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Mitochondrial DNA study in the Shuar ethnic group from Ecuador

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ABSTRACT

This study presents mitochondrial data from 55 unrelated individuals from two Ecuadorian Shuar communities: Kumbatza and Yukateis. Maternal linage was determined by analyzing the two mtDNA hypervariable regions: HRVI and HRVII. It was shown that the Shuar population exhibited the haplogroup B. This demonstrates that Shuar group is a conserved population with no mixing with the European and African diaspora populations.

1. Introduction

Ecuador is a multiethnic country [1–4] composed of 21 indigenous groups, among these the Shuar are settled in around 668 communities in different provinces of the Ecuadorian Amazon region (Provinces: Napo, Pastaza, Morona Santiago, Zamora Chinchipe, Sucumbíos and Orellana), the coast region (Provinces: Esmeraldas and Guayas), as well as in the Peruvian Amazon state. According to population census 80 000 individuals belong to this ethnic group, of which 22 000 live in Sucumbíos province. Their anthropological isolation due to their life-style and language, make them an appealing group for genetic studies. mtDNA analysis is a convenient tool for population studies because of its maternal inheritance, elevated mutation rate, high copy number per cell, no recombination, not easily degraded material. This has been commonly used to infer ancestry or reconstruct ethnic history [5]. The aim of this work was to identify the haplogroups existing in Shuar population and if they are related to their historical process.

2. Materials and methods

2.1. Samples

75 Ecuadorian Shuar individuals from Kumbatza and Yukateis communities from parish Huambi, canton Sucua and Morona Santiago province (Fig. S1 in the Supplementary Information) were enrolled after they signed the informed consent and their fingerprints were taken. Family trees were constructed to selected only 55 unrelated male and female individuals. This study was approved by the Human Research Ethics Committee of Universidad San Francisco de Quito 2018-127E.

2.2. mtDNA study

DNA was extracted from peripheral blood, collected via finger puncture in FTA Whatman paper, using Chelex 10% protocol along with boiling for cell lysis. DNA quality was assessed by NanoDrop 2000 Spectrophotometer (Thermo Scientific, USA). To detect mutations in HVRI and HVRII, primers with annealing temperatures of 56 °C were used; for HVRI: F: 5′ CACCATTAGCACCCAAAGCT 3′, R: 5′ CCCGTGA GTGGTTAATAGGT 3′ and for HRVII: F: 5′ CCCACACGTTCCCCTTAAAT 3′, R: 5′ CCCACACGTTCCCCTTAAAT 3′, and the standard protocols for 3130 Genetic Analyzer (Applied Biosystems, Life Technologies, USA). The data was analyzed in the Sequence Analysis software. Geneious software was used for sequence alignment of HVRI and HVRII with Cambridge Reference Sequence, polymorphic sites were recorded and haplogroups identified.

3. Results

The mtDNA study showed that the Shuar population exhibit the haplogroup B which belongs to the Native American population. The haplogroup identified in this the Shuar population is depicted in Table S1 (Supplementary Information) along with other haplogroups identified in Andean Native American populations.

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4. Discussion

There are several theories that arose on how American continent was initially populated. However, genetic studies have postulated that Bering Strait migration during the last glacial maximum through the ice-free corridor around 15–18 thousand years ago, could possibly explain mtDNA haplogroups geographical distribution in Pan-America [6]. It has been documented that the most commonly reported haplogroups in Amerindians A–D [4,6,7]. In a study in South America, the Andean population have a high predominance of haplotype B, when compare with North-South Amazon and Southern population [8]. Besides, our result is in accordance with 61% Native populations in Ecuador and Peru mentioned in Table S1 (Supplementary Information), as they showed high abundance of haplogroup B [9,10]. One can hypothesize that the reason we were not able to find other haplogroup in our sample is that Amerindian groups are closed populations with high inbreeding levels or bottlenecks thus presenting a low diversity range [5]. Cardoso [11] has found only one haplogroup when studying Waorani population. This demonstrates that Shuar group is a conserved population with no mixing with the European and African diaspora populations.

5. Conclusion

This study is the first in characterizing the mtDNA of the Ecuadorian Shuar ethnic group, it describes the presence of one of the founder haplogroups from the Native Americans and demonstrates that the Shuar are a conserved population with no mixing with the European and African diaspora populations from Ecuador.

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Declaration of Competing Interest

None.

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Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:https://doi.org/10.1016/j.fsigss.2019.09.055.

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