

HEALTHY BATS HARBOUR DIVERSE *GEOMYCES* STRAINS CLOSELY RELATED TO *GEOMYCES DESTRUCTANS*, A RECENT BAT PATHOGEN, L. J. A. N. Johnson<sup>1</sup>, A. N. Miller<sup>2</sup>, R. A. McCleery<sup>3</sup>, R. D. McClanahan<sup>4</sup>, J. A. Kath<sup>5</sup> A. Porras-Alfaro\*<sup>1</sup>, Western Illinois University<sup>1</sup>, Department of Biological Sciences, Macomb, IL 61455, University of Illinois<sup>2</sup>, Illinois Natural History Survey, 1816 South Oak Street, Champaign, IL 61820, University of Florida<sup>3</sup>, Department of Wildlife Ecology and Conservation, Gainesville, FL 32611, Shawnee National Forest US Forest Service - Hidden Springs RD<sup>4</sup>, 602 North 1st Street, Vienna, IL 62995 Illinois Department of Natural Resources<sup>5</sup>, One Natural Resources Way, Springfield, IL 62702, a-porras-alfaro@wiu.edu

Since 2006, over 5.5 million bats have died from White Nose Syndrome (WNS) in the northeast United States and Canada. A novel fungus, *Geomyces destructans*, causes WNS. Cave soils and WNS positive bats have shown to be reservoirs for *G. destructans*. Objectives for this study were: 1) to document fungi associated with hibernating Illinois bats, and 2) to isolate potential *Geomyces* species and document potential pathogens amongst Illinois bats. Since Illinois is thought to be WNS-free although surrounded by states positive for WNS, it is an ideal location to study bat fungal flora prior to WNS. We sampled 30 bats from four hibernacula in northern Illinois. From three bat species surveyed, *Myotis septentrionalis*, *M. sodalis* and *Perimyotis subflavus*, we isolated and sequenced 150 fungal isolates. Approximately 53 OTUs at 97% similarity were found. Common species isolated from bats included *Cladosporium*, *Geomyces*, *Fusarium*, *Mortierella*, *Penicillium* and *Trichosporon*. Eleven *Geomyces* isolates were obtained from all bat species and phylogenetic analysis using ITS rDNA, Mcm7 and LSU region revealed multiple *Geomyces* clades associated with bats with at least three potential novel clades. Our results suggest widespread distribution of *Geomyces* among bats can lead to false positives when detecting WNS and further research needs to be conducted to determine potential roles of these fungal communities in bats.