

# Hña hñu Amerindian population from La Sierra Otomí-Tepehua (Mexico) characterised by 14 STR–PCR polymorphisms

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**Abstract.** The purpose of this study is to report allele frequency data of Hña hñu (Otomí) ethnic Amerindian group population sample from La Sierra Otomí-Tepehua (Estado de Hidalgo-Mexico) for 14 STR–PCR polymorphisms (HumTH01, HumPenta D, HumPenta E, HumvWA, D18S51, D16S539, D13S317, D8S1179, D7S820, D5S818, D3S1358, HumCSF1PO, HumFGA and D21S11). © 2003 Elsevier B.V. All rights reserved.

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## 1. Introduction

The Hña hñu population received the name from its language. It belonged to a group of Otopame language, for which, these people were called Otomí population, too. They were established in different regions of Mexico. The group that was studied in this report lived in La Sierra Otomí-Tepehua from Estado de Hidalgo.

## 2. Material and methods

DNA was extracted from hair root samples by Chelex<sup>®</sup> method [1]. PCR were carried out in a 12- $\mu$ l volume containing 0.5 ng DNA template. PCR amplifications were performed according to the recommendations for the AmpFISTR<sup>®</sup> PowerPlex<sup>®</sup> kit (Promega). Genotypes from DNA-amplified products were analysed in capillary gel electrophoresis using an ABI Prim<sup>™</sup> 310 Genetic Analyzer automated laser sequencer [2]. Amplified DNA was mixed with internal fluorescent-labelled size standard and external ladders were also used for adjustment. Allele frequencies were determined. Unbiased estimates of expected

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Table 3

Statistical parameters of forensic interest ( $h$ , heterozygosity value, PD, power discrimination, CE, chance of exclusion) and equilibrium Hardy–Weinberg ( $p$ )

Locus	$n$	$p$	$h$	PD	CE
HumTHO1	83	0.4456	0.699	0.811	0.426
HumPenta D	79	0.8102	0.772	0.924	0.548
HumPenta E	83	0.1496	0.855	0.962	0.706
HumvWA	83	0.2142	0.759	0.882	0.525
D18S51	81	0.1083	0.877	0.950	0.748
D16S539	82	0.5631	0.756	0.878	0.520
D13S317	83	0.6006	0.771	0.928	0.547
D8S1179	83	0.4708	0.723	0.905	0.465
D7S820	83	0.4119	0.771	0.884	0.547
D5S818	82	0.1162	0.720	0.827	0.459
D3S1358	83	0.6873	0.627	0.798	0.324
HumCSF1PO	82	0.4054	0.622	0.850	0.318
HumFGA	83	0.3668	0.904	0.961	0.803
D21S11	83	0.4262	0.880	0.948	0.754

Table 4

Comparison between two Otomí populations; one lives in El Valle de Ixmiquilpan and the other in La Sierra Otomí-Tepehua

Locus	Probability
HumTHO1	0.1702
HumvWA	0.1179
D18S51	0.2521
D16S539	0.0662
D13S317	0.8368
D8S1179	0.3240
D7S820	0.2655
D5S818	0.2481
D3S1358	0.2877
HumCSF1PO	0.2741
HumFGA	0.0804
D21S11	0.0042

### 3. Results

The allele frequencies observed in each system in the Hña hñu Amerindian population are shown in Tables 1 and 2. In Table 3, we resumed the forensic parameters ( $h$ , heterozygosity index, CE chance exclusion and PD power discrimination) [3] and the equilibrium Hardy–Weinberg ( $p$ ) [4].

### 4. Discussion

A great genetic affinity has been obtained in comparison with the previously published Otomí population from El Valle de Ixmiquilpan (Table 4).

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