



Genetic analysis of autosomic and Y-chromosome STR-PCR polymorphisms of the Huaoranis, the last nomad tribe in Ecuador

Fabricio González-Andrade ^{a,*}, Miguel Bolea ^b,
Begoña Martínez-Jarreta ^b, Dora Sánchez ^a

^a DNA Laboratory, GENética, Hospital Metropolitano, Quito, Ecuador

^b Legal Medicine Department, University of Zaragoza, Spain

Abstract. Allele frequency data for the 15 STR systems, Amelogenine and 12 STRs from chromosome Y were determined in a population sample of healthy Amerindian Huaorani individuals. All loci met Hardy–Weinberg expectations and the high discrimination power of the combined system showed the forensic efficiency of these genetic markers. © 2006 Published by Elsevier B.V.

Keywords: Ecuador; STR; Forensic genetics; Amerindian Huaorani; Population genetics

1. Introduction

Huaorani population is the last nomad tribe of hunters–collectors from Ecuador. They speak Huao Tiro and no similar language exists from the linguistic point of view. They live in small communities, some of them without any contact with western society, such as the Tagaeri and Taromenane. Traditionally, the basic social unit is the “nanicabo”, formed by 6 to 10 families living under the same roof. There are currently only 2000 individuals left in 716,000 ha, in dispersed communities in the Amazonia region. They are also called Aucas and Jíbaros. They shrink heads [1].

2. Material and methods

Population sample: Whole blood was obtained in EDTA Vacutainer tubes by venipuncture from healthy unrelated Amerindian Huaoranis born and living in Ecuador.

* Corresponding author. Tel.: +593 2269354; fax: +593 2269354.

E-mail address: fabriciogonzaleza@yahoo.es (F. González-Andrade).

Table 1
Y chromosome haplotypes found

Huaoranis														
H	<i>n</i>	Frequency	DYS 19	DYS 385 a	DYS 385 b	DYS 389 I	DYS 389 II	DYS 390	DYS 391	DYS 392	DYS 393	DYS 437	DYS 438	DYS 439
h1	1	0.166667	13	14	19	12	30	25	10	14	14	15	11	12
h2	1	0.166667	14	14	16	13	30	23	10	15	13	14	12	13
h3	1	0.166667	14	14	16	13	30	23	10	15	13	14	12	11
h4	1	0.166667	13	15	15	13	28	23	10	14	13	14	11	10
h5	1	0.166667	14	14	16	12	30	23	10	15	12	14	12	12
h6	1	0.166667	14	14	16	13	30	23	10	15	13	14	12	12
Statistical parameters			<i>N</i>		<i>k</i>		Hd		□		<i>V</i>			
Huaoranis			6		6		1		5.87 ± 3.26		0.55 ± 0.53			

N, sample size; *k*, number of different haplotypes; Hd, haplotype diversity; □, average pairwise differences between haplotypes; *V*, average repeat size variance. P min: allelic frequency minimum, MEC: Mean paternity exclusion chance; PIC: Polymorphism information content; Pm: Probability of match; PD: Discrimination power; Obs H: observed heterocigoty; Exp H: expected heterocigoty; FIS: inbreeding coefficient.

We collected all samples within a period of 6 months. *N*: 37 Huaoranis. DNA extraction: DNA was extracted using Wizard Genomic DNA Purification Kit System[®], and the quantity was estimated by UV absorbance. PCR: Amplification was performed in a Genius[®] model Techne Thermal Cycler. Typing: By ABI Prism 310. Fragment size and allele designation of different loci was determined by comparison with allelic ladders distributed into the PowerPlex 16 (Promega) kit. The recommendations of the DNA Commission of the International Society of Forensic Haemogenetics for analysis of STRs systems were followed. Quality control: GEP-ISFG Working Group (<http://www.gep-isfg.org>) proficiency testing. Data analysis: Evaluation of Hardy–Weinberg expectations was carried out using statistical parameters of forensic interest, as previously described [2,3].

3. Results and discussion

Table 1 shows Y chromosome haplotypes found, and Table 2 shows allelic frequencies of autosomic STRs. Cumulative power of discrimination (PD) of autosomic STRs was 0.9999 and cumulative mean exclusion chance (MEC) was 0.999625.

References

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Table 2

Allele distribution of 15 STR loci and Amelogenin in a population sample of Huaoranis ($n=37$)

Allele	TH01	CSF1PO	TPOX	VWA	D13S317	D3S1358	D5S818	D7S820	D21S11	D18S51	PENTA E	D16S539	PENTA D	D8S1179	FGA
5	0	0	0	0	0	0	0	0	0	0	0	0	0.027	0	0
6	0.4459	0	0	0.0135	0	0	0	0	0	0	0	0	0	0	0
7	0.4865	0	0	0	0	0	0.2973	0	0	0	0	0	0	0	0
8	0	0.0135	0.0135	0	0	0	0	0	0	0	0	0.0135	0	0	0
9	0	0	0	0	0	0	0.0135	0.0135	0	0	0.027	0.3784	0.4595	0	0
9.3	0.0676	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10	0	0.1486	0	0	0.0811	0	0	0	0	0	0	0.4324	0.3919	0.0135	0
11	0	0.1622	0.2703	0	0.0135	0	0.2973	0.3919	0	0	0	0.0676	0.0541	0	0
12	0	0.6351	0.7162	0	0.1351	0	0.2297	0.5541	0	0.3243	0.0405	0.027	0	0.0811	0
13	0	0.0135	0	0	0.2703	0	0.1622	0	0	0.1622	0.1757	0.0135	0.0676	0.1216	0
14	0	0.0270	0	0	0.5	0	0	0.0405	0	0.0135	0	0.0676	0	0.4865	0
15	0	0	0	0.1351	0	0.6486	0	0	0	0.1486	0.4865	0	0	0.0946	0
16	0	0	0	0.6486	0	0.3378	0	0	0	0.0135	0	0	0	0.2027	0
17	0	0	0	0.1892	0	0.0135	0	0	0	0.1216	0	0	0	0	0
18	0	0	0	0	0	0	0	0	0	0.2162	0	0	0	0	0
19	0	0	0	0.0135	0	0	0	0	0	0	0.1216	0	0	0	0
20	0	0	0	0	0	0	0	0	0	0	0.1486	0	0	0	0.1351
21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0135
22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0135
23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1351
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.3514
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1757
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1757
29	0	0	0	0	0	0	0	0	0.1351	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0.2432	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0.1081	0	0	0	0	0	0
31.2	0	0	0	0	0	0	0	0	0.2027	0	0	0	0	0	0
32.2	0	0	0	0	0	0	0	0	0.2162	0	0	0	0	0	0
33.2	0	0	0	0	0	0	0	0	0.0946	0	0	0	0	0	0
χ^2 test	0.72062	0.98083	0.00009	0.91865	0.82901	0.81171	0.00001	0.74809	0.999939	0.28775	0.161700	0.52169	0.0001	0.9377	0.85807
P min	0.09292	0.09106	0.10785	0.10379	0.10786	0.08926	0.08749	0.09817	0.08926	0.09817	0.09817	0.09488	0.08749	0.08749	0.08393
MEC	0.47233	0.19117	0.57406	0.58081	0.62797	0.35735	0.29440	0.47039	0.24871	0.40178	0.50075	0.40407	0.26258	0.32335	0.17544
PIC	0.65676	0.36882	0.74640	0.75277	0.78751	0.55614	0.47777	0.65476	0.44157	0.59899	0.69752	0.59992	0.46180	0.50597	0.33863
Pm	0.14976	0.43898	0.11615	0.10007	0.09863	0.21400	0.29003	0.14095	0.30021	0.22863	0.11617	0.17601	0.27533	0.27093	0.40972
PD	0.85024	0.56102	0.88385	0.89993	0.90137	0.78600	0.70997	0.85905	0.69979	0.77137	0.88383	0.82399	0.72467	0.72907	0.59028
Obs H	0.62160	0.56750	0.91890	0.86480	0.91900	0.51360	0.45940	0.75670	0.51350	0.75670	0.75680	0.67550	0.45940	0.45930	0.35130
Exp H	0.69320	0.46502	0.77790	0.78454	0.81413	0.62704	0.52490	0.69173	0.53756	0.65192	0.74397	0.65961	0.55992	0.54716	0.41381
FIS	0.115418	-0.20386	-0.16528	-0.08739	-0.11354	0.19199	0.13662	-0.07913	0.05767	-0.14502	-0.00349	-0.01025	0.19061	0.17192	0.16253
Allele	PENTA E	D3S1358	FGA	D18S51	D21S11	PENTA D	VWA	D8S1179	D7S820	D13S317	D5S818	D16S539	TH01	CSF1PO	TPOX

P min: allelic frequency minimum; MEC: mean paternity exclusion chance; PIC: polymorphism information content; Pm: probability of match; PD: discrimination power; Obs H: observed heterozygosity; Exp H: expected heterozygosity; FIS: inbreeding coefficient.