



## Ancestral proportions based on 22 autosomal STRs of an admixed population (Mestizos) from the Península of Yucatán, México

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### ABSTRACT

Latin American populations trace their ancestry mainly to Post Columbian admixture among Native Americans (NA), Europeans, and Africans during nearly 500 years. Although historic and anthropological records suggest that the Peninsula of Yucatan (Southeast, Mexico) has as a large NA origin principally of Mayan ethnicity, they have been poorly studied with autosomal STRs. Thus, the ancestral proportion of Mestizos (admixed) from the Peninsula of Yucatan, was assessed by genotyping 687 subjects for 22 autosomal STRs (Powerplex Fusion system). STR databases from other Mexican Mestizos were included for the admixture analysis (North, West, and Center regions), Hispanic Americans, in addition to European, NA, and African genetic pools as ancestral references. The best fit of population clusters obtained with Structure ( $K = 5$ ), suggests that Mestizos from the Southeast are principally composed by NA (64.9%), followed by European (33.7%) and African (1.3%) ancestries. This was the highest among the compared Mexican Mestizo populations (range: 51.5–64.3%) and Hispanics (32.9%). Conversely, the European ancestry in the southeast is the lowest among Mexican-Mestizos (range: 33.7–48.5%) and Hispanics (60.2%). Differences with previous reports based on lesser number of STRs could be explained by intrapopulation structure due to socioeconomic and educational factors, as has been previously described in Mexican-Mestizos. This particular ancestral landscape justifies the creation of local STR databases for human identification purposes in Mexico.

### 1. Introduction

The largest part of the Mexican population (~90%), commonly named Mestizos, is result of admixture during nearly 500 years between Spaniard, Native American (NA), and in lesser extent African populations. The remaining ~10% consists of NA groups mainly concentrated in rural communities from the center to the southeast states [1]. Short tandem repeats (STRs) constitute the genetic markers of choice in forensic casework. However, STR population datasets are also useful to analyze anthropological issues, such as structure, relationships and admixture of human populations. Although Mexican populations have been widely analyzed with autosomal STRs [2], the emergence and development of new genetic systems makes necessary to re-analyze many of these populations [3]. Consequently, the aim of this study is to explore the ancestral proportions in Mestizos of the Peninsula of

Yucatan based on the 22 STRs included in the Powerplex Fusion® System.

### 2. Material and methods

We analyzed a total of 687 samples of unrelated Mestizos from the Peninsula of Yucatan (Southeast, Mexico). All individuals included in this study signed an informed consent. Buccal swabs and punches of blood stain samples on FTA paper were used as DNA sample for PCR. Amplification of 22 autosomal STRs, plus the Y-linked STR *DYS391* and *Amelogenin* was performed using the PowerPlex® Fusion System (Promega Corp., Madison WI, USA). PCR products were separated and detected by capillary electrophoresis with the ABI Prism 310 Genetic Analyzer (Applied Biosystems, Foster City, CA, USA). Genotyping was done using allelic ladders and the GeneMapper v.3.2 software (Applied

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Biosystems, Foster City, CA) software. Hardy-Weinberg equilibrium (HWE) and linkage disequilibrium (LD) were evaluated with the Arlequin v3.5 software [4]. Admixture analysis was performed by means of a supervised analysis with the Structure software [5] using the following ancestral references: African-Americans, European-Americans [6] and a NA pool from Mexico [3]. In addition, the following admixed populations were included: Hispanic-Americans [6], Monterrey City (Northeast, Mexico) [7], West region of Mexico [8], and Mexico City (Center) [9]. For consistence, for comparison purposes Mexican populations will be described by their geographic region. The admixture model and the correlated allele frequencies model (F-model) were utilized [10]. The evaluated number of population clusters (K) ranged from 2 to 10; for each K, 50 independent runs were carried out. We assessed and detected the number of genetic groups (K) that best fit to the data using the Structure harvester program [11]. In addition, the CLUMPAK program was used to graphically represent the best run for each K [12]. The laboratory annually participates in proficiency tests promoted by the Latin American Society for Forensic Genetics (<http://slagf.org.ar/a2/>).

### 3. Results

Genotype distribution of the 22 autosomal STRs was in agreement with HWE expectations. Similarly, LD tests displayed no association between pair of loci after Bonferroni correction (data not shown). The number of genetic clusters of the Structure supervised analysis that best-fit with the complete STR dataset are shown in the Fig. 1a (K = 5), which suggests that the populations analyzed were represented by the following ancestries: 1) European (sky blue), well distributed with different proportion throughout all populations; 2) African (navy blue), very low distribution in all population, with exception of Hispanics who showed the highest African proportion; 3) NA 1 (orange), was the largest NA ancestry represented throughout all the Mexican-Mestizo populations; 4) NA 2 (green), observed in few Mestizo samples from the

west and southeast regions, and; 5) NA 3 (purple), observed exclusively in some samples of the southeast region.

### 4. Discussion

The admixture proportions in the studied populations based on the three principal ancestries (Fig. 1b), suggests that the studied population of the Southeast is mainly composed by NA ancestry (64.9%), and lesser proportion by European (33.7%) and African (1.3%) ancestries. Interestingly, the similar ancestral proportion pattern was observed in a previous report based on the 13 CODIS-STRs (NA = 63.6%; European = 34.2%) [2], but showed differences with the study based on 20 STRs (NA = 55.5%; European = 42.4%) for the same Southeast region [3]. These differences could be explained by socioeconomic and educational factors of the population sample by intrapopulation structure, as has been described in Mexican-Mestizo populations [13].

The NA ancestry in the Southeast was the highest among the compared Mexican populations (range: 51.5–64.9%), whereas the European ancestry was the lowest (range: 33.7–45.8%). In Hispanics, the European ancestry was even higher (60.2%), diminishing the NA component (32.9%). Similarly, the African component was very low in Mexican-Mestizos (range: 0.7–3.3%) (Fig. 1b), but it was more than double in Hispanics (6.9%). Although a northwest-southeast genetic cline is evident (Fig. 1b), the ancestral distribution among the Mexican populations showed higher similarity between the Center and Southeast regions, respect to the West and Northeast regions, as previously noted [2,3]. Despite the small number of Mexican-Mestizo populations used herein, the distribution of NA ancestry roughly reflects the Pre-Hispanic NA demography, particularly toward the Mesoamerican area [13]. The peculiar ancestry landscape described throughout the Mexican territory, justifies the creation of local STR databases for human identification purposes in this country.

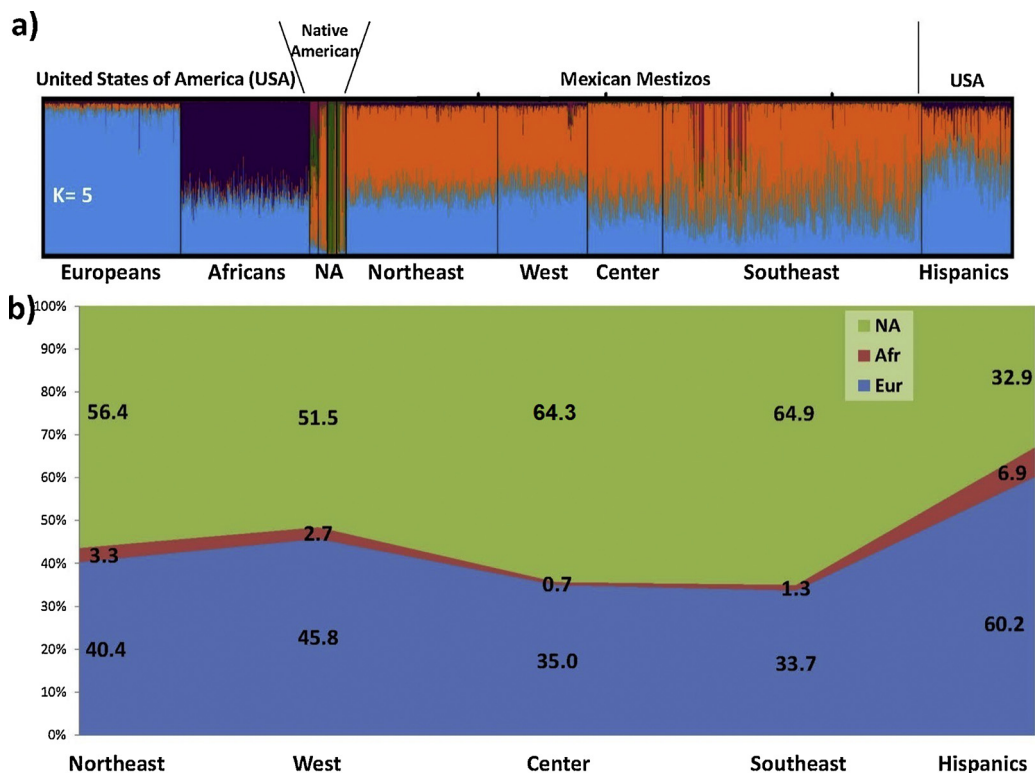


Fig. 1. Structure analysis that best-fit with the complete STR dataset, K = 5 (A). Admixture proportions in the studied populations based on the three principal ancestries (B).

## 5. Conclusion

Autosomal STRs allowed estimating a higher NA ancestry in the Southeast region respect to the Mexican-Mestizos from the Center, West, and North regions.

## Declaration of Competing Interest

Authors declare no conflict of interest.

## Acknowledgment

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