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FOR THE RECORD

Cristina Sánchez,[1] Ph.D.; Carme Barrot,[1] Ph.D.; Montserrat Ortega[1]; Antonio González-Martín,[2] Ph.D.; Amaya Gorostiza[2]; Jacint Corbella,[1] M.D., Ph.D.; Emili Huguet,[1] M.D., Ph.D.; and Manuel Gené,[1,3] M.D., Ph.D.

Genetic Diversity of 15 STRs in Choles From Northeast of Chiapas (Mexico)

POPULATION: Choles, an Amerindian population ($n = 109$)

KEYWORDS: forensic science, DNA typing, population genetics, Choles, Amerindian, D8S1179, D21S11, D7S820, CSF1PO, D19S433, HUMVWA31A, HUMTPOX, D18S51, D3S1358, HUMTHO1, D13S317, D16S539, D2S1338, D5S818, HUMFGA

Allele frequencies for 15 STR loci (D8S1179, D21S11, D7S820, CSF1PO, D19S433, HUMVWA31A, HUMTPOX, D18S51, D3S1358, HUMTHO1, D13S317, D16S539, D2S1338, D5S818, and HUMFGA) were analyzed in a Mexican population: Choles from Chiapas State. The aim of the study was to obtain accurate allele frequencies data and other genetic parameters of forensic interest on the Amerindian ethnic groups from Mexico, using an automatic method and commercial amplification kit. The agreement with HWE (Hardy-Weinberg equilibrium) was confirmed for all loci (based on the χ^2-test).

DNA profiling using STRs loci has become the most efficient system for determination of parentage and biological relationships of individuals and in forensic human indentification analyses (1–5).

The Chol population lives in Northeast of Chiapas (Mexico). They mainly live in the villages of: Tila, Tumbalá, Sabanilla, Catazajá, La Libertad, Salto de Agua, Palenque, Ocosingo, Yajalón, Huitiupán, and Chilón. Communication path is a big problem in the country. The main villages are connected with each other and with other towns located in the jungle by dirt tracks, and the lack of communication has traditionally been an obstacle to economic and social development [Pueblos Indígenas de México. Serie Monografias http://cdi.gob.mx/ini/monografias/choles.html]. The native population consists of 161,766 individuals [INEGI (Instituto Nacional de Estadística y Geografia Informática)—2000. XII Censo de Población y Vivienda. http://www.inegi.gob.mx]. DNA was extracted from hair root samples by Chelex® method (6) from 109 healthy unrelated Choles from Chiapas State.

PCR amplifications were carried out in a 12 μL volume. Amplification was carried out in a 9700 thermal cycler (Applied Biosystems, Foster City, CA) following the recommendations for the AmpFℓSTR® Identifiler™ kit (Applied Biosystems, Foster City, CA). Genotypes from DNA amplified products were analyzed in capillary gel electrophoresis using an ABI Prism™ 310 Genetic Analyser device (7). Allele frequencies (because autosomal codominant) were computed using the gene counting method. The agreement of genotype frequencies with Hardy-Weinberg expectations (HWE) was determined using the χ^2-test (8), based on the number of observed and expected genotypes, using the Popgene program. Forensic parameters were calculated using the software package PowerStats (Promega, Madison, WI).

The agreement with Hardy-Weinberg equilibrium (tested by the χ^2-test) was confirmed for all studied loci in Chol population. The allele frequency distribution for the 15 DNA systems studied is shown in Table 1. The expected heterozygosity and the power of discrimination calculated from the gene frequencies obtained in this population reveal that, in combination, the 15 systems have a high forensic efficiency (Table 1). The combined power of discrimination (PD) and the combined power of exclusion (PE) for the 15 STR loci tested were 1.0000 and 0.9999, respectively.

To summarize, based on presented allelic frequencies and statistical parameters for forensic testing, it may be concluded that analyses of these 15 STR loci do indeed represent a powerful and efficient approach to forensic human identification and parentage testing.

The complete data are available by accessing http://www.ub.edu/spublica/legal/choles.html

[1] Faculty of Medicine, University of Barcelona, Catalonia, Spain.
[2] History and Anthropology Area, Autonomous University of Hidalgo State, Mexico.
[3] Bellvitge Hospital, Catalonia, Spain.

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TABLE 1—*Allele frequencies of the 15 STRs in the Choles Amerindian population.*

Allele	D5S818	D13S317	D7S820	D16S539	HumTHO1	HumvWA	D8S1179	HumTPOX	HumFGA	HumCSF1PO	D21S11	D18S51	D2S1338	D19S433	D3S1358
5															
6					0.3981										
7	0.0648		0.0097		0.3287					0.0095					
8	0.0046	0.0694	0.0777		0.0509			0.4670		0.0095					
9	0.0509	0.2917	0.0243	0.0748	0.0463			0.0283		0.0286					
9.3					0.1713										
10	0.0278	0.1250	0.2767	0.2710	0.0046		0.0880	0.0425		0.2095		0.0047			
10.2														0.0046	
11	0.5602	0.1898	0.3301	0.2897			0.0324	0.2358		0.3333		0.0047		0.0093	
11.2														0.0046	
12	0.2407	0.1898	0.2330	0.3084			0.0972	0.2217		0.3567		0.0755	0.00047	0.0509	
12.2														0.0093	
13	0.0509	0.0833	0.0437	0.0467			0.3148	0.0047		0.0429		0.1085		0.1759	0.0139
13.2														0.1806	
14		0.0509	0.0049	0.0093		0.0694	0.2639					0.2311		0.2500	0.0556
14.2														0.0324	
15						0.0694	0.1481					0.1415		0.1343	0.5556
15.2														0.0741	
16						0.3843	0.0370					0.1226	0.0189	0.0324	0.2407
16.2														0.0278	
17						0.2685	0.0139					0.1792	0.0849		0.1111
17.2														0.0139	
18						0.1528	0.0046		0.0142			0.0849	0.0425		0.0185
18.2									0.0047						
19						0.0556			0.0613			0.0094	0.2736		0.0046
20									0.0094			0.0189	0.1557		
21									0.0802				0.0283		
22									0.1038			0.0142	0.0943		
22.2									0.0094						
23									0.1321			0.0047	0.2217		
23.2									0.0047						
24									0.1557				0.0472		
25									0.1745				0.0236		
26									0.1840				0.0047		
27									0.0425						
28									0.0189		0.0833				
29									0.0047		0.2593				
30											0.3426				
30.2											0.0139				
31											0.0509				
31.2											0.0972				
32											0.0093				
32.2											0.1111				
33											0.0046				
33.2											0.0278				
P	0.9415	0.7333	0.5984	0.7838	0.1338	0.5035	0.5723	0.9752	0.2476	0.4380	0.3494	0.9489	0.1936	0.2123	0.9384
H	0.565	0.843	0.786	0.738	0.676	0.713	0.778	0.717	0.837	0.686	0.722	0.858	0.858	0.778	0.620
CE	0.251	0.680	0.574	0.490	0.392	0.449	0.558	0.455	0.669	0.407	0.463	0.712	0.712	0.558	0.316
PD	0.809	0.933	0.888	0.881	0.847	0.894	0.915	0.838	0.961	0.865	0.921	0.957	0.944	0.954	0.794

P = Hardy-Weinberg equilibrium.
H = Heterozigosity value.
CE = Chance of exclusion.
PD = Power discrimination.

References

1. Budowle B, Chidambaram A, Strickland L, Beheim CW, Taft GM, Chacraborty R. Population studies on three native Alaska population groups using STR loci. Forensic Sci Int 2002;129:51–7. [PubMed]
2. Gené M, Moreno P, Borrego N, Pique E, Xifro A, Fuentes M, et al. Population study of Aymara Amerindians for the PCR-DNA polymorphisms HumTH01, HumvWA31A, D3S1358, D8S1179, D18S51, D19S253, YNZ22 and HLA-DQα. Int J Legal Med 2000;113:126–8. [PubMed]
3. Gené M, Fuentes M, Huguet E, Pique E, Bert F, Corella A, et al. Quechua Amerindian population characterised by HLADQa, YNZ22, 3′ApoB, HumTH01 and HumvWA31A polymorphisms. J Forensic Sci 1998;43(2):403–5. [PubMed]
4. Barrot C, Sánchez C, Ortega M, González–Martín A, Brand-Casadevall C. Gorostiza A, et al. Characterisation of three Amerindian populations from hidalgo state (Mexico) by 15 STR-PCR polymorphisms. Int J Legal Med In press. [PubMed]
5. Brinkmann B, Junge A, Meyer E, Wiegand P. Population genetic diversity in relation to microsatellite heterogeneity. Human Mutation 1998;11: 135–44. [PubMed]
6. Walsh PS, Metzger DA, Higuchi R. Chelex 100 as a medium for simple extraction of DNA for PCR-based typing from forensic material. Biotechniques 1991;10:506–13. [PubMed]
7. Anslinger K, Rolf B, Keil W. Evaluation and application of the AmpFℓSTR Profiler Plus PCR amplification kit in a Bavarian population sample. Int J Legal Med 2001;115:57–60. [PubMed]
8. Guo SW, Thompson EA. Performing the exact test of Hardy-Weinberg proportion for multiple alleles. Biometrics 1992;48:361–72. [PubMed]

Additional information and reprint requests:
Carme Barrot, Ph.D.
Forensic Genetics Laboratory. Department of Legal Medicine
Faculty of Medicine. University of Barcelona
C/Casanova 143
08036 Barcelona Spain
Tel: +34-3-4035289
Fax: +34-93-4035290
E-mail: cbarrotfeixat@ub.edu