

Mitochondrial DNA Analysis of Ancient Peruvian Highlander

K - S ¹* N A ² S ³ G ³ I S ⁴

¹De a e f A h g , Na a a e ca a ed b H a H B a s h a a d e a a f c h e h e a f P e h a e
 f Pa ca ca cha, Pa a ac a, a d H a a ea he fa ed de ed e . O d gge a g ge e c
 I ca a e a e a d a e f Mach P cch a af be ee a ed a e e H a c d d a a d
 a a ed b e a e cha eac , a d he e de A dea h g h a d e . A e a a f h e
 e e c a ed h a c e a d de DNA f a - Mach P cch e g c a c ec gge ha he e -
 Ce a A dea a ea e he h he ed d g- de he e e e a ed g f a e f a
 e h g h a d g . The c a d c d g eg f c a a a d h g h a d eg e ca ed b he I ca a e
 he ch d a DNA (DNA) f 35 d d a h f a ed e . O e a , d d ca e ha he
 g e e e e ced, a d he ha g f each d- a ed d d a f Pa ca ca cha a d Pa a ac a
 d a e e de e ed. The fe e c da a f he ha - e e d ge h g h a d e h ded e
 g f he e a e h cea h e f
 de ech a a d A a a a he Pe a

in alliance and road and in a chieftain and ceramic
style, the history of Paucacancha dates back to the reign
of the Inca king Tupa Inca (son of the king Pachacuti
Inca Yupanqui), a portrait in the late 15th century
(Kendall, 1985). Based on archaeological, ceramic, and other
evidence found in association, the belief that Bingham
established Paucacancha and Paucallanca can be assigned
to the period of the Inca control of the Uchumbamba Valley,
from ca. mid-15th to early 16th century (Bingham, 1913;
Kendall, 1985; MacCord, 1923).

Over the past 20 years, in addition to the aforementioned
work led by Kendall, there have been much effort
of the Inca and pre-Inca occupation along the "Sa-

expressed in the HVR 1 region. For the characterization of

inde enden], using the monoallelic PCR method primarily because of the robustness of PCR.

A multiplex of the PCR products was analyzed by electrophoresis in an 8-cm native polyacrylamide gel (10% T, 5% C) containing $1 \times$ TBE buffer (pH 8.0) in running buffer ($0.5 \times$ TBE, pH 8.0). DNA bands were detected by autoradiography following in situ hybridization with a probe (Fig. 2).

Data analysis

With improved knowledge of the global mtDNA tree in recent years, an understanding of the structure of mtDNA data and analyzing the mtDNA haplogroups in the global mtDNA tree have been improved. Consequently, we identified four major haplogroups and their subgroups (Alte-Silva et al., 2000; Bandelt et al., 2001; Kilgus et al., 2002; Kong et al., 2003; Macaulay et al., 1999; Malmström et al., 2003; Qin et al., 1999; Yao et al., 2002, 2003).

The effects were assigned each mtDNA haplogroup according to the HVR 1, HVR 2, and coding-region data, using the data and classification described above, which had each sample allocated to the haplogroup named haplogroup which it belonged. If the haplogroup had further characterized subgroups, an asterisk was attached to the name of the haplogroup indicating that the haplogroup could not be identified from the (Table 3). Since several segments of the same mtDNA were analyzed independently, multiple cases were taken to avoid artificial recombination caused by potential sample collection. After analyzing the mtDNA haplogroups, we classified them from the inferential line, based on the nucleotide change observed in the control and coding region.

To elucidate biological relationships, the 4420-1...4493a

TABLE 3. Nucleotide sequence of the P gene of the 1999 H5N1 influenza A virus.

Site and position	Ha log ₁₀	Major line	Mutation in segment 1		APLP analysis
			16209-16402 (16000+)	128-267 ²	
Paucan				10382-10465 (10000+)	
195	A*	A*-1	223 290 319 362	CRS	T
208	A*	A*-1	223 290 319 362	CRS	T
216	A*	A*-2	217 223 266 290 319 343T 362	CRS	
192	B4*	B4*-1	217 272 362	CRS	
193	B4*	B4*-2	217 289	CRS	
218	B4*	B4*-2	217 289	CRS	
219	B4*	B4*-3	217 289	CRS	
203	B4*	B4*-3	217	CRS	
210	B4*	B4*-4	217 228 379N	CRS	
212	B4*	B4*-5	214 217 262	CRS	
214	B4*	B4*-6	217 278	CRS	
227	B4*	B4*-7	217 357	CRS	
233	B4*	B4*-8	217 362	CRS	
230	B4a	B4a-1	217 261 319	CRS	
193	C*	C*-1	223 298 325 327	398 400	C
204	C*	C*-1	223 298 325 327	398 400	C
211	C*	C*-2	223 298 325 327	ND	C
Paucan					
680	B4*	B4*-2	217 289	CRS	
978	B4*	B4*-3	217	CRS	
681	B4*	B4*-9	217 296N 321 363 390	CRS	
686	B4*	B4*-10	217	CRS	
689	B4*	B4*-10	217	CRS	
687	B4*	B4*-11	217	CRS	
974	B4*	B4*-11	217	CRS	
981	B4*	B4*-12	217 268 348 378 379	CRS	
989	B4*	B4*-13	217 294	CRS	
677	B4*	B4*-14	217	CRS	
683	B4a	B4a-2	217 261	CRS	
976	B4a	B4a-3	217 261N 357	CRS	
678	B*	B*-1	217 381	CRS	
682	C*	C*-1	223 298 325 327	398 400	C
975	C*	C*-3	223 246N 298 325 327 373	398 400	C
676	C*	C*-1?	223 298N 325N 327	398 400	C
977	D*	D*-1	325 362N	398 400	C
Haucan					
899	C*	C*-1	223 298 325 327	398 400	C
897	C*	C*-4	223 298 325 327	392 400	C

¹ All of the mutations are in the coding region of the HA1 domain. CRS denotes conserved regions, and N indicates non-conserved regions. S f T indicates a substitution, and d indicates a deletion. Deletion at position 327 is indicated by a bold italicized letter. Nucleotide changes are indicated by bold italicized letters. ² Nucleotide changes are indicated by bold italicized letters. ³ Diagnostic of the mutation in segment 1 is indicated by a bold italicized letter. Diagnostic of the mutation in segment 2 is indicated by a bold italicized letter.

ecore, and enclosing a μ of 61.5% and 70.8%, respectively. In contrast of even individuals from the Haplogroup (only 28.6%) were completely excluded.

Haplogroup distribution for the total sample was as follows: 8.6% A, 65.7% B, 22.9% C, and 2.9% D. Haplogroup frequencies of contemporary Amerindian populations and ancient north coast samples are also shown in Table 4. Frequencies from haplogroup frequencies among regional populations are shown in Table 5. An exact test of differentiation between each pair of populations revealed statistically significant differences between the ancient highlands and contemporary central Andean populations ($F_{ST} = 0.180 \pm 0.054$).

To investigate the relationship among the allelic communities of the total μ of Machu Picchu, mtDNA frequencies of Paucabancha and Paucallanca were compared. Haplogroup frequencies of Paucabancha and Paucallanca are shown in Table 6. Genetic differentiation for the total μ is also shown in Table 7. Mean number of alleles and nucleotide diversity are highlighted in the Paucabancha.

DISCUSSION

Haplogroup profile of individuals examined in the present study

We found that haplogroup B is the most frequent among the total sample analyzed in the Inca-epoch identity of the Uchumbamba Valley, followed by haplogroups C, A, and finally D. The most distinctive feature of the haplogroup profile of individuals examined in the present study is the high frequency of haplogroup B (65.7%; 23 of 35 individuals; Table 3 and 4). Classification of individuals in a maternal lineage led in haplogroup B having at least 18 different lineages in 23 individuals. In other words, the high frequency of haplogroup B is not caused by the concentration of individuals on a specific maternal lineage.

Haplogroup B is the common haplogroup in contemporary Central Andean populations. When the haplogroup profile of the ancient identity of the Uchumbamba Valley is compared with that of others. South American populations, we found a clear similarity to the modern Central Andean populations that are distributed mainly in the Peruvian and Bolivian highlands (Table 4). This finding is not surprising, considering the highland location of the study area.

On the other hand, the ancient highlands considerably differ from individuals of the ancient north coast community in terms of mtDNA haplogroup frequencies. Various lines of archaeological evidence indicate in fact a clear relationship between the ancient north coast populations and contemporary Ecuadorian and Colombian populations (Shimada, 1995, 1999; Shimada et al., 1997, 2000). Relative high frequency of ha-

Antropología e Historia del Perú) and Japanese ethnographic. Yaka Yohji for the analysis in the collection of population genetic data in the mtDNA analysis. Research K.I.S. for the study of the genetic diversity in the Andean region. Science, 135:75017 from the Ministry of Education, Science, Sports and Culture, Japan.

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