



Genetic differences between Chibcha and Non-Chibcha speaking tribes based on mitochondrial DNA (mtDNA) haplogroups from 21 Amerindian tribes from Colombia

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Abstract

We analyzed the frequency of four mitochondrial DNA haplogroups in 424 individuals from 21 Colombian Amerindian tribes. Our results showed a high degree of mtDNA diversity and genetic heterogeneity. Frequencies of mtDNA haplogroups A and C were high in the majority of populations studied. The distribution of these four mtDNA haplogroups from Amerindian populations was different in the northern region of the country compared to those in the south. Haplogroup A was more frequently found among Amerindian tribes in northern Colombia, while haplogroup D was more frequent among tribes in the south. Haplogroups A, C and D have clinal tendencies in Colombia and South America in general. Populations belonging to the Chibcha linguistic family of Colombia and other countries nearby showed a strong genetic differentiation from the other populations tested, thus corroborating previous findings. Genetically, the Ingano, Paez and Guambiano populations are more closely related to other groups of south eastern Colombia, as also inferred from other genetic markers and from archeological data. Strong evidence for a correspondence between geographical and linguistic classification was found, and this is consistent with evidence that gene flow and the exchange of customs and knowledge and language elements between groups is facilitated by close proximity.

Keywords: mitochondrial DNA, Amerindian, Colombia, Chibcha, genetic relationships.

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Introduction

Studies about genetic variation among human populations are of great value for understanding genetic structure, migration routes and possible genetic relationships among different continental populations, and mitochondrial DNA (mtDNA) analysis has frequently put to such use in American populations (Schurr *et al.*, 1990; Torroni *et al.*, 1992, 1993a,b, 1994; Horai *et al.*, 1993; Bailliet *et al.*, 1994; Merriwether *et al.*, 1994; Santos *et al.*, 1994a,b; Bianchi *et al.*, 1995; Lorenz and Smith, 1996; Merriwether and Ferrell, 1996; Bonatto and Salzano, 1997; Bisso-Machado *et al.*, 2012). Despite its maternal inheritance (Giles *et al.*, 1980), the mitochondrial genome is extremely useful for determining genetic histories because of its rapid rate of mutation (Brown *et al.*, 1979) and lack of recombination

and repair mechanisms. Most mtDNA polymorphisms are single nucleotide substitutions, but insertions and deletions have also been described (Brown *et al.*, 1980; Cann and Wilson 1983; Cann *et al.*, 1984; Wallace *et al.*, 1985; Horai *et al.*, 1993; Torroni *et al.*, 1992, 1993a,b, 1994; Howell and Smejkal, 2000;). By revealing specific geographic locations for mitochondrial haplogroups, such studies helped to clarify migration patterns of human populations throughout history and over all continents (Fernandez-Dominguez, 2005).

Previous studies based on mtDNA analysis in Native American populations revealed the presence of four distinct haplogroups called A, B, C and D. Haplogroup A is characterized by the gain of a *Hae*III restriction site at position 663, haplogroup B by the 9 bp COII/tARN_Iys intergenic deletion, and haplogroup C by the loss of a *Hinc*II site at 13259 bp. Haplogroup D is characterized by the loss of an *Alu*I restriction site at position 5176 and a gain of a *Hinc*II site at 13259 bp (Torroni *et al.*, 1992, 1993a,b. A fifth haplogroup, X, has been predominantly characterized in

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some primarily North American populations (Eshleman *et al.*, 2003), but is absent in South America (Dornelles *et al.*, 2005).

Colombia has great cultural and genetic diversity. Its indigenous population is distributed in 89 different ethnic groups which are estimated to represent 1.83% of the total population (Arango and Sánchez, 2006). Based on the theory that peopling of the Americas occurred by migration from northeast Asia across the Bering Strait and subsequent migration through Central America to South America (Turner, 1984; Greenberg *et al.*, 1986; Dillehay and Meltzer, 1991), the nowadays Colombian territory at the northern tip of South America became an obligatory passage for people migrating to the southern cone.

In Colombia, several mtDNA studies of indigenous communities have been carried out (Mesa *et al.*, 2000; Keyeux *et al.*, 2002; Rodas *et al.*, 2002; Torres *et al.*, 2006; Melton *et al.*, 2007; Rondon *et al.*, 2007). In this study, we analyzed 424 individuals from 21 Amerindian populations to determine genetic structure and relationships among them based on geographical and historical information, as

well as linguistic and genetic relationships with other tribes of the Americas.

Subjects and Methods

Samples

We analyzed 424 blood samples from individuals unrelated by maternal lineage from 21 Amerindian tribes of Colombia (Table 1). Blood samples were collected between 1989 and 1992 after proper informed consent had been obtained. Informed consent included approval of each tribal Chief or Governor. The linguistic affiliation of each tribe is shown in Table 1. No Ge-Pano Carib speaking tribes were included in this study (Table 1).

DNA extraction and mtDNA haplogroup analysis

DNA was extracted using the salting out method (Gustincich *et al.*, 1991) with the DNA Wizard Genomic DNA Extraction Kit (Promega Corporation, Madison WI), following manufacturer's recommendations.

Four regions of the human mtDNA representing mtDNA haplogroups A, B, C and D were PCR amplified

Table 1 - Geographic location, sample size and linguistic classification for 21 Colombian Amerindian tribes analyzed.

mtDNA haplogroups (%)							Linguistic classification ^a	Geographic location (Department / region)	
Population	n	A	B	C	D	E			
Chimila	21	95.2	4.8	0.0	0.0	0.0	0.0952	Chibcha	Magdalena/ Caribbean region
Arsario	8	0.0	12.5	75.0	0.0	12.5	0.4643	Chibcha	Magdalena / Caribbean region
Kogui	32	71.9	0.0	28.1	0.0	0.0	0.4173	Chibcha	Cesar / Caribbean region
Arhuaco	21	90.4	4.8	4.8	0.0	0.0	0.1857	Chibcha	Cesar / Caribbean region
Embera	21	9.5	52.4	28.6	9.5	0.0	0.6571	Choco-Chibcha	Chocó / Pacific region
Ingano	48	39.6	35.4	22.9	2.1	0.0	0.5326	Andean	Putumayo / Amazonian region
Guambiano	24	4.2	12.5	66.6	16.7	0.0	0.6791	Without Classification	Cauca /Pacific region
Páez	36	27.8	8.3	27.8	33.3	2.8	0.7476	Without Classification	Cauca /Pacific region
Wayuu	17	29.4	17.6	47.1	0.0	5.9	0.6985	Tucano-ecuatorial	Guajira / Caribbean region
Tucano	14	7.1	21.4	7.1	57.1	7.1	0.6593	Tucano-ecuatorial	Vaupés-Guainía/ Orinoquian region
Guanana	10	20.0	0.0	20.0	50.0	10.0	0.7333	Tucano-ecuatorial	Vaupés-Guainía/ Orinoquian region
Cubeo	24	33.3	8.3	29.2	25.0	4.2	0.7645	Tucano-ecuatorial	Vaupés-Guainía/ Orinoquian region
Curripaco	22	4.5	40.9	36.4	13.7	4.5	0.7100	Tucano-ecuatorial	Vaupés-Guainía/ Orinoquian region
Desano	20	15.0	15.0	45.0	25.0	0.0	0.7263	Tucano-ecuatorial	Vaupés-Guainía/ Orinoquian region
Barasano	5	80.0	0.0	0.0	20.0	0.0	0.4000	Tucano-ecuatorial	Vaupés / Orinoquian region
Tatuyo	10	40.0	0.0	50.0	10.0	0.0	0.6444	Tucano-ecuatorial	Vaupés / Orinoquian region
Piratapuyo	8	12.5	12.5	50.0	12.5	12.5	0.7857	Tucano-ecuatorial	Vaupés / Orinoquian region
Tuyuca	6	17.0	50.0	0.0	17.0	16.0	0.8000	Tucano-ecuatorial	Vaupés / Orinoquian Region
Puinave	61	8.2	50.8	32.8	6.6	1.6	0.6333	Tucano-ecuatorial	Guainía / Orinoquian region
Yeral	8	12.5	12.5	50.0	25.0	0.0	0.7500	Tucano-ecuatorial	Guainía / Orinoquian region
Piapoco	8	12.5	25.0	25.0	12.5	25.0	0.8929	Tucano-ecuatorial	Guainía / Orinoquian region
Frequency		31.0	22.4	30.4	13.4	2.8	0.7447		
Total	424	131	95	129	57	12			

^aLinguistic affiliations (Ruhlen, 1987).

with the use of primers that were described elsewhere (Parra *et al.*, 1998).

Each amplification reaction consisted of 2.5 µL of DNA, 1.25 µL of each set of primers (10 nmol/µL), 2.0 µL of dNTPs (10 mM), and 0.125 µL of DNA *Taq* polymerase (Promega Corporation, Madison WI). The reaction mixture also contained 1.5 µL of MgCl₂ (25 mM) for haplogroup A, and 2.0 µL of MgCl₂ (25 mM) for the other haplogroups, respectively, in a final volume of 25 µL.

Amplification conditions consisted of a first denaturing cycle at 94 °C for 5 min; followed by 34 cycles of denaturing at 94 °C for 30 s, annealing at 50 °C for 30 s (Haplogroups B and D) or at 55 °C for 30 s (haplogroups A and C), extension at 72 °C for 30 s, and a final extension step at 72 °C for 5 min. The amplification products were evaluated by electrophoresis in a 2% agarose Nusieve/Seakem gel that was stained with ethidium bromide and photographed under UV light. 15 µL aliquots of the amplified products for groups A, C and D were digested with restriction enzymes for 3 h at 37 °C, while haplogroup B was only analyzed by electrophoresis. The digestion products were separated by electrophoresis in a 3% Nusieve/Seakem gel and processed as described above.

The haplogroup frequency of each population was estimated by direct counting (Table 1, Figure 1). Genetic diversity was estimated as $(n/(n-1))(1-\sum pi^2)$, where n is the sample size and pi the haplogroup frequency estimate for haplogroup i (Nei, 1978). Genetic distance estimates were based on mtDNA haplogroup frequencies calculated from F_{ST} pairs with the aid of Arlequin software (Excoffier *et al.*, 2005). Frequency data for mtDNA haplogroups belonging to Amerindian populations of South and Central America used in the analysis were obtained from the literature, see Table S1 (Ginther *et al.*, 1993; Horai *et al.*, 1993; Torroni *et al.*, 1993a, 1994; Bailliet *et al.*, 1994; Santos *et al.*, 1994a; Bianchi *et al.*, 1995; Kolman *et al.*, 1995; Merriwether *et al.*, 1995, 1997; Easton *et al.*, 1996; Lalueza-Fox, 1996; Ward *et al.*, 1996; Bonatto and Salzano, 1997; Kolman and Bermingham, 1997; Lalueza *et al.*, 1997; Dipierri *et al.*,

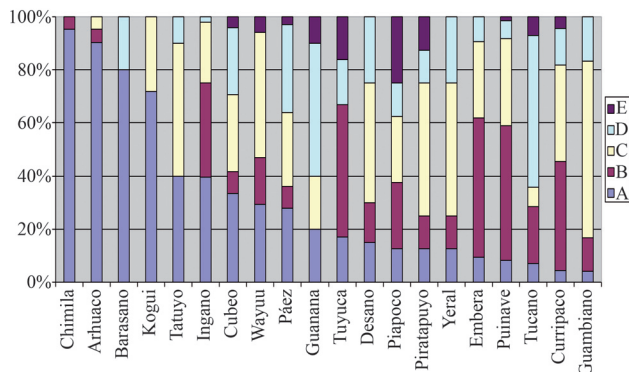


Figure 1 - Mitochondrial DNA (mtDNA) haplogroup frequency for 21 Amerindian populations of Colombia.

1998; Rickards *et al.*, 1999; Mesa *et al.*, 2000; Moraga *et al.*, 2000; Bert *et al.*, 2001; Demarchi *et al.*, 2001; Lobato-da-Silva *et al.*, 2001; Rothhammer *et al.*, 2001; Keyeux *et al.*, 2002; Williams *et al.*, 2002; Briceño *et al.*, 2003; Fuselli *et al.*, 2003; Garcia-Bour *et al.*, 2004; Lewis *et al.*, 2004; Sandoval *et al.*, 2004; Dornelles *et al.*, 2005; Cabana *et al.*, 2006; Torres *et al.*, 2006; Marrero *et al.*, 2007; Melton *et al.*, 2007; Barreto *et al.*, 2008). The results are presented in Figures 2 and 3.

In addition we calculated the degree of genetic differentiation among subpopulations (G_{ST}) based on the genetic diversity of the total population. An AMOVA analysis using Arlequin (Excoffier *et al.*, 2005) was carried out using linguistic classification or geographical location as testing parameters. In the first analysis, we evaluated the linguistic classification of each tribe, and whether differences could be attributed to belonging or not to the Chibcha speaking family. In the second analysis, we tested groups by geographic location (Tribes located in the north; tribes located in the east-Orinoquian/Amazonian region, and tribes located in the Pacific region-west). We also conducted a comparison to determine if the Andes mountain range was a factor in genetic differentiation (Table 2).

Finally, we compared the genetic (F_{ST} values), geographical (distance in km using the AMIGLOBE program) (Collard, 2006) and linguistic distance based on Ruhlen's classification (Ruhlen, 1987) matrices to calculate a possible relationship between these three variables. This was done with the aid of Arlequin, V3.1 software (Excoffier *et*

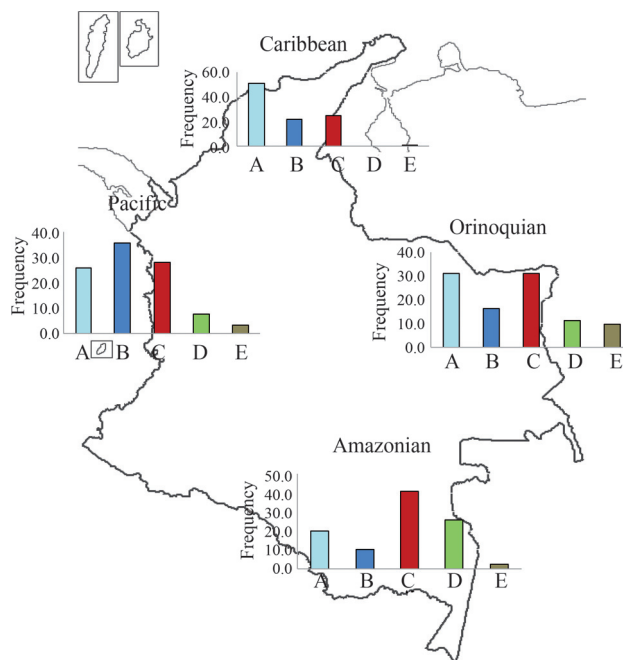


Figure 2 - mtDNA Haplogroup distribution of Amerindian tribes in Colombia according to their geographic location. Data reported by Torroni *et al.* (1994), Kolman and Bermingham (1997), Merriwether *et al.* (1997), Mesa *et al.* (2000), Keyeux *et al.* (2002), Briceño *et al.* (2003), Barreto *et al.* (2006), Torres *et al.* (2006) and Melton *et al.* (2007) was also included.

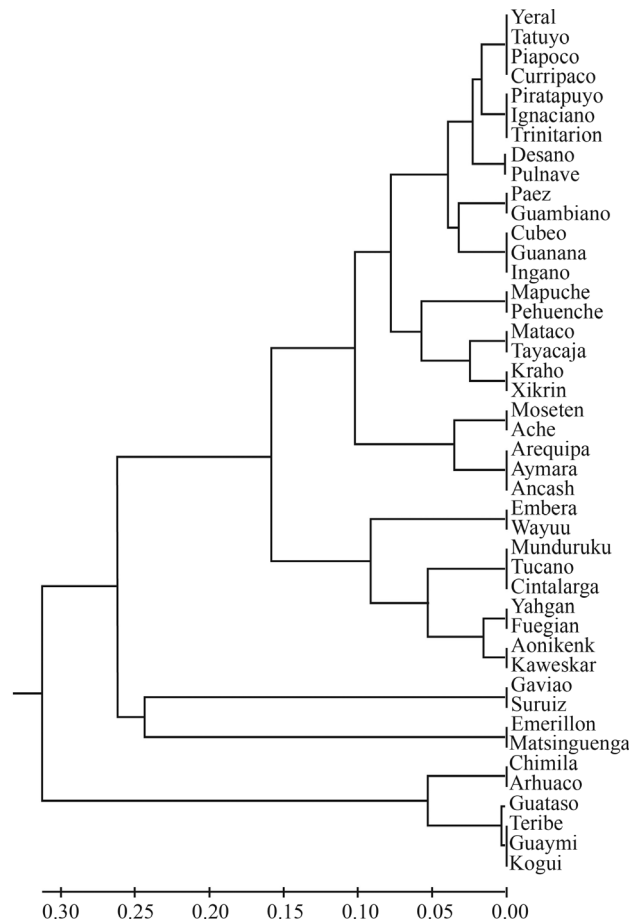


Figure 3 - UPGMA tree based on F_{ST} distances for Colombian and Central and South American Amerindian tribes analyzed for mtDNA haplogroups.

al., 2005) by using the Mantel test with 100,000 permutations (Figure 3).

Results

Mitochondrial DNA haplogroup frequencies from 424 individuals belonging to 21 Amerindian tribes of Colombia are shown in Table 1 and Figure 1. Haplogroup A was found most frequently; its average frequency was 31% (131/424 individuals), followed by haplogroup C with 30.4% (129/424), haplogroup B with 22.4% (95/424) and haplogroup D with 13.4% (57/424). The 12 out of 424 individuals who did not show any of the four mtDNA founder haplogroups (2.8%) were listed as haplogroup E. At least two of four mitochondrial haplogroups were present in the 21 populations studied. The frequency distribution of these haplogroups ranged from 2.1% to 95.2%.

Genetic diversity index values are shown in Table 1. The least genetic diversity was found among the Chimila tribe ($h = 0.0952$) while the greatest one was found among the Piapoco ($h = 0.8929$). The average diversity index for all populations studied was $h = 0.7447$ ($n = 424$).

Figure 2 shows the mtDNA haplogroup frequency distribution based on four geographical location groups: Caribbean (northern region), Amazonian (southern region), Pacific (western region) and Orinoquian (eastern region). We also included data from other studies (Torroni *et al.*, 1994; Kolman and Bermingham, 1997; Merriwether *et al.*, 1997; Mesa *et al.*, 2000; Keyeux *et al.*, 2002; Briceño *et al.*, 2003; Torres *et al.*, 2006; Melton *et al.*, 2007; Barreto *et al.*, 2008) in this analysis. There was a marked clinal pattern for mtDNA haplogroup distribution among Amerindian tribes of Colombia. Haplogroup A frequency was higher in the northern region of Colombia (50% frequency) decreasing

Table 2 - Analysis of Molecular Variance (AMOVA) for mtDNA haplogroups. Grouping based on linguistics or geographical criteria for Colombian Amerindian tribes.

Groups	AMOVA values (%)			Fixation index		
	a	b	c	F_{SC}	F_{ST}	F_{CT}
1. Chibchas and Non-Chibcha	69.06	9.87	21.07	0.12505	0.30939	0.21069
				*	*	($p = 0.001$)
2. All linguistic families	77.26	15.83	6.91	0.17003	0.22739	0.06911
				*	*	($p = 0.082$)
3. North East and Pacific	72.54	11.26	16.2	0.13435	0.27458	0.162
				*	*	($p = 0.013$)
4. Andes barrier	79.2	17.66	3.14	0.18229	0.20796	0.03139
				*	*	($p = 0.150$)

AMOVA analysis based on linguistic classification (groups 1 and 2) and geographical location (3 and 4). Group 1: Chibcha (Arsario, Kogui, Arhuaco, Chimila); Non-Chibcha (Wayuu, Curripaco, Piapoco, Yeral, Cubeo, Desano, Tatuyo, Piratapuyo, Puinave, Guanana, Ingano, Tucano). Group 2: Chibcha (Arsario, Arhuaco, Kogui, Chimila, Embera); Ecuatorial-Tucano: (Wayuu, Curripaco, Piapoco, Yeral, Cubeo, Desano, Tatuyo, Piratapuyo, Puinave, Guanana, Tucano); Andean (Ingano). Group 3: North (Kogui, Chimila, Arsario, Arhuaco, Wayuu); Pacific (Paéz, Guambiano, Embera); East (Ingano, Cubeo, Curripaco, Desano, Yeral, Tucano, Piapoco, Puinave, Guanana, Tatuyo, Piratapuyo). Group 4: Andean mountains: (Kogui, Arhuaco, Arsario, Chimila, Wayuu, Embera, Guambiano, Paéz); Amazonian/Orinoquian (Ingano, Guanana, Curripaco, Desano, Cubeo, Tatuyo, Piratapuyo, Yeral, Piapoco, Puinave, Tucano).

to 20% in the southern region of the country while haplogroup C frequency was lower in the north and highest in the south. The pattern for haplogroup D was similar, being almost absent in the northern part of Colombia, and showing the highest value in the southern part of the country (25%). Haplogroup B was more frequent in the west, declining towards the east and south.

We constructed a UPGMA tree based on F_{ST} genetic distances which includes other Amerindian populations from Central and South America (Figure 3). One cluster included the Kogui, Arhuaco and Chimila tribes of Colombia and the Teribe, Guaymi and Guatasa Chibcha-speaking tribes of Central America, which are all characterized by high frequencies of haplogroup A. An exception was found for the Arsario tribe, where none of the individuals tested in this Chibcha speaking tribe carried haplogroup A. The remaining Colombian tribes clustered together with other Amerindian tribes of South America that do not belong to the Chibcha linguistic family. The Guambianos, Paez and Ingano tribes were grouped within this cluster, reflecting their relationships to these non-Chibcha Amerindian populations.

We performed a non-metric multidimensional scaling analysis based on the mtDNA haplogroups identified (Figure 4). Herein we included the results of other Amerindian populations (Table S1) as well as populations of African descent of Colombia (Nuqui, Guanguí and Providencia) described by Rodas *et al.* (2002), and African populations as an outgroup (Chen *et al.*, 2000) (Figure 4). Most of the Amerindian tribes are clustered together due to the heterogeneous presence of the four mtDNA haplogroups among them. However, the Chibcha speaking tribes have a tendency to cluster much closer together due to the high frequency of haplogroup A and low frequencies for haplogroups C and D. The African descent populations from

Colombia are located intermediately between the Amerindian populations and the African population used as outgroup. This is due to the admixture process that resulted in the presence of some of the four mtDNA haplogroups among the Colombian African-descent populations.

The AMOVA analysis based on linguistic affiliation was used to test for differences based on belonging or not to the Chibcha linguistic family (Table 2). The Guambiano and Paez tribes were not included since their languages have not been classified yet. The results showed that 69% variations were due to variations within populations and 21% was due to whether or not a tribe belonged to the Chibcha linguistic family ($p < 0.001$). Another AMOVA analysis based on the geographical location of Colombian Amerindian tribes detected no significant differences when the tribes were grouped according to the side of the Andes mountain range they were located. Significant differences were found among tribes residing in the northern part of Colombia (most of the Chibcha speaking tribes analyzed here), compared to the Pacific region and the Orinoquian/Amazonian region ($p = 0.013$), but not so for the Andes as a separating barrier ($p = 0.150$) (Table 2).

Finally, the Mantel test was used to evaluate the possible relationship between genetic, linguistic and geographical distance. There was a strong correlation between linguistic and geographic distances, and a less strong correlation between genetic and geographic distances. There was no correlation between genetic and linguistic distance (Table 3).

Discussion

This study provides additional information on mtDNA haplogroup distribution in several Colombian Amerindian populations to previous studies (Keyeux *et al.*, 2002). Haplogroup A, with an average frequency of 31% (131/424 individuals) was found most frequently. It was followed by haplogroup C with 30.4% (129/424), haplogroup B with 22.4% (95/424) and haplogroup D with 13.4% (57/424).

Previous studies of Colombian Amerindian populations have shown high frequencies of haplogroups A and C and lower frequencies for haplogroup D (Keyeux *et al.*, 2002; Torres *et al.*, 2006; Melton *et al.*, 2007; Rondon *et al.*, 2007). Our results are in agreement with those reports. However, the 13.4% average haplogroup D frequency we found was higher than that previously published for Co-

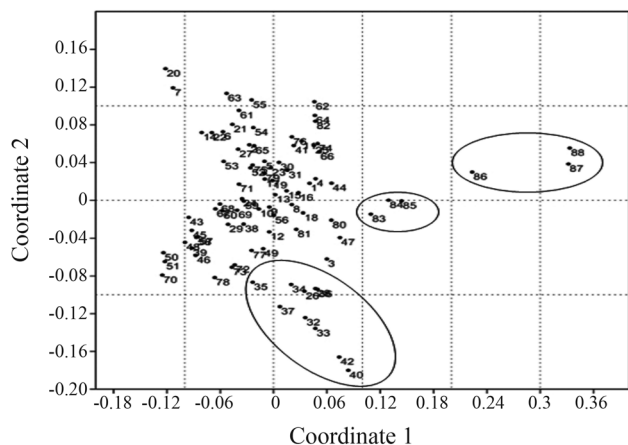


Figure 4 - NM-MDS plot of Amerindian populations from Central and South America, Colombian African descendant and African populations. The lower circle includes most of the Chibcha Speaking groups. The circle in the middle includes the populations of African descent in Colombia, and the circle to the left includes African populations used as outgroup. For haplogroup data see Table S1.

Table 3 - Mantel test correlating genetic, linguistic and geographical distances for 21 Colombian Amerindian populations studied.

Matrix 1	Matrix 2	r	p-value
Genetic	Linguistic	0.156272	0.06825
Genetic	Geographic	0.287512	0.00939
Linguistic	Geographic	0.648335	0.00001

Colombian Amerindian populations of 6.6% by Keyeux *et al.* (2002) and 9.95% by Torres *et al.* (2006). These differences could be attributed to the fact that these three studies chose different populations to study, or may even be due to differences within groups of the same population. For example, Keyeux *et al.* (2002) found no haplogroup D in the Paez tribe, whereas we found this haplogroup in 33% of the Paez individuals. Similar situations occurred in the cases of the other haplogroups. For instance, in our study, the Arsario tribe did not carry haplogroup A (but only 8 individuals were tested), while 68% of the individuals of the Arsario tribe tested by Melton *et al.* (2007) were reported to carry haplogroup A. These results indicate an even greater genetic heterogeneity within the same populations than has been described before.

Only 12 out of 424 individuals showed none of the four founder mtDNA haplogroups (2.8%). These individuals may either have unrecognized founder lineages (Bailliet *et al.*, 1994), recent racial admixture (Torroni *et al.*, 1993a) or reversal of a mutation. The second possibility could be the case for the Wayuu, Arsario and Paez tribes in which admixture has been documented by blood groups and HLA class II genes (Yunis *et al.*, 1994, 2001). The third possibility, which is termed haplogroup C revertant, is common in populations found in the Colombian Orinoquian and Amazonian basin (Torres *et al.*, 2006). This may be the case for the Piapoco tribe of our study that showed a 25% frequency of non A-D haplogroups. A high frequency (59%) for the revertant C haplogroup had previously been found by Torres *et al.* (2006) for this tribe. The same scenario is possible for the Piartapuyo (12.5%), Tuyuca (16%) and Guanana (10%) Amerindian tribes that live geographically close together in the Northern Amazonian region of Colombia. They present low genetic admixture based on Y STR haplotypes (Campo, D and, JJY, unpublished data) and HLA Class II genes (unpublished data).

The Amerindian tribes considered in this study showed a high degree of genetic heterogeneity (Table 2) and diversity (similar to or greater than populations found throughout South America) as has been described before (Santos *et al.*, 1994a; Batista *et al.*, 1995; Kolman *et al.*, 1995; Ward *et al.*, 1996; Bonatto and Salzano, 1997; Mesa *et al.*, 2000; Keyeux *et al.*, 2002).

Genetic diversity values were higher among the Tucano-Equatorial speaking tribes (0.60 to 0.80) while the Chibchan-speaking groups showed lower values (0.09 to 0.50). These results are consistent with those reported for Chibcha speaking tribes from Central and South America, including Colombia (Torroni *et al.*, 1994; Kolman *et al.*, 1995; Keyeux *et al.*, 2002). The higher diversity values found in Amazonian populations may be a result of gene flow between these populations, as has been shown for other genetic markers such as the Y-chromosome (Mesa *et al.*, 2000). Alternately, it could be the result of fission, fragmentation and founder effects (Cavalli-Sforza *et al.*, 1992).

The population that showed the lowest genetic diversity value (and the highest frequency for haplogroup A) was the Chimila ($h = 0.0952$). The low diversity found in this population has been reported by others (Keyeux *et al.*, 2002) looking at different genetic markers and is probably due to inbreeding (unpublished data).

The high genetic diversity found in our study and others indicates that it is unlikely that bottleneck events took place during the early Amerindian settlement of South America. However, it is evident that Amerindian populations located in northern Colombia that belong to the Chibcha linguistic family differ from non-Chibcha speaking tribes, as has been described before with nuclear genetic markers (Yunis *et al.*, 1994, 2001). Previous studies have shown that Amerindian populations of northern Colombia are close to Central American tribes and North American Amerindian populations (Stone and Stoneking, 1993; Lorenz and Smith, 1996; O'Rourke *et al.*, 2000; Keyeux *et al.*, 2002; Melton *et al.*, 2007). Our results provide further support indicating that Chibcha speaking tribes in Central and South America genetically differentiated from non-Chibcha speaking tribes prior to entering South America.

There were marked clinal patterns for mtDNA haplogroup distribution among Amerindian tribes of Colombia. When populations were grouped according to their geographical location (northern-Caribbean; southern-Amazonian, western-Pacific and eastern-Orinoquian) (see Figure 2), haplogroup A frequency was high in the northern part of Colombia (50% frequency) but decreased to 20% in the southern part of the country. Haplogroup C frequency was lower in the north and had its highest value in the south. Similarly, haplogroup D was almost absent in the north, but had the highest value in the southern part of the country (25%). Haplogroup B was more frequent in the west and had decreasing frequencies towards the east and south. These clinal patterns are similar to those described earlier (Torroni *et al.*, 1994; Lalueza-Fox, 1996; Lorenz and Smith, 1996; Lalueza *et al.*, 1997; Keyeux *et al.*, 2002; Bisso-Machado *et al.*, 2012).

A UPGMA tree constructed from data for the Amerindian tribes analyzed in this study plus data from several Amerindian populations from Central and South America described elsewhere showed a cluster of Chibcha speaking tribes (Chimila, Arhuaco, Kogui, Teribe, Guaymi tribes), which are genetically distant from other Amerindian tribes analyzed. The second cluster includes the remaining tribes including the Guambiano, and Paez tribes. The results for these two tribes, which currently have unclassified languages, provide further support of a genetic relationship to Tucano-Equatorial or Andean linguistic families rather than to the Chibcha linguistic family where they had been classified before. Similar results have also been obtained with HLA genes (Yunis *et al.*, 2001). Some authors have postulated that the Paez originated from the Amazonian region and migrated northeast to their present location before

the Spanish conquest (Arboleda, 1993). Recently, archeological findings in the west Amazonian region of Colombia have provided further support for an Amazonian ancestral origin of the Guambiano and Paez tribes.

The AMOVA analysis showed a significant association ($p < 0.001$) due to variation based on whether or not a tribe belonged to the Chibcha linguistic family (21%) (Table 2). On the other hand, our results do not support the hypothesis that the Andes mountain range served as a differentiation factor for the Amerindian tribes studied.

The strong genetic differentiation between the Chibcha and non-Chibcha speaking tribes is likely due to the high frequency of haplogroup A among these populations. Similar results were obtained in the past using the major histocompatibility complex and other genetic markers (Yunis *et al.*, 1994, 2001).

The correlation analysis between the geographical, linguistic and genetic data (Table 3) showed the highest correlation value for the linguistic-geographical pair followed by the genetic-geographic comparison. These results are explained by the fact that many populations that belong to the same linguistic family are also geographically close, so it is difficult to infer whether there is a linguistic-genetic relationship based solely on mtDNA haplogroups. The Amerindian tribes that are closely related are also geographically close, which facilitates gene flow and exchange of customs, knowledge and languages. Both geographic and linguistic factors are associated with genetic differentiation in the Amerindian populations analyzed in Colombia. As has been found for other Amerindian tribes, these three parameters have evolved together in a historical and strongly correlated fashion.

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Internet Resources

- Collard O (2006) AMIGLOBE. p Amiglobe is a world atlas and database with information about every country in the world, http://www.downloadatoz.com/home-education_directory/amiglobe-2006/.

Supplementary Material

The following online material is available for this article:

Table S1 - mtDNA haplogroup frequencies of Colombian and South America Amerindian tribes.

This material is available as part of the online article from <http://www.scielo.br/gmb>.

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