



The maternal inheritance of the Ashaninka native group from Peru

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ABSTRACT

The Amazonia rainforest, in South America, harbours native populations with high ethnic diversity. The evaluation of the genetic composition of these populations represents a challenge, and only few studies are available describing its native groups. In this work, the maternal inheritance of 170 Ashaninka individuals living in the Amazonia region of Pasco department, Peru, was evaluated by mtDNA control region sequencing. As previously observed for other native groups from Amazonia, low haplotype diversity was obtained, and only Native American haplogroups were found. Strong founder effects were observed, especially for sub haplogroups A2aa, B2b + 152, C1b and D1. During the European colonial period, the Ashaninka population seems to have remained relatively isolated, which can be explained by its remote location in the tropical forest. A comparison with other native South American populations from different linguistic families showed a lack of geographic or linguistic affiliations, highlighting the importance of having specific mtDNA database for the native groups in South America.

1. Introduction

It is currently accepted that the first America colonization happened through the Bering Strait and it was characterized by a strong founder effect succeeded by a rapid dispersal southwards. This has been corroborated by several genetic studies on uniparental markers for native and admixed American populations (e.g. [1,2]), which demonstrate that the native mitochondrial DNA (mtDNA) lineages are restricted to the macro-haplogroups A, B, C, D and X (the latter being limited to North America), while the Y-chromosome native lineages are mainly included in macro-haplogroup Q. Although characterized by this limited genetic diversity, there is a high differentiation inside and between populations, modulated by several demographic processes, especially as migrations and bottlenecks.

The Peruvian territory comprises three, very distinct, landscape zones (the coast, the Andean Mountain and the Amazonian forest), which are known to have contributed to the high linguistic and ethnic diversity found in the country. Furthermore, the multi-ethnicity was also due to admixture processes between Native Americans, Europeans, Africans and Asians.

In South American populations, no strong correlations were found between genetics and geography or language affiliation (e.g. [1–5]). This lack of associations highlights the importance of the elaboration

and implementation of detailed genetic forensic databases, representative of diverse geographic regions, linguist families and ethnic groups.

The Ashaninka (Arawak linguistic family) are the largest native Amazonian group in Peru [6]. Even though the Amazonia comprehends around 60% of the Peruvian territory, not many studies have so far focused on the genetic composition of its populations. Regarding mtDNA, the publications are restricted to HVS-I or HVS-I/HVS-II [7,8]. The present study aims at contributing to a deeper understanding of this under-described population, by investigating the distribution of maternal lineages in a large sample of Ashaninka people, living in Peru. Also, a comparison with other native South American populations from different linguistic families will allow disclosing genetic affinities among them, which will support the implementation of forensic databases for this type of isolated populations.

2. Material and methods

A total of 170 blood samples were collected from unrelated individuals, belonging to 41 communities located in the banks of Pichis and Palcazu rivers, in the district of Puerto Bermúdez, Pasco region, Peru. Samples were extracted using either a phenol-chloroform protocol or a Chelex based protocol. The control region of mtDNA was amplified

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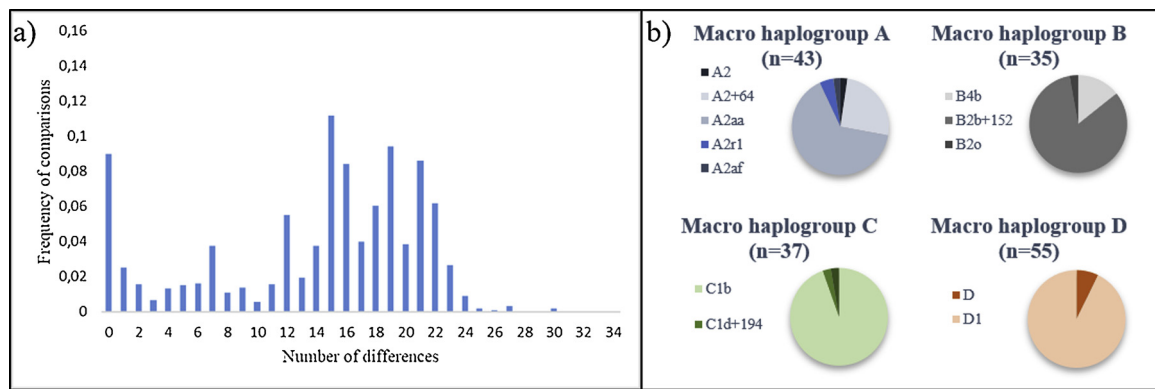


Fig. 1. a) Mismatch distribution profile for 170 samples from Ashaninka, Peru; b) distribution of haplogroups A, B, C and D in the studied sample.

and sequenced according to the protocol described in [9]. Haplotype were classified following the guidelines proposed by the International Society for Forensic Genetics and the haplogroups were assigned via EMPOP [10]. Diversity parameters were calculated using the Arlequin software [11].

3. Results and discussion

3.1. mtDNA diversity

The sequences obtained showed low haplotype diversity (0.9134 ± 0.0100) and exclusion power (0.8847). When removing indels at positions 309, 315 and 523–524, the haplotype diversity was even lower (0.8883 ± 0.0103) than that calculated for admixed population from Lima, Peru (0.9997 ± 0.0018) [12], under the same conditions. For comparative purposes, when reducing the haplotypes to HVSI, the haplotype diversity was lower (0.8897 ± 0.0102) than for other native (see [8,13]) and urban (see [13]) populations in Peru. The mismatch distribution profile (Fig. 1a) shows a high number of pairwise comparisons without differences. These results can be explained by the isolation of the Ashaninka in the Amazonian forest and possible recent founder effects.

3.2. Native haplogroups in Ashaninka

All major South Native American lineages were found in the sample (Fig. 1b). Haplogroup D was the most frequent (32%), followed by haplogroups A2 (25%), C1 (22%) and B2 (21%). Haplogroup B4b was found just in 1 sample (Fig. 1b). Strong founder effects were observed, especially for sub haplogroups A2aa, B2b + 152, C1b and D1, showing a high number of shared haplotypes, which made it challenging to evaluate linguistic or geographic affiliations, corroborating previous findings [5,14].

When comparing native South American populations, Barbieri et al. (2014) [7] described a trend on mtDNA haplogroup distribution: (i) haplogroup B is characteristic of the Andes, (ii) haplogroup A is more frequent in the Northern regions, and (iii) haplogroups C and D are more common in Amazonia. However, neither of these trends was found in the Ashaninka, showing an evenly distribution of the macro-haplogroups.

3.3. Maternal vs. paternal ancestries

In 2015, Tineo et al. [15] studied 58 samples from the Ashaninka linguistic group from Peru, for 27 Y chromosome specific STRs, which were further genotyped for Y-SNPs (unpublished data), to determine their possible geographic origin. From these samples, 51 overlap those studied for mtDNA markers. Most Y-SNP profiles were classified inside haplogroup Q. However, approximately 10% of the samples have non-

Native Y chromosome haplogroups. The Ashaninka population studied in this work seems to have remained relatively isolated, with just a small input of non-native male lineages. This can be explained by its remote location in the tropical forest and a sex biased admixture.

4. Conclusions

The native populations living in the Amazonian rainforest have remained considerable isolated, with no or reduced European and African influxes. Our results corroborate the low genetic input of non-native maternal lineages in the Ashaninka native group. However, it is possible to find some non-Native paternal inputs. The lack of association found between the haplotype distribution and a linguistic or geographic origin highlight the importance of having specific mtDNA database for the different native groups in South America

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Declaration of Competing Interest

None.

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