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Molecular genetic evidence suggesting treponematosi s in pre-Columbian, Chilean mummies. PK ROGAN and SE LENTZ, Pennsylvania State University College of Medicine, Hershey PA 17033.

Multiple hypotheses explain the origin of treponematosi s and its worldwide dispersion. Paleopathological studies have suggested treponematosi s as the most likely cause for the epidermal and spongiform bone lesions commonly seen in preserved, pre-Columbian, South American human remains. Although the spirochaetes responsible for pinta, yaws, endemic syphilis, and venereal syphilis display substantial antigenic overlap, the ribosomal DNA (rDNA) sequences of each of these pathogens are unique. The objective of this study was to retrieve ancient prokaryotic rDNA sequences to identify, if possible, the etiologic agent(s) of the infection in preserved, mummified remains manifesting ancient treponematosi s. Nucleic acids were extracted from soft tissues (muscle) of 4 individuals with evidence of tertiary treponematosi s excavated from sites at El Morro, Arica (Chinchorro culture) and San Miguel de Azapa (Gentilar culture), Chile. Control amplifications with a modified polymerase chain reaction procedure (pPCR; UCLA Symp. Mol. Cell. Biol. 122: 223-234) demonstrated the recovery of ancient human DNA in each specimen. Prokaryotic pPCR products were obtained for 2 of these Chinchorro individuals, both of which were excavated from the same cemetery. A comparison of cloned ancient bacterial rDNA sequences against all known sequences revealed that 8 of the 10 most similar contemporary relatives were classified as spirochaetes, with 5 of these belonging to the genus *Treponema*. Sequences derived from two different individuals were nearly identical, suggestive of a similar infectious agent. None of the sequences were identical to the ancient isolates. The degree of similarity between the contemporary treponemal species was analogous to that found for the ancient sequences (78-85%). Attempts to amplify 2 different contemporary *T. pallidum* structural genes were unsuccessful, consistent with the possibility either that the ancient and contemporary sequences represent distinct species or that mutations in these genes have occurred which abrogate annealing of the oligonucleotide primers to the ancient template. Other cloned sequences were similar to *Spiroplasma* species as well as potential agents of decomposition. Phylogenetic analysis of the ancient rDNA sequence suggests the closest association with *T. phagedenis*, *T. denticola*, *S. zuelzeriae* and *T. pallidum* rather than other Spirochaetes. These results suggest that ancient treponematosi s in Chile may have been due to a spirochete similar, but not identical, to *T. pallidum*.

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