

ANCIENT DNA – LESSON FROM THE PAST

Summary

Under certain conditions small amounts of DNA can survive for long periods of time and may be used as substrates in the polymerase chain reaction (PCR) for the study of phylogeny and population genetics of extinct animals and plants. About 20 years ago, DNA sequences were separately described from the quagga and an ancient Egyptian individual; what made these DNA sequences exceptional was that they were derived from 140- and 2,400-year-old specimens. More recently, ancient DNA (aDNA) has been used to study phylogenetic relationships of protists, fungi, algae, plants, and higher eukaryotes such as extinct horses, cave bears, woolly mammoths, the moa, and Neanderthal. In the past few years, this approach has been extended to the study of infectious disease in ancient mummies from Egypt and South America; they suggested a butchery pattern indicative of a human population under resource

stress, revealed dietary habits of ancient animals, and helped to understand how climatic change impacts biological diversity. However, the field of aDNA is still regularly marred by erroneous reports, which underestimate the extent of contamination within laboratories and samples themselves. Deeper understanding of these processes and the effects of damage on aDNA templates has started to provide a more robust basis for research. DNA sequencing of the entire mitochondrial cytochrome b of *Myotis myotis sensu lato* in our molecular laboratory allowed the comparison of aDNA sequences (dating back to ca. 830 years BP) with those of modern bats to assess their genetic relationships. Initial results have revealed surprisingly complex population histories, and indicate that modern studies may give misleading impressions about even the recent evolutionary past.