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Sex-Specific Genetic Admixture of Mestizos, Amerindian Kichwas, and Afro-Ecuadorans from Ecuador

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Abstract Three main ethnic groups live in the South American country of Ecuador: Mestizos, Amerindian natives, and African-derived populations, or Afro-Ecuadorans. Mestizos and Afro-Ecuadorans can be considered trihybrid populations containing genes originating in the Americas, Europe, and Africa, as is the case with equivalent populations in other Latin American countries. The proportion and the dynamics of the admixture process remain unknown. However, a certain sex asymmetry of the admixture process can be expected for historical reasons. We typed 11 Y-chromosome short tandem repeats (STRs) in these three ethnic groups to provide adequate allele and haplotype frequencies for forensic genetic purposes and to quantify admixture proportions in male lineages. In addition, a data set of 15 autosomal STRs in the same samples were reanalyzed for the same purpose. Contributions to Mestizo Y chromosomes were estimated to be 70% European, 28% Amerindian, and 2% African, whereas in autosomes the contributions were 19%, 73%, and 8%, respectively, which underlines the sexual asymmetry in mating, with Europeans contributing mostly males. European Y-chromosome haplotypes in Mestizos were similar to those in Spain. Moreover, about 10% of European Y chromosomes were found in the Amerindian Kichwa. As for Afro-Ecuadorans, their contributions to the male line are 44% African, 31% European, and 15% Native American; the last value is the highest percentage reported so far for an African-derived American group. Autosomal admixture was estimated as 56% African, 16% European, and 28% Amerindian.

Three main ethnic groups live in Ecuador: Mestizos, Amerindian natives, and Afro-Ecuadorans. Mestizos are the most numerous group, with 8 million (or 60% of the total population); they are the Spanish-speaking descendants of Europeans (mostly Spanish) and Amerindian natives. The proportion and dynamics of the processes that caused this admixture of populations remain unknown.

A number of different native Amerindian populations retain their culture, language, and distinct identity in Ecuador. Of these the most numerous by far are

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the Kichwa (often spelled Quichua), which number 3 million. The Kichwa language is the result of the absorption of local populations into the former Inca empire (the related but different language spoken by the descendants of the Inca in the core Inca regions of Peru and Bolivia is called Quechua). The Kichwa live mostly in the Andes highlands, but some are found in the Amazonian region (Moya 2000; Vásquez and Saltos 2003). The cultural and dialectal variation between the highlands and the plain and within the highlands itself is considerable. Finally, half a million Ecuadorans descend from African slaves and retain distinct phenotypic features as well as African cultural traits, such as music, dance, and religion. They live in rural areas in two separate provinces, in the Valle del Chota (in the Andes) and in the coastal Esmeraldas province (Moya 2000; Vásquez and Saltos 2003). The extent to which they have absorbed European and native Amerindian gene contributions remains uncharacterized.

We have typed 11 Y-chromosome short tandem repeats (STRs) in these three ethnic groups with a twofold purpose: to provide adequate allele and haplotype frequencies for forensic genetic purposes and to characterize the three groups genetically. Significant genetic differences are expected among Kichwa, Mestizos, and Afro-Ecuadorans, and, accordingly, separate population databases should be used in forensic casework. We have typed the standardized Y-chromosome STRs that are considered best and that are currently most widely used in forensic practice worldwide so that our results can be compared with data from other populations.

Mestizos and Afro-Ecuadorans can be considered trihybrid populations containing genes originating in the Americas, Europe, and Africa in various proportions, as is the case with equivalent populations in other Latin American countries. We aim to quantify these proportions and to ascertain the sex asymmetry of the admixture process by comparing Y-chromosome markers with autosomal markers. Y-chromosome genetic variation is particularly deeply partitioned among populations and among continental groups, which enables precise identification of the origin of each Y chromosome and makes Y-chromosome STRs a good tool for admixture quantification. However, Y chromosomes convey only the male side of the story, and for this reason we have reanalyzed a published data set of 15 forensic autosomal STRs in the same populations (González-Andrade et al. 2003, 2005; González-Andrade and Sánchez 2004).

Materials and Methods

Population Sample. Whole blood was obtained in vacutainer tubes containing EDTA by venipuncture from healthy unrelated Kichwas, Mestizos, and Afro-Ecuadoran populations, of both sexes, born and living in Ecuador. Samples from Kichwas and Afro-Ecuadorans were obtained directly in their communities. Samples of Mestizos were taken from the paternity test bank of our laboratory. All the samples were collected after obtaining informed written consent, and the study was approved by the Bioethics Committee of our hospital. We selected the individuals using criteria such as skin color, surnames, town of origin, and language.

DNA Extraction. DNA was extracted using the Wizard Genomic DNA Purification Kit System (Promega, Foster City, California, 1998), and quantity was estimated by ultraviolet absorbance (Gene Quant Calculator, Pharmacia, Uppsala, Sweden).

PCR. Amplification was performed in a Techne Thermal Cycler, model Genius (Techne, New York City), following the manufacturer's recommendations.

Typing. The 11 Y-chromosome STRs in the Power Plex Y kit were typed with an ABI Prism 310 automated sequencer. Fragment size and allele designation of different loci were determined by comparison with allelic ladders distributed with the kit. The recommendations of the DNA Commission of the International Society for Forensic Haemogenetics for analysis of STR systems were followed (Bär et al. 1997; International Society for Forensic Haemogenetics 1992). We also used the experience of our team (Bell et al. 2000; Martínez-Jarreta 1999).

Quality Control. Our laboratory participated in proficiency testing provided by the GEP-ISFG Working Group (International Society for Forensic Genetics, <http://www.gep-isfg.org>).

Data Analyses. Number of different haplotypes, haplotype diversity, pairwise haplotype differences, and allele size variance in Y-chromosome STRs were computed with Arlequin 2.000 (Schneider et al. 2000). Median-joining networks (Bandelt et al. 1999) were produced with Network 4.1.0.8 (available at <http://www.fluxus-engineering.com>). STRs were given weights that were inversely proportional to their allele size variances. Admixture proportions in autosomal STRs were computed with Admix 2.0 (Dupanloup and Bertorelle 2001).

Results and Discussion

Y-Chromosome STRs

Within-Population Diversity. We typed *DYS19*, *DYS389I*, *DYS389II*, *DYS390*, *DYS391*, *DYS392*, *DYS393*, *DYS385*, *DYS437*, *DYS438*, and *DYS439* Y-chromosome STRs in 94 Afro-Ecuadorans, 102 Kichwa, and 102 Mestizos, all from Ecuador. Allele frequencies can be found in Appendixes 1–3, phenotype frequencies at the duplicated *DYS385* locus in Appendix 4, and haplotype frequencies in Appendix 5. General descriptors of intrapopulation genetic diversity can be found in Table 1. Haplotype diversity is high and quite close to 1 in all three populations; it should be noted that in haploid systems such as mtDNA and the Y chromosome this parameter is numerically identical to a priori forensic information parameters, such as the power of discrimination or the power of exclusion in paternity cases. Therefore this 11-locus set has ample power to discriminate unrelated male individuals in all three populations and can be used in situations such as sex crimes, where it is most appropriate.

Mestizos and Afro-Ecuadorans show slightly (and nonsignificantly) higher diversities, as measured by the average number of loci showing different alleles in

Table 1. General Descriptors of Intrapopulation Genetic Diversity in the Study Populations

Population	N^a	k^b	Haplotype Diversity	π^c	V^d
Kichwa	102	91	0.9977 \pm 0.0015	7.12 \pm 3.37	1.14 \pm 1.14
Mestizos	102	99	0.9994 \pm 0.0015	7.64 \pm 3.59	1.21 \pm 1.06
Afro-Ecuadorans	94	89	0.9989 \pm 0.0018	7.79 \pm 3.66	1.41 \pm 1.20

- a. Sample size.
 b. Number of different haplotypes.
 c. Average pairwise differences between haplotypes.
 d. Average repeat size variance.

a random chromosome pair and the average variance of the allele size. This trend toward higher diversity is expected of admixed populations.

Haplotype Sharing Within Ecuador. Seven different haplotypes were shared between Kichwas and Mestizos, one between Mestizos and Afro-Ecuadorans, and one between Kichwas, Afro-Ecuadorans, and Mestizos. This last shared haplotype happens to be the most frequent haplotype in Europeans, in particular, the Spanish. The total number of different haplotypes is 271.

Minimum Haplotype Sharing with Global Populations. Minimum haplotypes (i.e., *DYS19-389I-389II-390-391-392-393-385*) have been defined for forensic practice, and such haplotypes from global populations are stored in the YHRD (Y-Chromosome Haplotype Reference Database; available at <http://www.yhrd.org>). Minimum haplotypes in Ecuadoran populations were searched for in the YHRD (release 16); this release contained minimum haplotypes for 32,196 chromosomes from 271 world populations. Perfect matches were counted; for haplotypes without matches, one-step neighbors were considered (i.e., haplotypes that were different by only one repeat at one locus). Results are displayed in Table 2. No haplotype showed matches to more than one continental group.

A match or a one-step neighbor could not be found for more than half the Kichwa haplotypes. It is also remarkable that only five matches were found with other native American populations, but 26 haplotypes had one-step neighbors. These two facts can be explained by two nonmutually exclusive phenomena: the higher interpopulation differentiation among Amerindians (Salzano 2002) and the underrepresentation of these populations in the database (6 populations, compared to 201 European populations). This increases the probability of no-match chromosomes (which, a priori, could have any population origin) being of native American origin.

Overall, the number of matches with Europe is striking. This method is more sensitive to European admixture, though, because Europe (and Spain in particular) is overrepresented in the YHRD. However, perfect or near-perfect matches in Europe were found for 14% of Kichwa Y chromosomes, 67% of Mestizo Y chromosomes, and 27% of Afro-Ecuadoran Y chromosomes.

Table 2. Minimum Haplotype Y-Chromosome STR Matches for Ecuadoran Populations in the Y-Chromosome Haplotype Reference Database (Release 16)

Match ^a	Kichwa	Mestizos	Afro-Ecuadorans
American matches	5 (4.9%)	1 (1.0%)	0
1-s n. Americas	26 (25.5%)	10 (9.8%)	2 (2.1%)
European matches	12 (11.8%)	57 (55.9%)	18 (19.1%)
1-s n. Europe	2 (2.0%)	11 (10.8%)	7 (7.4%)
African matches	1 (1.0%)	1 (1.0%)	29 (30.9%)
1-s n. Africa	0	1 (1.0%)	7 (7.4%)
Central Asian matches	1 (1.0%)	0	0
1-s n. Central Asia	1 (1.0%)	0	0
Pacific matches	2 (2.0%)	0	0
East Asian matches	0	1 (1.0%)	0
1-s n. East Asia	0	1 (1.0%)	0
1-s n. South Asia	0	0	1 (1.1%)
No matches	52 (51.0%)	19 (18.6%)	30 (31.9%)

a. "1-s n." stands for one-step neighbors, that is, haplotypes without any perfect match but with chromosomes in the database differing by only one repeat at one locus. "Americans" include native American and Hispanic populations; "Africa" includes Africans and populations of African descent living in the Americas or in Europe.

Admixture Estimates. The proportion of Y chromosomes of native American, European, and African origin in each population was roughly estimated by trying to predict the haplogroup of each chromosome, because most haplogroups are geographically restricted (Jobling and Tyler-Smith 2003). This task was performed by using data sets in which both biallelic markers and STRs had been typed (Bortolini et al. 2003; Zegura et al. 2004; Beleza et al. 2005, 2006) and takes advantage of the fact that STR variation in the Y chromosome is deeply partitioned by haplogroup background (Bosch et al. 1999). A chromosome was allocated to a haplogroup when a perfect or near-perfect match was found for a chromosome with a known haplogroup or when a diagnostic allele or subhaplotype was present (such as 14 or larger alleles at *DYS392* combined with *DYS19*13* for haplogroup Q, *DYS19*15-DYS390*21* for haplogroup E3a, or *DYS392*13-DYS385*11,14* for haplogroup R1b). Because we are interested in the broad origins of each chromosome, rather than in a fine phylogeography, and because this method is prone to error, we assigned each chromosome to one of the following categories: Q (native American), R1b (European), other European (includes haplogroups E3b, G, I, J, R1a), and E3a (African). The frequencies of each class in each population can be found in Table 3, and class assignments for each haplotype are given in Appendix 5.

It is worth noting that the Kichwa contain about 10% of Y chromosomes of putative European origin. However, this value is not exceptional in South America; European origin accounts for 11% of Y chromosomes in Guarani and Ingano groups, 14% in the Kaingang, and 26% in the Wayuu (Bortolini et al. 2003). The proportion of putative European lineages is as high as 70% in Mestizos (plus an additional 2%

Table 3. Inferred Haplogroup Frequencies in Ecuadoran Populations by Comparison of STR Haplotypes with Data Sets in Which Both STRs and Haplogroup-Defining Biallelic Polymorphisms Have Been Typed

Haplogroup	Kichwa	Mestizos	Afro-Ecuadorans
Q	78 (76.5%) ^a	23 (22.5%)	14 (14.9%)
R1b	7 (6.9%)	48 (47.1%)	11 (11.7%)
Other European	4 (3.9%)	25 (24.5%)	18 (19.1%)
E3a	0	2 (2.0%)	41 (43.6%)
Unknown	13 (12.7%)	4 (3.9%)	10 (10.6%)

a. Includes two chromosomes that carry haplotypes found in C3b chromosomes, also of native American origin.

of African origin). The significance of this figure is not immediately apparent because, to the best of our knowledge, no quantitative estimates of admixture proportions have been published, although Y-chromosome STR data sets have been published for comparable urban Mestizo populations. However, in the admixture of Kichwa, mating between Mestizos and Kichwas should be considered the most important source of European Y chromosomes.

Afro-Ecuadorans are also highly admixed. The origins of their Y-chromosome lineages can be estimated as 44% African, 31% European, and 15% native American. In this case comparable figures do exist: In different Afro-Brazilian communities, paternal contributions range from 47% to 77% for Africans, 23% to 48% for Europeans, and 0% to 4% for native Americans (Abe-Sandes et al. 2004). Compared to Brazil, the native American contribution to Afro-Ecuadorans seems larger, probably because of the native American population in the Andes, which is historically much denser than in the Amazon and Atlantic regions. The relative proportion of haplogroup R1b versus other European haplogroups is different between Mestizos and Afro-Ecuadorans ($\chi^2 = 6.59$, $p = 0.01$). The proportion in Mestizos is similar to that in Spaniards; taking into account only the putatively European-derived chromosomes, the frequency of haplogroup R1b is 65.8%, whereas it is 59.6% in Spain (Flores et al. 2004). In Afro-Ecuadorans, it is 37.9%.

Native American and African Lineages in Detail. Median-joining networks were produced for the putative Q and E3a chromosomes. No discernible structure is found for Q chromosomes (Figure 1) in the network, which would suggest the presence of sublineages such as Q-M19 (Bortolini et al. 2003), whereas in the E3a network (Figure 2), two sublineages seem apparent. By comparison to Beleza et al. (2005), the bottom half of the network seems to apply to E3a7 chromosomes, and the top part of the network may belong to the E3a* paralog. The frequencies of these two haplogroups in Afro-Ecuadorans are estimated to be 20.2% and 24.5%, respectively.

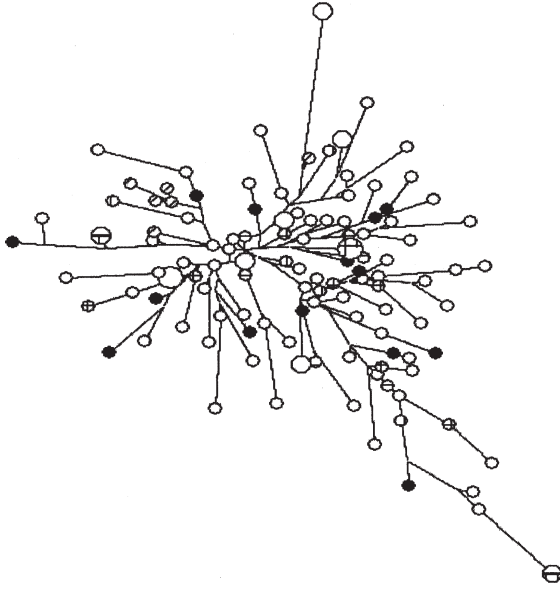


Figure 1. Median joining network of putative Q chromosomes. Open circles, Kichwa chromosomes; cross hatching, Mestizos; filled circles, Afro-Ecuadorans.

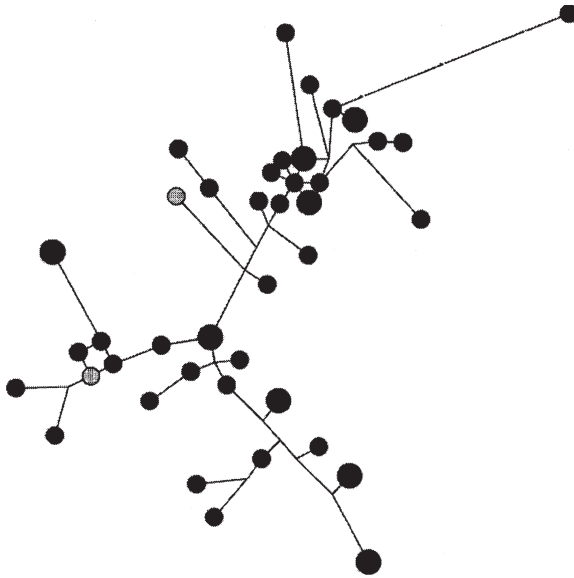


Figure 2. Median joining network of putative E3a chromosomes. Open circles, Kichwa chromosomes; cross hatching, Mestizos; filled circles, Afro-Ecuadorans.

Table 4. Average Intrapopulation Diversity Parameters for 15 Autosomal STR Loci

<i>Population</i>	$2N^a$	k^b	H^c	<i>Reference</i>
Kichwa	230	8.87 ± 3.08	0.751 ± 0.088	González-Andrade et al. (2003)
Mestizos	634	10.47 ± 4.28	0.781 ± 0.080	González-Andrade et al. (2005); González-Andrade and Sánchez (2004)
Afro-Ecuadorans	208	10.13 ± 3.44	0.808 ± 0.064	González-Andrade et al. (2005); González-Andrade and Sánchez (2004)
Spanish	408	9.87 ± 3.72	0.794 ± 0.067	Paredes et al. (2003)
Guineans	268	10.40 ± 3.62	0.802 ± 0.059	Alves et al. (2005)

a. Sample size in number of chromosomes.

b. Average number of alleles.

c. Mean expected heterozygosity.

Autosomal STRs

Intrapopulation Diversity. Fifteen STRs contained in the PowerPlex 16 kit were typed in 115 Kichwa, 317 Mestizo, and 104 Afro-Ecuadoran individuals. Allele frequencies were reported by González-Andrade et al. (2003) (Mestizos), González-Andrade et al. (2005) (Afro-Ecuadorans), and González-Andrade and Sánchez (2004) (Kichwas). Mean number of alleles and genetic diversity can be found in Table 4. Besides the Ecuadoran populations, data from two possible source populations were included: allele frequencies from a metropolitan population from Barcelona (including individuals born all over Spain; Paredes et al. 2003) and those from Equatorial Guinea (Alves et al. 2005), a former Spanish colony and slave trade post in Africa. The Kichwa showed the lowest diversity, in accordance with the low variability reported for many Amerindian groups. Diversity in Mestizos and Afro-Ecuadorans is greater, also according to expectations for admixed populations. However, of all pairwise comparisons, only allele number and haplotype diversity are lower in the Kichwa than in Mestizos (Wilcoxon test, $p = 0.002$ and $p = 0.001$, respectively).

Genetic Distances. F_{ST} genetic distances were computed among Ecuadoran and external populations (Table 5). F_{ST} distances were used rather than any STR-specific distance measure, given that 7 of the 15 loci showed imperfect repeats that cannot be accommodated by the simple stepwise mutation model on which distances such as R_{ST} are based (Slatkin 1995). Genetic distances in general are short, probably because of frequent stepwise mutations that tend to homogenize allele-frequency distributions. This is a general trend for STRs, and more so for forensic STRs, in which interpopulation homogeneity is a desirable property. Mestizos display a short distance from the Kichwa, but their distance from the Spanish is clearly shorter than the distance between Kichwa and Spanish. This is also the case for their respective distance to Guineans. This is consistent with a triple genetic ori-

Table 5. F_{ST} Genetic Distances Based on 15 Autosomal STR Loci

	<i>Kichwa</i>	<i>Mestizos</i>	<i>Afro-Ecuadorans</i>	<i>Spanish</i>	<i>Guineans</i>
Kichwa	0				
Mestizos	0.0075	0			
Afro-Ecuadorans	0.0278	0.0137	0		
Spanish	0.0437	0.0204	0.0163	0	
Guineans	0.0651	0.0417	0.0096	0.0274	0

gin for Mestizos: Amerindian, European, and African, as demonstrated by Y-chromosome STRs.

Afro-Ecuadorans are closest to Guineans but are closer to Kichwa and Spanish than Guineans are. With different admixture proportions the triple-source model proposed for Mestizos also applies to Afro-Ecuadorans. See Figures 3, 4, and 5.

Genetic Admixture. Genetic admixture was quantified as suggested by Dupanloup and Bertorelle (2001). These investigators derived a linear model that can accommodate any number of parental populations, as well as mutation rate, molecular distance among alleles, and time elapsed since admixture. Admixture proportions

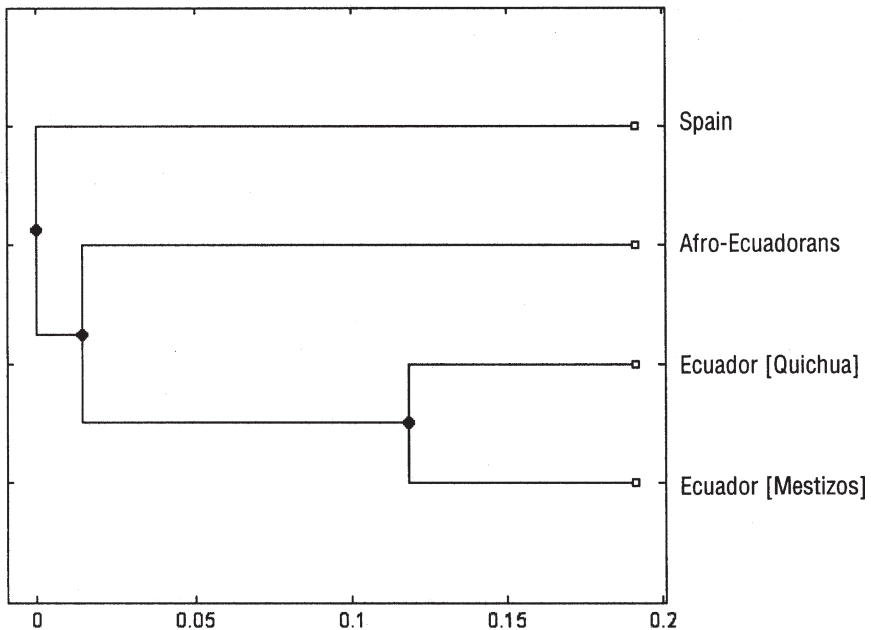


Figure 3. Dendrogram and genetic distances between Mestizos, Kichwas and Afro-Ecuadorans calculated with minimal Y-chromosome haplotypes.

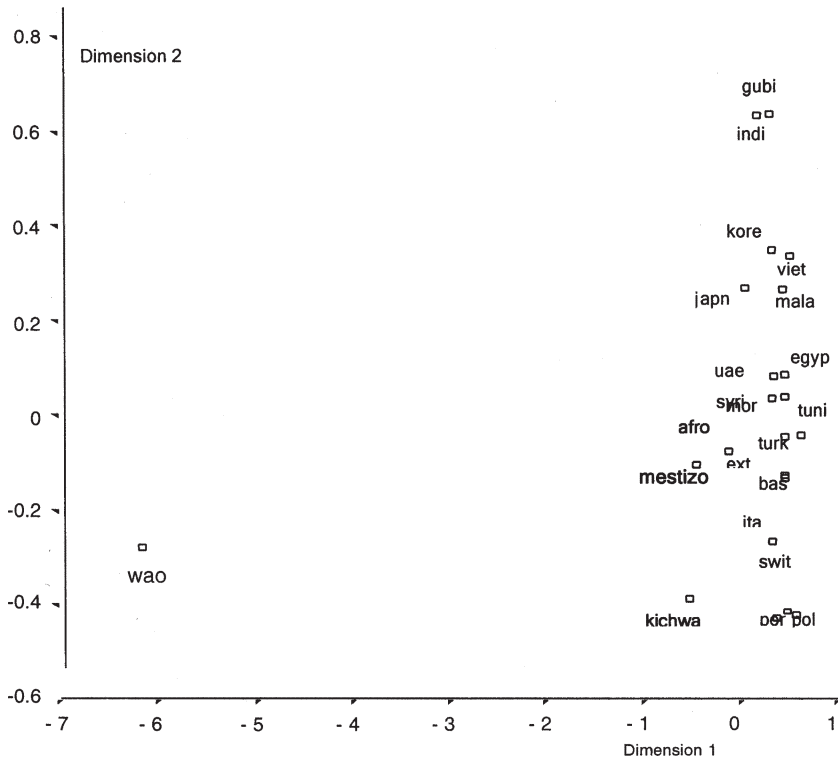


Figure 4. Genetic distances using autosomal STRs. European populations: bas, Basque Country; ext, Extremadura; pol, Poland; por, Portugal; ita, Italy; swit, Switzerland. North African populations: mor, Morocco; tuni, Tunisia; egypt, Egypt. Sub-Saharan African population: gubi, Guinea Bissau. Middle Eastern populations: turk, Turkey; syri, Syria; uae, United Arab Emirates; indi, India. Asian populations: kore, Korea; japn, Japan; viet, Vietnam; mala, Malaysia. American populations: kichwa, Kichwas; wao, Waoranis. Hybrid populations: mestizo, Mestizos; afro, Afro-Ecuadorans. We considered the following STRs: *D3S1358*, *D5S818*, *D7S820*, *D8S1179*, *D13S317*, *D18S51*, *D21S11*, *FGA* (FIBRA), *VWA31*, *CSF1PO*, *D16S539*, *TH01*, and *TPOX*. We used a distance coefficient. In multidimensional scaling: stress = 0.06869, variance explained = 0.99352.

and their standard deviations were estimated from 100,000 bootstrap iterations. By using Kichwa, Spanish, and Guineans as source populations, admixture proportions in Mestizos were 0.730 ± 0.243 Amerindian, 0.193 ± 0.280 European, and 0.078 ± 0.077 African. Large standard deviations are a reflection of short genetic distances among the source populations. These results contrast sharply with those obtained for Y-chromosome STRs but can be reconciled by postulating considerable sex asymmetry in matings, with most mixed matings involving European men and Amerindian women. However, such extreme differences could not arise if Mestizos

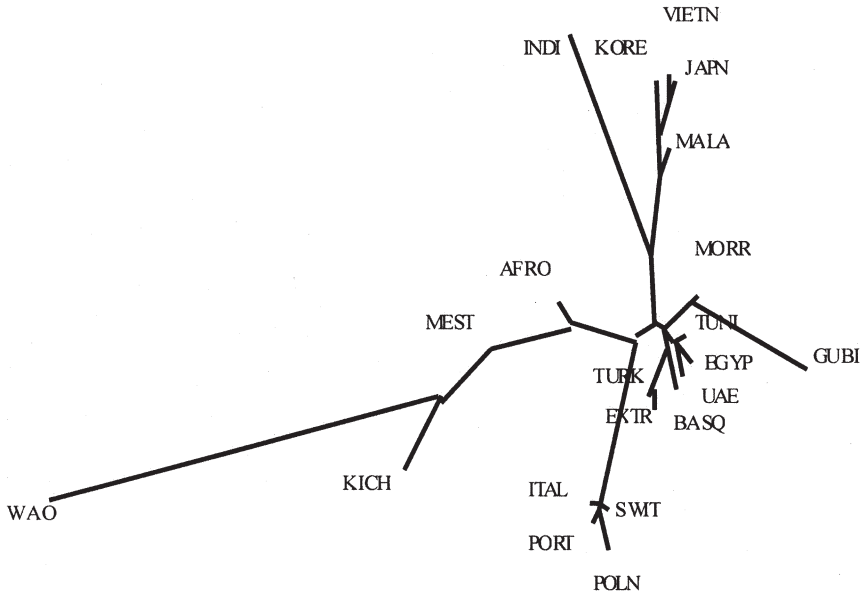


Figure 5. In the neighbor-joining dendrogram obtained from the same distance matrix, populations are more separate. India and Guinea Bissau are clearly separated, and India lies between Asia and Africa. Mestizos from Ecuador and Afro-Ecuadorans are between native populations and the rest of the world. Like other Amerindian groups, native populations such as Ecuadoran Kichwas show a lower genetic derivative effect or a greater mixture with Europeans.

were created in a single generation by the mating of Amerindian women and European men. That is, a mixture of genes contributed by 70% European men and 30% Amerindian men and only Amerindian women would result in the proportions seen for the Y chromosome, but in autosomes admixture proportions would be 35% European and 65% Amerindian. Subsequent asymmetry in matings between Mestizos and Amerindians, again with mostly men contributing to the first group and women to the second, needs to be referred to in order to explain the results. This significant sex asymmetry has also been reported for several other Latin American populations (Seielstad 2000).

Other urban Mestizo populations have been studied for other autosomal markers; a survey of the literature is presented in Table 6. It can be seen that Ecuadoran Mestizos represent one of the largest Amerindian contributions among the populations studied, although, given the various types of markers and levels of resolution used in the different publications, such a comparison should be made with caution. Admixture proportions for Afro-Ecuadorans were 0.564 ± 0.107 African, 0.279 ± 0.328 Amerindian, and 0.158 ± 0.367 European. As also seen from the Y chromosome, the Amerindian contribution to Afro-Ecuadorans is remarkable. Asymmetry

Table 6. Admixture Proportions for Various Urban Admixed American Populations Based on Autosomal Loci

<i>Population</i>	<i>Type</i>	<i>Reference</i>	<i>Native American</i>	<i>European</i>	<i>African</i>
Mestizos, Ecuador	General urban	This study	73	19.3	7.8
Afro-Ecuadorans	African American	This study	27.9	15.8	56.4
La Plata (Argentina)	General urban	Martinez-Marignac et al. (2004)	25.9	67.6	6.5
Churuguara (Venezuela)	General urban	Loyo et al. (2004)	19.9	52.5	27.6
Santiago (Chile)	Low status	Cifuentes et al. (2004)	34.7	65.3	NA
Santiago (Chile)	High status	Cifuentes et al. (2004)	20.9	79.1	NA
Puerto Rico	Living in New York City	Bonilla et al. (2004b)	17.6	53.3	29.1
San Luis Valley (USA)	Hispanics	Bonilla et al. (2004a)	34.1	62.7	3.2
Costa da Lagoa, Santa Catarina Island (Brazil)	General urban	De Souza et al. (2003)	7.7	75	17.3
Sao Joao do Rio Vermelho, Catarina Island (Brazil)	General urban	De Souza et al. (2003)	18.7	53.3	28
California	Hispanics	Bertoni et al. (2003)	43	46.3	10.7
California	Hispanics	Bertoni et al. (2003)	38.2	48.4	13.4
Nevada	Hispanics	Bertoni et al. (2003)	57.9	34	8.1
Southwestern United States	Hispanics	Bertoni et al. (2003)	35.6	64.4	0
Florida	Hispanics	Bertoni et al. (2003)	19.9	72	8.1
New Jersey	Hispanics	Bertoni et al. (2003)	9.1	84.5	6.4
Pennsylvania	Hispanics	Bertoni et al. (2003)	0.2	82.9	16.9
Southwestern United States	Hispanics	Bertoni et al. (2003)	0	93.3	6.7
Virginia	Hispanics	Bertoni et al. (2003)	21.3	63.8	14.9

NA, not available

is lower than in Mestizos, but again European men seem to have contributed disproportionately to admixed matings (probably mostly between them and Amerindians). Although it is well established that Hispanics generally have mixed native American, African, and European ancestry (Lisker and Babinsky 1986; Lisker et al. 1990; Mesa et al. 2000; Bedoya et al. 2006), the dynamics of the admixture of these and other different populations within South America is heterogeneous and poorly documented.

Conclusions

We have confirmed and quantified that Mestizos and Afro-Ecuadorans are trihybrid populations with various proportions of Amerindian, European, and African contributions. As seen from the Y chromosome, the male European contribution (clearly Spanish in the case of Mestizos) was much larger than when admixture estimates were computed from autosomal STRs. Other types of markers would enable the present results to be refined. For instance, Y-chromosome biallelic markers would enable the geographic attribution of Y chromosomes to be confirmed, and, in particular, would no doubt shed some light on the origin of European Y chromosomes in Afro-Ecuadorans. Autosomal ancestry informative markers (AIMs; Shriver et al. 2003) would yield much more precise autosomal admixture estimates. And, last but not least, mtDNA sequences and haplogroups would provide the female side of history. However, our study provides a reasonably detailed sketch of the composition of the main ethnic groups of Ecuador and contributes to the understanding of their diverse heritage.

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Appendix 1. Allele Frequencies in the Kichwa^a

Allele	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS437	DYS438	DYS439
8									0.010	
9					0.108				0.049	0.029
10					0.618				0.098	
11					0.265				0.706	0.314
12	0.029	0.186			0.010	0.069	0.010		0.137	0.520
13	0.608	0.608				0.029	0.010	0.010		0.127
14	0.216	0.206				0.186	0.725	0.010		0.010
15	0.098					0.529	0.216	0.824		0.824
16	0.039					0.137	0.039	0.127		0.127
17						0.020		0.039		0.039
18	0.010					0.010				
21				0.010		0.020				
22				0.039						
23				0.206						
24				0.578						
25				0.167						
28			0.049							
29			0.245							
30			0.353							
31			0.284							
32			0.069							

a. Sample size $N = 102$ for all loci.

Appendix 2. Allele Frequencies in Mestizos^a

Allele	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS437	DYS438	DYS439
9					0.029				0.127	0.010
10					0.539	0.020			0.216	0.020
11					0.373	0.245	0.010		0.196	0.294
12	0.020	0.157			0.049	0.020	0.118		0.451	0.490
13	0.324	0.608			0.010	0.471	0.716	0.069		0.167
14	0.451	0.225				0.206	0.137	0.578		0.010
15	0.167					0.039	0.020	0.314		0.010
16	0.039							0.039		
18									0.010	
21				0.020						
22				0.059						
23				0.216						
24				0.608						
25				0.098						
27			0.020							
28			0.078							
29			0.382							
30			0.363							
31			0.108							
32			0.049							

a. Sample size N = 102 for all loci.

Appendix 4. Phenotype Frequencies at the Duplicated *DYS385* Locus

<i>Phenotype</i>	<i>Kichwa (N = 102)</i>	<i>Mestizos (N = 102)</i>	<i>Afro-Ecuadorans (N = 94)</i>
9,21	0.020		
10,11			0.011
10,17		0.010	
11,13		0.029	
11,14	0.049	0.304	0.074
11,15		0.029	0.032
11,16			0.011
11,18	0.010		0.011
12,12	0.020		
12,13		0.010	
12,14	0.029	0.078	0.011
12,15	0.010	0.029	0.021
12,16	0.010		0.032
12,17	0.059	0.049	
12,18			0.011
12,19	0.010	0.010	
12,20		0.020	
13,14		0.020	0.032
13,15	0.020	0.020	0.011
13,16		0.020	0.010
13,17	0.020	0.049	
13,18		0.029	0.021
13,19	0.039	0.010	0.011
13,20	0.020	0.010	
13,21		0.010	
14,14	0.098	0.010	0.011
14,15	0.078	0.010	0.021
14,16	0.059	0.020	0.032
14,17	0.039	0.029	0.053
14,18	0.059	0.020	0.011
14,19	0.010	0.020	0.011
14,20	0.029		
15,15	0.069		0.011
15,16	0.049	0.039	0.085
15,17	0.069	0.029	0.043
15,18	0.029	0.010	0.032
15,19	0.010	0.010	0.021
15,20			0.021
16,16	0.010	0.020	
16,17	0.010	0.020	0.128
16,18	0.020		0.053
16,19	0.010		
16,22			0.011
17,18		0.020	0.096
17,19		0.010	0.043
17,20			0.011
18,19		0.010	
19,19	0.039		
19,20			0.011

Appendix 5. Y-Chromosome STR Haplotypes in Ecuadoran Populations

Haplotype	Absolute Haplotype Frequency														Inferred Haplogroup ^a	
	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS385a	DYS385b	DYS437	DYS438	DYS439	Kichwa	Mestizo		African
K28	12	13	29	25	9	13	14	15	15	14	11	11	1			Q
M83	12	13	30	23	10	14	13	15	17	13	10	12	1	2		Q
K57	12	13	30	24	10	14	14	12	14	14	11	12	1			Q
K67	13	12	28	24	10	14	13	14	16	14	11	12	1			Q
K1	13	12	28	24	10	14	14	15	15	14	9	11	1			Q
K91	13	12	29	23	9	14	14	14	18	14	11	11	1			Q
K24	13	12	29	23	9	15	13	15	16	14	12	11	1			Q
N47	13	12	29	23	10	15	13	15	16	14	12	12			1	Q
M31	13	12	29	24	10	11	13	17	18	14	10	10		1		OE
N70	13	12	29	24	10	14	13	13	18	13	11	13			1	Q
M67	13	12	29	25	10	11	13	17	18	14	10	11		1		OE
N50	13	12	29	25	10	14	13	14	17	14	11	12			1	Q
M28	13	12	30	24	10	11	14	15	18	15	10	11		1		OE
M90	13	12	30	24	10	14	13	14	18	14	11	13		1		Q
K20	13	12	30	24	10	14	14	12	17	14	11	13	1			Q
M88	13	12	30	24	10	14	14	12	17	14	12	12		1		Q
K88	13	12	30	24	11	14	14	16	18	14	11	12	1			Q
M101	13	12	30	25	10	10	13	18	19	14	9	10		1		OE
K8	13	12	30	25	10	14	13	14	17	14	11	11	1			Q
K21	13	12	31	24	10	13	13	16	18	14	11	13	1			Q
N67	13	12	31	24	10	14	13	13	19	14	12	12			1	Q
K35	13	12	31	24	10	15	13	15	16	14	12	11	1			Q
K64	13	13	29	23	10	14	13	15	15	15	11	11	1			Q
M84	13	13	29	23	10	14	15	14	17	14	9	12	1	1		Q
M63	13	13	29	24	10	13	12	14	15	14	11	12	1		1	Q
K59	13	13	29	24	10	13	13	14	14	14	11	12	1			Q
K16	13	13	29	24	10	14	13	14	15	14	11	12	1			Q
K83	13	13	29	24	10	14	13	15	16	14	11	12	2			Q
K54	13	13	29	24	10	14	14	14	17	15	11	12	1			Q
M82	13	13	29	24	10	15	13	15	16	14	11	12		1		A
M51	13	13	29	24	11	12	13	12	17	14	11	12		1		UA

M77	13	13	24	29	11	13	13	13	21	14	11	12	1	1	R1b
K58	13	13	25	29	10	14	15	14	16	14	11	12	1	1	Q
K95	13	13	25	29	11	14	14	14	15	14	11	12	1	1	Q
M8	13	13	23	30	10	11	13	16	17	14	10	12	1	1	OE
K26	13	13	30	30	10	14	13	15	15	14	11	12	1	1	Q
N18	13	13	23	30	10	14	14	12	16	14	11	11	1	1	Q
M1	13	13	23	30	10	14	14	14	14	14	10	12	1	1	Q
M15	13	13	23	30	10	15	13	13	17	14	11	9	1	1	Q
K66	13	13	30	30	10	15	13	15	17	14	11	12	1	1	Q
K46	13	13	23	30	11	14	13	14	16	14	11	12	1	1	Q
N11	13	13	23	30	11	14	13	14	17	14	11	12	1	1	Q
N79	13	13	24	30	9	11	13	13	14	14	10	10	1	1	OE
K25	13	13	30	30	10	11	13	14	14	14	11	12	1	1	Q
N4	13	13	24	30	10	11	13	16	17	14	10	11	1	1	OE
N65	13	13	24	30	10	11	13	16	18	14	10	12	1	1	OE
M41	13	13	24	30	10	11	14	13	17	14	10	13	1	1	OE
K6	13	13	24	30	10	12	13	13	17	14	11	12	1	1	UA
K65	13	13	24	30	10	13	13	14	14	14	11	12	1	1	Q
M97	13	13	24	30	10	14	11	15	17	14	11	12	1	1	Q
M47	13	13	24	30	10	14	13	13	20	14	11	11	1	1	Q
K7	13	13	24	30	10	14	13	14	18	14	11	11	1	1	Q
K61	13	13	24	30	10	14	13	15	15	14	11	12	1	1	Q
K12	13	13	24	30	10	14	13	16	16	14	11	12	1	1	Q
N61	13	13	24	30	10	14	13	16	16	14	11	11	1	1	Q
K42	13	13	24	30	10	15	13	14	15	14	11	13	1	1	Q
K15	13	13	24	30	10	15	14	14	18	14	12	14	1	1	Q
K9	13	13	24	30	10	17	13	14	14	14	11	12	1	1	Q
M18	13	13	24	30	11	13	13	12	14	15	12	11	1	1	R1b
K50	13	13	24	30	11	14	13	12	16	14	11	12	1	1	Q
M87	13	13	24	30	11	14	13	12	20	14	10	12	1	1	Q
K31	13	13	24	30	11	14	13	13	20	14	11	11	1	1	Q
N66	13	13	24	30	11	14	15	15	16	14	8	11	1	1	Q
M22	13	13	25	30	10	14	13	15	16	14	11	12	1	1	Q
K2	13	13	25	30	10	14	15	15	18	14	8	11	1	1	Q
K14	13	13	23	31	10	11	13	15	17	14	10	12	1	1	OE
K32	13	13	23	31	10	14	14	12	17	14	11	12	1	1	Q

Appendix 5. *continued*

Haplotype	Absolute Haplotype Frequency														Inferred Haplogroup ^b	
	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS385a	DYS385b	DYS437	DYS438	DYS439	Kichwa	Mestizo		African
K84	13	13	31	24	9	13	13	14	18	14	11	13	1			Q
M46	13	13	31	24	10	11	13	15	19	14	10	13		1		OE
K13	13	13	31	24	10	13	12	13	15	14	11	13	1			Q
K47	13	13	31	24	10	14	11	14	17	14	11	12	1			Q
M49	13	13	31	24	10	14	14	12	17	14	11	13		1		Q
K52	13	13	31	24	10	14	14	14	15	14	11	11	1			Q
M27	13	13	31	24	11	11	13	16	17	14	10	13		1		OE
K49	13	13	31	24	11	14	14	12	17	14	11	13	1			Q
K72	13	13	31	25	10	14	14	14	18	14	11	12	1			Q
K19	13	13	32	22	9	11	13	13	15	14	10	12	1			UA
M72	13	13	32	24	11	14	14	12	17	14	11	12		1		Q
K37	13	13	32	24	11	15	14	12	17	14	11	11	1			Q
K93	13	13	32	25	9	14	14	12	19	14	11	12	1			UA
M74	13	13	32	25	10	13	13	14	17	15	12	12		1		UA
N93	13	14	30	24	9	11	13	14	16	14	10	10			1	OE
K86	13	14	30	24	10	14	13	14	16	14	11	11	1			Q
K74	13	14	30	24	10	15	13	11	18	14	11	12	1			Q
M50	13	14	30	25	10	14	13	14	19	13	11	12		1		Q
K39	13	14	30	25	11	14	13	13	19	14	11	12	1			Q
M60	13	14	31	23	10	14	13	13	17	14	11	12		1		Q
K18	13	14	31	23	10	14	13	13	17	14	11	13	1			Q
M53	13	14	31	23	10	14	13	13	18	14	9	12		1		Q
K53	13	14	31	23	10	14	13	15	18	14	11	11	1			Q
K85	13	14	31	23	10	16	14	14	18	14	11	13	1			Q
K76	13	14	31	23	10	16	14	15	19	14	11	13	1			Q
N26	13	14	31	23	11	15	13	13	16	14	12	13			1	R1b
N13	13	14	31	24	10	11	13	16	18	14	10	11			1	OE
N56	13	14	31	24	10	13	13	11	14	15	12	12			1	R1b
M54	13	14	31	24	10	14	13	13	18	14	11	12		1		Q
M62	13	14	31	24	10	14	13	13	19	14	11	12		1		Q
K56	13	14	31	24	10	14	13	14	19	14	11	12	1			Q
K41	13	14	31	24	10	14	13	14	20	14	11	12	1			Q
M44	13	14	31	24	10	14	14	15	16	14	11	13		1		Q

K10	13	14	31	24	11	14	13	13	19	14	11	12	1	Q
N72	13	14	31	24	11	14	13	14	19	14	11	11	1	Q
K78	13	14	31	24	11	14	13	19	19	14	11	12	2	Q
M5	13	14	31	24	11	14	14	13	17	14	11	11	1	Q
K27	13	14	31	24	11	15	13	12	17	14	11	13	1	Q
N81	13	14	31	25	10	14	12	14	15	15	11	11	1	Q
K43	13	14	32	23	11	14	14	14	16	14	11	9	1	Q
K87	13	14	32	24	11	14	13	13	19	15	11	13	1	Q
M80	13	15	32	24	10	11	13	16	16	14	10	11	1	OE
M71	14	12	28	22	10	11	13	13	15	16	10	11	1	OE
K94	14	12	28	22	10	11	13	14	14	16	10	11	1	OE
K45	14	12	28	22	11	14	13	15	17	15	11	12	1	Q
N15	14	12	28	24	11	11	13	15	20	14	11	12	1	UA
M11	14	12	28	24	11	13	13	11	14	15	12	15	1	Rib
N23	14	12	28	25	11	11	13	14	17	15	11	11	1	UA
N37	14	12	28	25	11	13	13	14	15	15	12	12	1	Rib
K4	14	12	29	24	11	13	13	12	14	15	12	11	2	Rib
K44	14	12	31	24	10	15	13	15	15	14	12	12	1	Q
M76	14	13	28	24	11	13	13	11	14	15	12	11	1	Rib
M96	14	13	28	24	12	13	13	11	14	15	12	12	1	Rib
N80	14	13	28	24	13	13	13	11	14	15	12	12	1	Rib
M59	14	13	29	22	10	13	13	12	14	15	12	11	1	Rib
N89	14	13	29	22	11	13	12	11	14	15	12	13	1	Rib
M64	14	13	29	23	10	11	12	14	17	14	10	12	1	OE
N76	14	13	29	23	10	13	13	11	18	15	12	13	1	OE
M65	14	13	29	24	10	12	13	11	14	15	12	13	1	Rib
M98	14	13	29	24	10	13	13	11	13	15	12	11	1	Rib
M92	14	13	29	24	10	13	13	12	13	15	12	11	1	Rib
M17	14	13	29	24	10	13	13	12	14	14	12	11	1	Rib
M24	14	13	29	24	10	13	13	12	14	14	12	12	1	Rib
M69	14	13	29	24	10	13	13	12	14	15	12	12	1	Rib
K48	14	13	29	24	10	14	13	16	19	14	11	11	1	Q
M39	14	13	29	24	11	13	13	11	13	14	12	12	1	Rib
M33	14	13	29	24	11	13	13	11	14	14	12	11	1	Rib
M9	14	13	29	24	11	13	13	11	14	14	12	12	1	Rib
M34	14	13	29	24	11	13	13	11	14	15	10	13	1	Rib
M19	14	13	29	24	11	13	13	11	14	15	12	11	1	Rib

Appendix 5. *continued*

Haplotype	Absolute Haplotype Frequency													Inferred Haplogroup ^a		
	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS385a	DYS385b	DYS437	DYS438	DYS439	Kichwa		Mestizo	African
M55	14	13	29	24	11	13	13	11	14	15	12	12		1		R1b
K90	14	13	29	24	11	13	13	11	14	15	12	13	1			R1b
M25	14	13	29	24	11	13	13	11	14	15	12	14		1		R1b
M29	14	13	29	24	11	13	13	11	14	15	18	12		1		R1b
M13	14	13	29	24	11	13	13	11	15	15	12	13		1		R1b
M4	14	13	29	24	11	13	15	11	14	14	12	13		1		R1b
M32	14	13	29	24	11	14	13	11	14	14	12	12		2		R1b
M100	14	13	29	24	13	13	12	14	14	13	11	12		1		R1b
K77	14	13	29	25	10	15	14	14	20	14	11	12	2			Q
M21	14	13	29	25	11	13	13	11	14	14	12	12		1		R1b
M3	14	13	29	25	11	13	13	11	14	15	12	12		1		R1b
K71	14	13	29	25	11	13	13	11	14	15	12	12	1		2	R1b
N16	14	13	29	26	11	13	13	12	15	15	12	11		1		R1b
N42	14	13	30	22	11	11	13	12	15	14	9	11		1		OE
N53	14	13	30	23	10	11	12	13	14	14	10	13			1	OE
M43	14	13	30	23	10	11	12	13	17	14	10	11		1		OE
M94	14	13	30	23	10	11	12	14	19	14	10	13		1		OE
K17	14	13	30	24	9	13	15	14	15	14	12	11	1			UA
N86	14	13	30	24	10	11	14	14	18	14	11	12			1	Q
N57	14	13	30	24	10	13	14	15	15	14	11	12			1	Q
M68	14	13	30	24	10	15	14	10	17	14	11	12		1		Q
N9	14	13	30	24	11	11	13	19	20	14	10	12			1	UA
N43	14	13	30	24	11	13	13	16	22	15	12	11			1	UA
K34	14	13	30	24	11	14	13	15	16	14	11	11		1		Q
M81	14	13	30	24	12	13	13	11	14	15	12	13		1		R1b
K68	14	13	31	24	10	14	13	15	18	14	12	11				Q
K63	14	13	31	24	11	14	13	13	20	14	11	11		1		Q
K11	14	13	31	25	9	14	13	15	17	14	11	12		1		Q
K23	14	13	31	25	10	14	13	15	17	14	11	12		2		Q
N94	14	14	29	24	9	11	12	12	18	14	10	11			1	OE

M14	14	14	24	11	13	13	11	14	15	12	12	1	R1b
M12	14	14	30	10	11	12	13	16	15	9	12	1	OE
K33	14	14	30	10	14	13	14	15	14	11	11	1	Q
M61	14	14	30	11	13	13	11	14	15	12	12	1	R1b
M56	14	14	30	24	10	13	11	14	14	12	11	1	R1b
M40	14	14	30	24	10	13	11	14	15	12	11	1	R1b
M37	14	14	30	24	11	13	11	13	14	12	11	1	R1b
M73	14	14	30	24	11	13	11	14	14	9	12	1	R1b
M45	14	14	30	24	11	13	11	14	14	12	12	1	R1b
M48	14	14	30	24	11	13	11	14	15	12	11	1	R1b
M95	14	14	30	24	11	13	11	15	15	12	12	1	R1b
M75	14	14	30	24	11	13	11	14	15	12	13	1	R1b
N40	14	14	30	25	10	13	14	16	14	12	13	1	Q
M35	14	14	30	25	11	13	11	14	14	12	11	1	R1b
M52	14	14	31	23	10	13	11	14	14	12	12	1	R1b
N1	14	14	31	24	10	14	13	18	14	11	13	1	Q
K62	14	14	32	23	10	14	14	16	14	11	12	1	Q
K3	14	14	32	24	11	13	13	19	14	9	12	1	Q
M58	14	14	32	24	11	13	11	15	14	12	11	1	R1b
M7	14	14	32	24	11	13	12	14	14	12	12	1	R1b
M23	15	12	27	24	11	11	13	18	16	9	13	1	OE
M20	15	12	27	25	10	13	12	19	14	10	13	1	UA
M38	15	12	28	22	10	11	13	14	15	10	11	1	OE
M66	15	12	28	23	10	11	12	16	15	9	13	1	OE
N71	15	12	28	23	10	12	15	16	14	10	11	2	Q
M30	15	12	28	24	10	11	12	18	16	9	13	1	OE
M102	15	12	29	22	10	10	14	16	13	12	11	1	OE
K30	15	12	29	22	10	11	13	17	16	10	11	1	OE
N69	15	12	29	22	11	11	13	14	17	10	12	1	OE
M16	15	12	29	23	11	13	15	16	13	9	12	1	J
K40	15	12	29	24	11	13	11	14	15	12	12	1	R1b
M85	15	12	31	23	12	15	12	15	14	12	12	1	R1b
K81	15	12	31	24	10	18	13	14	16	11	11	2	UA
M91	15	13	28	24	12	13	11	14	14	12	12	1	R1b
M99	15	13	29	21	10	11	14	16	14	12	11	1	E3a
M2	15	13	29	22	10	11	13	14	16	10	11	1	OE

Appendix 5. *continued*

Haplotype	Absolute Haplotype Frequency														Inferred Haplogroup ^a		
	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS385a	DYS385b	DYS437	DYS438	DYS439	Kichwa	Mestizo	African	OE	R1b
M26	15	13	29	23	9	11	12	12	17	14	9	11		1			OE
M10	15	13	29	23	10	13	14	11	14	15	12	12		1			R1b
K80	15	13	29	23	10	14	13	14	15	14	9	11	2				UA
N92	15	13	29	24	11	13	13	11	14	15	12	12			1		R1b
K89	15	13	29	25	11	15	13	15	15	15	11	11	1			Q	
N38	15	13	30	21	10	11	13	15	16	14	11	11			1		E3a
N10	15	13	30	21	10	11	13	16	17	14	11	12			1		E3a
N75	15	13	30	21	10	11	15	16	17	13	11	12			1		E3a
N33	15	13	30	21	11	11	14	15	17	14	11	11			1		E3a
M79	15	13	30	22	9	11	13	13	15	14	10	11		1			UA
N3	15	13	30	22	10	12	13	15	17	14	11	13			1		E3a
N21	15	13	30	23	10	11	14	13	15	16	10	11			1		OE
M86	15	13	30	23	12	13	13	14	16	13	9	11		1			R1b
N84	15	13	30	24	10	11	12	13	14	16	8	12			1		OE
M89	15	13	30	24	11	13	13	11	14	14	12	12		1			R1b
N17	15	13	30	25	11	13	13	10	11	15	12	12					UA
N77	15	13	31	21	10	11	13	15	17	14	11	12			1		E3a
N91	15	13	31	21	10	11	13	16	17	14	11	11			1		E3a
N31	15	13	31	21	10	11	13	16	17	14	11	12			1		E3a
N62	15	13	31	21	10	11	14	15	19	14	11	12			1		E3a
N24	15	13	31	21	10	11	14	16	17	13	11	11			1		E3a
N12	15	13	31	21	10	11	14	16	17	14	11	13			1		E3a
N8	15	13	31	21	10	11	15	17	18	14	11	12			2		E3a
N68	15	13	31	21	10	12	13	16	17	14	11	12			1		E3a
N78	15	13	31	21	11	11	13	16	17	14	11	12			1		E3a
N25	15	13	32	21	10	11	14	15	20	14	11	12			1		E3a
N52	15	14	29	25	11	13	14	11	16	14	10	12			1		R1b
K82	15	14	30	24	11	12	13	9	21	14	11	9	2				UA
M70	15	14	30	25	11	13	13	11	14	15	12	12		1			R1b
N74	15	14	31	21	10	11	13	15	16	14	11	11			1		E3a
N48	15	14	31	23	10	11	11	14	16	16	10	12			1		OE
N54	15	14	31	24	10	11	14	15	16	14	11	12			1		OE
N36	15	14	32	21	10	11	13	16	17	14	11	12			1		E3a

N44	16	12	28	22	10	11	14	14	15	16	11	11	11	OE
N34	16	12	30	22	11	11	13	15	16	17	8	11	11	E3a
N59	16	12	30	25	11	11	13	11	14	15	11	11	11	OE
M42	16	13	29	23	10	11	12	15	15	15	9	11	2	OE
N87	16	13	29	23	10	13	13	11	15	15	12	11	1	R1b
N85	16	13	29	23	11	11	12	12	16	15	9	11	1	OE
K22	16	13	30	21	9	11	13	12	12	14	10	12	1	C3b
N73	16	13	30	21	10	11	14	15	18	14	11	12	1	E3a
M6	16	13	30	21	10	11	14	17	19	14	11	12	1	E3a
N90	16	13	30	21	10	12	15	17	20	14	11	12	1	E3a
N49	16	13	30	21	11	11	15	17	18	14	12	12	1	E3a
K29	16	13	30	24	9	11	13	12	12	14	10	13	1	C3b
M78	16	13	30	24	9	11	13	12	14	14	10	12	1	OE
N60	16	13	30	24	11	14	13	11	15	14	12	12	1	OE
K79	16	13	30	25	10	13	14	19	19	15	10	11	2	Q
N29	16	13	31	21	10	11	15	17	19	14	11	11	1	E3a
N41	16	13	32	21	10	11	13	15	19	14	11	11	1	E3a
N6	16	14	31	21	10	11	14	16	18	14	11	12	1	E3a
N22	16	14	31	21	10	11	14	17	19	14	11	12	1	E3a
N82	16	14	31	22	10	11	14	17	17	14	11	10	1	UA
N2	17	13	30	20	10	11	14	15	18	14	11	12	1	E3a
N5	17	13	30	21	10	11	13	17	18	13	11	11	1	E3a
N39	17	13	30	21	10	11	14	15	17	14	11	12	1	E3a
N7	17	13	30	21	10	11	14	17	19	14	11	12	1	E3a
N14	17	13	30	21	10	11	15	15	18	14	11	12	1	E3a
N19	17	13	30	21	10	11	15	16	18	14	12	13	2	E3a
N64	17	13	30	22	10	11	13	16	17	14	11	12	1	E3a
N63	17	13	30	22	10	11	13	16	17	14	11	13	1	E3a
N88	17	13	31	21	10	11	15	17	18	14	12	11	1	E3a
N30	17	14	30	21	11	11	14	17	18	14	11	11	2	E3a
N45	17	14	31	21	10	11	14	17	17	14	11	12	1	E3a
N20	17	14	31	21	10	11	14	17	19	14	11	12	1	E3a
N28	17	14	31	21	10	11	15	17	18	14	12	12	1	E3a
N27	17	14	32	21	11	11	15	17	18	14	11	12	1	E3a
K55	18	13	28	24	10	15	13	14	14	14	11	12	1	UA

a. OE, other European; UA, unassigned.