

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

Journal of Vertebrate Paleontology abstracts 2011

[See also: <http://en.wikipedia.org/wiki/Metagenomics>]

Technical Session I (Wednesday, November 2, 9:15 am)

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

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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, JRF 56, 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.

<http://pterosaurheresies.wordpress.com/2012/02/22/the-t-rex-collagen-controversy/#comment-875>:

Salzberg et al. (2011) Struck Back with Metagenomics... In their JVP abstract Salzberg et al. (including Tom Kaye, 2011) recovered a full characterization of the DNA from a section of *Brachylophosaurus canadensis* fossil using ‘[Metagenomics](#)’ techniques. Soft tissue structures similar to those reported as dinosaurian blood vessels and bone cells were observed providing the platform for analyzing the molecular content of this fossil further. Metagenomics data identified ALL the DNA in the sample giving proportionate ranks to the various molecular species therein. The sample was processed to isolate organic remnants from the intravascular cavities of the fossil’s cortical bone, in order to exclude possible contaminants from the bone surface. DNA from various species of bacteria, plants, fungi, and chordates was detected in the bone. Some modern bird DNA was also found. The presence of modern DNA provided an obstacle to identifying ancient dinosaur molecules. The bacterial DNA provided support for the production of biofilms over the 80-million-year age of the fossil.

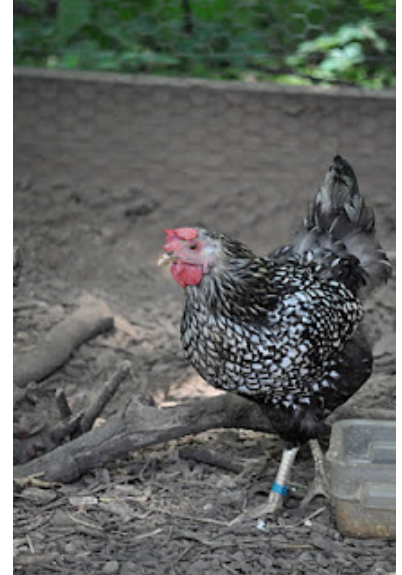
The Salzberg findings also came up with a more complete proteome of the ostrich and the previously reported “T. Rex proteins” now found a perfect match in the ostrich sequence suggesting contamination on Schweitzer’s part. The same was true of unreported hemoglobin proteins in the Schweitzer data that also turned out to be a perfect match to ostrich.

Salzberg S et al. 2011 abstract. DNA, dinosaurs and metagenomics: a new tool for mass identification of DNA from fossil bone. Journal of Vertebrate Paleontology abstracts 2011.

SVP 2011 (Day 1): Vertebrates in Vegas

<http://superoceras.blogspot.com/2011/11/svp-2011-day-1-vertebrates-in-vegas.html>

There were some dinosaur talks during the first technical session, one of which is sure to sadden more than a few individuals who are still hoping to be able to resurrect a non-avian dinosaur from [recovered soft tissues](#), proteins, or DNA. Using new "metagenomic" techniques, researchers have been able to identify all the DNA in a sample of proposed dinosaur soft tissues, and have discovered that the majority of it is, in fact, not dinosaurian (Salzberg *et al.* 2011). The presence of bacterial, plant, and fungal DNA seems to suggest that there is a very small chance that any of the soft tissues previously recovered are actually from a dinosaur. And the chordate DNA found in the sample is likely the result of sediment leaching, as more of it was mammalian than avian. That being said, they did find some chicken DNA in there as well, posing the question as to whether it belonged to a modern bird and was also present as a result of leaching, or whether it is the original dinosaurian molecules, preserved for millions of years. I think the odds of it belonging to a modern neognathan are pretty strong given the evidence, but a reevaluation of the soft tissue work done in previous years, and future research, may still yield indisputable non-avian dinosaur proteins. One can only hope!



If you're looking for dinosaur DNA, *Gallus gallus* may be your ~~only~~ best source. A silver laced Wyandotte, photographed at the Nashville Zoo at Grassmere.

Salzberg, S., Novak, B., Poinar, H., and Kaye, T., and MacCoss, M. 2011. DNA, dinosaurs, and metagenomics: A new tool for mass identification of DNA from fossil bone. Presented at the 71st Annual Meeting of the Society of Vertebrate Paleontology, Wednesday, 02 November, 2011, at 9:15AM.

----- Forwarded message -----

From: **David Peters** <davidpeters@att.net>
Date: Fri, Mar 2, 2012 at 8:04 PM
Subject: Salzberg abstract
To: BobEnyart@gmail.com

Thanks for your interest, Bob.

Here's the abstract you requested.

Technical Session I (Wednesday, November 2, 9:15 am)
DNA, DINOSAURS, AND METAGENOMICS: A NEW TOOL FOR MASS
IDENTIFICATION OF DNA FROM FOSSIL BONE
SALZBERG, Steven... [see above]

David Peters
davidpeters@att.net

From: **Bob Enyart** <Bob@kgov.com>
Date: Sat, Mar 3, 2012 at 8:03 AM
To: David Peters <davidpeters@att.net>

David, thank you so very much. That's definitely helpful and on such a fascinating topic! I'm confused though about the availability of the full paper. Again, I'm happy to purchase a pdf of the full paper; just don't know where to go to do so. Thanks!

-Bob Enyart
AM 670 KLTT

From: **David Peters** <davidpeters@att.net>
Date: Sat, Mar 3, 2012 at 8:08 AM
To: Bob Enyart <Bob@kgov.com>
Cc: Tom Kaye <tom@tomkaye.com>

I'm not aware of the full paper yet.

You might touch base with
Tom Kaye <tom@tomkaye.com>

Dave
David Peters
davidpeters@att.net

From: **Bob Enyart** <Bob@kgov.com>
Date: Sat, Mar 3, 2012 at 8:23 AM
To: David Peters <davidpeters@att.net>

Thanks so much David. Will do.

-Bob Enyart

From <http://en.wikipedia.org/wiki/Metagenomics>

Metagenomics is the study of **metagenomes**, [genetic](#) material recovered directly from [environmental](#) samples. The broad field may also be referred to as **environmental genomics**, **ecogenomics** or **community genomics**. While traditional [microbiology](#) and microbial [genome sequencing](#) and [genomics](#) rely upon cultivated [clonal cultures](#), early environmental gene sequencing cloned specific genes (often the [16S rRNA](#) gene) to produce a profile of diversity in a natural sample. Such work revealed that the vast majority of [microbial biodiversity](#) had been missed by cultivation-based methods.^[1] Recent studies use "shotgun" [Sanger sequencing](#) or massively parallel [pyrosequencing](#) to get largely unbiased samples of all genes from all the members of the sampled communities.^[2] Because of its power to reveal the previously hidden diversity of microscopic life,

metagenomics offers a powerful lens for viewing the microbial world that has the potential to revolutionize understanding of the entire living world.^{[3][4]}