

Mitochondrial DNA Analysis of Ancient Peruvian Highlander

K - S ^{1*} N A ² S ³ G ⁴ I S ⁴

¹De a e f A h g , Na a a e ca a ed b H a B gha a he a c e
f Pa ca ca cha, Pa a ac a, a d H a a ea he fa ed
I ca a e a e a d a e f Mach P ch 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 Topa 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
to identify 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 to observe the effect of PCR.

A 1- μ l aliquot of the PCR product was added to 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 ethidium bromide staining in ethidium bromide (Fig. 2).

Data analysis

With improved knowledge of the global mDNA tree in recent years, an understanding of the structure of mDNA data and analyzing the mDNA tree to place in the global mDNA tree have been improved. Consequently, identification of a majority of the major haplogroups and their subgroups (Alte-Silva et al., 2000; Bandelt et al., 2001; Kilgild et al., 2002; Kong et al., 2003; Macaluso et al., 1999; Malmgren et al., 2003; Qinana-Maci et al., 1999; Yao et al., 2002, 2003).

The effect was assigned each mDNA 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 major 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 by the (Table 3). Since sequential segments of the same mDNA were analyzed independently, multiple cases were taken to avoid artificial recombination caused by potential sample errors. After analyzing the mDNA haplogroups, the classification was determined from the information line, based on the nucleotide change observed in the control and coding region.

To elucidate biological relationships between 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	
213	B4*	B4*-2	217 289	CRS	
198	B4*	B4*-2	217 289	CRS	
203	B4*	B4*-3	217	ND	
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
Paallac					
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
Ha					
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/T indicates amino acid substitution, and D indicates deletion. Deletion at position 263 is indicated by a bold italicized letter. A/E indicates amino acid substitution, and N indicates non-conserved regions. Diagonal indicates amino acid substitution in the HA2 domain.

² Nucleotide change at position 263 in segment 1 is indicated by a bold italicized letter. Do not indicate a nucleotide change at a position indicated by a bold italicized letter.

³ Diagonal indicates amino acid substitution in the HA2 domain.

ecore, and enclosing a ϕ of 61.5% and 70.8%, respectively. In contrast of seven individuals from the Haplogroup (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 frequency of contemporary Amerindian population and ancient north coast sample are also shown in Table 4. Frequency from haplogroup frequency among regional population are shown in Table 5. An exact test of differentiation between each site of population revealed statistically significant difference between the ancient highlands and contemporary central Andean population (significance $F = 0.180$, $P = 0.054$).

To investigate the relationship among the allelic combination of the control region of the mitochondrial DNA sequence of Paucabancha and Paucallanca were compared. Haplogroup frequency of Paucabancha and Paucallanca are shown in Table 6. Genetic diversity level for the control region are shown in Table 7. Mean number of alleles difference 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 period identity of the Uchumbamba Valle, 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 indicates the concentration of individuals on a specific maternal lineage.

Haplogroup B is the common haplogroup in contemporary Central Andean population. When the haplogroup profile of the ancient identity of the Uchumbamba Valle is compared with that of others. South American population, we found a clear similarity to the modern Central Andean population 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 mitochondrial haplogroup frequency. Various lines of archaeological evidence indicate in a clear relationship between the ancient north coast population and contemporary Ecuadorian and Colombian population (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 mitochondrial DNA. In: Proceedings of the 13th International Conference on Human Genetics, Kyoto, Japan, 1998. Edited by G. Inoue. Journal of Science, Sports and Culture, Japan.

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