

Molecular Perspectives on the origins of Chibchan-speakers from Sierra Nevada de Santa Marta, Colombia

Introduction:

Over the last decade increased scientific inquiry has focused on Chibchan-speaking populations from lower Central and Northern South America due to their geographic location bridging the two American continents. This research has rejected the traditional notion of the region as a pathway for migrating populations and suggests long term occupancy and biological continuity dating back 10,000 years (Barrantes *et al.* 1990; Torroni *et al.* 1994; Kolman *et al.* 1995; Kolman & Bermingham 1997). While archaeological (Bray 2003; Hoopes 2005) and linguistic (Constenla 1991) research has found a relationship between the Central and Northern South American Chibchan populations the biological relationship of these groups remains unresolved. This research examines mitochondrial DNA haplogroup and haplotype diversity in three Chibchan-speaking (Kogí, Ijka, and Arsario) populations from the Santa Marta mountain region and a neighboring Arawak-speaking (Wayú) group from the Guajiro peninsula of northeastern Colombia in an attempt to determine the biological relationship between Central and South American Chibchan groups.

Objectives:

1. Determine biological relationship between four study populations.
2. Determine if a biological relationship exists between Central and Northern South American Chibchan-speaking populations at the maternal level.
3. Develop timeframe for Chibchan genetic history in northern South America.
4. Discuss the role of Chibchan-speakers in peopling the Americas.



Figure 1: Geographic location of Chibchan-speaking populations in lower Central and northern South America.

Chibchan Population Background:

Chibchan populations are defined by their linguistic affiliation, Chibcha, which is a language family spoken from eastern Honduras into portions of Colombia, Ecuador, and Venezuela (Figure 1). Current archaeological, biological, and linguistic evidence point to a Central American origin for these populations and suggest a timeframe of between 5,000 and 9,000 YBP for the development of these populations (Barrantes *et al.* 1990; Constenla 1991; Hoopes & Fonseca 2003).

Study included biological samples collected from 190 individuals (50 Kogí, 50 Arsario, 40 Ijka, 50 Wayú) from northeast Colombia, by researchers from Javeriana University, Bogotá (Briceño *et al.* 1996). DNA samples were sent to Dr. Michael Crawford by Dr. S.S. Papiha for analysis.

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Materials and Methods:

mtDNA RFLP and HVS-I sequencing:

- RFLP analysis (n=190) was used to characterize each of these four study populations for four of the five major Native American mtDNA haplogroups A, B, C, and D (Schurr *et al.* 1990, Torroni *et al.* 1993).
- HVS-I sequences (n=61) were generated on an ABI 310 capillary system sequencer through automated fluorescence using the ABI ver. 3.0 Big Dye sequencing cycle kit and primers 15976F and 16422R. All sequencing was conducted at Integrated DNA Technologies (IDT) in Corallville, IA.
- Comparative sequence data were drawn from the literature for South and Central American populations: Huetar, n=27 (Santos *et al.* 1994); Kuna, n=63 (Batista *et al.* 1995); Ngöbé, n=46 (Kolman *et al.* 1996); Zoro, n=29 (Ward *et al.* 1996); Yanamamö, n=53 (Easton *et al.* 1996; Torroni *et al.* 1993); Xavante, n=25 (Ward *et al.* 1996); Gavião, n=28 (Ward *et al.* 1996); Mapuche, n=39 (Ginther *et al.* 1993); Emberá, n=44 (Kolman & Bermingham 1997); Wounan, n=31 (Kolman & Bermingham 1997).

Median Joining Network:

- Median Joining networks were constructed in order to determine genetic relationships between haplotypes found within studied groups and comparative populations (Bandelt *et al.* 1995, 1999). Networks were constructed using the program Network 4.0 (www.fluxusengineering.com).

Measures of Selective Neutrality:

- Two measures of Selective Neutrality, Tajima's D (Tajima 1989) and Fu's Fs (Fu 1997) that test for significant evolutionary factors in the sequence data were investigated. Measures were generated using Arlequin 2.0 (Schneider *et al.* 2000).

Time Estimate Measures:

- Two time measures, mismatch analysis (Rogers & Harpending 1992) and p-statistic (Saillard *et al.* 2000) were used to generate chronological estimates based on mtDNA coalescence dates. Measures were generated using Arlequin 2.0 and Network 4.0.

Results: RFLP Analysis

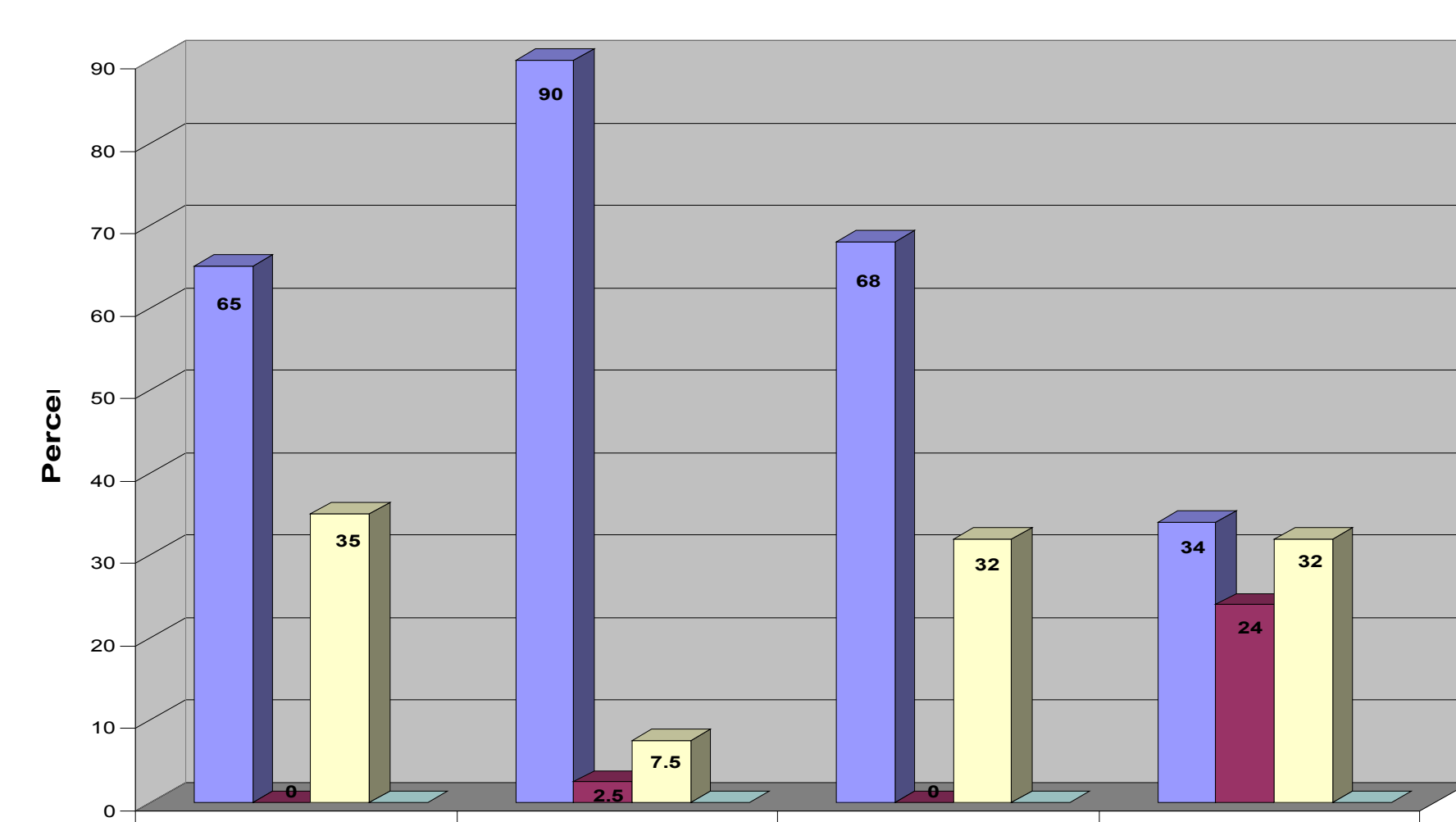


Figure 2: mtDNA RFLP Comparison date for four study populations. The Kogí and Arsario possess mtDNA haplogroups A and C. The Ijka are largely haplogroup A (90%), some haplogroup C, and one B individual. The Wayú possess 3 haplogroups (A, B, & C) in relative equal frequency.

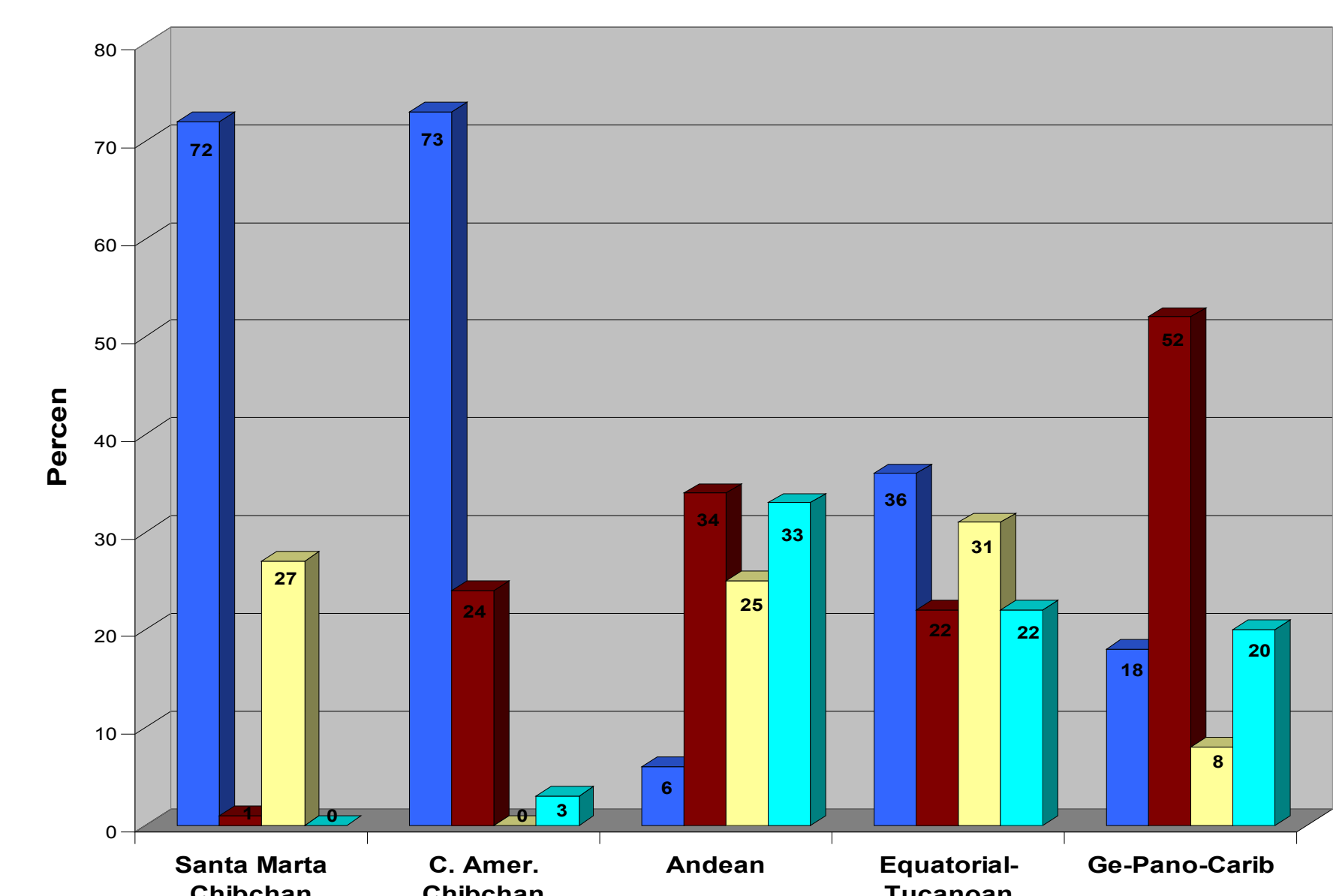


Figure 3: mtDNA RFLP Comparison date for four study populations and other South and Central American indigenous populations. Chibchan-speakers from both the Santa Marta region and Central America are characterized by high frequencies of haplogroup A, but differ in the presence of haplogroups B and C. This in contrast to other South American populations that contain four of the major Native American mtDNA haplogroups in differing frequencies.

Results: Median Joining Network

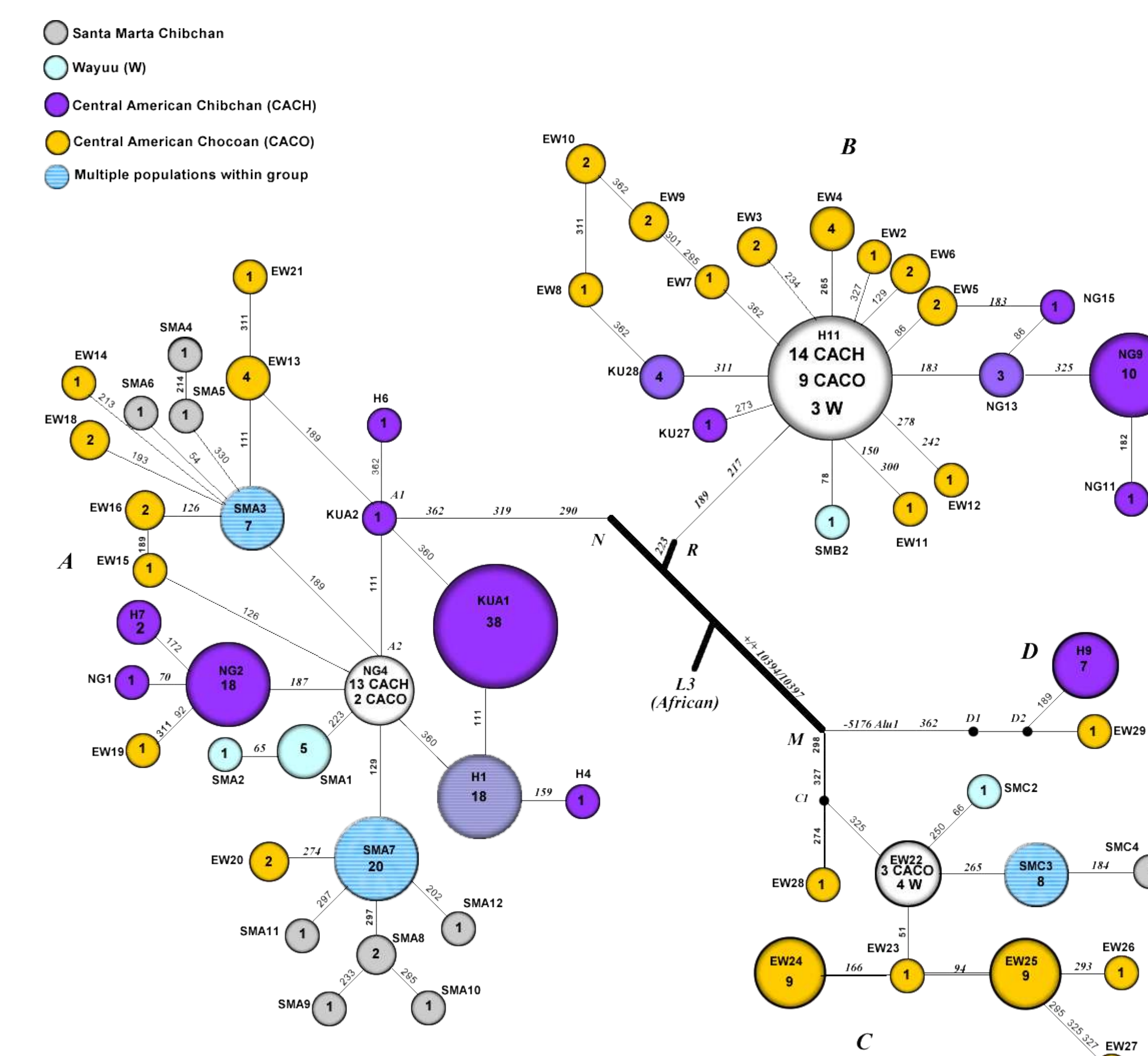


Figure 4: Median-Joining Network for four study populations, along with three Central American Chibchan populations (Huetar, Kuna, Ngöbé), and two Chocoan-speaking populations (Emberá, Wounan). Size of the node represent number of individuals within that node and numbers along lines represent position of mtDNA mutations within HVS-I.

Of 60 haplotypes present in these populations only three are shared between groups (H11, NG4, EW22). All three of these shared haplotypes are also shared with other Native American populations as they correspond to founding Native American haplotypes (A2, B, C2). This indicates that while Central American and Santa Marta Chibchan populations share a high frequency of haplogroup A, they do not share matrilineages within that haplogroup. In addition, Chibchan populations within haplogroup A are all characterized by large nodes within one position of major Native American haplotype and this may be indicative of these populations all of having undergone a recent genetic bottleneck.

Results: Measures of Selective Neutrality

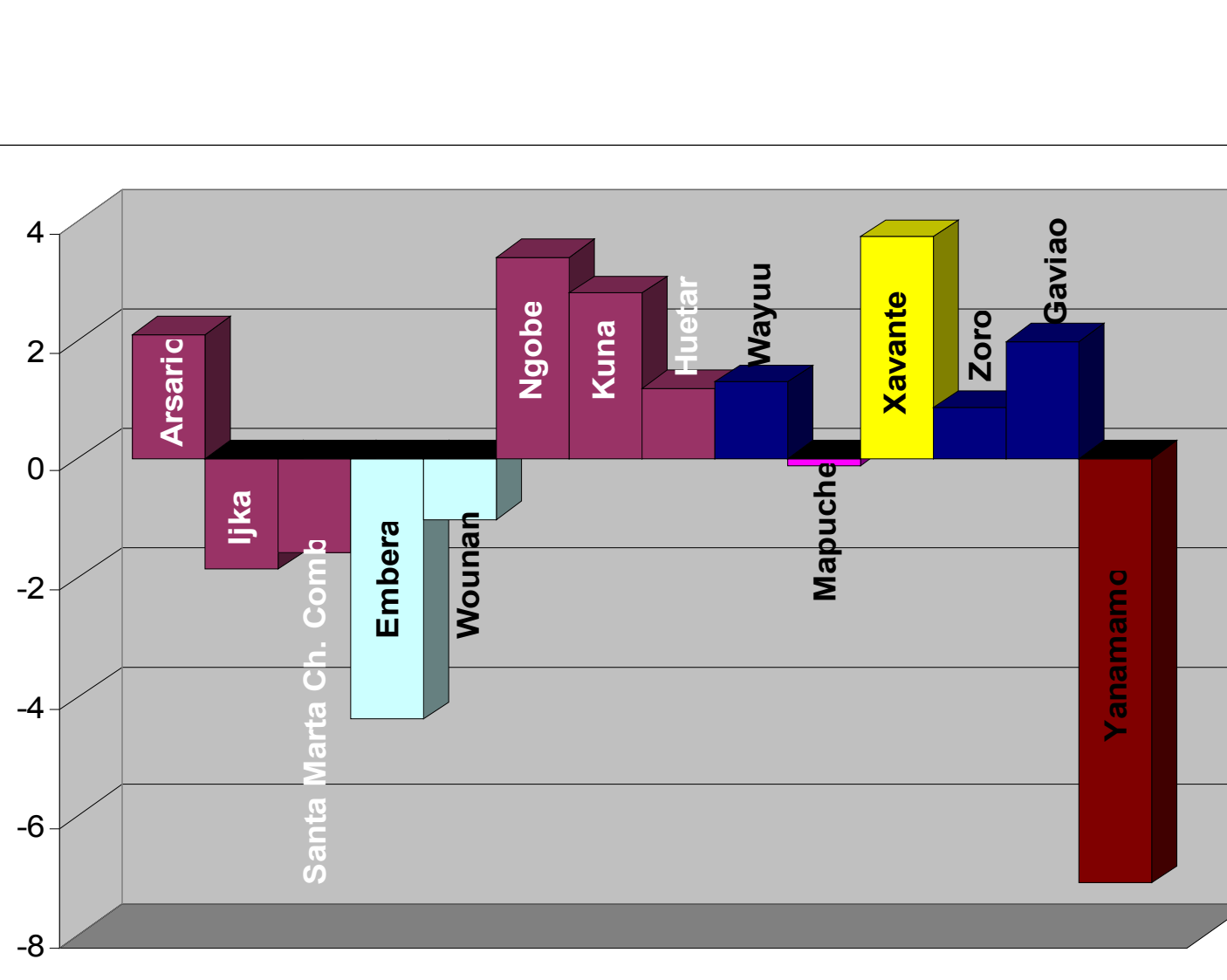
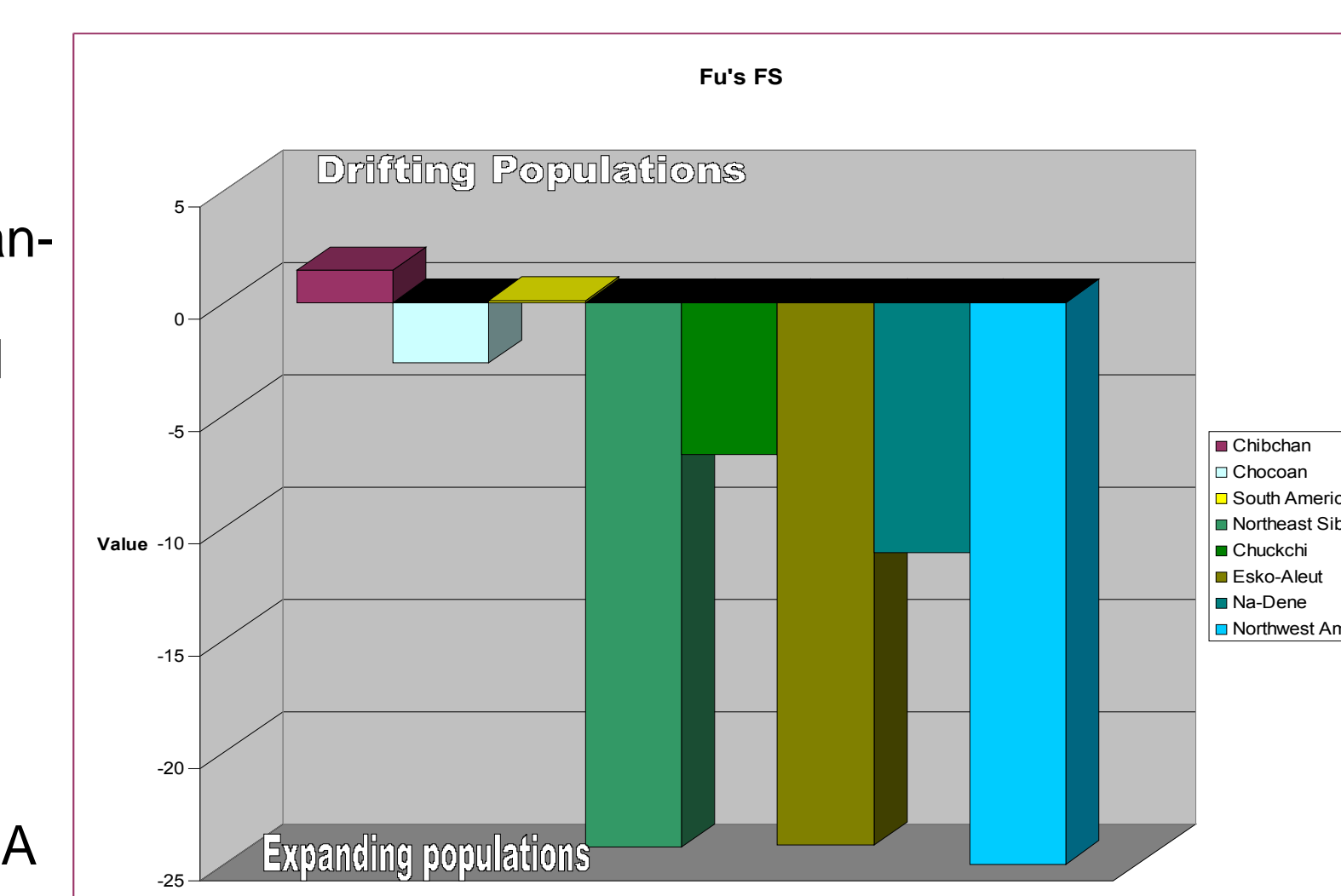


Figure 6: Fu's Fs values for Native American and Siberian populations (Melton 2005, Zlotjuro *et al.* 2005). Only two groups of populations shown here demonstrate positive Fs values and these are Chibchan-speaking populations (both Central and Santa Marta) and other South American populations. All other populations appear to be expanding. This may indicate that all Chibchan-speaking populations experienced the same evolutionary event but due to fragmentation of mtDNA haplotypes that this occurred sometime in the past.

Figure 5: Fu's Fs values for study populations and comparative South American groups (Melton 2005). Statistically significant Fs negative values are indicative of expanding populations as these groups show an excess number of alleles. Among these groups only the Yanamamö, were found to have statistically significant Fs value. Populations with low negative or positive Fs values indicate a reduced number of alleles, which suggests that these populations are either currently experiencing genetic drift or have recently experienced a genetic bottleneck



Results: Time estimate measures

Time estimates for Mismatch and p values for South America Populations				
Population	T	95% CI	Time Estimate	Date Range
Arsario	9.57	3.8-19.88	89,001	35,340-184,884
Ijka	2.18	0.247-4.43	20,274	2,297-41,119
Santa Marta Chibcha comb	9.98	4.184-15.98	92,814	38,911-148,614
Emberá	9.11	4.21-13.85	84,723	39,153-128,805
Wounan	9.95	4.9-14.59	92,535	45,570-235,687
Ngöbé	9.92	4.26-16.72	92,256	39,618-155,496
Kuna	8.14	2.9-13.7	75,702	26,970-127,410
Huetar	6.83	2.25-14.82	63,519	20,925-137,826
Wayú	8.28	3.75-13.75	77,004	34,875-127,875
Mapuche	7.93	4.23-11.22	73,749	39,339-104,346
Xavante	9.52	4.19-14.52	88,536	38,967-135,036
Zoro	7.02	2.23-12.52	65,286	20,739-116,436
Gavião	8.24	2.94-15.92	76,632	27,342-148,056
Yanamamö	6.22	2.08-11.27	57,846	19,344-104,811
Santa Marta Haplogroup A	2.6	0.48-6.34	24,180	4,464-58,962
Santa Marta Haplotype A3	0.97	0.00-3.96	9,021	0-36,828
Santa Marta Haplotype A7	2.25	0.188-4.21	20,925	1,748-39,153
Median Joining Cluster	p			
Santa Marta Haplotype A3	0.4	0.15-0.65	8,072	3,129-13,015
Santa Marta Haplotype A7	0.35	0.17-0.52	6,985	3,428-10,542

Table 1: Mismatch τ and p values for South American populations. Mismatch time estimates are based on 1 mutational event every 9,300 years (Kolman *et al.* 1996), p values are based on 1 mutational event every 20,180 years (Saillard *et al.* 2000).

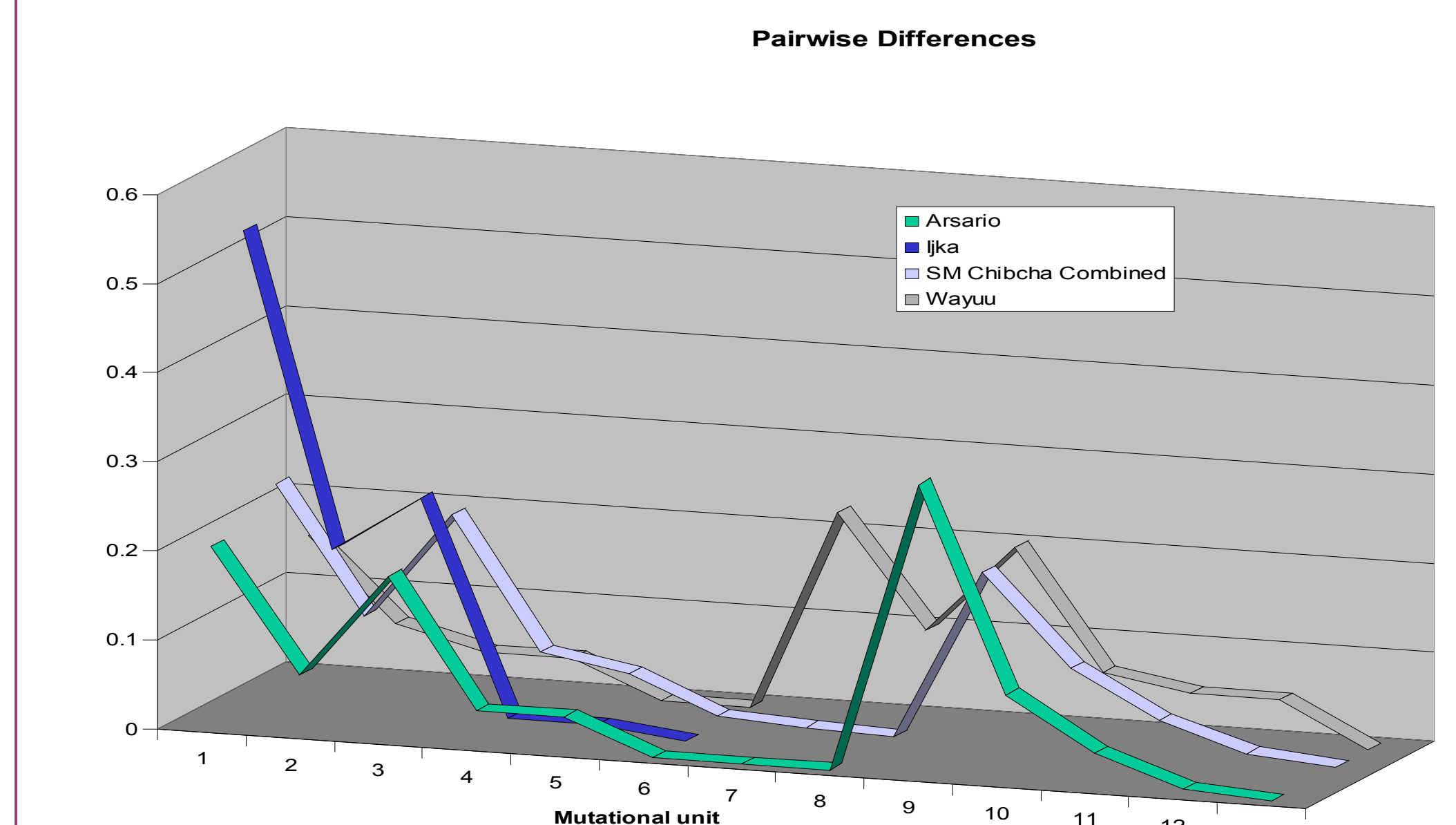


Figure 7: Mismatch values in four study populations. Three populations share a major peak between 6 and 9 mutational units, indicating an ancient expansion between 55,000 – 90,000 YBP corresponding to the initial peopling of Siberia. The three Santa Marta Chibcha populations also share a major peak between 0 and 1 mutational units, which is also shared with other Central American Chibchan groups.

Key Points:

1. Santa Marta Chibchan populations are biologically related to each other but not neighbouring populations.
2. Santa Marta Chibchan populations do not share any direct connection with Central American Chibchan populations. However, they share a number of characteristics that indicate similar genetic histories for these populations.
3. The p-statistic coalescent dates (Table 1) are consistent with other dates given for the development of the biological distinctiveness of Chibchan populations that occurred between 6,000-10,000 YBP (Barrantes *et al.* 1990; Kolman & Bermingham 1997).
4. Research offers further support for a Chibchan "population plug" that may have impeded or blocked gene flow through the Panamanian isthmus.

Acknowledgements:

This research was sponsored in part by the National Science Foundation, a Carroll D. Clark Award from the KU Dept. of Anthropology. I would like to thank the individuals who participated in the original study. Also, several individuals who assisted me during research for this project including Dr. Michael Crawford (KU), Dr. John Hoopes (KU), Dr. Carlos Langeback (Univ. of the Andes, Bogotá), Dr. Augusto Oyuela-Caycedo (Univ. of Kentucky), Dr. Eric Devor & Meredith Mills (Integrated DNA Technologies, Corallville, IA).



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