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Pre-Columbian Population Dynamics in Coastal Southern Peru: A Diachronic Investigation of mtDNA Patterns in the Palpa Region by Ancient DNA Analysis



AUTHORS

Markus Reindel + 4



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the sampled individuals are based on the archaeo-
logical context in the graves and secondary on the

TABLE 2. Primers used for the HVR I sequence analysis

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TABLE 3. Primer-/probes used for the analysis of the haplogroup-specific mitochondrial SNPs and 9bp deletion

System ^a	Primer/Probes	Primer- /probe sequences (5'-3') and fluorophores	Conc. (μ M) ^b
HG A np 663 A/G	Upper	AATACACTGAAAATGTTAGACG	0.6
	Lower	GGTGATTAGAGGGTGAAC	0.3
	Sensor	LCRed610-GGCCAGGACCAAACCTATT	0.4
	Anchor	GCTTGCATGTGAATCTTACTAAGAGCTAATAGA-FL	0.2
	Upper	TAATTCCCCTAAAAATCTTGAAATAG	0.3
	Lower	GGTGTGGTTCTCTTAATCT	0.6
HG B 9bp del	Sensor	ATAGCACCCCCCTCTACCCCCTC-FL	0.2

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TABLE 4. Distribution of mtDNA haplogroups in the analyzed population and other prehistoric and contemporary Peruvian populations

Group/Population	n	Haplogroup frequencies					Reference
		A	B	C	D	Other	
Paracas (Peninsula)	10	0.00	0.00	0.30	0.70	0.00	This study
Paracas (Palpa)	28	0.07	0.00	0.14	0.79	0.00	This study
Nasca-Rural (Palpa)	37	0.02	0.11	0.22	0.65	0.00	This study
Nasca-Urban (Palpa)	28	0.00	0.18	0.43	0.39	0.00	This study
Middle Horizon (Palpa)	11	0.00	0.27	0.36	0.36	0.00	This study
Pacapaccari (Highlands)	16	0.00	0.69	0.31	0.00	0.00	This study
Ancient Coast (MH)	36	0.19	0.22	0.06	0.31	0.22	Shimada et al., 2004
Ancient Highlands (Inca)	35	0.09	0.66	0.23	0.03	0.00	Shinoda et al., 2006
ChenChen (MH)	23	0.39	0.39	0.17	0.04	0.00	Lewis et al., 2007
San Martin	22	0.09	0.55	0.05	0.27	0.05	Fuselli et al., 2003
Ancash	33	0.09	0.52	0.18	0.21	0.00	Lewis et al., 2004
Arequipa	22	0.09	0.68	0.14	0.09	0.00	Fuselli et al., 2003
Tayacaja	60	0.21	0.33	0.30	0.13	0.03	Fuselli et al., 2003

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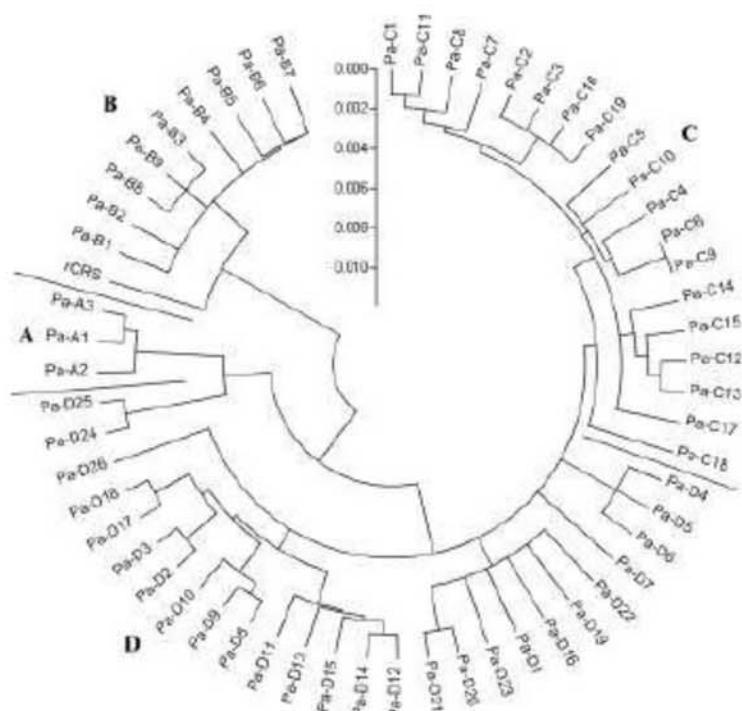
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Fig. 2. Linearized NJ-Tree exhibiting the 57 mitochondrial HVR I haplotypes detected in the prehistoric south Peruvian

1989b). But the values for Paracas-Palpa ($D = -1.2$) and Nasca-rural-Palpa ($D = -1.5$) are close to the significant negative value of $D = -1.6$ (cf. Tajima 1989a, Table 2).

The obtained haplotypes were crosschecked with the available datasets of Native American and Asian populations and the Genographic Project mitochondrial database (Behar et al., 2007). Some of the determined haplotypes lack one or more haplogroup characteristic polymorphisms like PA-C18 missing the C-T transition at np16327 typical for haplogroup C, or haplotypes PA-D24 and D25 missing the T-C transition at np16325, characteristic for D (cf. Table 6). The haplogroup status was independently confirmed by coding region polymorphisms and phylogenetic clustering as shown in the NJ-dendrogram (see Fig. 2). Noticeable is the occurrence of a T-C transition at np 16140 in eight haplotypes belonging to all four haplogroups, and also the np16362 T-C transition—characteristic for groups A and D—observed in four haplotypes belonging to haplogroup C., e.g. PA-C14.

Interpopulation genetic distances were calculated for the populations analyzed in this study and the contemporary Peruvian populations, revealing concordant results for the different distance calculations (not all data shown). An NJ-dendrogram employing the pairwise F_{ST} matrix (Table 8) is shown in Figure 3. An exact test of differentiation between each pair of populations

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TABLE 6. Mitochondrial HVR I haplotypes and their chronological distribution observed in the ancient Peruvian populations^a analyzed in this study

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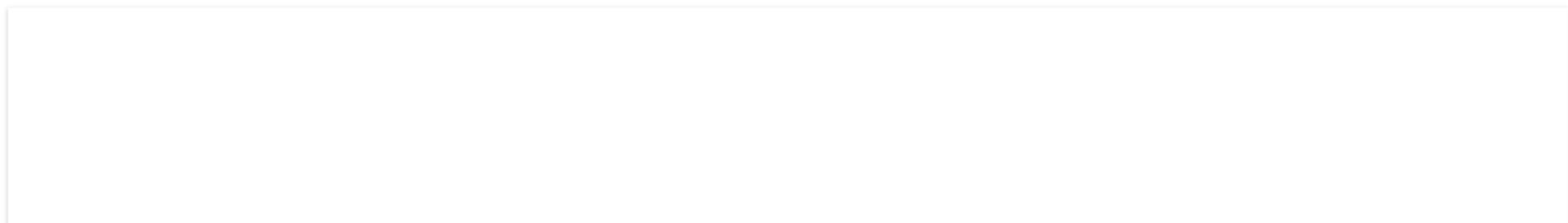
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