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Molecular Immunology 43 (2006) 1881–1889

Molecular Immunology

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HLA genes in Lamas Peruvian–Amazonian Amerindians

Juan Moscoso [a,1], Segundo Seclen [b,1], Juan I. Serrano-Vela [a], A. Villena [b], Jorge Martinez-Laso [a], Jorge Zamora [a], Almudena Moreno [a], Juan IRA-Cachafeiro [a], Antonio Arnaiz-Villena [a,*]

[a] *Departments of Inmunologia and Medicina Interna, Hospital 12 Octubre, Hospital Clinico San Carlos, Universidad Complutense, Madrid, Spain*
[b] *Universidad Cayetano Heredia, Lima, Peru*

Received 11 August 2005; received in revised form 11 October 2005; accepted 14 October 2005
Available online 5 December 2005

Abstract

The Lamas Amerindians are the Chancas descents who established before 1532 A.D. (Spanish conquest) at Lamas City, Wayku quarter in a Peruvian–Amazonian province (San Martin).

The Lamas HLA profile shows significant differences with other Amerindians HLA profile, i.e.: (a) a higher number of newly found haplotypes compared to other studied Amerindian populations, particularly HLA-A*02-B*48-DRB1*0403-DQB1*0302, A*02-B*48-DRB1*0804-DQB1*0402 and A*02-B*40-DRB1*0407-DQB1*0302; (b) a relative high frequency of HLA-DRB1*0901 (a high frequency southern Asian allele) and HLA-B*48 (a Na-Dene, Siberian and Eskimo allele); both alleles are also found frequently in Quechuas and Aymaras, but not in many other (particularly Meso American) Amerindians and (c) correspondence and neighbor-joining dendrogram analyses show that Lamas (Chancas) may have an origin close to Amazonian Indians that later reached the Andean altiplano.

Keywords: Aymaras; Chancas; HLA; Lamas Amerindians; Quechuas

1. Introduction

The First Native Americans are believed to have populated America coming from Asia through the Bering land bridge between 30,000 and 12,000 years before present (BP). These conclusions have been based on cultural, morphological and genetic similarities between American and Asian populations (Crawford, 1998). Both Siberia (Crawford, 1998) and Mongolia (Kolman et al., 1996; Merriwether et al., 1996) have been put forward as the most approximate places of Amerindians origin in Asia.

Greenberg postulated the triple migration theory for explaining the Americas peopling on linguistic bases (Greenberg et al., 1986): Amerindians (most north and south American Indians; 12,000 BP), Na-Dene (Athabaskans, Navajo, Apache; 8000 BP) and Eskimo-Aleuts (6000 BP). Studies on Y chromosome showed that more than one paternal founder haplotype arrived in America during different migrations (Karafet et al., 1999), probably from Siberia (Santos et al., 1999).

The northern Andean cultural area has been settled by men since at least 20,000 year B.C. [Ayacucho Valley (Davies, 1998)]. Other important civilizations have also been identified south Lima and the Titicaca Lake area cultural development was probably independent from others and included early groups of Aymara-speaking people [Collas, Lupacas, Pacajes, Collaguas, Callahuayas, Charcas, Caracaras, etc., whose identity and origin are obscure (Canahuire-Ccama, 1999; Salomon and Schwartz, 1999)]; Chiripa city (southern Titicaca shore) remains show that a particular cultural development was going on here by 1800 B.C. (Davies, 1998). Later, Quechua speaking people originated from the Titicaca Lake Area and formed a big empire (Martinez-Laso et al., 2005). Other non-Quechua speaking people, like the “Charcas”, existed south Titicaca Lake (Fig. 1) (Salomon and Schwartz, 1999).

The Inca (Quechua-speaking) empire conquered areas near Cuzco, including this city itself after a ferocious fight with the “Chanca” Amerindians. This occurred not long before the Spanish conquerors seized the Inca Empire and its king, Atahualpa,

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* Corresponding author. Tel.: +34 913941632; fax: +34 913941641.
E-mail address: aarnaiz@med.ucm.es (A. Arnaiz-Villena).
URL: http://chopo.pntic.mec.es/biolmol.

[1] The contributions of these authors’s are equal and the order of authorship is arbitrary.

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doi:10.1016/j.molimm.2005.10.013

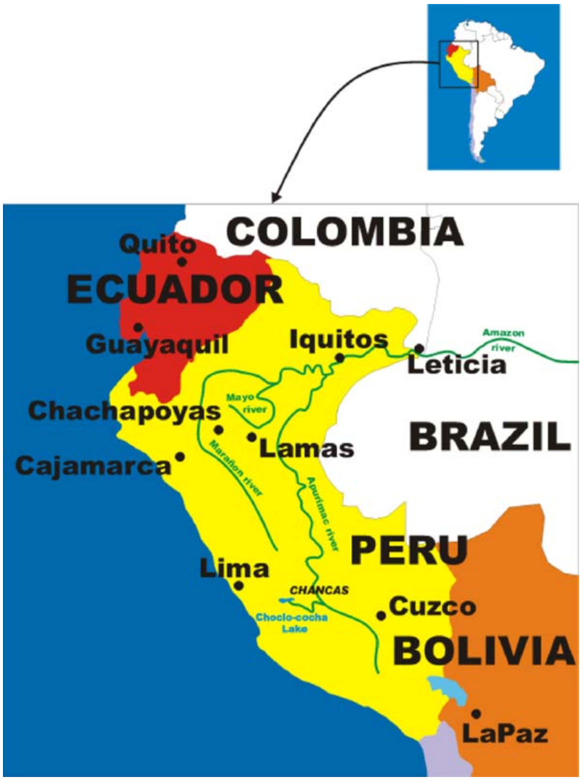

Fig. 1. South American map showing Lamas and other relevant names mentioned in the text.

at Cajamarca in 1535 A.D. (Davies, 1998). The "Chancas" Amerindians were the Lamas (Waiku) precursors who were defeated by the Incas in their original settlements close to Choclococha Lake (4605 m high), Apurimac River (Kauffmann-Doig, 1992) and also Cuzco and fled to the forest (Fig. 1), in the nowadays region and city of Lamas, and established in the so called Wayku quarter (Junquera-Rubio, 1998). The original Lama language was extinct and the Chachapoyas and Lamas ethnic groups speak today very similar Quechua dialects, imposed first by the Incas and later by the Spaniards (Taylor, 2000). Lamas practice witchcraft and initiation rites with hallucinogen plants (mainly "Ayawaska") and they have taken numerous Spanish words, which are included in their Quechua dialect (Tessmann, 1999).

The aim of the present work is: (a) to study of the Lamas HLA profile by HLA classes I and II indirect (or direct) DNA HLA sequencing; (b) comparing their profile with other First Native Americans and (c) comparing Lama HLA frequencies with worldwide populations in order to gather more data about the question of the Amerindian HLA uniqueness (Arnaiz-Villena et al., 2000, 2005; Gomez-Casado et al., 2003; Martinez-Laso et al., 2005).

2. Materials and methods

2.1. Population sample

Eighty-three healthy unrelated individuals from the Lama population (Peru) were HLA classes I and II typed. They were ancestrally living in Lamas City (San Martin province), in a quarter called Wayku near Mayo River (tributary of Amazon River), nowadays inhabited by 4000 people. Their ancestors were settled down in the area for at least three generations. They were blood donors who volunteered for this study and spoke a Quechua dialect partially shared with the Chachapoyas Indians and little Spanish language. Ethical laws were kept with explicit consent from individuals. No genetic analyses had previously been performed to our knowledge in Lamas.

The origin of all other populations used for comparisons are detailed in Table 1. 15,230 chromosomes were used for this study, including populations from very different geographical origins: Europeans, Orientals, Polynesians, Micronesians, Na-Dene, Eskimos, Negroids and Amerindians. In particular, the Amerindian group includes tribes from the following linguistic families Macro-Mixteco (Mixtecan and Zapotecan), Macro-Maya (Mixe), Macro-Yuma (Seris), Chibcha (Arsario, Kogi, Arhuaco and Cayapa), Arawak (Wayu), Ge Pano Caribe (Xavantes, Mataco, Kaingang and Toba) and other Andean groups like Aymara (Swadesh, 1959; Ruhlen, 1991).

2.2. HLA typing and DNA sequencing

HLA class I (A and B) and HLA class II (DRB1 and DQB1) typings were performed using a reverse dot-blot technique with the Automated Innolipa system (Innogenetics N.V., Zwijndrecht, Belgium). HLA-A, -B, -DRB1 and -DQB1 allele DNA sequencing was only done in an automated Applied Biosystems ABI-373 DNA sequencer, when this indirect DNA typing yielded ambiguous results (Arnaiz-Villena et al., 1992).

2.3. Statistical analysis

Statistical analysis was performed with Arlequin v.2.000 software kindly provided by Schneider et al. (2000). In summary, this program calculated HLA-A, -B, -DRB1 and -DQB1 allele frequencies, Hardy–Weinberg equilibrium and the linkage disequilibrium between two alleles at two different loci. Their level of significance (p) for 2×2 comparisons was determined as previously described (Imanishi et al., 1992a,b). In addition, the frequency of maximum likelihood complete presumed haplotypes were deduced from: (1) the 2–4 HLA loci haplotype frequencies (Imanishi et al., 1992a,b); (2) the previously described haplotypes in other populations (Imanishi et al., 1992a,b) and (3) haplotypes if they appeared in two or more individuals and the alternative haplotype was well defined (Imanishi et al., 1992a,b). In order to compare phenotype and haplotype HLA frequencies with other populations, the reference tables of the 11th and 12th International HLA Workshops were used [(Clayton and Lonjou, 1997; Imanishi et al., 1992c), see also Table 1]. Non-rooted dendrograms were constructed with the allelic frequencies using the neighbor-joining (NJ) method (Saitou and Nei, 1987) with the genetic distances between populations [DA (Nei, 1972)], using DISPAN software comprising the programs GNKDST and TREEVIEW (Nei, 1973; Nei et al., 1983). Correspondence analysis in n dimensions and its bi-dimensional representation was carried out using the VISTA v5.02 computer program [(Young