A MODERN-TO-ANCIENT TRANSECT OF MICROBIAL PHYLOGENETIC DIVERSITY PRESERVED IN PROXIMAL SLOPE FACIES HOT-SPRING TRAVERTINE DEPOSITS OF YELLOWSTONE AND TURKEY. Abigail E. Asangba^{1*}, Yiran Dong², Robert Sanford¹, Eva Deboever^{3,4}, Anneleen Foubert³, Ripan Malhi^{2,5}, Mark Band⁶, Bruce W. Fouke^{1,2,7}, ¹Department of Geology, University of Illinois at Urbana-Champaign, USA (*asangba1@illinois.edu), ²Institute for Genomic Biology, University of Illinois at Urbana-Champaign, USA, ³Department of Geosciences, University of Fribourg, Switzerland, ⁴Department of Earth and Environmental Sciences, KU Leuven, Belgium, ⁵Department of Anthropology & Animal Biology, University of Illinois at Urbana-Champaign, USA, ⁶Department of Microbiology, University of Illinois at Urbana-Champaign, USA,

Introduction: A systematic evaluation is being completed of the mechanisms and products of microbial community preservation within modern-to-ancient terrestrial hot-spring calcium carbonate (CaCO₃) limestone deposits called *travertine*. Modern-Holocene travertine deposited within the Proximal Slope Facies (PSF) at Mammoth Hot Springs (MHS), Yellowstone National Park, is being compared to analogous Holocene-Late Pleistocene PSF travertine at Gardiner, Montana, and Middle Pleistocene PSF travertine in Denizli, Turkey.

Sampling has included: (1) active travertine (0 year old hot springs, Angel Terrace, MHS); (2) sub-recent travertine (~100 years old, New Highland Terrace, MHS); (3) Holocene travertine (~4000 years old, USGS Y-10 Core); (3) Late Pleistocene travertine (~30,000 years old, Gardiner Quarry); and (4) Middle Pleistocene travertine (all of the Mammoth Hot Springs (YNP) and (~1.1 Ma years old, Cakmak Quarry, Turkey).

Genomic DNA, entombed during rapid (~5 mm/day) travertine deposition and preserved within fluid inclusions and between CaCO₃ crystals, was extracted under sterile clean room conditions. Pooled 16S rRNA gene sequence libraries were constructed from polymerase chain reactions (PCRs), terminal-restriction fragment length polymorphisms (T-RFLP), and MiSeq amplicon sequencing. Blast searches against multiple webbased bioinformatics tools identified over 400 operational taxonomic units (OTUs) affiliated with 15 phyla within the Domain Bacteria.

Results indicate that only a third of the total of 15 bacterial phyla were detected in all PSF travertine samples of all ages. Furthermore, with progressively increasing depositional age and associated increases in diagenetic alteration, the microbial community structure shifted from being dominated by Cyanobacteria in the Modern and Recent, to dominance by Firmicutes in the Pleistocene. This is not unexpected, as endospores of Firmicutes are known to be resistant and also persist under harsh environmental conditions and therefore show higher relative abundance in ancient samples in comparison to modern samples. Preliminary blast search results imply that libraries from all PSF traver-

tine samples of all ages contain photoautotrophic, chemoautotrophic and heterotrophic metabolic activi-