American bison [1]. They are especially to be commended for the care they took to prevent contamination of their paleo-
logic DNA samples. Their work is consistent with the hypothesis of Sreevatsan et al. [2] concerning the origins of modern species of mycobacteria, and it suggests that a prehistoric precursor of Mycobacterium tuberculosis was globally distributed.

A remaining issue of interest is which species of mycobacteria infected humans in the pre-Columbian Americas [3, 4]. Because the Bering Strait became open water >9000 years ago, one must suppose that the early mycobacterial species that caused human disease in the Western Hemisphere were established and geographically isolated by that time. It could have been either Mycobacterium bovis or M. tuberculosis; I have argued that it was most likely the latter [4]. It is unlikely to have been the organism present in the prehistoric bison, because that organism did not persist in the Americas.

One may speculate concerning where and when modern mycobacterial species evolved from early precursors, such as the organism that infected the prehistoric bison. However, it is not reasonable to assume that a modern species evolved from this precursor separately in the Western and Eastern hemispheres.

One may hope that future investigators who isolate DNA from specimens of paleologic human remains in the Americas will use the spoligotyping method used by Rothschild et al. [1] and will exercise similar care to prevent contamination of their samples. Only thus will the etiology of pre-Columbian tuberculosis in the Americas be established.

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References


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Origins of Tuberculosis in North America

Str—Rothschild and colleagues deserve congratulations for their elegant study of tuberculosis in a 17,000-year-old North American bison [1]. They are especially to be commended for the care they took to prevent contamination of their paleo-
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