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# Sampling efficiency for Amerindian female lineages

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**Abstract.** Sampling strategy is the first potential biasing factor in population diversity analyses, especially when surveying is done in small communities and uniparental markers are being characterised. Amerindian tribes, known to have been subject to strong bottlenecks and genetic drifts, are being the focus of most works dealing with Amerindian female lineages description, although the few characterised town samples have shown to contain as much as 1/3 of these lineages in its pool. In this work we show that Amerindian female lineage diversity is higher when analysing town samples than when pooling small but scattered tribal samples. A sampling strategy in surveying towns (especially those known to have incorporated Amerindian females) would reveal that much diversity is still underscored in present databases in a faster and easier way, avoiding anthropological missions and their corresponding difficulties and problems. 

*Keywords:* mtDNA; Amerindian; Sampling; Town; Tribe

## 1. Introduction

Characterisation of mtDNA lineages in South American urban populations has revealed that as much as one third of its gene pool is of Amerindian ancestry, showing the introgression of native American females in the highly mixed (with Eurasian and sub-Saharan) new cosmopolitan communities. By opposition, only a small fraction of the male pool of urban South American populations is of Amerindian ancestry (almost 98% is of Eurasian background). The old native communities were drastically reduced in its effective size, and the remaining few are small and scattered.

We could then hypothesize the following scenarios: the native female lineages picked up for the constitution of the new cosmopolitan mixed populations were from communities around the location of the new town and probably still diverse; while the native female

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lineages observed in present small native communities went through severe demographic events, such us bottlenecks, genetic drift and founder effects. Being these scenarios true, a sampling effort would reveal much more diversity when surveying cosmopolitan populations than small tribes, leading to a reconstruction of the Amerindian mtDNA phylogeny that is much more promising in the first case than in the second.

## 2. Material and methods

We compiled published data for South and Central Amerindians and compared their diversity with the cosmopolitan pool of Amerindian ancestry:

- for native populations: 120 Cayapa from Ecuador [1]; 129 Yanomami from Venezuela and Brazil [2]; 39 Mapuche from Argentina [3]; 34 Mapuche, 24 Pehuenche and 15 Yaghan from Chile [4]; 46 Ngobe from Panama [5]; 27 Huetar from Costa Rica [6]; 44 Emberá and 31 Wounan from Panama [7]; 22 Arequipa, 61 Tayacaja and 22 San Martin de Pangoa from Peru [8];
- for cosmopolitan populations: 44 from Chile and 20 from Colombia [9]; and 82 from Brazil [10].

## 3. Results

The Amerindian haplogroup distribution in the pooled tribal samples was equivalent to the one in the pooled cosmopolitan samples, but the diversity was higher in towns (Table 1). Haplogroups A and B were the main contributors for the higher diversities observed in towns, while for haplogroups C and D, diversities were almost equal in tribes and towns. This trend of higher haplogroups A and B diversities in towns (as well as the equivalent diversity for haplogroups C and D) was also observed when randomly resampling 4 sub-groups (the same size of towns) inside the pooled tribal sample, showing that this effect is not due to a bias resulting from disproportionate sample sizes.

Network analyses showed that in the pooled tribes, haplogroups B and C present a star-like phylogeny, while A and D show several equally frequent haplotypes, being one-step departed in A but many steps in D (leading to a high mean pairwise difference). This testifies the diverse effects acting upon different haplogroups. In pooled towns, networks show a much diverse phylogeny for all haplogroups, as resulting from the picking up of divergent lineages.

Table 1
Haplogroup distribution and diversity in the pooled tribe and town samples

| | | *n* | Haplogroup frequency (%) in the sample | % of haplotypes | Haplotype diversity | Mean pairwise differences |
|---|---|---|---|---|---|---|
| Hap A | Tribes | 166 | 24 | 26 | $0.899 \pm 0.013$ | $2.135 \pm 1.194$ |
| | Towns | 37 | 25 | 57 | $0.960 \pm 0.016$ | $3.444 \pm 1.800$ |
| Hap B | Tribes | 198 | 28 | 31 | $0.792 \pm 0.031$ | $1.754 \pm 1.023$ |
| | Towns | 37 | 25 | 57 | $0.890 \pm 0.045$ | $2.134 \pm 1.214$ |
| Hap C | Tribes | 175 | 25 | 19 | $0.794 \pm 0.030$ | $1.622 \pm 0.964$ |
| | Towns | 43 | 29 | 44 | $0.803 \pm 0.062$ | $1.599 \pm 0.968$ |
| Hap D | Tribes | 159 | 23 | 30 | $0.948 \pm 0.007$ | $4.717 \pm 2.321$ |
| | Towns | 29 | 20 | 59 | $0.941 \pm 0.025$ | $2.576 \pm 1.422$ |
| Total | Tribes | 698 | – | 27 | $0.962 \pm 0.004$ | $6.030 \pm 2.877$ |
| | Towns | 146 | – | 53 | $0.972 \pm 0.007$ | $6.180 \pm 2.954$ |

## 4. Conclusions

In summary, a considerable amount of information for the native Amerindian lineages can be inferred by studying the descendents of the newly constituted populations after the arriving of Eurasians. This is true for the mtDNA, but unfortunately, cannot be applied to the Y-chromosome, for which many lineages are lost forever.

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