Forensic Science International: Genetics Supplement Series 7 (2019) 491–493

Contents lists available at ScienceDirect

Forensic Science International: Genetics Supplement Series

journal homepage: www.elsevier.com/locate/fsigss

Forensic statistical parameters of 22 autosomal STRs in Mestizos from the Peninsula of Yucatán, México

L. González-Herrera[a,b,*], J.E. Sosa-Escalante[a], P. López-González[a], M.J. López-González[a], R.Y. Gamboa-Magaña[c], R.G. Herrera-Diaz[c], K.A. Piña-Dzul[c], S.F. León- Acosta[c], R.I. Flores-Baas[c], J. Bautista-González[a], M.R. Rivera-Guzman[d], H. Rangel-Villalobos[e]

[a] DIMYGEN Laboratorio, Mérida, Mexico
[b] Universidad Autónoma de Yucatan, Merida, Mexico
[c] Instituto de Ciencias Forenses, Fiscalía General del Estado de Yucatán, Mexico
[d] Laboratorio Genomelab, Tijuana, Mexico
[e] Instituto de Investigación en Genética Molecular, Universidad de Guadalajara, (CUCiénega-UdeG), Ocotlán, Mexico

ARTICLE INFO

Keywords:
Autosomal STR
Forensic parameters
Yucatán

ABSTRACT

The Mestizo (admixed) population of the Peninsula of Yucatan (Southeast, México) characterizes by a predominant Native American origin involving the Mayan culture. Autosomal Short tandem repeats (STRs) are the election tool for human identification (HID) purposes, such as forensic casework and paternity testing, among others. Although there are autosomal STR databases for some Mexican populations, the HID kits with more STRs have poorly studied in this country. Therefore, we estimated forensic parameters for 22 autosomal STRs belonging to the PowerPlex® Fusion System Promega kit (Promega, Corp.) in a population sample of 733 Mexican Mestizos subjects from the Peninsula of Yucatán (Southeast, Mexico). Buccal swabs were used as DNA sample for direct PCR multiplex amplification for genotyping PowerPlex® Fusion System Promega kit. Forensic parameters were obtained with Powerstats 1.2 software. Hardy-Weinberg expectations (HWE) were estimated with GDA ver 1.1 software. Gene diversity was estimated with Shannon-Wiener (H`) and statistical differences with *t*-test modified by Hutcheson using Biodiv 5.1 software. Interpopulation comparisons were analyzed with Dice and Rogers-Tanimoto indexes and classification method of Unweighted Pair-Group Method (UPGMA). Genotype distribution was in agreement with HWE ($p > 0.001$), except for D1S1656. FGA and Penta E were the most polymorphic loci with 32 and 25 different alleles, respectively. Heterozygosity ranged from 0.6112 for D22S1045 to 0.9141 for D1S1656. The most discriminating loci were Penta E (0.9852) and FGA (0.9756). The combined power of discrimination and combined power of exclusion were 1.9093×10^{-26} and 99.9999833%, respectively. Gene diversity ranged from 1.21 for D22S1045 to 2.68 for Penta E. Inter-comparison populations did not show significant differences for gene diversity based on allelic frequencies of 22 studied autosomal STR. Our results provide a STR population dataset that allow confident interpretation of paternity tests and criminal cases carried out with this HID system in the Peninsula of Yucatan.

1. Introduction

People from the Peninsula of Yucatán are an admixed population composed of Mayan ethnicity as native American ancestry, European, and Asian ancestry at Southeast, Mexico. Short tandem repeat (STR) polymorphisms are mainly used in forensic fields, for paternity tests and individual identification. The implementation of STR in forensic casework requires population validation that includes estimation of forensic statistical parameters [1], given the development of new genetic systems with a higher number of STRs, which are poorly studied in Mexican Mestizo populations. Indices of diversity computed with STR have shown that geography is the main factor shaping the variation of genetic diversity across populations. A smooth gradient of genetic variation is observed between geographic groups rather than abrupt changes [2]. Since, Yucatan STR databases are based on a limited sample size and on HID systems with few STRs, we obtained the forensic parameters for 22 autosomal STRs in the Península of Yucatán, at Southeast, Mexico.

* Corresponding author.
E-mail address: lizbeth@correo.uady.mx (L. González-Herrera).

https://doi.org/10.1016/j.fsigss.2019.10.063
Received 13 September 2019; Received in revised form 4 October 2019; Accepted 7 October 2019
Available online 14 October 2019
1875-1768/

Table 1
Forensic parameters of 22 autosomal STRs of Power Plex Fusion system in 733 Mexican-Mestizos from Peninsula of Yucatan, Mexico. PD: Power of discrimination; PIC: Polymorphic information content; PE: Power of exclusion; TPI: Typical paternity index; MAF: Minimum allele frequency; Ne: No. of effective alleles; He: Observed heterozygosity; HWE: Hardy-Weinberg equilibrium; GD: Gene diversity.

	PD	PIC	PE	TPI	MAF	Ne	He	HWE	No. alleles	GD
D3S1358	0.8569	0.6381	0.3488	1.4096	0.0038	3.152	0.6453	0.4518	9	1.39
D1S1656	0.9736	0.8746	0.8242	5.8175	0.0047	8.723	0.9141	0.0079	18	2.33
D2S441	0.8466	0.6322	0.3433	1.3935	0.0037	2.927	0.6412	0.5403	16	1.47
D10S1248	0.8714	0.6706	0.4495	1.7452	0.0039	3.353	0.7135	0.1369	11	1.45
D13S317	0.9481	0.8046	0.6133	2.5993	0.0042	5.795	0.8076	0.5103	11	1.88
PENTA E	0.9852	0.9058	0.7963	5.0205	0.0046	11.359	0.9004	0.4534	25	2.68
D16S539	0.9161	0.7415	0.546	2.1815	0.0041	4.473	0.7708	0.5261	12	1.65
D18S51	0.968	0.854	0.7136	3.5583	0.0044	7.576	0.8595	0.6639	16	2.2
D2S1338	0.9594	0.8351	0.7001	3.3935	0.0044	6.726	0.8527	0.1349	13	2.1
CSF1PO	0.8832	0.7016	0.4873	1.899	0.004	3.895	0.7367	0.3679	15	1.61
PENTA D	0.944	0.7997	0.676	3.1325	0.0043	5.672	0.8404	0.5832	17	1.89
TH01	0.9062	0.685	0.467	1.8144	0.004	3.684	0.7244	0.4977	7	1.45
VWA	0.8961	0.7065	0.485	1.8892	0.004	3.896	0.7353	0.4715	10	1.59
D21S11	0.9529	0.822	0.6184	2.6367	0.0042	6.226	0.8104	0.2196	24	2.18
D7S820	0.9126	0.7399	0.593	2.4597	0.0042	4.433	0.7967	0.9828	12	1.68
D5S818	0.8648	0.6475	0.4259	1.6584	0.0039	3.157	0.6985	0.2817	9	1.46
TPOX	0.8702	0.6714	0.4032	1.5797	0.0038	3.517	0.6835	0.1266	9	1.46
D8S1179	0.9219	0.7521	0.568	2.305	0.0041	4.59	0.7831	0.1483	12	1.73
D12S391	0.9581	0.8277	0.6733	3.1059	0.0043	6.464	0.839	0.4560	21	2.15
D19S433	0.9597	0.8329	0.6787	3.1595	0.0043	6.63	0.8417	0.2662	23	2.17
FGA	0.9756	0.8832	0.7629	4.3118	0.0045	9.335	0.884	0.0546	32	2.46
D22S1045	0.7935	0.557	0.3045	1.286	0.0037	2.683	0.6112	0.1410	11	1.21

2. Materials and methods

We included 733 unrelated volunteers who participated in paternity testing at a private laboratory where attend people from Península of Yucatán (Campeche, Yucatán and Quintana Roo, Mexico); as well as volunteers from the general population, with the following inclusion criteria: Residence, to be born and to have ancestors at least two generations living and to be born in the geographical region of Península de Yucatán. Buccal swabs samples were analyzed for direct PCR multiplex amplification of 22 autosomal STRs using the PowerPlex® Fusion System Promega kit (Promega Corp., Madison WI, USA). Separation of amplified DNA fragments was performed employing capillary electrophoresis in an ABI Prism 310 Genetic Analyzer (Applied Biosystems). Genotyping was performed after comparison of STR fragments to the allelic ladder and internal size standard using GeneMapper ID v3.2 software. All steps were according to the laboratory internal control standards and proficiency testing provided by Promega Corporation. Written informed consent form was signed by each participant according to the ethical guidelines of the Helsinki Declaration.

Forensic parameters of population genetics including heterozygosity (He), Power of Discrimination (PD), Polymorphic Information Content (PIC), Power of Exclusion (PE) and Typical Paternity Index (TPI) were calculated with the PowerStats 1.2 Software. The Hardy–Weinberg equilibrium deviation for each locus was verified with the exact-test, using GDA ver 1.1 software. Genetic diversity was estimated from the obtained allele frequencies for each locus with Shanon-Wiener (*H'*) index, and the *t* test modified by Hutcheson, which were estimated with Biodiv 5.1 software.

The similarity between the STR's markers based on allele frequencies recorded, was estimated by the Dice index and composition with Rogers-Tanimoto index, both for quantitative data. A cluster analysis was applied with Unweighted Pair-Group Method (UPGMA). Genetic relatedness was obtained comparing allele distribution and frequency of Península of Yucatan with STRs datasets reported at the National Institute of Standards and Technology (NIST) [3], and other ethnically related Mexican Mestizo populations from the West Region [4], Monterrey [5] and Mexico City [6].

3. Results

Genotype distribution was in agreement with Hardy–Weinberg expectations after Bonferroni correction ($p > 0.001$), except for D1S1656. We observed 93 different alleles. FGA was the marker with the highest number of alleles (32 alleles). D1S1656 and Penta E displayed the highest heterozygosity: 0.9141 and 0.9004 respectively. Penta E and FGA showed the highest power of discrimination, 0.9852 and 0.9756, respectively. The combined PD and PE were 1.9093×10^{-26} and 99.9999833%, respectively. Gene diversity ranged from 1.21 for D22S1045 to 2.68 for Penta E. Forensic parameters and gene diversity of autosomal STR are shown in Table 1. Interpopulation comparison did not show significant differences in gene diversity of allele distribution among global populations nor among Mexican Mestizo population ethnically related, $p > 0.05$.

4. Discussion

Forensic parameters and gene diversity based on 22 autosomal STR of PowerPlex® Fusion Promega System kit, were estimated for the population from Peninsula of Yucatán, Mexico, which has been poorly studied about STR datasets contained in new HID systems with more autosomal STRs, such as PowerPlex® Fusion Promega System kit. Forensic parameters show that, although FGA has the highest number of alleles; Penta E was the STR with the highest gene diversity, as well as the highest power of discrimination; and the second in heterozygosity, suggesting Penta E as the most informative and polymorphic STR. D22S1045 was the least informative (1.21).

Gene diversity indices based on 22 autosomal STRs, were similar overall among all studied populations, however Mexican Mestizo populations, including Hispanics from Southwest, form a cluster. In this cluster, distribution of autosomal studied STRs of the population of Peninsula of Yucatán was more similar with the allelic distribution of Mexico City and Monterrey. Similar relation between the Peninsula of Yucatán and Central Mexico, have been found previously in which "the Mayan component" is present at 10–20% in central Mexican natives consistent with the identity by descent and with migration edges connecting the regions, suggesting that gene flow between the two regions has been ongoing for a long time [7]. Genetic diversity observed in Mexican Mestizos is related to differential Native American and

European ancestral contribution [8]. Native American component in individuals from the Southeast of Mexico is predominantly related to the Mayans, while in individuals from Central Mexico is related most closely to Nahuas [7]. The Northern Mexican populations have the highest European ancestral contribution, whereas Southern Mexican populations have the highest Amerindian ancestry. Findings provide a STR population dataset that allow confident interpretation of paternity tests and criminal cases carried out with this HID system in the studied population.

5. Conclusion

Our results provide an STR population dataset that allow confident interpretation of paternity tests and criminal cases carried out with this HID system in the Peninsula of Yucatan, Mexico. Penta E is the most polymorphic and informative STR, being the most discriminating and with the highest gene diversity. The combined power of discrimination and power of exclusion were 1.9093×10^{-26} and 99.9999833%, respectively. Gene diversity based on these autosomal STRs show similarities among Mexican ethnically related populations.

Declaration of Competing Interest

Authors declare that they do not have conflict of interest of any kind.

Acknowledgments

We sincerely thank to DIMYGEN Laboratorio Staff, Andrés Cruces, Aurea Acosta and Gisseth Magaña for their assistance and support.

References

[1] J.M. Butler, Advanced Topics in Forensic DNA Typing: Interpretation, Elsevier Academic Press, London UK, 2014.
[2] N. Silva, L. Pereira, E. Poloni, M. Currat, Human neutral genetic variation and forensic STR data, PLoS One 7 (2012) e49666 doi:10.1371/ journal.pone.0049666.
[3] C.R. Hill, D.L. Duewer, M.C. Kline, M.D. Coble, J.M. Butler, U.S. Population data for 29 autosomal STR loci, Forensic Sci. Int. Genet. 7 (2013) e82-e83.
[4] J.A. Aguilar-Velázquez, G. Martínez-Cortés, A. Inclán-Sánchez, O. Romero Rentería, X.X. Díaz-Navarro, H. Rangel-Villalobos, Population data of 23 STR loci (PowerPlex® Fusion System) in Mexican mestizos from the west region, Int. J. Legal Med. 132 (2016) 1293–1296.
[5] B. Ramos-González, J.A. Aguilar-Velázquez, M.L. Chávez-Briones, J.R. Delgado-Chavarría, E. Alfaro-Lopez, H. Rangel-Villalobos, Population data of 24 STRs in Mexican-Mestizo population from monterrey, nuevo leon (Northeast, Mexico) based on powerplex fusion and global filer kits, Forensic Sci. Int. Genet. 21 (2016) e15-e17.
[6] E. Ramírez-Flores, M. Saiz, D. Villegas-Carmona, M.J. Alvarez-Cubero, Genetic variation of 24 STR loci in a Mexican Mestizo population from Mexico D.F, Forensic Sci. Int. Genet. 10 (2014) 4–6.
[7] A. Moreno-Estrada, C.R. Gignoux, J.C. Fernández-López, F. Zakharia, et al., The genetics of Mexico recapitulates Native American substructure and affects biomedical traits, Science 344 (2014) 1280–1285, https://doi.org/10.1126/science.1251688.
[8] I. Silva-Zolezzi, A. Hidalgo-Miranda, J. Estrada-Gil, J.C. Fernandez-Lopez, et al., Analysis of genomic diversity in Mexican Mestizo populations to develop genomic medicine in Mexico, Proc. Natl. Acad. Sci. U.S.A. 106 (2009) 8611–8616, https://doi.org/10.1073/pnas.0903045106.