

DNA, DINOSAURS, AND METAGENOMICS: A NEW TOOL FOR MASS IDENTIFICATION OF DNA FROM FOSSIL BONE

Steven L. Salzberg, Ben J. Novak, Arthur Brady, Melanie Kuch, Christine E. King, Hendrik N. Poinar, Tom G. Kaye, Matthew P. Fittzibbon, Gennifer E. Merrihew, Michael J. MacCoss, Pavel A. Pevzner, Jeong Kyowan, Martin McIntosh

The idea that endogenous soft tissues are preserved in Mesozoic fossil bone remains contentious after 6 years of research. Here full characterization of DNA is reported using 'Metagenomics' techniques from a section of *Brachylophosaurus canadensis* fossil, JRF56, from the Judith river formation near Malta, Montana. Soft tissue structures similar to those reported as dinosaurian blood vessels and bone cells are observed in JRF 56, providing the platform for analyzing the molecular content of this fossil further. Previous studies have focused on long-lasting proteins since it is generally accepted that DNA can not survive such time scales. Here 'Metagenomics' data is presented that identifies ALL the DNA in the sample giving proportionate rank of endogenous molecular species. The sample was processed to isolate organic remnants from the intravascular cavities of the fossil's cortical bone, excluding possible contamination from sediments on the bone surface. DNA from various species of bacteria, plants, fungi, and chordates was detected in the bone and therefore longer lasting proteins from these species can be expected. Critically, avian molecules identified as modern bird DNA were found in the organic isolates. The presence of modern bird and other chordate DNA provide a large analytical obstacle to identifying possible endogenous molecules. Bacteria DNA provides support for the production of biofilms within the fossil. The specific types of bacteria suggest biotic-mineral interplay over the geologic life span of the fossil as suggested in previous work. Metagenomics provides a new and significant method for examining the extent of modern biomolecular infusion into ancient fossils. Metagenomics should thus be incorporated as part of the standard "toolbox" in the investigation of molecular paleontology.