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Allele frequency data for 15 autosomal strs and ancestral proportions using aims-indels in the shuar ethnic group from Ecuador

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ABSTRACT

The ethnic group Shuar is located in Ecuador. To identify their genetic composition, 46 ancestry-informative insertion deletion markers (AIM-INDELs) were used. Also, characterization of 15 tandem repeats (STRs) in the AmpFISTR Identifiler Kit were applied. Forensic parameters showed a matching probability of 0.1535, a power of discrimination of 0.8465, a polymorphism information content of 0.6584, probability of exclusion of 0.415 and a typical paternity index of 1.78. The Shuar are not influenced by admixture population events, being a Native American group 98.7%, along with a genetic diversity of 0.699346 + /-0.356964.

1. Introduction

South America is home to several indigenous populations that show the less genetic diversity across the globe [1,2]. Ecuador, which was conquered by the Spanish, is inhabited by different ethnic groups such as the Shuar who are isolated and settled in the amazon region. Moreover, Ecuador is well known for its heterogeneous distribution and wide inter-population differentiation of three main ancestral contributions from Native Americans, Europeans and Africans [3]. The latest census showed, 71.9% of Ecuadorians self-identified as mestizos, 7.2% as Afro-Ecuadorians and 7% as indigenous [4]. There are few studies in indigenous populations about their genetic composition [5]. We decided to characterize the Shuar ethnic group by determining the allele frequencies of 15 STRs, and by using 46 AIM-INDELs to determine their ancestral proportion.

2. Materials and methods

2.1. Population

40 individuals from the Shuar community were randomly selected, 25 females and 15 males, whose blood samples were taken on FTA cards. All individuals signed an informed consent for population genetic studies. DNA was extracted following the manufacturer's recommendations (Whatman – GE Healthcare).

2.2. Genetic markers and genotyping

Amplification of the 46 AIM-Indels was performed according to Pereira [6], meanwhile, the 15 STRs were amplified in a multiplex reaction using the AmpFISTR Identifiler PCR Amplification Kit (Applied Biosystems, Foster City, CA, USA). DNA amplification was done according to manufacturer's protocol, except that 30 cycles were used in a final volume of 5 ul. For genotyping, capillary electrophoresis separated the PCR products on an ABI PRISM 3130 Genetic analyzer (Applied Biosystems, Foster City, CA), and data were analyzed with the GeneMapper ID v3.2 (Applied Biosystems) [7].

2.3. Statistical analysis

Allele frequencies, genetic diversity, Hardy-Weinberg equilibrium and linkage disequilibrium were calculated using the Arlequin v.3.5.1.3 software. Statistical parameters of forensic interest were obtained using the PowerStats v1.2 (Promega Corporation, USA) software [8]. The distribution of genetic ancestry was calculated using the STRUCTURE v.2.3.4 software.

3. Results

The obtained genetic diversity was 0.699346 + /-0.356964. Allelic frequencies and forensic parameters can be seen in Table 1. All markers

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Table 1
Allele frequencies for the Shuar population sample and forensic parameters.

Allele	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA
5	.....	.....	.....	.....	.....	0.0125	.....	.....	.....	.....	.....	.....	.....	.....	.....
6	.....	.....	.....	.....	.....	0.3375	.....	.....	.....	.....	.....	.....	.....	.....	.....
7	.....	.....	.....	.....	.....	0.4875	.....	.....	.....	.....	.....	0.0125	.....	0.075	.....
8	.....	.....	.....	0.025	.....	.....	.....	.....	.....	.....	.....	0.4125	.....	.....	.....
9	.....	.....	0.1	0.1375	.....	.....	0.5625	0.1875	.....	.....	.....	.....	.....	0.225	.....
9,3	.....	.....	.....	.....	.....	0.1625	.....	.....	.....	.....	.....	.....	.....	.....	.....
10	0.2	.....	0.3375	0.1	.....	.....	0.075	0.3875	.....	.....	.....	0.0125	.....	0.025	.....
10,2	.....	.....	.....	.....	.....	.....	.....	.....	.....	0.0125	.....	.....	.....	.....	.....
11	0.0125	.....	0.2125	0.3	.....	.....	.....	0.025	.....	.....	.....	0.4625	.....	0.3125	.....
12	0.05	.....	0.3375	0.425	.....	.....	0.075	0.375	.....	.....	.....	0.1	0.075	0.15	.....
13	0.5875	.....	0.0125	0.013	.....	.....	0.1625	0.0125	.....	0.3375	.....	.....	0.1875	0.2	.....
13,2	.....	.....	.....	.....	.....	.....	.....	.....	.....	0.0875	.....	.....	.....	.....	.....
14	0.1	.....	.....	.....	0.0125	.....	0.125	0.0125	.....	0.0875	0.0375	.....	0.3375	0.0125	.....
14,2	.....	.....	.....	.....	.....	.....	.....	.....	.....	0.15	.....	.....	.....	.....	.....
15	0.05	.....	.....	.....	0,5625	.....	.....	.....	.....	0.225	0.2125	.....	0.1375	.....	.....
15,2	.....	.....	.....	.....	0.0375	.....	.....	.....	.....	0.0125	.....	.....	.....	.....	.....
16	.....	.....	.....	.....	0.2625	.....	.....	.....	.....	0.0125	0.425	.....	0.0125	.....	.....
16,2	.....	.....	.....	.....	.....	.....	.....	.....	.....	0.075	.....	.....	.....	.....	.....
17	.....	.....	.....	.....	0.125	.....	.....	.....	0.0875	.....	0.175	.....	0.225	.....	.....
18	.....	.....	.....	.....	.....	.....	.....	.....	0.0875	.....	0.1	.....	0.025	.....	.....
19	.....	.....	.....	.....	.....	.....	.....	.....	0.3875	.....	0.05	.....	.....	.....	0.2625
20	.....	.....	.....	.....	.....	.....	.....	.....	0.1625	.....	.....	.....	.....	.....	.....
21	.....	.....	.....	.....	.....	.....	.....	.....	0.0125	.....	.....	.....	.....	.....	0.05
22	.....	.....	.....	.....	.....	.....	.....	.....	0.025	.....	.....	.....	.....	.....	0.05
23	.....	.....	.....	.....	.....	.....	.....	.....	0.2375	.....	.....	.....	.....	.....	0.1
24	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	0.175
25	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	0.2
26	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	0.125
27	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	0.0375
28	.....	0.025	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
29	.....	0.15	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
30	.....	0.4	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
30,2	.....	0.0375	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
31	.....	0.05	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
31,2	.....	0.25	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
32,2	.....	0.0625	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
33,2	.....	0.025	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
MP	0.2175	0.11	0.1538	0.1663	0.2763	0.205	0.1813	0.1738	0.105	0.085	0.1325	0.235	0.1025	0.0975	0.0613
PD	0.7825	0.89	0.8463	0.8338	0.7238	0.795	0.8188	0.8263	0.895	0.915	0.8675	0.765	0.8975	0.9025	0.9388
PIC	0.5603	0.7114	0.6648	0.6507	0.5406	0.549	0.5948	0.6098	0.7154	0.7643	0.6923	0.5249	0.7415	0.7499	0.8066
PE	0.322	0.322	0.2619	0.5535	0.468	0.2619	0.2351	0.3552	0.599	0.322	0.322	0.2619	0.6462	0.6949	0.599
TPI	1.33	1.33	1.18	2.22	1.82	1.18	1.11	1.43	2,50	1.33	1.33	1.18	2.86	3.33	2.5
Het Obs	0.625	0.625	0.575	0.775	0.725	0.575	0.55	0.65	0.8	0.625	0.625	0.575	0.825	0.85	0.8

PD: Power of Discrimination; PIC: Polymorphic Information Content; PE: Power of Exclusion; TPI: Typical Paternity Index; Het Obs: Heterozygosity Observed.

were in Hardy-Weinberg equilibrium except for D7S820 and vWA, $p < 0.05$. An average matching probability of 0.1535, average discrimination power of 0.8465, average polymorphic information content of 0.6585, average power of exclusion of 0.415 and an average typical paternity index of 1.78 were obtained.

Ancestry proportion was estimated from three reference populations: Africa, America and Europe (K = 3). The Shuar population consists of Native American 98.7%, European 0.5% and African 0.8% (Fig. 1).

4. Discussion

The Ecuadorian ethnic group Shuar was characterized for its allelic frequencies for the first time. The observed genetic diversity value 0.699346 is lower than those seen in other studies for an indigenous population, which might be due to their culture and manners that include endogamy. However, it shows similar values when compared to the Waoranis, another Ecuadorian ethnic group [5,9]. Regarding the 15 analyzed STRs, the Shuar showed two new allelic variants 15.2 and 10.2 for D3S1358 and D19S433, respectively. Moreover, the genetic markers vWA and D7S820 are not in Hardy-Weinberg equilibrium which might be because the sample is too little to show a representative

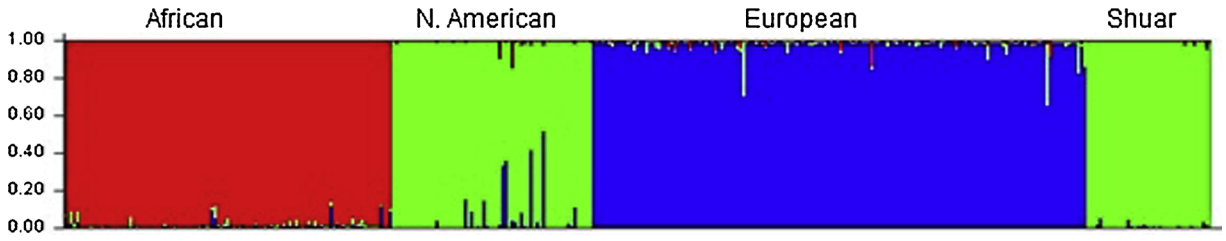

Fig. 1. Ancestry component analysis result for the Shuar population. The bars with colour represent different ancestry origins from the analysis: red, Africa; green, Native American; blue, European. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

allelic distribution or the levels of endogamy were not revised [10]. The AIM-INDELs showed that the Shuar is a Native American group 98.7%, hence not influenced by admixture population events. Isolation of this group has enabled to conserve their genetic material which should be considered for further studies.

5. Conclusion

The Shuar group is a conserved population with no influence from the European and African diaspora populations, allele frequencies of 15 STRs were obtained.

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Declaration of Competing Interest

None.

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