



Announcement of Population Data

Genetic analysis of the Amerindian Kichwas and Afroamerican descendents populations from Ecuador characterised by 15 STR-PCR polymorphisms

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Abstract

Allele frequency data for the 15 STR systems and Amelogenine were determined in a population sample of healthy Amerindian Kichwas and Blacks individuals. All loci met Hardy–Weinberg expectations and the high discrimination power of combined system showed the forensic efficiency of these genetic markers.

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Keywords: Ecuador; STRs; Forensic genetics; Black population; Amerindian Kichwas

Population sample: Whole blood was obtained in EDTA vacutainers tubes by venipuncture from healthy unrelated Amerindian Kichwas and Blacks born and living in Ecuador. We collected all samples in a period of time of 6 months [1].

N: 115 Amerindian Kichwas and 104 Afroamerican Blacks.

DNA extraction: The DNA was extracted using Wizard Genomic DNA Purification Kit System[®] (Promega Corporation, Madison, WI, USA), and the quantity was estimated by UV absorbance (Gene Quant Calculator[®], Pharmacia, Uppsala, Sweden).

PCR: Amplification was performed in a Techne Thermal Cycler, model Genius[®] following the manufacturer's recommendations [2].

Typing: By ABI Prism 310. Fragment size and allele designation of different loci was determined by comparison with allelic ladders distributed into the kit PowerPlex 16 (Promega) [2]. The recommendations of the DNA Commission of the International Society of Forensic Haemogenetics for analysis of STRs systems were followed [3,4].

Results: See Tables 1 and 2.

Quality control: Proficiency testing of the GEP-ISFG Working Group (<http://www.gep-isfg.org>).

Analyses of data: Evaluation of Hardy–Weinberg expectations was carried out using the Exact test and determination of further statistical parameters of forensic interest was carried out by using the computer programme HWE-analysis Version 3.3 (Christoph Puers, Institute for Legal

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Table 1
Allele distribution of 15 STR loci and Amelogenin in a population sample of Ecuadorian Black population ($n = 104$)

Allele	PENTAE	D3S1358	FGA	D18S51	D21S11	PENTA D	VWA	D8S1179	D7S820	D13S317	D5S818	D16S539	TH01	CSF1PO	TPOX
2.2	–	–	–	–	–	0.0890	–	–	–	–	–	–	–	–	–
3.2	–	–	–	–	–	0.0050	–	–	–	–	–	–	–	–	–
5	0.0560	–	–	–	–	0.0330	–	–	–	–	–	0.0090	–	–	–
6	–	–	–	–	–	–	–	–	–	–	–	–	0.2570	–	0.0370
6.3	–	–	–	–	–	–	–	–	–	–	–	–	0.0050	–	–
7	0.0930	–	–	–	–	0.0470	–	–	–	–	0.0140	0.0050	0.3830	0.0370	0.0050
8	0.1360	–	–	–	–	0.1170	–	–	0.1450	0.0370	0.0190	0.0090	0.1450	0.0470	0.4210
9	0.0370	–	–	–	–	0.1360	–	0.0050	0.0890	0.1450	0.0610	0.2010	0.0840	0.0420	0.1540
9.3	–	–	–	–	–	–	–	–	–	–	–	–	0.1170	–	–
10	0.0280	–	–	–	–	0.2010	0.0050	0.0230	0.3040	0.0510	0.0510	0.1260	0.0090	0.2660	0.0700
11	0.0700	–	–	0.0050	–	0.1450	0.0090	0.0280	0.2380	0.2710	0.3130	0.3270	–	0.2570	0.2340
12	0.1070	0.0050	–	0.0470	–	0.0750	–	0.1030	0.1920	0.2900	0.2940	0.1680	–	0.2990	0.0790
13	0.0890	0.0050	–	0.0560	–	0.1030	0.0190	0.3320	0.0330	0.1590	0.2290	0.1310	–	0.0420	–
13.2	–	–	–	0.0090	–	–	–	–	–	–	–	–	–	–	–
14	0.0700	0.0610	–	0.1360	–	0.0370	0.0330	0.3040	0.0010	0.0470	0.0140	0.0230	–	0.0050	–
15	0.1260	0.3640	–	0.1640	–	0.0140	0.1730	0.1820	–	–	–	–	–	–	–
16	0.0610	0.3360	–	0.1540	–	–	0.2710	0.0190	–	–	0.0050	–	–	–	–
17	0.0330	0.1680	–	0.1780	–	–	0.2760	–	–	–	–	–	–	0.0050	–
18	0.0420	0.0510	0.0050	0.1120	–	–	0.1120	–	–	–	–	–	–	–	–
18.2	–	–	0.0190	–	–	–	–	–	–	–	–	–	–	–	–
19	0.0140	0.0090	0.0700	0.0700	–	–	0.0840	–	–	–	–	–	–	–	–
19.2	–	–	0.0050	–	–	–	–	–	–	–	–	–	–	–	–
20	0.0190	–	0.0890	0.0370	–	–	0.0190	–	–	–	–	–	–	–	–
21	0.0140	–	0.0980	0.0140	–	–	–	–	–	–	–	–	–	–	–
22	0.0050	–	0.1590	–	–	–	–	–	–	–	–	–	–	–	–
23	–	–	0.1400	0.0140	–	–	–	–	–	–	–	–	–	–	–
24	–	–	0.1070	–	–	–	–	0.0050	–	–	–	–	–	–	–
24.2	–	–	0.0050	–	–	–	–	–	–	–	–	–	–	–	–
25	–	–	0.1170	–	–	–	–	–	–	–	–	–	–	–	–
26	–	–	0.1070	–	–	–	–	–	–	–	–	–	–	–	–
27	–	–	0.0510	–	0.0370	–	–	–	–	–	–	–	–	–	–
28	–	–	0.0190	–	0.1590	–	–	–	–	–	–	–	–	–	–
28.2	–	–	–	–	0.0050	–	–	–	–	–	–	–	–	–	–
29	–	–	0.0090	–	0.1590	–	–	–	–	–	–	–	–	–	–
30	–	–	–	–	0.2570	–	–	–	–	–	–	–	–	–	–
30.2	–	–	–	–	0.0370	–	–	–	–	–	–	–	–	–	–
31	–	–	–	–	0.0980	–	–	–	–	–	–	–	–	–	–
31.2	–	–	–	–	0.1070	–	–	–	–	–	–	–	–	–	–
32	–	–	–	–	0.0140	–	–	–	–	–	–	–	–	–	–
32.2	–	–	–	–	0.0650	–	–	–	–	–	–	–	–	–	–
33	–	–	–	–	0.0140	–	–	–	–	–	–	–	–	–	–
33.2	–	–	–	–	0.0230	–	–	–	–	–	–	–	–	–	–
34	–	–	–	–	0.0090	–	–	–	–	–	–	–	–	–	–
34.2	–	–	–	–	0.0050	–	–	–	–	–	–	–	–	–	–
35	–	–	–	–	0.0090	–	–	–	–	–	–	–	–	–	–
Exact test	1.0000	0.4798	0.7260	0.6590	0.4532	0.2368	0.9942	0.6914	0.7994	0.2482	0.4308	0.5976	0.2900	0.4780	0.5060
Chi Square test	0.9976	0.6246	0.1506	0.5794	0.3662	0.1282	0.9790	0.1706	0.7551	0.3376	0.2620	0.6930	0.3838	0.2780	0.5408
G-test	0.9998	0.6638	0.7710	0.8184	0.4754	0.2416	0.9800	0.6904	0.9142	0.2728	0.4734	0.5588	0.5026	0.6324	0.3386
MEC	0.8280	0.4794	0.7815	0.7426	0.7128	0.7538	0.6094	0.5297	0.5779	0.5923	0.5333	0.5942	0.5240	0.5509	0.5140
PC	0.9088	0.6716	0.8825	0.8620	0.8386	0.8655	0.7710	0.7125	0.7513	0.7596	0.7160	0.7611	0.7070	0.7292	0.6952
Pm	0.0186	0.1221	0.0275	0.0340	0.0453	0.0374	0.0717	0.1050	0.0820	0.0800	0.1026	0.0783	0.1106	0.0958	0.1131
PD	0.9814	0.8778	0.9724	0.9659	0.9546	0.9625	0.9282	0.8949	0.9179	0.9199	0.8973	0.9216	0.8893	0.9041	0.8868

MEC: mean paternity exclusion chance; PIC: polymorphism information content Pm: probability of match; PD: discrimination power. Cumulative power of discrimination (PD) was 0.9999 and cumulative mean exclusion chance (MEC) was 0.9999.

Medicine, University of Münster), as previously described [5,6]. For Kichwa analysis, we used BD Gen 1.0 and GDA software.

Population comparisons: We compared Kichwa population from Ecuador with Aymara Amerindians (Bolivia) [7], Quechuas (Bolivia) [8], Mapuches, Tehuelches and Wichis (Argentina) [9], Huichol, Puerepecha, Tarahumaras (Mexico) [10], and did not revealed significant differences at HUMTH01, HUMVWA and CSF1PO genetic markers.

A comparison of our Black population with Kichwas, Afroamericans from Connecticut, USA [11], Afroamericans from Indiana, USA [12], North American Blacks [13], Mestizos from Bogotá, Colombia [14] was performed. We have seen significant differences ($p < 0.05$) with all the groups in several genetics markers in special with Afroamerican descendents from USA. There are no significant differences with African descendentes from Colombia and Afroamericans from Chocó, [14,15] (see Table 3). This paper

Table 2
Allele distribution of 15 STR loci and Amelogenin in a population sample of Amerindian Kichwas (n = 115)

Allele	TH01	CSF1PO	TPOX	VWA	D13S317	D3S1358	D5S818	D7S820	D21S11	D18S51	PENTA E	D16S539	PENTA D	D8S1179	FGA
5	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
6	0.3870	–	–	–	–	–	–	–	–	–	–	–	–	–	–
7	0.3609	–	–	–	–	–	0.1391	0.0043	–	–	0.0130	–	–	–	–
8	0.0087	0.5870	0.5870	–	0.0522	–	0.0043	0.0217	–	–	0.0087	–	0.0087	–	–
9	0.0304	0.0087	0.0087	–	0.3304	–	0.1348	0.0217	–	–	–	0.2000	0.2304	–	–
9.3	0.2043	–	–	–	–	–	–	–	–	–	–	–	–	–	–
10	0.0043	0.3261	0.0087	–	0.0652	–	0.0522	0.2304	–	–	–	0.2652	0.3391	0.0696	–
11	0.0043	0.3130	0.2609	0.0087	0.0826	–	0.4957	0.4304	–	–	0.0435	0.2478	0.1348	0.0478	–
12	–	0.2783	0.1348	0.0043	0.1652	0.0043	0.1348	0.2391	–	0.0696	0.1739	0.2348	0.0870	0.2217	–
13	–	0.0609	–	0.0087	0.1391	–	0.0348	0.0435	–	0.0609	0.0435	0.0478	0.1565	0.3304	–
14	–	0.0087	–	0.0174	0.1652	0.0348	–	0.0087	–	0.3435	0.0435	0.0043	0.0348	0.2304	–
15	–	–	–	0.0304	–	0.5000	–	–	–	0.1261	0.1913	–	0.0087	0.0826	–
16	–	–	–	0.413	–	0.2783	–	–	–	0.1043	0.1043	–	–	0.0174	–
17	–	–	–	0.3913	–	0.1522	0.0043	–	–	0.1652	0.0739	–	–	–	–
18	–	0.0043	–	0.0957	–	0.0261	–	–	–	0.0696	0.0739	–	–	–	0.0174
19	–	–	–	0.0261	–	–	–	–	–	0.0087	0.0696	–	–	–	0.0783
20	–	–	–	0.0043	–	0.0043	–	–	–	0.0261	0.0304	–	–	–	0.0435
21	–	–	–	–	–	–	–	–	–	0.0043	0.0783	–	–	–	0.0609
21.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.0043
22	–	–	–	–	–	–	–	–	–	0.0130	0.0261	–	–	–	0.0739
23	–	–	–	–	–	–	–	–	–	0.0087	0.0130	–	–	–	0.0870
23.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.0087
24	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.2609
25	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.1739
26	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.1478
27	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.0348
28	–	–	–	–	–	–	–	–	0.0783	–	–	–	–	–	0.0087
29	–	–	–	–	–	–	–	–	0.1565	–	0.0043	–	–	–	–
30	–	–	–	–	–	–	–	–	0.2696	–	–	–	–	–	–
30.2	–	–	–	–	–	–	–	–	0.0391	–	–	–	–	–	–
31	–	–	–	–	–	–	–	–	0.0609	–	–	–	–	–	–
31.2	–	–	–	–	–	–	–	–	0.1304	–	–	–	–	–	–
32	–	–	–	–	–	–	–	–	0.0087	–	–	–	–	–	–
32.2	–	–	–	–	–	–	–	–	0.1435	–	–	–	–	–	–
33.2	–	–	–	–	–	–	–	–	0.1000	–	–	–	–	–	–
34.2	–	–	–	–	–	–	–	–	0.0043	–	–	–	–	–	–
35	–	–	–	–	–	–	–	–	0.0043	–	–	–	–	–	–
35.2	–	–	–	–	–	–	–	–	0.0043	–	–	–	–	–	–
Exact test	0.1620	0.7500	0.4754	0.2588	0.3316	0.7028	0.3286	0.6300	0.9930	0.2088	0.0470	0.2882	0.0662	0.7194	0.5454
Chi Square 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
G-test	0.90948	0.94637	0.88274	0.86642	0.97744	0.74093	0.96071	0.56207	0.99897	0.12168	0.25018	0.59107	0.53939	0.88672	0.79097
MEC	0.78597	0.39433	0.71242	0.64939	0.69172	0.57895	0.41051	0.56679	0.45743	0.62112	0.48363	0.54608	0.40617	0.45607	0.31137
PIC	0.88357	0.59220	0.83807	0.79384	0.82605	0.74910	0.60550	0.74065	0.65293	0.77818	0.66278	0.73167	0.61416	0.65970	0.50699
Pm	0.02672	0.17675	0.04455	0.06105	0.05225	0.08429	0.17319	0.08703	0.14026	0.07162	0.13181	0.08841	0.16793	0.13709	0.25939
PD	0.97328	0.82325	0.95545	0.93895	0.94775	0.91571	0.82681	0.91297	0.85974	0.92838	0.86819	0.91159	0.83207	0.86291	0.74061

MEC: mean paternity exclusion chance, PIC: polymorphism information content, Pm: probability of match, PD: discrimination power. Cumulative power of discrimination (PD) was 0.9999 and cumulative mean exclusion chance (MEC) was 0.9999954.

follows the guidelines for publication of population data requested by the journal [16].



Other remarks:

Kichwas—Kichwa (ancestral name) or Quichua (a mixture of native and Spanish derived name) population are almost three million inhabitants (20% of total). They are most representative Amerindian group in Ecuador. Most of them live in the mountains, in the Andean region, from Carchi province, on the north, until Loja province, on the South. Some of them are distributed on the Amazonia region, on provinces of Pastaza, Napo, Sucumbíos and Orellana. They are approximately 70,000 persons, and speak Kichwa language distinguishable from highlands Quichua dialects. Everybody have the Spanish like a second language Kichwa nationality is product from to raise some groups. Kichwa nationality from Ecuador appears due to process of “quichuization” of multiplicity of peoples that had their own elements. It was due to contacts between ethnic groups toward pre incasic period

Table 3
Population comparisons between Black populations ($p < 0.05$)

Genetic marker	Kichwas Ecuador	Afroamericans (Connecticut, USA) [11]	Afroamericans (Indiana, USA) [12]	North American Choco and Blacks [13]	Mestizos Bogota Colombia [14]	Afroamericans Chocó and Colombia [14,15]
D13S1358	0.0940	0.0600	0.5200	0.7500	–	–
FGA	0.0010	0.0060	0.5500	0.0005	–	–
D18S51	0.0010	0.5130	0.8680	0.5680	–	–
D21S11	0.0140	0.0150	0.0034	0.1375	–	–
D8S1179	0.0090	0.0094	0.1270	0.9290	–	–
VWA	0.0010	0.0001	0.1276	0.6700	0.3370	0.7350
D7S820	0.0010	0.0052	0.0218	0.1021	0.5460	0.2750
D13S317	0.0010	0.0001	0.0001	0.0001	0.0001	0.0001
D5S818	0.0010	0.0363	0.0250	0.1420	0.0028	0.9778
D16S539	0.0010	0.6004	0.5079	0.0549	0.0010	0.2595
TH01	0.0010	0.0002	0.0079	0.0041	0.0010	0.1990
CSF1P0	0.1500	0.9133	0.8597	0.7870	0.0010	0.7300
TPOX	0.0010	0.0420	0.0510	0.0010	0.0070	0.6400

and they adopt “Quichua” like maternal language. Quichua was the Inca language.

Afroamericans (blacks)—Black populations from Ecuador are descendents of African slaves. They live in two major regions, in Andean region on Valle del Chota, and in the coast, in Esmeraldas province. It is possible that they came from Colombia and Africa, on slaves’ ships in 1533. There are 500,000 individuals around the country. They speak Spanish and preserve African traditions like music, dance, religion and ancestral practices. Blacks are ethnic group formed by Blacks Communities, characterised for an Afroecuadorian ascending, a same history, with similar cultural manifestations between themselves and a conscient identity. Actually, mostly of them live in rural regions and work in agricultural activities.

There is a general lack of information on Ecuadorian population from a genetic point of view and no previous publications on the distribution of Short Tandem Repeats is available. One million Ecuadorians have migrated over the last 10 years to the USA and Spain and, in these countries Ecuadorians are sometimes involved in criminal cases, or in other forensic identification issues. Adequate evaluation of the DNA forensic evidence need of proper databases on STR polymorphisms distribution.

In this paper, we report the allele frequency distribution of several STR loci that have proven to be extremely useful for forensic casework, human identification and population genetics in a population sample of Amerindian Kichwas (Quichuas) and Blacks (afroamericans) from Ecuador.

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References

- [1] F. González-Andrade, D. Sánchez, B. Martínez-Jarreta, Evaluation of 1495 cases of disputed paternity in Ecuador (South America) resolved with STR-PCR polymorphisms, in: E. Baccino (Ed.), Proceedings of International Association of Forensic Sciences, Monduzzi Ed., 2002, pp. 225–230.
- [2] Promega Corporation, Gene Print™ STR Systems for silver stain detection, in: Technical Manual, 1998 (TMD no. 004).
- [3] International Society for Forensic Haemogenetics, Recommendations of the DNA Commission of the International Society for Forensic Haemogenetics relating to the use of PCR-based polymorphisms, *Forensic Sci. Int.* 55 (1) (1992) 1–3.
- [4] W. Bär, B. Brinkmann, B. Budowle, A. Carracedo, P. Gill, P. Lincoln, W. Mayr, B. Olaisen, DNA recommendations. Further report of the DNA Commission of the ISFH regarding the use of short tandem repeat systems, *Forensic Sci. Int.* 87 (3) (1997) 181–184.
- [5] F. González-Andrade, Q. Sánchez, B. Martínez-Jarreta, Genetic profile of the Ecuadorian Mestizo population by using the Power-Plex 16 system kit, *Forensic Sci. Int.* 135 (1) (2003) 64–66.
- [6] F. González-Andrade, D. Sánchez, B. Martínez-Jarreta, Population Genetic of 12 STR loci in a sample of Mestizos from Ecuador (South – America), *J. Forensic Sci.* 48 (2) (2003) 453–454.
- [7] M. Gené, P. Moreno, N. Borrego, E. Piqué, A. Xifró, M. Fuentes, et al. Population study of Aymara Amerindians for the PCR-DNA polymorphisms HUMTH01, HUMVWA31A, D3S1358, D8S1179, D18S51, D19S253, YNZ22 and HLA-DQ α , *Int. J. Legal Med.* 113 (2000) 126–128.
- [8] M. Gené, M. Fuentes, E. Huget, E. Piqué, F. Bert, A. Corella, P. Moreno, Quechua Amerindian Population Characterised by HLA-DQ α , YNZ22, 3’APOB, HUMTH01 and HUMVW31A polymorphisms, *J. Forensic Sci.* 43 (23) (1998) 403–405.
- [9] A. Sala, G. Penacino, D. Corach, Comparison of allele frequencies of eight STR loci from Argentinian Amerindian an European population, *Hum. Biol.* 70 (5) (1998) 937–947.

- [10] H. Rangel-Villalobos, F. Rivas, L. Sandoval, B. Ibarra, et al. Genetic variation among four by Mexican populations (Huichol, Purepecha, Tarahumara and Mestizo) revealed by two VNTRs and four STRs, *Hum. Biol.* 72 (6) (2000) 983–995.
- [11] C.A. Scherzinger, J.L. Hintz, B.J. Peck, M.S. Adamowicz, M.T. Bourke, H.M. Coyle, C. Ladd, N.C. Yang, B. Budowle, H.C. Lee, Allele frequencies for the CODIS core STR loci in Connecticut populations, *J. Forensic Sci.* 45 (4) (2000) 938–940.
- [12] K. Balamurugan, B. Budowle, M.A. Tahir, Allele frequencies for nine STR loci in African American and Caucasian populations from Marion County, Indiana, USA, *J. Forensic Sci.* 45 (May (3)) (2000) 744–746.
- [13] B. Budowle, T.R. Moretti, A.L. Baumstark, D.A. Defenbaugh, K.M. Keys, Population data on the thirteen CODIS core short tandem repeat loci in African Americans, U.S. Caucasians, Hispanics, Bahamians, Jamaicans, and Trinidadians, *J. Forensic Sci.* 44 (November (6)) (1999) 1277–1286.
- [14] M.L. Bravo, M.A. Moreno, J.J. Builes, A. Salas, M.V. Lareu, A. Carracedo, Autosomal STR genetic variation in negroid Choco and Bogota populations, *Int. J. Legal Med.* 115 (October (2)) (2001) 102–104.
- [15] J.J. Yunis, O. Garcia, A. Baena, G. Arboleda, I. Uriarte, E. Yunis, Population frequency for the short tandem repeat loci D18S849, D3S1744, and D12S1090 in Caucasian-Mestizo and African descent populations of Colombia, *J. Forensic Sci.* 45 (March (2)) (2000) 429–431.
- [16] P. Lincoln, A. Carracedo, Publication of population data of human polymorphisms, *Forensic Sci. Int.* 110 (1) (2000) 3–5.