

# Mitochondrial DNA Analysis of Ancient Peruvian Highlander

K - S <sup>1\*</sup> N A <sup>2</sup> S <sup>3</sup> G <sup>4</sup> I S <sup>4</sup>  
<sup>1</sup>D A <sup>g</sup>, N H B <sup>g</sup>  
I , , H M

in allusion and road and its architectural 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 gold image in the late 15th century (Kendall, 1985). Based on architectural, ceramic, and other artifacts 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 Cuzco Inca and Pre-Inca occupation along the "Sa-



expressed in the HVR 1 region. For the characterization of

inde enden], using the mono le PCR method p ma i mi e the ob tne of PCR.

A 1- $\mu$ l ali o of the PCR od c t a e a a ed b elec o ho e i in an 8-cm na i e ol ac lamide gel (10% T, 5% C) con aining 1  $\times$  TBE b ffe ( H 8.0) i h nning b ffe (0.5  $\times$  TBE, H 8.0). DNA band e e de ec ed b l a iole i adia ion af e r aining i h e hidi m b omide (Fig. 2).

### Da a anal i

Wi h im o ed kno ledge of the global m tDNA t ee in ecen ea r, an nde anding of the t c t r e of m tDNA da a and a igning the m tDNA t e p a r lace in the global m tDNA t ee ha e been im li ed. Con ol egion mo if e e iden i ed fo a majo i t of the majo ha log o and r hei bha log o (Al e -Sil a e t al., 2000; Bandel e t al., 2001; Ki iild e t al., 2002; Kong e t al., 2003; Maca la e t al., 1999; Ma ama e t al., 2003; Q in ana-M ci e t al., 1999; Yao e t al., 2002, 2003).

The efo e, e a r igned each m tDNA p ha log o acco ding p the HVR 1, HVR 2, and coding egion da a, ing the da a and cla i ca ion ee de c ibed abo e, ch ha t each am le a lloca ed p the malle t named ha log o p hich i t belonged. If the ha log o had f r the cha ac e i ed bha log o , an a e i k a a ached p the name of the ha log o p indica e ha t the ha log o a t co ld no be iden i ed f he (Table 3). Since e e al egmen t of the ame m tDNA e e anal ed inde enden], me i c lo t ca e a t aken p a o id a i cial eombina ion ca ed b o en jal am le co o e. Af e r a igning the m tDNA p ele an ha log o , e cla i ed hem f r the in p ma e nal line , ba ed on the n cleo ide change ob e e ed in the con trol and coding egion .

To el cid e biological r ela ion hi he4420-1..4493a

ABLE 3. N

Site and specimen number	Material line	Ha log <sub>10</sub>	Major ion in specimen <sup>1</sup>		APLP analysis				
			16209-16402 (16000+)	128-267 <sup>2</sup>	5178	8794	14318	9 b	
Pa cancha					10382-10465 (10000+)				
195	A*-1	A*	223 290 319 362	146 235	CRS	.	T	.	2
208	A*-1	A*	223 290 319 362	146 235	CRS	.	T	.	2
216	A*-2	A*	217 223 266 290 319 343T 362	146 153 235 260	CRS	.	.	.	2
192	B4*-1	B4*	217 272 362	CRS	CRS	.	.	.	I
213	B4*-2	B4*	217 289	143	CRS	.	.	.	I
198	B4*-2	B4*	217 289	143	ND	.	.	.	I
203	B4*-3	B4*	217	146 215	CRS	.	.	.	I
210	B4*-4	B4*	217 228 379N	214	CRS	.	.	.	I
212	B4*-5	B4*	214 217 262	23IN	CRS	.	.	.	I
214	B4*-6	B4*	217 278	146 215	CRS	.	.	.	I
227	B4*-7	B4*	217 357	143	CRS	.	.	.	I
233	B4*-8	B4*	217 362	CRS	CRS	.	.	.	I
230	B4a-1	B4a	217 261 319	CRS	CRS	.	.	.	I
193	C*-1	C*	223 298 325 327	146 249d	398 400	.	.	C	2
204	C*-1	C*	223 298 325 327	146 249d	398 400	.	.	C	2
211	C*-2	C*	223 298 325 327	249d	ND	.	.	C	2
Pa allac									
680	B4*-2	B4*	217 289	143	CRS	.	.	.	I
978	B4*-3	B4*	217	146 215	CRS	.	.	.	I
681	B4*-9	B4*	217 296N 321 363 390	214 234	CRS	.	.	.	I
686	B4*-10	B4*	217	152	CRS	.	.	.	I
689	B4*-10	B4*	217	152	CRS	.	.	.	I
687	B4*-11	B4*	217	CRS	CRS	.	.	.	I
974	B4*-11	B4*	217	CRS	CRS	.	.	.	I
981	B4*-12	B4*	217 268 348 378 379	CRS	CRS	.	.	.	I
989	B4*-13	B4*	217 294	143 210	CRS	.	.	.	I
677	B4*-14	B4*	217	152, 204	CRS	.	.	.	I
683	B4a-2	B4a	217 261	CRS	CRS	.	.	.	I
976	B4a-3	B4a	217 261N 357	143	CRS	.	.	.	I
678	B*-1	B*	217 381	CRS	398	.	.	.	I
682	C*-1	C*	223 298 325 327	146 195 249d	398 400	.	.	C	2
975	C*-3	C*	223 246N 298 325 327 373	CRS	398 400	.	.	C	2
676	C*-1?	C*	223 298N 325N 327	CRS	398 400	.	.	C	2
977	D*-1	D*	325 362N	CRS	398 400	A	.	.	2
Ha a									
899	C*-1	C*	223 298 325 327	398 400	398 400	.	.	C	2
897	C*-4	C*	223 298 325 327	392 400	392 400	.	.	C	2

<sup>1</sup> All of the material lines are identified by Andrieu et al., 1999. CRS denotes the chemical composition of the sample, and N indicates the number of analyses performed.

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

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 pair of population revealed statistically significant difference between the ancient highlands and contemporary central Andean population ( $F_{ST} = 0.180 \pm 0.054$ ).

To investigate the relationship among the allelic community of the total population of Machu Picchu, mtDNA frequency of Paucabancha and Paucallanca were compared. Haplogroup frequency of Paucabancha and Paucallanca are shown in Table 6. Genetic differentiation level for the total population are shown in Table 7. Mean number of alleles difference and nucleotide differentiation 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-tioid 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 a high 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 mtDNA haplogroup frequency. Various lines of archaeological evidence indicate a migration of individuals 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-







