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Ecuadorian Quichua population data on three tetrameric STR loci—HUMCSF1PO, TPOX and TH01—derived using a multiplex system

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Abstract

Allele frequency data for the STR systems, HUMCSF1PO, HUMTPOX and HUMTH01, were determined in a population sample of unrelated Amerindian Quichua individuals. All loci met Hardy-Weinberg expectations and the high discrimination power of combined system showed the forensic efficiency of these genetic markers. There is a lack of genetic information on Ecuadorian populations and therefore no previous publications on the distribution of STRs in Quichuas are available.

Keywords: STRs; Multiplex; Population data; Amerindian Quichua; Ecuador

1. Introduction

Ecuador is a small South American country with almost 12 million inhabitants comprised of three main ethnics groups: Caucasian mestizos, Amerindian natives (more than 100 multiethnic and pluricultural groups) and a small group of negroids descendents from African slaves. Mestizos are the most representative and largest group [1–4]. They are descendents from Spanish and Amerindian people. The Quichua population comprises almost 1 million inhabitants (9.4% of total). Most of them live in the mountains, in the Andean region, but some of them are distributed on the coast regions and Amazonia. Few STR studies have been carried out in South America native populations. Extensive work may be required in this field to demonstrate the different genetic admixture process

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between original individuals. There is a general lack of information on Ecuadorian population from a genetic point of view and no previous publications on the distribution of STRs is available. Therefore studies like this should be encouraged, furthermore at this moment when migration from Ecuador to more developed countries such as Spain is increasing.

In this paper, we report the allele frequency distribution of three STR loci that have proven to be extremely useful for forensic casework and human identification: HUMCSF1PO, HUMTPOX and HUMTH01 in a population sample of Amerindian Quichuas from Ecuador [5].

2. Material and methods

2.1. Population sample

Whole blood was obtained in EDTA vacutainer tubes by venipuncture from 150 unrelated Amerindian Quichuas born and living in Ecuador. Samples came from a paternity testing bank of the Genetics Laboratory (Cruz Roja Ecuatoriana).

2.2. DNA analysis

The DNA was extracted using the Wizard Genomic DNA Purification Kit System© (Promega, Madison, WI, USA) and 5% Chelex for the samples on filter paper. The quantity was estimated by UV-absorbance (Gene Quant Calculator©). The multiplex analysis of HUMCSF1PO, HUMTPOX and HUMTH01 was performed using the kit CTT Multiplex System (Promega) and following the manufacturer's recommendations. Amplification was performed in a Techne Thermal Cycler, model Genius©. The PCR products were typed by

Table 1
Allele frequency distribution and Hardy-Weinberg equilibrium tests on the loci analyzed in a Quichua population sample from Ecuador

Allele	CSF1PO (n=150)	TPOX (n=150)	TH01 (n=150)
6	–	–	0.4800
7	–	–	0.3200
8	0.0030	0.5130	0.0070
9	0.0070	–	0.0230
9.3	–	–	0.1330
10	0.3130	0.0030	0.1230
11	0.2930	0.3600	0.0370
12	0.3130	0.1230	–
13	0.0570	0.0030	–
14	0.0130	–	–
P_{min}	0.0197	0.0197	0.0197
X^2	0.3744	0.8728	0.2032
G-test	0.3408	0.9080	0.5280
Exact test	0.4956	0.8192	0.3928

P_{min}=minimum allele frequency; number of random shuffles performed: 5000.

Table 2
Parameters of forensic efficiency

Parameter	CSF1PO (n=150)	TPOX (n=150)	TH01 (n=150)
Obs H	0.7333	0.5800	0.6400
Exp H	0.7165	0.5936	0.6497
MEC	0.4552	0.3065	0.3876
MEP	0.4543	0.2833	0.3547
PIC	0.6591	0.5114	0.5871
PM	0.1401	0.2462	0.1906
PD	0.8599	0.7538	0.8094

Power of discrimination cumulative=0.99342, Mean exclusion chance cumulative=0.80942, Obs H=observed heterozygosity, Exp H=expected heterozygosity, MEC=mean exclusion chance, MEP=mean exclusion probability, PIC=polymorphism information content, PM=probability of match, PD=power of discrimination.

vertical electrophoresis on 0.40 mm thick 4% denaturing polyacylamide gels (19:1 acrylamide:bisacrylamide, 7 M urea) and silver staining [3,6]. Electrophoresis was carried out in a GIBCO BRL Sequencing System, model SA, (Gibco©, USA) at 1200 V, up to 2200 V at the end, with a fixed temperature of 50 °C.The recommendations of the DNA Comission of the International Society of Forensic Genetics for analysis of STR systems [7–9] were followed.

2.3. Statistical approach

The evaluation of Hardy-Weinberg expectations and calculation of statistical parameters of forensic interest was done as previously described [10].

3. Results and discussion

The distributions of observed allele frequencies for the three loci, HUMCSF1PO, HUMTPOX and HUMTH01, and the results of the different test procedures for testing the correspondence of the genotype frequencies with Hardy-Weinberg expectations are summarized in Table 1. Table 2 shows the forensic value of the analysed systems expressed as various statistical parameters. All loci met Hardy-Weinberg expectations and there was no evidence for association of alleles among the three loci. Forensic efficiency parameters revealed the high efficiency of the three STR loci analysed. The data presented in this work will allow the calculation of matching probabilities in cases where Ecuadorian Quichua individuals are considered as source of DNA evidence.

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