

Michelle H. Hersh

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Education:

- Duke University, University Program in Ecology, Durham, NC
Ph.D., 2009, Ecology; Minor: Microbiology
- Bryn Mawr College, Bryn Mawr, PA
A.B. in Biology, Environmental Science concentration, magna cum laude, May 2000

Professional Positions:

- Postdoctoral Associate, Program in Biology, Bard College and Cary Institute of Ecosystem Studies (Oct 2009-present). Advisors: Felicia Keesing and Richard S. Ostfeld
- Teaching Assistant, Department of Biology, Duke University
 - Microbiology (Rytas Vilgalys, Xinnian Dong): Fall 2004, Spring 2008
 - Ecology (Chantal Reid): Spring 2005, Fall 2007

Selected Professional Honors:

- Mycological Society of America Graduate Student Research Prize (Best Oral Presentation), 2009 annual meeting.
- Stern Dissertation Fellowship, Duke University, 2008-2009
- National Science Foundation Doctoral Dissertation Improvement Grant, 2007
- National Science Foundation Graduate Research Fellowship, 2003-2007
- James B. Duke Fellowship, Duke University, 2002-2006
- W.D. Billings Fellowship, Department of Biology, Duke University, 2002-2003

Research Interests and Activities:

I am broadly interested in the connections between disease and biodiversity. My research has focused on how ecological interactions can shape communities of plants and animals, and how linkages between diversity and disease are altered by human activities, such as climate warming. Similarly, I also look at how a diverse community of hosts can affect the dynamics of diseases. I use tools from molecular biology, field ecology, and statistics to address these questions. My current research projects include:

Dynamics of Babesia microti

Babesia microti is the cause of babesiosis, a malaria-like disease, and an emerging human pathogen. It is likely carried by multiple animal hosts, and transmitted to humans via black-legged ticks (*Ixodes scapularis*). We designed and are implementing a protocol to detect *B. microti* infection in ticks from a suite of wildlife hosts using quantitative real-time PCR. Ultimately, the goal of this research is to better understand the role that different animal hosts and host diversity play in *B. microti* transmission.

Effects of tick parasitism on mouse populations

White-footed mice (*Peromyscus leucopus*) are significant reservoirs of many tickborne pathogens, and often carry considerable tick burdens. Do larger tick burdens reduce mouse survival? In this project, we are assessing effects of tick burdens on mouse survival and population dynamics using statistical models.

Seedling pathogens and forest dynamics

Plant pathogens are often invoked as an important mechanism for controlling tree seedling growth and survival. These early life stage effects could ultimately serve a critical role in shaping forest community structure and maintaining tree species diversity. For this research, we used culturing and DNA sequencing to characterize the community of fungi associated with dead and dying seedlings from several southeastern US forest tree species. We then developed a Bayesian hierarchical model to examine the impacts of these fungi on seedling survival, both alone and in combination.

Selected Publications:

- Clark, J.S., D.M. Bell, **M.H. Hersh**, L. Nichols. 2011. Climate change vulnerability of forest biodiversity: climate and resource tracking of demographic rates. *Global Change Biology* 17(5): 1834-1849.
- Clark, J.S., D.M. Bell, C. Chu, B. Courbaud, M.C. Dietze, **M.H. Hersh**, J. HilleRisLambers, I. Ibanez, S.L. LaDeau, S. McMahon, C.J.E. Metcalf, J.E. Mohan, E.V. Moran, L. Pangle, S.F. Pearson, C.F. Salk, Z. Shen, D.R. Valle, and P. Wyckoff. 2010. High dimensional coexistence based on individual variation: a synthesis of evidence. *Ecological Monographs* 80: 569–608.
- Clark, J.S., D.M. Bell, M.C. Dietze, **M.H. Hersh**, I. Ibanez, S.L. LaDeau, S.M. McMahon, C.J.E. Metcalf, E.V. Moran, L. Pangle, and M.S. Wolosin. 2010. Models for demography of plant populations. *In The Oxford Handbook of Applied Bayesian Analysis*, Eds. T. O’Hagan and M. West, Oxford University Press, pp. 431-481.
- Clark, J.S. and **M.H. Hersh**. 2009. Inference in incidence, infection, and impact: When multiple pathogens affect multiple hosts. *Bayesian Analysis* 4(2): 337-366.
- McMahon, S., M.C. Dietze, **M.H. Hersh**, E.V. Moran, and J.S. Clark. 2009. A predictive framework to understand forest responses to global change. *In The Year in Ecology and Conservation Biology 2009*, Eds. R.S. Ostfeld and W.H. Schlesinger. *Annals of the New York Academy of Science* 1162: 221–236.
- Ibáñez, I., J.S. Clark, M.C. Dietze, K. Feeley, **M.H. Hersh**, S.L. LaDeau, A.C. McBride, N.E. Welch, and M.S. Wolosin. 2006. Predicting biodiversity change: outside the climate envelope, beyond the species-area curve. *Ecology* 87(8): 1896-1906.

Manuscripts in Preparation:

- **Hersh, M.H.**, R. Vilgalys, and J.S. Clark. Evaluating the impacts of fungal seedling pathogens on temperate forest seedling survival. *In revision*.
- Clark, J.S., D. Bell, **M. Hersh**, M. Kwit, E. Moran, C. Salk, A. Stine, D. Valle, K. Zhu. Individual-scale variation, species-scale differences: Inference needed to understand diversity. *In revision*.
- **Hersh, M.H.**, R. Vilgalys, and J.S. Clark. Characterizing the fungal associates of tree seedlings in a temperate mixed hardwood forest: Implications for forest diversity. *In preparation*.
- **Hersh, M.H.**, M. Tibbetts, M.E. Strauss, R.S. Ostfeld, F. Keesing. Quantifying reservoir competence for *Babesia microti* for multiple wildlife host species using real-time PCR. *In preparation*.