Announcement of Population Data

Genetic variation of 15 autosomal microsatellite loci in a Nayarit population (Mexico)

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Abstract

Fifteen STRs are studied to determine the allele frequencies’ distribution and to evaluate the homogeneity of Nayarit populations. This study allows the identification of forensic efficiency parameters to be used in forensic genetics and to explore the genetic similarities between Nayarit and the neighboring countries such as Mexico, Brazil, Puerto Rico, Guatemala, Honduras, Bolivia and Costa Rica. The Hardy–Weinberg equilibrium, expected heterozygosity, matching probability, and power of discrimination, were calculated in the Nayarit population. We found that with respect to the studied markers, Nayarit genetic structure is homogeneous. In this study, it is established that Nayarit is genetically similar to the South American Mestizo population. The distribution of a set of these 15 STRs was analyzed with other South American populations as well as in the extensive set of neighboring populations from the literature (USA, Europe and Africa). We found significant differences exist between the isolated populations (Huastecos, Otomi from Sierra Madre and from Ixmiquilpan Valley) and Mestizo populations. Statistical analysis supports that Americans actual inhabitants and Europeans are genetically similar, while Africans and isolated populations from South America have more genetic differences.

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Population

Samples (231 individuals) from Nayarit, Mexico were analyzed for 15 STR loci, however for doing anthropological analysis and population’s studies we should reduce the markers to 13. The selection of 13 STR loci (D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, TH01, TPOX, CSF1PO and AMEL) is due to they constitute the core Genetic Loci of the United States national database, CODIS (Combined DNA Index System) [1]. The population samples consist of five regional populations from this region are represented in Figs. 1 and 2.

DNA extraction

Blood samples and buccal swabs were collected by Forensic Genetic Laboratory of the Attorney General’s Office of Nayarit state, using the Helsinki protocol and collected with informed consent which was approved by Ethics Committee. Some personal questions were asked in the collection of the samples in order to have sufficient anthropological information of their ancestors and an accurate selection of the individuals.

PCR

Approximately 0.5–1 ng/μl of template DNA was amplified using Power Plex16 kit (Promega®) [2] (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D19S433, vWA, TPOX, D18S51, D5S818, Penta D, Penta E, and FGA), by a GeneAmp System 2400 thermal cycler. The kit Power Plex16 was selected because it is the common kit for forensic uses, however if we want to do anthropological analysis and population’s studies we should reduce the markers to 13. The selection of 13 STR loci (D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818,
D13S317, D7S820, D16S539, THO1, TPOX and CSF1PO) is due to they constitute the core Genetic Loci of the United States national database, CODIS (Combined DNA Index System) [1].

Typing
Electrophoresis, detection of PCR products, and genotyping were carried out on the ABI PRISM 310 Genetic Analyzer (Applied Biosystems®) using GeneMapper® ID Software v3.2 (Applied Biosystems®, Foster city, CA). The raw data obtained was also analyzed by GeneMapper® ID-X Software v1.1 and all the haplotypes were confirmed in the Identification Laboratory, University of Granada, Spain.

Quality control
Positive and negative controls as specified in the Power Plex16 kit (Promega®) user’s manual. The data were analyzed and verified by two independent analysts.

Analyses of data
The population’s genetic structure was analyzed using methods implemented in the Arlequin v.3.5 software [3], obtaining data, such as Hardy–Weinberg equilibrium, expected heterozygosity and observed heterozygosity. Matching probability, power of discrimination, polymorphism information content, probability of exclusion, and typical paternity index, which were calculated with a modified version of Powerstats v.1.2 [4]. To test for population stratification, the STRUCTURE v.2.1 [5] program was used. A correspondence analysis was calculated with STATISTICA v.7.1 (StatSoft, Inc., Tulsa, USA). The statistical significance of the pairwise genetic distances FST values was estimated by permutation analysis using 2000 permutations. Reynolds’ distance [6] was calculated with the Gendist genetic tool of the Phylip v.3.1 software pack [7]. Multidimensional scaling (MDS) [8] analysis of Reynolds’ distance values was performed using the software package SPSS v.15.0.

Results
The allele frequency distributions for the 15 STR loci studied in the Nayarit population and statistical parameters (Hardy–Weinberg equilibrium, expected heterozygosity, observed heterozygosity, matching probability, power of discrimination, polymorphism information content, probability of exclusion, and typical paternity index) are summarized in Table 1. To evaluate whether the main regions of the present day Nayarit population are homogeneous with respect to the studied STRs, the analysis of molecular variance (AMOVA) [9] on grouped Mexican populations was performed.

The expected heterozygosity, the power of inclusion (PI), and the power of discrimination (PD) calculated from the allele frequencies obtained for the Nayarit population revealed that in combination, the 15 STR loci have a high forensic efficiency.
Table 1
Allele frequencies and statistical parameters of the 15 STRs loci in the Nayarit population (n = 231). The minimum frequency is 0.0021645.

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<th>Allele</th>
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<th>Penta E</th>
<th>D5S818</th>
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Abbreviations: PD – power of discrimination; PE – power of exclusion; PIC – polymorphism information content; TPI – typical paternity.

* vldf based on unbiased estimate with 2000 shufflings.
** Exact test based on 2000 shufflings.
The combined Power of discrimination (PD) and the combined Power of exclusion (PE) for the 15 tested STR loci were 0.999999999 and 0.999999333, respectively.

To evaluate whether the main regions of the present day Nayarit population are homogeneous with respect to the studied STRs, AMOVA performed. We were unable to detect statistically significant differences between the subregions of Nayarit (Acaponeta, Bucerias, Itzlan del Rio, and Tepic), which indicates genetic homogeneity among the analyzed populations. We also observed that all loci are in Hardy–Weinberg equilibrium. STRUCTURE v.2.1 was also used to analyze homogeneity, and we always observed the highest probability in $K = 1$ with all the studied models. Thus, it can be concluded that the Nayarit population is homogeneous [5] and we cannot find a statistically significant component of indigenous population.

Other remarks
To further study the genetic distances and the differences between the American populations, we also included the African and European populations. STATISTICA v.7.1 program was performed with all the populations cited in Appendix A to calculate the correspondence analysis. We analyzed the differences between the populations’ STR frequencies. We reduced the analysis to 13 STRs to achieve unification of the data [10].

All the Mestizo populations from America and Europe are clustered, while African population and populations from Central and...
North America, Mayan, and Nadane (Navajo and Apache) [Fig. 3] [10] are quite dispersed. The most dispersed are the Mexican Huastecos groups (Otomí from Sierra Madre and Ixmiquilpan and Huastecos) [11], while pre-Mayan populations are in fact isolated. There are some Mestizo populations like Brazil [12] genetically quite similar to the African populations and others like Mestizos from Bolivia [13] or Metztitlan [14] to the Native American populations. We can see that this situation correlates with the genetic homogeneity between these populations, and that the distribution of populations on the correspondence analysis plot did not fully correlate with geography, but with the ancestry of these population groups [15]. The distribution of all the populations depends on a range of markers that make a population suitable in one specific part of the plot.

We studied the genetic distances and the differences between the Mexican population and USA hispanic descendent, and calculated the matrix of coancestry coefficients [6] using the tool GenDist (Phylip v.3.1 software). The Euclidean distance model of a multidimensional scale (MDS) and a representation plot from the MDS analysis is shown in Fig. 4. MDS was calculated with the SPSS software. As can be seen in Fig. 4, the Mexican population can be divided into natives and Mestizos. We could observe all Mestizo population groups clustered on the right part at the top of the image, and the Mayan population at the bottom. Isolated protomayan populations are dispersed and situated on the left of the image.

There were significant differences between the population of North America, indicating that isolated groups are different from the others owing to the geographical and cultural factors. Furthermore, differences between the Mayan and Mestizo population could also be a consequence of these factors, while we also observed that populations from Jalisco, Metztitlan, and Nayarit have more genetic similarities, owing to their nearer geographical locations.

Acknowledgments

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Appendix A. Supplementary data

Supplementary data (completed list of populations used in the present study for comparative analyses) associated with this article can be found, in the online version, at doi:10.1016/j.legalmed.2011.07.003.

References