

4-8-2011

# Avian Community Ecology and the Shifting Baseline in Sugarcreek Metropark

Jennifer Lynne Hays

Thomas P. Rooney

*Wright State University - Main Campus*, [thomas.rooney@wright.edu](mailto:thomas.rooney@wright.edu)

Jeffrey L. Peters

*Wright State University - Main Campus*, [jeffrey.peters@wright.edu](mailto:jeffrey.peters@wright.edu)

Follow this and additional works at: <https://corescholar.libraries.wright.edu/biology>



Part of the [Biology Commons](#), [Medical Sciences Commons](#), and the [Systems Biology Commons](#)

---

## Repository Citation

Hays, J. L., Rooney, T. P., & Peters, J. L. (2011). Avian Community Ecology and the Shifting Baseline in Sugarcreek Metropark. .  
<https://corescholar.libraries.wright.edu/biology/139>

This Presentation is brought to you for free and open access by the Biological Sciences at CORE Scholar. It has been accepted for inclusion in Biological Sciences Faculty Publications by an authorized administrator of CORE Scholar. For more information, please contact [corescholar@www.libraries.wright.edu](mailto:corescholar@www.libraries.wright.edu), [library-corescholar@wright.edu](mailto:library-corescholar@wright.edu).

junctions, MAGI-1b causes loss of CAREx8. We hypothesize that each CAR isoform interacts with different MAGI-1 PDZ-binding domains (PDZ0-PDZ5). N-terminally His-GST-tagged CAREx7-c-terminus (aa 261–365), CAREx8-c-terminus (aa 261–352), and individual MAGI-1 PDZ domains (aa 20–110, 465–555, 630–730, 840–930, 990–1080, 1140–1230) were prepared by cloning PCR fragments for CAR and MAGI-1 into the vector pHH2. Clones were verified by PCR, restriction digestion and DNA sequencing. We then transformed appropriate plasmids into Rosetta2 competent cells (EMD). Protein synthesis was induced with IPTG followed by six samples taken hourly. Proteins were extracted with PBS and run on SDS-PAGE. Coomassie blue staining/destaining demonstrated protein bands at the expected size of between 30kDa and 46kDa for all clones after 1 hour of induction. Isolated GST-fusion proteins will be used to study CAR-MAGI-1 interaction using in vitro FRET analysis

**Co-Authors/Collaborators:** Abimbola O. Kolawole, Raquel Mateus, Priyanka Sharma, and Katherine JDA. Excoffon

### **Investigating the association between emerin and Btf**

**Student Presenter(s):** Kelly Conti

*Undergraduate Student in Biological Sciences  
Participant in*

**Faculty Mentor:** Paula Bubulya

**Department:** Biological Sciences

Btf is a nuclear speckle protein that can operate as a transcriptional repressor, and that when over expressed in a cell, causes apoptosis. Apoptosis is a genetically controlled process of cell suicide that plays a critical role in maintaining homeostasis and preventing disease. Emerin is an integral membrane protein of the inner nuclear membrane in vertebrates, and it is predominantly located at the inner nuclear membrane. It is also a nuclear-lamina associated protein. A yeast two-

hybrid screen determined that Btf binds with emerin. A mutation in the gene encoding emerin, EMD, is responsible for the disease Emery-Dreifuss Muscular Dystrophy (EDMD). A specific mutation (S54F) in the Btf-binding region of emerin is found in some EDMD patients and may disrupt emerin binding to Btf. Emery-Dreifuss Muscular Dystrophy is one of the nine types of muscular dystrophy, a group of degenerative genetic diseases that predominantly affect voluntary muscles. Its onset is generally around ten years of age, with symptoms of weakness and wasting of the shoulder, upper arm, and calf muscles, as well as joint stiffening. The disease typically progresses slowly and cardiac complications are common. Interestingly, results from our lab show that Btf is upregulated during muscle cell differentiation, which may increase the extent to which Btf can bind with emerin. In order to fully understand the mechanism for disease in patients with various emerin mutations, it is important to understand how emerin interacts with other cellular proteins. My project aims to understand the association of emerin and Btf in muscle cells and other cell types. If we can tie disruption of Btf-emerin interaction to EDMD mutations, the ultimate goal of this research will be to develop therapeutic treatments to repair Btf-emerin association in patients with EDMD.

**Co-Authors/Collaborators:** TJ Hufford, Amy Pitstick, Sapna Varia, Paula Bubulya

### **Avian Community Ecology and the Shifting Baseline in Sugarcreek Metropark**

**Student Presenter(s):** Jennifer Hays

*Graduate Student in Biological Sciences*

**Faculty Mentor:** Tom Rooney and Dr. Peters

**Department:** Biological Sciences

Quantifying changes in forest avian diversity is a challenging, but necessary task for developing effective conservation plans. While small changes in diversity accumulate over time,

short-term changes in communities do not allow us to assess changes in diversity. More progressive changes from established baseline conditions may be more interpretable because the changes in diversity are assessed over longer time periods. We examined the temporal changes in avian forest communities at Sugarcreek Metropark in southwestern Ohio based on baseline survey provided by Dr. Reed Noss. Working in 1978, Noss conducted 33 censuses during the breeding and postbreeding seasons and evaluated the diversity of the avifauna to discern trends in both composition and species richness (Noss 1981). Our objective of this study was to determine how forest avian diversity has changed in Sugarcreek Reserve (Metropark) over time and how those changes have altered species richness and community composition. In 1978, Noss observed 7,609 individuals representing 77 species. In 2010, we sampled with the same protocol and intensity, but only observed 6,445 individuals representing only 63 species. Rarefaction analysis was used to normalize 2010 data set to match 1978. Individual species were separated according to categories: wintering residents and migrants. Both rarefaction analysis and rank-abundance curves revealed declines in diversity were attributable to declines in migratory species. Numbers of Northern Cardinals (*Cardinalis cardinalis*) increased nearly threefold, and Indigo Bunting numbers (*Passerina cyanea*) declined by a third. The decline in migrants observed at Sugarcreek mirror declines of migrants elsewhere in eastern North America.

### **The Purpose and Variation of Students' Explanations in Scientific Modeling**

**Student Presenter(s):** Elizabeth Swartzwelder  
*Undergraduate Student in Biological Sciences  
Participant in Honors Program*

**Faculty Mentor:** Lisa Kenyon

**Department:** Biological Sciences, Education

Scientific practices are the disciplinary practices of scientists as they construct, evaluate, communicate, and apply scientific knowledge. We focus on two practices, scientific modeling and developing explanations, for elementary students. Scientific models are simplified, theoretical representations focusing on key concepts to explain and predict natural phenomena. Students engage in model-based inquiry to enhance their understanding of science content, develop metamodeling knowledge, generate parallel predictions, and communicate their knowledge with others. Students construct a model by taking their internal thoughts of how a process occurs and externalizing them into a representation. As students learn new material and listen to peer input, they revise their representations to fit new understandings. Since models are purposeful for explaining phenomena, it is important to analyze students' explanations in its basic fundamental units: claim, evidence, and reasoning. Claim answers the question at hand, evidence supports the claim with quantitative or qualitative data, and reasoning bridges claim and evidence to form a complete explanation. These explanations can be further classified based upon levels of complexity: association, process, or mechanism. Association is the most basic and describes interactions between components in a phenomenon. Process is more complex by showing that a phenomenon occurs in a series of steps or over time. Mechanism represents the highest complexity and explains the how's and why's of a phenomenon. The MoDeLS project research team developed an evaporation/condensation unit with student book exercises and pre/post written test assessments. Approximately sixty 4th graders from a Midwestern elementary school completed the assessments. These assessments were coded by the fundamental explanation units and levels of complexity. Over time, some students showed stronger explanatory skills by incorporating more reasoning into their models, and most students