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Genetic variability of 17 Y chromosome STRs in two Native American populations from Argentina

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Abstract. Seventeen Y-STRs (DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385, DYS437, DYS438, DYS439, DYS448, DYS456, DYS458, DYS635, GATA H4) were analyzed in two Native American populations, namely, Tobas ($N=49$) and Collas ($N=29$), settled in the North and Northwest regions of Argentina, respectively. Standard diversity indices and haplotype frequencies were estimated. Genetic distance between both population was estimated by mean of F_{st} (R_{st}) test. Statistical tests were performed using Arlequin software Ver 2.000. Thirty-three and fifteen different complete haplotypes were observed for the Tobas and Collas, respectively. Haplotype diversity was 0.9769 ± 0.01 for Tobas and 0.9497 ± 0.02 for Collas. A new variant, present in thirteen individuals, was identified at DYS385 loci in Tobas. At DYS448, two alleles were found in two samples from Toba population and in one sample from Collas. No shared haplotypes were found between the two populations. A significant F_{st} value of 0.1466 was obtained in the pairwise comparison between the two populations ($P=0.00 \pm 0.0$). © 2006 Published by Elsevier B.V.

Keywords: Y-STR; Argentina; Amerindian; Population genetics; Forensic

1. Introduction

Y-STR haplotyping in different populations has a relevant importance in forensic genetics and anthropological studies. The aim of this work was to report haplotypes and molecular diversity indexes for 17 Y-STRs in two Native American populations from

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Table 1
Haplotypes with two alleles at DY448

<i>n</i>	Population	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385	DYS393	DYS391	DYS439	DYS635	DYS392	GATA H4	DYS437	DYS438	DYS448
1	C	17	12	23	30	16	16	15,16	13	9	12	21	12	28	16	10	19,20
2	T	15	13	24	32	17	13	13,16	13	10	12	22	14	29	15	12	20,21

C: Colla; T: Toba.

Argentina, namely, Tobas and Collas, settled in Chaco and Tucumán provinces, respectively, at the North and Northwest region of Argentina. Both populations inhabit in isolated areas, with little interaction with individuals outside their communities, so they still keep their cultural and social traditions.

2. Materials and methods

Forty-nine and twenty-nine males from the Toba and Colla community, respectively, were studied. DNA was extracted from blood samples of non-related individuals by means of standard procedures. Amplification of the 17 Y-STRs was performed with the AmpFISTR® Yfiler kit according to manufacturer's instructions (AmpFISTR® Yfiler PCR Amplification Kit, User's Manual Applied Biosystems). PCR products were analyzed in an ABI PRISM 310 genetic analyzer. Reference ladders provided with the kit were used for allele assignment. Standard diversity indexes, *F_{st}* (*R_{st}*) and haplotype frequencies were calculated using the Arlequin software, version 2.000 [1].

3. Results and discussion

Haplotypes for the 17 STRs analyzed are available upon request to corresponding author.

No shared haplotypes were observed between the Toba and Colla populations. Haplotype diversity was 0.9769 ± 0.01 for Tobas and 0.9497 ± 0.02 for Collas, lower values than those observed in most populations. A significant *F_{st}* value of 0.1466 was obtained at the pairwise comparison between the two populations ($P=0.00 \pm 0.0$). A new variant was identified at *DYS385* loci in Tobas, present in thirteen haplotypes. Sequencing of this allele revealed the following structure: 5'-(*gaaa*)₄ *gaaaa* (*gaaa*)₁₁-3'. Two samples from Toba population and one sample from Collas had two alleles at *DYS448* (Table 1). Haplotypes with duplicated alleles were not used for calculation of diversity indexes, neither for population comparisons. These results contribute to enlarge the data available at public databases of current use in forensic and provide useful data for evolutionary studies.

Acknowledgements

This work was partially supported by POCTI, Programa Operacional Ciência, from Fundação para a Ciência e Tecnologia.

Reference

- [1] S. Schneider, D. Roessli, L. Excoffier, Arlequin Version 2000. A Software for Population Genetic Data Analysis, University of Geneva, 2000.