



Native American Y-STR haplotyping: Its forensic relevance in Argentina



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ARTICLE INFO

Article history:

Received 4 September 2013

Accepted 2 October 2013

Keywords:

Native American

Y-STRs

Haplogroup Q-M3

Forensic reference database

ABSTRACT

Y-STR markers, namely YHRD minimal haplotype with additional DYS437, DYS438, and DYS439 markers, were investigated in a set of 236 samples of individuals belonging to Mataco–Guaycurú speaking tribes, inhabiting communities in Northern and Central Argentina. One specific Amerindian Y-SNP was also typed in order to identify Native Y chromosomal haplotypes. Our results show that 86% of the samples belong to haplogroup Q-M3 and 67% of the haplotypes were unique and never found before in the YHRD database.

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1. Introduction

The Argentinean population is the result of complex admixture events. Major interactions took place between Native Americans, European conquerors, and immigrants. Nowadays, autochthonous people represent only 2.3% of the extant population. Due to discrimination and poverty these groups tend to live in social isolation and prone to perpetrate criminal acts, as in any other social group. Taking into account that those populations show differential allele or haplotype frequencies, its research is relevant for the forensic interpretation. Aiming to investigate the informativeness of the Y-STR markers, four ethnic groups belonging to Mataco–Guaycurú linguistic branch were analyzed.

2. Individuals, materials and methods

A set of 236 samples of south Amerindians belonging to Mataco–Guaycurú speaking tribes, namely Toba (To), Pilaga (Pi), Wichi (Wi) and Mocovi (Mo) ethnicities, inhabiting Northern and Central Argentina were selected. Haplotype analysis comprised YHRD minimal haplotype with additional DYS437, DYS438, and DYS439 Y-STRs. Native American haplogroup defining SNP M3 was typed by multiplex Real Time PCR followed by High Resolution

Melting analysis in order to identify the most frequent Amerindian haplotypes [1].

3. Results and discussion

From the 202 analyzed Q-M3 haplotypes, 135 were unique (66.83%), and 17 were shared between different groups with frequencies ranging from 0.99% to 10.9% (Table 1). From these, only three were found out of Argentina, in isolated cases from Native American people or admixed populations in America. None of these haplotypes were found in Argentinean males of European Ancestry (YHRD, release 44). Fig. 1 shows the relationship between these haplotypes, where the mutation per locus ranged from 1 to 6 (in DYS385).

The highest genetic distances were observed between Mocovi and other groups. Similar figures were observed in mitochondrial DNA analysis, where Mocovi seems to be the most different [2]. Previous investigations allowed us to find some particular mitochondrial haplotypes that, together with Y-STRs information, might provide a clue of the ethnicity of a sample. Such information might provide to the forensic lab valuable information for reference databases employed for statistical analysis.

Role of funding

This work was supported, in part, by grants UBACyT 2011–2014 to DC and PIP 11420090100232 (CONICET) to AS. DC, CB, MC and AS are members of the Carrera del Investigador Científico y

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Table 1
Most frequent haplotypes in Mataco–Guaycurú speakers (Q-M3 hg).

Code	DYS19	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393	DYS385	DYS437	DYS438	DYS439	Freq
MG1	14	13	30	23	10	14	13	14.17	14	11	12	0.0199
MG2	13	13	31	24	10	14	13	14.16	14	11	13	0.0348
MG3	14	13	29	24	10	14	13	12.14	14	11	12	0.0100
MG4	13	13	30	24	10	14	13	14.17	14	11	12	0.0647
MG5	13	13	31	24	10	14	13	15.17	14	11	13	0.0348
MG6	13	13	30	24	10	14	13	15.21	14	11	12	0.0796
MG7	13	13	31	24	10	14	13	15.21	14	11	14	0.0199
MG8	13	13	30	24	10	14	13	15.20	14	11	12	0.0846
MG9	13	13	30	24	10	15	13	15.16	14	11	13	0.1095
MG10	13	13	32	24	10	14	13	13.16	15	12	12	0.0249
MG11	13	13	31	24	10	14	13	14.17	15	11	13	0.0249
MG12	13	14	31	22	10	13	13	14.18	14	11	11	0.0348
MG13	13	14	31	22	10	13	13	14.19	14	11	11	0.0398
MG14	13	13	30	24	10	16	13	15.17	14	11	13	0.0100
MG15	13	13	30	23	10	14	13	13.18	15	12	13	0.0100
MG16	13	13	32	24	10	14	13	15.17	14	11	13	0.0100
MG17	13	13	29	23	10	16	13	13.13	14	11	13	0.0149

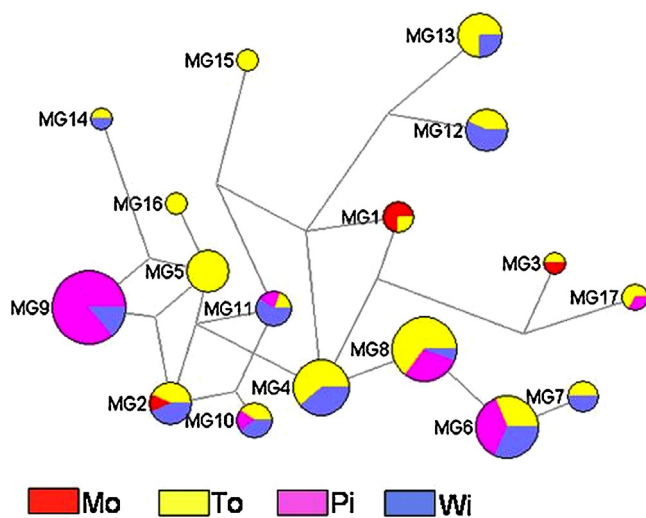


Fig. 1. N-J network of Y-haplotypes (Q-M3 hg).

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Conflict of interest

None.

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