

Origin of Mexican Nahuas (Aztecs) according to HLA genes and their relationships with worldwide populations

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Abstract

A Nahua Aztec isolated group from Morelos State (Mexico) was studied for their HLA profile. The relationship with other Amerindians and worldwide populations was studied by using 13,818 chromosomes and calculating Nei's chord genetic distances (DA), neighbor-joining dendrograms and correspondence multidimensional values.

Three new HLA extended haplotypes were found in our group: A*30-B*49-DRB1*1001-DQB1*0501 (the most frequent one in this population), A*02-B*52-DRB1*1402-DQB1*0301 and A*68-B*61-DRB1*1602-DQB1*0303.

Both genetic distances and correspondence analyses clearly show that our Nahua isolated group is genetically close to some of the most ancient groups living in Mexico (Mayans, Zapotecs, Mixtecs). This suggests that Nahua language (Nahuatl) may have been imposed to scattered groups throughout Mexico; otherwise Aztecs may have been living in Mexico long before their postulated immigration in the XII century AD.

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1. Introduction

Nahuas are composed by nowadays Mexican ethnic groups who speak Nahuatl. There was a migration about XII–XIII century AD from a northern people probably coming from nowadays Arizona or New Mexico areas, and specifically from a city called Aztlan. These people called themselves Aztecs, but they changed the name at departure calling themselves “Mexitin” or “Mexicas”; they spoke Nahuatl (Navarrete-

Linares, 1998). They were initially agriculturalists, but southwards they learned hunter-gathering when passing through the Chichimecan territory, close to the nowadays USA border (Sonora dessert) (Fig. 1). They also had cultural and theoretically genetic relationships with Chichimecans. In their southwards way they also met Toltecs with whom they also had close relationships. Later, they managed to seize ethnic groups belonging to the main autochthonous Mexican cultures, like Mayan, Mixtecan, Zapotecan and others. They also founded Tenochtitlan at the Chapultepec woods in what is nowadays Mexico City around 1323 AD (Lopez-Lujan, 1983).

At the arrival of the Spanish Hernan Cortes with a small group of people (Arnaiz-Villena et al., 2000) 1519 AD they had a sophisticated society centred in a very heavily populated Tenochtitlan. Spanish attacks and Spanish borne diseases finished with the Mexican (Nahua) Empire.

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Fig. 1. Inset: postulated Mexicas immigration into Mexico. Figure shows the relatively isolated little town where Aztec samples were taken from: Santo Domingo Ocotitlan.

However, nowadays there are Nahuatl language speakers in many parts of Mexico (Fig. 2). There are many Nahuatl-speaking originated groups at the city southern area and in many other states such as Morelos, Puebla, Hidalgo, Tlaxcala, San Luis Potosi, Jalisco, Guerrero, Oaxaca, Veracruz and Chiapas. Considering the linguistic classification, we can contemplate four population groups: (a) West Nahuatl, from Toluca, Michoacan, Guerrero and Morelos; (b) Central Nahuatl, from Mexico City, Puebla and Tlaxcala; (c) Septentrional Nahuatl, from San Luis Potosi; (d) East Nahuatl, from Puebla, Veracruz, Oaxaca and Central America.

This may be due to an extension of the original group and subsequent isolation or to language imposition (Nahuatl). It belongs to the Uto-Aztecan family (with 25 different extant languages), that is also spoken by groups living in Mexico, Arizona and New-



Fig. 2. Black spots: "Nahuatl proper" language speaking groups. Dotted spots: Nahuatl language related groups (from north to south: Papagos, Pimas, Tepehuanes, Yaquis, Mayos, Tarahumaras, Guajiros, Coras and Huicholes).

Mexico, like Hopi, Pima, Tarahumara, Shosone and Comanche Amerindians.

In the present work, we aim to study the HLA profile of Mexicas or Nahuatl speaking people from Santo Domingo Ocotitlan (Morelos, Fig. 1) and relating it with other Amerindians (Arnaiz-Villena et al., 2000; Vargas-Alarcon et al., 2006; Infante et al., 1999; Kostyu and Amos, 1981) and worldwide populations in order to establish degrees of genetic relatedness with different populations. The problem of differentiation between Mexicas coming from nowadays Arizona and Mexico and Nahuatl-speaking groups will also be addressed by studying the HLA profile of our Nahuatl-speaking sample from Morelos (Fig. 1).

2. Materials and methods

2.1. Population samples

We studied 85 unrelated healthy individuals from a Nahuatl-speaking and relatively isolated group. They were HLA class I and class II typed and they were living in Santo Domingo Ocotitlan village (Morelos State, Mexico). Each individual was born in Santo Domingo Ocotitlan area, had a Mexican Amerindian physical appearance and their four grandparents were born in the same area and spoke Nahuatl. The origin of all other populations used for comparisons are detailed in Table 1: 13,818 chromosomes were studied in total, including populations from different origins (Caucasoids, Orientals, Negroids, Polynesians, Micronesians, Na-Dene, Eskimos and Amerindians). In particular, the Amerindian group includes groups belonging to the following linguistic families: Macro-Mixteco (Mixtecos, Zapotecans and Mazatecos), Macro-Maya (Mixe and Mayans), Macro-Yuma (Seris), Andean (Quechuans and Aymaras), Chibcha (Arsario, Kogi, Arhuaco and Cayapa), Arawak (Wayu), and Ge Pano Caribe (Xavantes, Mataco and Toba).

2.2. HLA typing and DNA sequencing

HLA class I (A and B) and class II (DRB1 and DQB1) allele families typing was performed by polymerase chain reaction-sequence specific oligonucleotide (PCR-SSO) reverse dot blot hybridization (Amplior, Hoffmann La Roche, Basel, Switzerland) (according to IMGT/HLA version 2.6, July 2004). HLA-DRB1 and DQB1 high-resolution typing was done by DNA sequencing in a Perkin-Elmer 310 automated DNA sequencer (Foster City, CA, USA). The sequences were analyzed using the IMGT/HLA sequence database (<http://www.ebi.ac.uk/imgt/hla/align.html>).

2.3. Statistical analyses

Statistical analyses were performed with Arlequin v2.0 software kindly provided by Schneider (Schneider et al., 2000). In summary, this program calculated HLA-A, -B, -DRB1, and -DQB1 allele frequencies, Hardy-Weinberg equilibrium and the linkage disequilibrium (D' ; also named LD) (Imanishi et al., 1992b); their level of significance (P) for 2×2 comparisons was determined (Mattiuz et al., 1970). In addition, the most

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