0.0199	0.9411	0.0059
D9S304	0.3843	0.0235	0.5676	0.0235	0.5800	0.0245

Table 4
Matching probability (MP), power of discrimination (PD) and power of exclusion (PE)

Locus	MP	PD	PE
D12S1090	0.022	0.978	0.825
D3S1744	0.073	0.927	0.678
D18S849	0.114	0.886	0.402
CSFIPO	0.130	0.870	0.580
TPOX	0.191	0.809	0.308
THO1	0.116	0.884	0.679
FGA	0.038	0.962	0.683
D7S820	0.104	0.896	0.585
D1S533	0.056	0.944	0.633
D9S304	0.075	0.925	0.538
Combined	8.8e – 12	99.9999999991%	99.993%

Power of exclusion, matching probability and power of discrimination for single loci and the combined values of each parameter for all 10 STRs are indicated in Table 4.

4. Conclusion

We conclude that these allele frequency estimations can be used to reliably calculate likelihood ratios for paternity and forensic DNA casework.

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