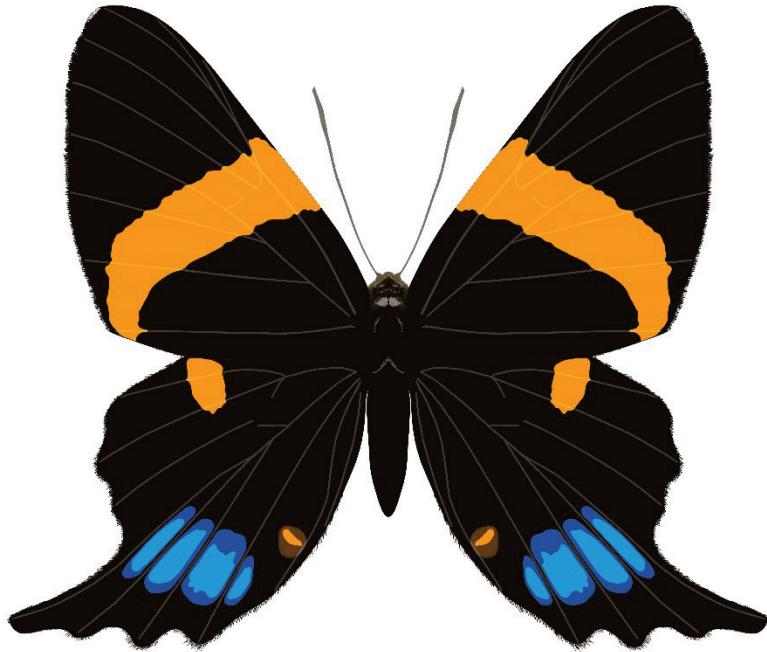


Southern Lepidopterists'
Society

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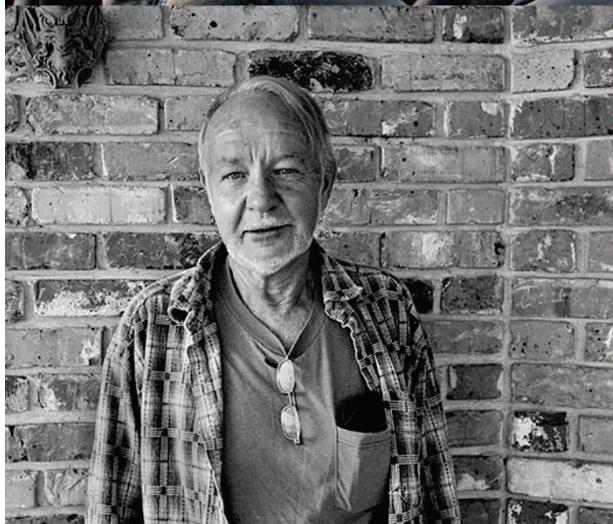
**ASSOCIATION FOR
TROPICAL LEPIDOPTERA**

2025 Annual Meeting



Celebrating 20 years • 2004-2024

The McGuire Center
for Lepidoptera and Biodiversity





We would like to honor in this meeting many people who have donated their collections and time to the McGuire Center since its inception 20 years ago and who are no longer with us. Among them are Tom and John Emmel, Lee and Jackie Miller, George Austin, Ed Knudson, Charles Bordelon, Ron Leuschner, Dan Lindsley, David Bauer, Irving Finkelstein, Bob Eisele, Larry Hollister, Austin Platt, Floyd and June Preston, Bob Woodruff, Paul Opler, and many others.

ANNUAL MEETING OF THE SOUTHERN LEPIDOPTERISTS' SOCIETY AND THE ASSOCIATION FOR TROPICAL LEPIDOPTERA, APRIL 24–27, 2025

Gainesville, Florida

Local Arrangements

Meeting Coordinators:

Deborah L. Matthews, Keith R. Willmott, John F. Douglass

Organizing Committee:

Sarah R. Steele Cabrera, John F. Douglass, David R. Fine, Laura E. Gaudette, Akito Y. Kawahara, Terry A. Lott, Deborah L. Matthews, Marc C. Minno, David Plotkin, Jeffrey R. Slotten, Keith R. Willmott

Lunch / Breaks / Picnic:

Sarah R. Steele Cabrera, Marcela Diaz Zamora, Ada Neal, Megan X. Neal, David Plotkin, Jeffrey R. Slotten

Field Events:

James K. Adams, Eric B. Anderson, Nicole Barbieri, Jamie Bass, Bob Belmont, John F. Douglass, Deborah L. Matthews, Marc C. Minno, Brian G. Scholtens

Collection Access:

Bob Belmont, James E. Hayden, Deborah L. Matthews, Andrei Sourakov

Program:

Deborah L. Matthews, John F. Douglass, Andrei Sourakov

Technical Support:

David Plotkin, Nolan B. Ferguson, Keith R. Willmott

Moderators:

David R. Fine, Paul K. Masonick, Vaughn M. Shirey, J.D. Turner, Keith R. Willmott

Photography and Graphics Support:

Jeff Gage, Andreina Hornez Peralta

Banquet / Evening Program:

James K. Adams, Rick Cech, David R. Fine, Cornelia Holbrook, Douglas S. Jones, Akito Y. Kawahara, Adrienne Phillips

Front Cover / Logo:

Rendering of *Ancyluris inca inca*, Pico Bonito Lodge, Honduras. Deborah L. Matthews

Schedule of Events

Thursday, April 24

4:00–11:00 pm: RECEPTION & EVENING COLLECTING / PHOTOGRAPHY. Lodge at Cuscowilla Nature and Retreat Center, 210 SE 134 Ave., Micanopy, FL 32667. For those of you attending this event, please plan to pick up your programs, nametags and parking information at the lodge.

Friday, April 25

8:00: MORNING RECEPTION & POSTER SESSION.

MORNING SESSION

Moderator: Keith R. Willmott
Technical Support: David Plotkin

8:45: OPENING REMARKS - Andrew Short (UF Ent/Nem), David R. Fine (SLS), J.D. Turner (ATL), and Akito Y. Kawahara (MGCL).

9:00: **Akito Y. Kawahara**

“Twenty years of research and education at the McGuire Center for Lepidoptera and Biodiversity”

9:20: **Keith R. Willmott**

“New Neotropical butterfly species are where you find them”

9:40: **James C. Dunford**

“Catching up with *Speyeria* (=*Argynnис*?!?) and working alongside icons in lepidopterology”

10:00: **Sandy Koi**

“The role of citizen science in the recovery of the imperiled Atala butterfly (*Eumaeus atala*) in South Florida”

10:20: BREAK.

10:40: **Delano S. Lewis**

“From the tropics to the north: Counting butterflies and unraveling ecological entanglements”

11:00: **Montana M. Atwater***, Jacqueline Y. Miller, Jaret Daniels, and James Ackerman

“Moth-pollination through the looking glass: Structure of a flower-settling moth network reveals functional groups”

11:20: **Anisha Sapkota*** and Sajan KC

“Revision of *Pholisora* (Scudder, 1872) (Lepidoptera: Hesperiidae)”

11:40: **David R. Fine**

“The future of the Southern Lepidopterists’ Society: Reaching the next generation”

12:00: GROUP PHOTO.

12:10: LUNCH / SLS DISCUSSION – Lunch (pizza & veggies) will be served at the NATL (Natural Area Teaching Lab) Pavilion located SW of Steinmetz Hall (weather permitting). Picnic tables are available in the NATL Pavilion as well as in the picnic area just west of Steinmetz Hall. Those wishing to join informal SLS business discussions may filter back into room 1031 after picking up lunch.

AFTERNOON SESSION

Moderator: David R. Fine

Technical Support: Nolan B. Ferguson

1:30: **Łukasz Przybyłowicz**

“*Dysauxes* – an African conqueror of the Cold Lands”

1:50: **Leonardo C. J. Corvalan***, Ivone de Bem Oliveira, Taylor Pierson, Lillian Hendrick, Sarah R. Steele Cabrera, Rhewter Nunes, Jaret C. Daniels

“The mitochondrial genome of *Euphyes dukesii calhouni* and *Euphyes pilatka klotsi* and molecular evolution within the family Hesperiidae”

2:10: **Rachel L. Walsh***, R. Keating Godfrey, Yi-Ming Weng, Paul B. Frandsen, Jaret C. Daniels, and Akito Y. Kawahara

“New high-quality genome for the imperiled Loammi skipper butterfly (*Atrytonopsis loammi*: Hesperiidae)”

2:30: **Olivia C. Maule*** and Keith R. Willmott

“Andean uplift and Neotropical butterfly species divergence”

2:50: BREAK.

3:10: **Sofía Nogales***

“Long-term changes in abundance, species diversity, and taxonomic composition in a butterfly community in one of the world’s most biodiverse protected areas”

3:30: **Sajan KC***

“A review of the genus *Rapala* Moore, 1881 (Lepidoptera: Lycaenidae: Theclinae) of Nepal with insights on little-known species”

3:50: **Sarah R. Steel Cabrera***, Michael Belitz, Thomas C. Emmel, Emily S. Khazan, Matthew J. Standridge, Kristin Rossetti, Jaret C. Daniels

“Long-term population dynamics of the endangered Schaus’ swallowtail butterfly are influenced by hurricane-mediated disturbance”

4:10: **Kaylie L. Johnson*** and Keith R. Willmott

“A systematic review of *Memphis acidalia*”

EVENING EVENTS

6:00–10:00: BANQUET, Sweetwater Branch Inn, 625 E. University Ave. Parking is available across the street on the north side of University Ave. at the Kirby Center.

Welcome and introductions: Douglas S. Jones and Akito Y. Kawahara

Featured Speaker: Rick Cech - "A Week in Paraíso"

Door prizes: James K. Adams and David R. Fine

Saturday, April 26

8:00: MORNING RECEPTION & POSTER SESSION.

8:55: ANNOUNCEMENTS.

MORNING SESSION

Moderator: J.D. Turner

Technical Support: David Plotkin

9:00: **Samuel John P. Evangelista*** and Jade Aster T. Badon

"Alcoholic butterflies: Frugivorous butterflies of Mount Makiling, Luzon, Philippines"

9:20: **Andrei Sourakov**, Jing Zhang, Qian Cong, and Nick V. Grishin

"Bella Moth updates"

9:40: **Isabel Lopez-Cacacho***, Yi-Ming Weng, Edward L. Stanley, Andrei Sourakov, Bert Foquet, Christopher J. Martyniuk, and Akito Y. Kawahara

"Understanding detoxification and immune responses to pyrrolizidine alkaloids in *Utetheisa ornatrix* caterpillars using micro-CT and gene expression profiling"

10:00: **Aidan D. Bloch***

"Further results in the *Pedaliodes asconia/pollonia* species group"

10:20: BREAK.

10:40: **Ava C. Johnson***, Rachel L. Walsh, Bert Foquet, and Akito Y. Kawahara

"Assessing the availability of protected habitats for an imperiled Florida butterfly"

11:00: **Olivia L. van der Vlugt***, **Anastasia Baluk Garavaglia***, Md Jahir Rayhan, Lauren

Eccles, Whitney Stoppel, Bert Foquet, and Akito Y. Kawahara

"An in-depth study of lepidopteran silk glands"

11:20: **David Chung-Te Cheng***, David Plotkin, Paul K. Masonick, Andrew J. Mongue, and Akito Y. Kawahara

"Phylogeny of bagworms (Lepidoptera: Psychidae): A preliminary result from anchored hybrid enrichment data"

11:40: **Taylor Pierson***, Ivone de Bem Oliveira, Leonardo C. J. Corvalan, and Jaret C. Daniels

"Creating conservation genomics resources for an imperiled butterfly"

12:00: LUNCH / ATL BUSINESS MEETING. Lunch (Subway courtesy of Ada Neal) will be served at the NATL Pavilion located SW of Steinmetz Hall (weather permitting). Picnic tables are available in the NATL Pavilion as well as in the picnic area just west of Steinmetz Hall. Those wishing to join the ATL Business Meeting may filter back into room 1031 after picking up lunch.

AFTERNOON SESSION

Moderator: Vaughn M. Shirey
Technical Support: Keith R. Willmott

1:20: **Vaughn M. Shirey**, Jayme Lewthwaite, Ann Marie Gawel, Laura Melissa Guzman, and Matthew Williamson

“Tracking scientific integrity and influence with regard to Endangered Species Act rulemaking and lepidopteran conservation in the United States”

1:40: **Jeffrey R. Slotten**

“Tribute to Howard David Baggett, founder of the Southern Lepidopterists’ Society”

2:00: **James K. Adams** and **Brian G. Scholtens**

“James’ and Brian’s Excellent Adventure -- collecting moths in the plains and mountains to and from the 2023 Billings Lep Soc Meeting”

2:50: BREAK.

3:10: **James E. Hayden** and Sidney Bennett

“*Eudarcia* (Meessiidae) in Florida: Many more species”

3:30: **Bert Foquet**, Lauren Eccles, Amanda Markee, Whitney Stoppel, and Akito Y. Kawahara
“Spinning to the moon: A molecular characterization of Luna Moth silk”

3:50: **Nolan B. Ferguson**, Bert Foquet, and Akito Y. Kawahara

“Play, imagination, and science communication”

4:10: **Marc C. Minno** and Douglas M. Fernández-Hernández

“Exploring for Cuban butterflies - July 2024”

4:30: SLS STUDENT AWARDS. The Southern Lepidopterists’ Society Chairman, David R. Fine, will present the Jacqueline Y. Miller Award for best student oral presentation and two honorable mentions. The 17 student presenters are marked with asterisks(*) in the schedule.

EVENING EVENTS

6:00–12:00: MOTHING PICNIC at Morningside Nature Center, 3540 E. University Ave., Gainesville, FL 32641. We have a special use permit for the evening and will be joined by Morningside staff members. Light finger foods will be available at the screened-in pavilion in the picnic area starting at 6:00. Bucket traps may be set up as early as 4:00 pm. Communal sheets will be set up in the vicinity of the pavilion. RSVP to Debbie Matthews if you would like to set up a trap, as we must coordinate the number and locations with Morningside staff. Bucket traps may be left overnight and picked up after the gate opens at 8:00 am Sunday. Please note GPS coordinates for trap and sheet locations.

Sunday, April 27

8:00: MORNING RECEPTION.

MORNING SESSION

Moderator: Paul K. Masonick

Technical Support: David Plotkin

9:00: Jade Aster T. Badon

“Recent updates on Philippine Lepidoptera: Discoveries from 2019-2024”

9:20: Akito Y. Kawahara and Jesse R. Barber

“Evolution of anti-bat defenses in moths: Sonar jamming, acoustic deflection, and mimicry”

9:40: Paul K. Masonick

“Convergent evolution of antipredatory bioacoustic traits in bombycoid moths (Lepidoptera: Saturniidae, Sphingidae)”

10:00: Md Jahir Rayhan, Gisella DePiazza, Jacob Bethin, David Plotkin, Shashank R. Pathour, Bert Foquet, and Akito Y. Kawahara

“A CRISPR-based rapid identification approach for Tomato Pinworm, *Tuta absoluta* (Meyrick, 1917)”

10:20: BREAK.

10:40: Jose I. Martinez

“A decade of systematic advances in Noctuoidea and expanding horizons”

11:00: Jing Zhang, Qian Cong, Jinhui Shen, Leina Song, and Nick V. Grishin

“Surprises from butterfly genomics”

11:30: BIOBLITZ HIGHLIGHTS. – Open show-and-tell of results from collecting and photography at Cuscowilla and Morningside. Led by James K. Adams and Brian G. Scholtens.

Poster Abstracts

1. Cori Keim, Patrick Bohlen, Christina Watkins, Christina L. Kwapich
corinkeim@ucf.edu
Department of Biology, UCF, Orlando, FL

Microlepidoptera as cryptic generalist pollinators: Uninvolved or underdog?

With the exception of obligate mutualist species and day-flying hawk moths (Lepidoptera: Sphingidae), the role of moths as generalist pollinators is poorly understood. There is growing evidence of moth pollination in natural and agricultural systems, but the species involved are often unidentified. Most moths belong to microlepidoptera, a polyphyletic assemblage of families with members that tend to be under 20 mm in size. It is likely that microlepidopterans participate in pollination, but there is scarce evidence to support this claim. Our aim was to determine if microlepidopterans act as generalist pollinators. Microlepidopterans were sampled through hand collection and at black-light sheets set up across Orange County. Under a stereomicroscope, moths were identified using morphological keys and visually scanned for the presence of plant pollen. Pollen was swabbed from moths with a glycerin gel mixture, stained, and identified. We excluded pollen belonging to the plant families Pinaceae or Poaceae, both of which utilize wind pollination. Pollen that did not originate from a pine or grass species was catalogued. Our findings detail the relationships between a diverse and underappreciated assemblage of microlepidopterans and Florida plant species. Uncovering cryptic relationships between Florida plants and pollinators is essential for the conservation of both partners.

2. Andrei Sourakov
sourakov@ufl.edu
MGCL, FLMNH, UF, Gainesville, FL

Pharmacological experiments on wing pattern development of Lepidoptera

Studies of the effects of heparin on Lepidoptera wing patterns have been restricted to a small number of species, mostly within Nymphalidae. Observations from experiments on a broader range of taxa, including swallowtails, lycaenids, giant silk moths, tiger moths and microlepidoptera, are reported and discussed. Heparin injections made in prepupae and pupae sometimes altered the entire wing pattern in a dramatic way, and sometimes only caused local changes, and the results are compared to the effects of cold shock and CRISPR experiments. Using this pharmaceutical intervention demonstrates similarities and differences in the ways wing patterns are formed in different butterfly and moth lineages. By creating a range of variation, it can be demonstrated how one wing pattern can evolve into another, which helps to understand speciation and adaptation processes. Experimenting with Atala butterflies (*Eumaeus atala*) enabled association of the markings of this and other Lycaenidae to the symmetry systems of Nymphalidae - a family separated from lycaenids by 100 million years of evolution. Similarly, the eyespots of Saturniidae that are present in numerous lineages of this family, despite looking similar in the Polyphemus moth (*Antherea polyphemus*) and the Io moth (*Automeris io*), reacted differently to heparin injections, thus demonstrating that some of the constituent pattern elements are non-homologous. These two moths represent two different saturniid subfamilies and are separated by over 50 million years of evolution, so convergence, rather than shared ancestry, is responsible for similarities in their patterns.

3. Christina L. B. Watkins¹ and Luke S. Smith
christinalwat@gmail.com
Department of Biology, UCF, Orlando, FL

Lepidoptera under our noses: A systematic survey with a partial checklist and synoptic collection at the University of Central Florida, with special emphasis on microlepidoptera

Lepidoptera serve vital ecological roles as pollinators, prey, parasitoid hosts, defoliators, and decomposers. Despite their significance and diversity, regional surveys on Lepidoptera are often lacking, especially for microlepidoptera. While Orange County, located in Central Florida, is home to expansive and diverse habitat types, standardized surveys of Lepidopteran diversity remain limited for this region. This work presents a survey conducted in the University of Central Florida Arboretum using systematic sampling methods, providing a partial checklist and a digitized synoptic collection. These findings provide essential baseline data for future research and conservation efforts within the region.

Talk Abstracts

1. James K. Adams and Brian G. Scholtens
jadams@daltonstate.edu, ScholtensB@cofc.edu
Dalton State College, Dalton, GA, & College of Charleston, Charleston, SC

James' and Brian's Excellent Adventure -- collecting moths in the plains and mountains to and from the 2023 Billings Lep Soc Meeting

As is typical for every LepSoc meeting, I (JKA) turn the meeting into a big moth trip. The summer of 2023 was no exception. However, that summer I asked good friend and colleague Brian Scholtens to join me, and he (excitedly) did so. He indicated he had never spent significant time in the plains states and was eager for the chance! He joined me in western Nebraska, and we mothed from there through South and North Dakota, Montana (of course), Wyoming, Colorado, and Kansas. We collected excellent moths everywhere, including state records for virtually every state (obviously true for Brian's micros). Come and enjoy this photologue of our excellent adventure!!

2. Montana M. Atwater*, Jacqueline Y. Miller, Jaret C. Daniels, James Ackerman
montana.atwater@gmail.com
University of Puerto Rico & UF, Vero Beach, FL

Moth-pollination through the looking glass: Structure of a flower-settling moth network reveals functional groups

Plant-pollinator mutualisms are key to sustaining ecosystem function and biodiversity. The study of plant-pollinator networks has conventionally focused on diurnal interactions, while flower-settling moths are among the most diverse yet least understood pollinator groups. Our main objective was to focus on the structure and function of a flower-settling moth network within a habitat of high conservation priority, the Florida Sandhill. Specifically, we considered key taxonomic, life history, and functional traits of moths as potential drivers of network structure. We integrated two network types: flower-visitor, based on direct field observation of

moths visiting flowers for nectar, and pollen-transport, inferred from the identification of pollen found on moths. Flower-settling moth networks were diverse and significantly structured (modular). Moth phenology and caterpillar host-plant interactions were associated with module formation. Additionally, functionally similar moths were linked more often to particular modules. Notably, average proboscis length and wingspan of moths varied significantly among modules, thus revealing potential functional groups. Accordingly, we propose three potential functional groups of flower-settling moths: micro, small, and macro - as supported by modes in the distribution of proboscis length and wingspan, and as reflected in modularity analysis. In addition, we recommend the use of wingspan as a potential proxy for proboscis length and/or moth functional group. We conclude that flower-settling moth assemblages are more functionally diverse than previously understood and offer a glimmer of hope in the darkness for pollinator conservation.

3. Jade Aster T. Badon

jtbadon@up.edu.ph

University of the Philippines, Los Baños, Laguna, Philippines

Recent updates on Philippine Lepidoptera: Discoveries from 2019-2024

The Philippines is an archipelago of more than 7,000 islands of various ages and sizes which have influenced species and diversification of its flora and fauna. The country is home to more than 900 species of butterflies, of which one-third are endemic, while moths remain understudied. Philippine Lepidoptera Butterflies and Moths, Inc., was founded by citizen scientists in 2013 to document butterflies and moths in the country. This organization was able to document some new discoveries which will eventually improve the country's Lepidoptera research and education. Here are some of the discoveries from 2019-2024: life history notes of the Near-Threatened butterfly, *Euploea swainson*; life histories of *Euploea eunice* and *Horaga syrinx*; the biology and life history of the endemic butterfly *Athyma gutama*; interesting life history of *Nacaduba pavana*; migration of *Euploea* in the western Philippines; the curious case of *Euploea eunice*, and a moth that crawls backwards to mimic an ant. These recent discoveries suggest that the country still has many discoveries to expect in the future.

4. Aidan D. Bloch*

aidan.bloch@ufl.edu

MGCL, FLMNH, UF, Gainesville, FL

Further results in the *Pedaliodes asconia/pollonia* species group

Species definitions and geographical ranges within the Andean genus *Pedaliodes* (Nymphalidae, Satyrinae) are vague, with considerable phenotypic overlap and meager genetic data. Here, I present the results of additional mtDNA sequencing within the *Pedaliodes pollonia/asconia* species complex. These data supplement pre-existing specimens from the McGuire Center collections, integrating the results of field collections at cloud forest sites throughout the Ecuadorian Andes during the summer of 2023. New data fill geographical blank spots and will triple the available sample size, forming a more complete picture of *Pedaliodes* ranges and species definitions.

5. Rick Cech

rcech@nyc.rr.com

butterfliesarestillfree.com, New York, NY

A week in Paraíso

Tales of an intensive visit to Cristalino, in the lowlands of the Amazon basin, will be presented, tracing the arc of a Neotropical leps advocate's peak life experience. Featured will be a select group of the hundreds of butterfly species found there, in photos sorted into major taxonomic groups. Cristalino is a personal field laboratory, ideally equipped to display the enormous diversity of the Neotropical community.

Featured speaker **Rick Cech** is an active field naturalist, trip leader, lecturer, author, and photographer. Among other publications, he is the principal author and photographer of *Butterflies of the East Coast: An Observer's Guide* (Princeton, 2005) and "A Distributional Checklist of the Butterflies and Skippers of the New York City Area." He is a curatorial affiliate in Entomology at the Yale Peabody Museum of Natural History and a past president of the Linnaean Society of New York. Rick has taught nature photography and butterfly identification at the New York Botanical Garden and at Yale's Graduate School Department of Ecology and Evolutionary Biology.

6. David Chung-Te Cheng*, David Plotkin, Paul K. Masonick, Andrew J. Mongue, Akito Y. Kawahara
chungte.cheng@ufl.edu
MGCL, UF, Gainesville, FL

Phylogeny of bagworms (Lepidoptera: Psychidae): a preliminary result from anchored hybrid enrichment data

Bagworm moths (Psychidae) are a family of approximately 1,350 species that are distributed worldwide and grouped into 10 subfamilies and 300 genera. Their common name refers to the bag-like cases that larvae make from leaves, stems, and detritus that they spin together with silk. Adult bagworms are unusual in the animal kingdom in that they display a remarkable range of sexual dimorphism and sexual reproduction. Over half of the known species have adult females that are brachypterous or apterous (i.e., lacking wings), and some species have vermiform adult females that also lack legs, eyes, antennae, and mouthparts, whereas adult males possess "normal" characteristics. The neotenic females never leave their silk cases, and in these species, the female calls the male, and the male inserts its telescopic abdomen into the case to mate. This extreme sexual dimorphism in bagworms has resulted in some of the most bizarre life history traits found among insects. Despite their unusual life history and potential as a model system for evolutionary genetics, a robust phylogenetic framework of Psychidae is lacking, and the relationships between European, African, and New World species remain largely unknown. As such, major relationships of higher psychid clades are not firmly established. In this work, a preliminary AHE tree which contains 57 psychid species across 8 subfamilies was reconstructed. The monophyletic relationships of most subfamilies were confirmed, with several exceptions such as Psychinae and Naryciinae. In addition, we now have more than 40 genome assemblies for further analysis. The newly generated result is by far the most robust phylogenetic tree of the family Psychidae, providing a backbone for further discussion on various biological topics.

7. Leonardo C. J. Corvalan*, Ivone de Bem Oliveira, Taylor Pierson, Lillian Hendrick, Sarah R. Steele Cabrera, Rhewter Nunes, Jaret C. Daniels
lcorvalan@ufl.edu
MGCL, FLMNH, UF, Gainesville, FL

The mitochondrial genome of *Euphyes dukesi calhouni* and *Euphyes pilatka klotzi* and molecular evolution within the family Hesperiidae

The genus *Euphyes* includes around 20 species, with *Euphyes dukesi calhouni* and *Euphyes pilatka klotzi* found in the southern Atlantic and Gulf Coastal Plains. Both species have experienced significant declines in their natural ranges. The Daniels lab, in collaboration with the U.S. Fish and Wildlife Service, is gathering data for these species' status assessments and potential listing. Aiming to develop molecular resources to help conserve these species, we assembled their complete mitochondrial genomes, identified nucleotide diversity hotspots, and performed a phylogeny analysis including more than 100 Hesperiidae species. We will show the annotation results for these mitogenomes, and areas identified as presenting high diversity. The new markers developed can be used as potential conservation and phylogenetic research tools within the family Hesperiidae.

8. James C. Dunford

jcdunfordento@gmail.com
Windsor, CO

Catching up with *Speyeria* (=*Argynnис*?) and working alongside icons in lepidopterology

The genus (or subgenus) *Speyeria* ranks among the upper echelons of phylogenetic irresolution, and to this day presents challenging taxonomic interpretations of ongoing hybridization and adaptive radiation against a backdrop of anthropogenic influences. An overview of my *Speyeria* endeavors in the early 2000s and an update of current work on the group is presented. The story of how an interest in butterflies over 40 years ago allowed for working alongside some of the world's greatest lepidopterists and entomologists is also told, and how that led to a rewarding career in the field of entomology.

9. Samuel John P. Evangelista* and Jade Aster T. Badon

spevangelista1@up.edu.ph
University of the Philippines, Los Banos, Laguna, Philippines

Alcoholic butterflies: Frugivorous butterflies of Mount Makiling, Luzon, Philippines

The impact of habitat changes on butterfly diversity is crucial, particularly as biodiversity loss continues due to anthropogenic land use activities. This study explores the potential of butterflies as umbrella species to highlight broader conservation efforts. Focusing on frugivorous feeding behavior, modified bait traps were utilized to sample butterflies from various habitats and elevations. The study was conducted in Mount Makiling to assess and provide baseline data of frugivorous butterfly composition and diversity across three distinct habitats: Garden, Mixed Agricultural Forest Trail, and Primary Forest. From April to September 2024, a total of 27 bait traps containing banana-rum or pineapple-vodka mixtures recorded a total of 246 individuals representing 18 species (9 endemic species) from the Nymphalidae family. The results of our study indicated notable differences in frugivorous butterfly composition among the three habitats; however, diversity values remained similar. Our results also showed that the two types of baits did not show a significant difference in terms of the number of species and individuals per species captured. Interestingly, we recorded some species that are bait-specific, and this could be important in future conservation initiatives in terms of sampling for specific species.

10. Nolan B. Ferguson, Bert Foquet, Akito Y. Kawahara
nolan.ferguson@ufl.edu
MGCL, FLMNH, UF, Gainesville, FL

Play, imagination, and science communication

Emotion is often seen as unscientific, but it can be a powerful bridge between research and the public. Scientists are drawn to their fields by passion — my love for moths and butterflies began with *Mothra*, just as many paleontologists were inspired by *Jurassic Park*. People care deeply about their work, yet research is often presented dryly, making it harder to engage audiences, especially children. Play is fundamental to learning — why not embrace it in science communication? How can we ensure information is not just accurate but also fun? I'll share past exhibit work with moths and butterflies as an example and explore ways to use imagination and play to make science more engaging and accessible.

11. David R. Fine
davidf@calvaryftl.org
KEYSMOTHS.COM, Coconut Creek, FL

The future of the Southern Lepidopterists' Society – Reaching the next generation

Since 1978, the Southern Lepidopterists' Society has been a community of amateur and professional lepidopterists and enthusiasts that has advanced the knowledge of butterflies and moths in the southeast United States to any who are interested. While the goals of the organization will not change, we are coming to a crossroads on HOW the SLS will operate in an ever-changing world of digital interaction. In our discussion, we will celebrate the retirement from the 23 years of volunteer service that editor Barry Lombardini has provided and discuss the future of the newsletter and how members will interact within the SLS in community and on social media and our website.

12. Bert Foquet, Lauren Eccles, Amanda Markee, Whitney Stoppel, and Akito Y. Kawahara
bfoquet@ufl.edu
MGCL, FLMNH, UF, Gainesville, FL

Spinning to the moon: A molecular characterization of Luna moth silk

Silk is one of the most intriguing biomaterials made by insects, and has a long history of being used in the textile industry. Even though there is an immense diversity of silk within the order Lepidoptera, it has only been studied in depth in the silkworm *Bombyx mori*. We generated RNA sequencing and silk strength data for different life stages of the Luna moth, *Actias luna*, aiming to expand our knowledge of lepidopteran silk to another species. We identified several genes involved in silk generation, and discuss how their expression varies throughout their life cycle.

13. Jing Zhang, Qian Cong, Jinhui Shen, Leina Song, and Nick V. Grishin
grishin@chop.swmed.edu
UT Southwestern, Dallas, TX

Surprises from butterfly genomics

While nature is full of deceit, the true colors of Lepidoptera are revealed by their genes. From several tribes of blues that look like hairstreaks and rampant misassignment of butterflies to genera because of rapid divergence and mimicry, to unexpected cryptic species present in essentially any group, genomic analysis yields numerous surprises. We selected an array of visually striking examples to show and discuss, focusing on higher butterfly classification and cryptic species complexes from the USA. Genomic sequencing aided the discovery of 29 new butterfly species in the US, which adds more than 3% to the current total species count.

14. James E. Hayden and Sidney Bennett
jehayden63@gmail.com
FDACS-DPI/MGCL, FLMNH, UF, Gainesville, FL

***Eudarcia* (Meessiidae) in Florida: Many more species**

We have found eight to ten species of *Eudarcia* Clemens and *Bathroxena* Meyrick in Florida since May 2023. This results from new collecting and determining of pro-tempore material in the FSCA / McGuire Center. Most of the species are undescribed; we illustrate and comment on them. Four are in the Lower Keys and the rest on the mainland, and most fly in springtime. We show morphological plesiomorphies which corroborate the genetic results that Meessiidae is the sister group to all other Ditrysia. We reinterpret ditrysian genitalia in light of the telescoping tineoid ovipositor. We encourage collecting larvae on lichens and adult moths with dry Malaise traps.

15. Ava C. Johnson*, Rachel L. Walsh, Bert Foquet, and Akito Y. Kawahara
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Assessing the availability of protected habitats for an imperiled Florida butterfly

The Loammi skipper (*Atrytonopsis loammi*) is an imperiled Florida butterfly that has lost much of its preferred habitat to development. It is unclear how much of its habitat is left in Florida, and whether it is protected. I built a model in ArcGIS Pro to rank the top 10 habitats in which *A. loammi* occurs, using publicly available data, and found that the top habitats correspond with the literature. I subsequently ranked these habitats based on how much is protected in Florida and discovered that *A. loammi* has a high reliance on protected lands. Its occurrence in pasture, rural, and urban areas suggests these do not prevent dispersal, but ongoing habitat loss may increase isolation. Therefore, conserving suitable habitat to preserve movement corridors is critical.

16. Kaylie L. Johnson* and Keith R. Willmott
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A systematic review of *Memphis acidalia*

The genus *Memphis* represents a significant component of Neotropical butterfly diversity, particularly in canopy habitats across Central and South America. This study investigates the taxonomy of *Memphis acidalia*, with a focus on clarifying species boundaries and addressing challenges posed by sexual dimorphism and intraspecific variation. *Memphis acidalia* exhibits notable variability, complicating its taxonomic resolution. We addressed three objectives: (1)

to refine the identification of conspecific males and females, (2) to determine species delimitation within the complex, and (3) to establish accurate nomenclature. A combined approach of morphological and molecular analyses was employed. Historical taxonomic literature was also reviewed to resolve ambiguities. The findings contribute to a more robust understanding of *Memphis* systematics, providing insights into Neotropical butterfly diversity, with implications for conservation and monitoring programs.

17. Akito Y. Kawahara

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Twenty years of research and education at the McGuire Center for Lepidoptera and Biodiversity

The McGuire Center for Lepidoptera and Biodiversity, located on the University of Florida campus in Gainesville, has become one of the world's leading research and education facilities dedicated to butterflies and moths. Committed to advancing knowledge and conservation of Lepidoptera, the Center offers unparalleled resources, expertise, and training. Since its construction 20 years ago, the facility has grown to house millions of specimens from across the globe, rivaling some of the largest Lepidoptera research collections worldwide. It is home to a team of researchers studying many aspects of lepidopterology, including behavior, conservation, ecology, genomics, and systematics. In the face of a rapidly changing environment, understanding historical distributions, ecological impacts, and evolutionary adaptations of butterflies and moths is more crucial than ever. The McGuire Center is dedicated not only to uncovering the past but also to predicting how environmental changes may shape the future of these insects, ensuring their protection and conservation. In this talk, I will highlight the progress made over the past two decades and discuss the future vision and plans for the McGuire Center.

18. Akito Y. Kawahara and Jesse R. Barber

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MGCL, FLMNH, UF, Gainesville, FL

Evolution of anti-bat defenses in moths: Sonar jamming, acoustic deflection, and mimicry

Adaptations to divert the attacks of visually guided predators have evolved repeatedly in animals. However, few studies have examined how invertebrates have evolved to use ultrasonic hearing against bats. Over the last 12 years, our research team has synergistically conducted behavioral experiments, phylogenetics, and functional genomics to examine how the more than 140,000 moth species evolved to escape bats – their primary predator at night. Over the last 60 million years, moths have evolved ultrasonically sensitive ears and ultrasound-producing organs to combat bat attack. Some moths have gone a step further and gained the ability to jam bat sonar using tymbals on their thorax or by stridulating their genitalia, allowing them to inhabit new environments. Others generate acoustic diversion with spinning tails to deflect echolocating bat attack. This presentation will include high-speed infrared videography of moths and bats to elucidate the function and evolution of anti-bat strategies.

19. Sajan KC*

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MGCL, FLMNH, UF, Gainesville, FL

A review of the genus *Rapala* Moore, 1881 (Lepidoptera: Lycaenidae: Theclinae) of Nepal with insights on little known species

The taxonomy of *Rapala* in Nepal is problematic due to historical misidentifications, reclassifications, and a lack of identification keys. This study reviews *Rapala* species in Nepal using field observations, citizen science data, literature, and museum specimens. Thirteen species are recognized, with *R. rosacea* formally recorded for the first time, previously misidentified as *R. rectivitta*. New evidence of *R. rectivitta* in Nepal is provided. *Rapala huangi* is reaffirmed as valid, while *R. hinomaru* is proposed as *nomen dubium*. *Rapala huangi* is newly recorded from NE India. Identification images, genitalia, and keys are included. A potential new *R. rectivitta*-complex species is discovered in Myanmar, while *R. nissa hirayamana* (Taiwan) and *R. n. pahangana* (Malaysia) may be distinct species, warranting further research on *Rapala* across broader Asia.

20. Sandy Koi

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Florida International University, University Park, FL

The role of citizen science in the recovery of the imperiled Atala butterfly (*Eumaeus atala*) in South Florida

Significant declines in insect populations globally have been documented for decades, due to habitat fragmentation and loss, pesticides, and climatic changes, as well as intra- and inter-specific competition with native and non-native species. Southeast Florida is a biodiversity hotspot, making our rare and endemic species of high conservation concern. However, one small but iconic butterfly in Southeast Florida has made a dramatic recovery from assumed extinction 75 years ago to state-wide presence: the Atala Hairstreak (*Eumaeus atala*). The three originally documented sites for Atala presence, Miami-Dade, Broward, and Palm Beach counties, were surveyed by citizen scientists for this study. Using population data from the North American Butterfly Association spanning 27 years, long-term data analyses quantified the crash-eruption cycle of the butterfly, indicating a slow but stable increase over time. Additional data were recently published in the Journal for Nature Conservation.

21. Delano S. Lewis

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Burman University, Lacombe, Alberta

From the tropics to the north: Counting butterflies and unraveling ecological entanglements

A recap is offered of my activities prior to and after leaving the McGuire Center. I will talk about current roles and projects: 1) An examination of the effects of climate stochasticity on butterfly abundance and diversity. We highlight an affordable and effective way to measure diversity, show undergraduate students and citizen scientists advancing research at a PUI, and disclose plans to make this project a longitudinal study. 2) This project seeks to explore the correlations between: (a) pesticide use in central Alberta; (b) pesticide accumulation in insects; (c) the local abundance of such insects, and (d) whether such pesticides are transferred to the birds that feed on them. This multidisciplinary, collaborative project seeks to close the gap between applied science and end-users and decision-makers.

22. Isabel Lopez-Cacacho*, Yi-Ming Weng, Edward L. Stanley, Andrei Sourakov, Bert Foquet, Christopher J. Martyniuk, and Akito Y. Kawahara
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Understanding detoxification and immune responses to pyrrolizidine alkaloids in *Utetheisa ornatrix* caterpillars using micro-CT and gene expression profiling

The Bella moth, *Utetheisa ornatrix*, is a tiger moth known to tolerate, sequester, and utilize toxic pyrrolizidine alkaloids (PAs) found in *Crotalaria*. The anatomical and genetic adaptations that facilitate PA tolerance in Lepidoptera, along with their effects on the immune system, remain largely unexplored. In this study, we utilize micro-computed tomography (micro-CT) to qualitatively and quantitatively characterize the organs of Bella moth caterpillars. Additionally, we evaluated the expression patterns of ten detoxification and five immune genes across the fat body, gut, integument, Malpighian tubules, and testes of caterpillars under a PA and PA-devoid diet. Our results indicate organ-specific expression of both detoxification and immune genes, with PA detoxification genes showing particularly high expression in the testes and Malpighian tubules. The fat body and integument showed similar expression patterns, as well as the Malpighian tubules and gut. Our findings provide valuable insights into the genetic mechanisms of PA tolerance in Lepidoptera, providing a holistic approach to studying detoxification and immune response in Lepidoptera.

23. Jose I. Martinez
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A decade of systematic advances in Noctuoidea and expanding horizons

Over the past ten years, my research on the systematics and evolution of the superfamily Noctuoidea has led to the reclassification of 13 subfamilies, elevating them to family level and establishing a more stable and accurate systematic framework. This work not only resolved longstanding systematic and taxonomic issues, but also highlighted key gaps that present exciting opportunities for further exploration in Lepidoptera. Additionally, this extensive work provided me with the skills and insights necessary to explore other insect orders such as Neuroptera and Diptera. In this presentation, I will discuss both ongoing and future research efforts, focusing primarily on Lepidoptera, while also introducing new ventures into Neuroptera and Diptera, reflecting a broader commitment to understanding insect diversity and evolution.

24. Paul K. Masonick, Pamela Rivera¹, Jesse Barber², and Akito Y. Kawahara
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¹ Boise State University, Boise, ID
² American Museum of Natural History, New York, NY

Convergent evolution of antipredatory bioacoustic traits in bombycoid moths (Lepidoptera: Saturniidae, Sphingidae)

Moths have evolved an astonishing array of antipredatory traits ranging from the sequestration of defensive toxins to deimatic displays. Within the Bombycoidea, many silkworms (Saturniidae) and hawkmoths (Sphingidae) employ disparate yet effective bioacoustic tactics

to thwart bat attacks. Among Saturniidae, several lineages have independently evolved elongated hind wings with twisted tails that lure bat strikes away from vital body parts. Concordantly, numerous Sphingidae facilitate their escape by producing ultrasound that is capable of disrupting echolocating by bats. Despite these being relatively high-profile features well known among lepidopterists, detailed investigations into the three-dimensional morphology and microsculpturing underlying these traits have been lacking. Herein, using microtomography (microCT) and scanning electron microscopy (SEM), we examine the complex 3D shapes and scale morphologies that putatively enable silkmoths to create decoy echoes that confuse bats. Similarly, we survey the diversity of ultrasound producing stridulatory structures in male hawkmoths where modified genital scales (the scraper or plectrum) rub against modified scales, spines, or microsculpturing on the ventral surface of the last abdominal tergite (the file, stridulitrum, or pars stridens). In both groups, we investigate these traits in a phylogenetic context and demonstrate their tendencies to coalesce on adaptive optima. Our findings ultimately provide novel insights into the iconic bat-moth arms race.

25. Olivia C. Maule*, Keith R. Willmott
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Andean uplift and Neotropical butterfly species divergence

In this study, the primary hypothesis is that the rise of the Andes has caused speciation in butterflies, with the result that elevation correlates with DNA divergence, and specifically that higher divergence is present at lower elevations. To test this, I am examining divergence in DNA sequences from specimens in the Florida Museum of Natural History and existing sequences of related species on either Andean slope. Additionally, I hypothesize that the amount of DNA divergence among species at the same elevation could depend on differences in traits. Specifically, I would expect more dispersive species to show less divergence than sedentary species occurring at the same elevations. Variables such as wing length as a measure of dispersal ability and flight height/speed will help model whether increasing elevation results in decreased divergence, and identify traits associated with species divergence and potential speciation. This study is the first to examine Lepidoptera DNA divergence and trait differences between east and west Andean populations at different elevations. Mitochondrial COI sequences from specimens are offering insights into genetic differences between Lepidoptera on both Andean slopes at different elevations. Currently, we have suitable sequence data for about 180 species with >4 samples for each species. Knowing that 65% of insects may be extinct in a century, understanding biogeographical elements of Lepidoptera divergence can help provide insights into likely climatic and geographic effects upon ecosystems.

26. Marc C. Minno and Douglas M. Fernández-Hernández
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Exploring for Cuban butterflies - July 2024

On July 2–15, 2024, we searched for butterflies in the vicinity of Matanzas, San Miguel de los Baños, Topes de Collantes Grand Natural Park, Zapata National Park, Cienfuegos, Playa Ancon, Havana Botanic Garden, Escaleras de Jaruco, and other sites. During this trip we explored rocky shorelines, beaches, salt marshes, mangrove swamps, salt ponds, sawgrass

marshes, the foothills and peaks of the Escambray Mountains, tropical hardwood forests, and serpentine scrub woodlands. Overall, we observed at least 116 species of butterflies and discovered a caterpillar of *Panoquina corrupta* (Lepidoptera: Hesperiidae), which has not been previously documented.

27. Sofía Nogales*

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Long-term changes in abundance, species diversity, and taxonomic composition in a butterfly community in one of the world's most biodiverse protected areas (Yasuní National Park, Ecuador)

A significant decline in insect biodiversity and abundance is underway worldwide, driven by multiple factors such as deforestation and climate warming. Although tropical regions are particularly vulnerable to rising temperatures, the status of insect populations in these areas remains largely unknown. Long-term studies are essential to understanding of changes in biodiversity and its responses over time. This research explores long-term changes in the butterfly abundance, species diversity, and community structure in the tropical rainforest of Yasuní National Park, Ecuador, over a two-decade period, comparing data collected from 2002–2021. The study aims to enhance our understanding of tropical butterfly ecology, assess population changes potentially driven by climate change or other anthropogenic factors, and underscore the importance of long-term monitoring in achieving environmental conservation strategies.

28. Taylor Pierson*, Ivone de Bem Oliveira, Leonardo C. J. Corvalan, Jaret C. Daniels

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Creating conservation genomics resources for an imperiled butterfly (*Callophrys irus*)

The Frosted Elfin, *Callophrys irus*, is a small, imperiled, non-migratory butterfly facing historic habitat loss and fragmentation. In order to inform the species' status assessment, our lab has partnered with the U.S. Fish and Wildlife Service to uncover the population structure of this species. Here, we present the assembly and annotation for the first genome for the Frosted Elfin built using third-generation sequencing (TGS). Our analyses revealed a highly complete sequence used to estimate population genetics parameters and to build the first mitogenome for this species. We show that this resource is highly applicable for assisting in this species' conservation. Moreover, we prove that we can build a high-quality genome at a reduced cost, allowing for a cost-effective application of resources for conservation analysis across all orders of insects.

29. Łukasz Przybyłowicz

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ISEA PAS¹, Kraków, Poland

¹Institute of Systematics and Evolution of Animals, Polish Academy of Sciences

Dysauxes – an African conqueror of the Cold Lands

The genus *Dysauxes* Hübner, 1819, is a small lineage of tiger moths belonging to the tribe Syntomini. According to the last review, it contains 8 species distributed exclusively in the

Palaearctic (Ignatev, 2006). While most lepidopterists treat *Dysauxes* as rather uniform morphologically (West Palaearctic), its true diversity can be assessed only by taking into account much less known Asiatic species. Surprisingly, thorough analysis of the entire range of this genus implicates intriguing questions on its evolutionary and biogeographic origin, that seem to be much more complicated and unclear. The newest discoveries resulted from the study of a wide range of taxa representing most of the Syntomini genera, strongly indicating the Madagascar roots of this lineage (Przybyłowicz *et al.*, 2019). Such a hypothesis is confidently confirmed by both morphological and molecular data. To make the story even more complicated, *Dysauxes* appears to be even more widely distributed across the Indian Ocean, by the existence of the omitted until very recently, endemic *D. florida* on the small oceanic island Mauritius, located about 900 km east of Madagascar (Przybyłowicz *et al.*, 2021). The species differs in some characters from typical congeners, however it is reasonable to ascribe it to the genus in question based on our present knowledge. Its presence on the remote, small oceanic island is not improbable and can be confidently elucidated assuming the stepping-stones scenario. This seemingly unlikely distribution pattern gained important confirmation by the very recent unexpected finding from East Africa: a single male of an unknown taxon, deceptively similar to typical *Dysauxes*, was collected in NE Tanzania. This discovery further corroborates the hypothesis that *Dysauxes* is not what it was thought to be. The European taxa are most probably only the youngest conquerors of the Cold Lands in which (wing-) veins still flow with hot African blood.

Ignatev, N.N. and Zolotuhin, V.V. 2006. A review of syntomids (Lepidoptera: Syntomidae) of Russia and adjacent territories. Part 2. Genus *Dysauxes* Hübner, 1826. *Eversmannia*, 6: 27–51.

Przybyłowicz, Ł., Lees, D.C., Zenker, M.M., and Wahlberg, N. 2019. Molecular systematics of the arctiine tribe Syntomini (Lepidoptera, Erebidae). *Systematic Entomology*, 44: 624–637.

Przybyłowicz, Ł., Wiorek, M., Przystałkowska, A., and Wahlberg N. 2021. Alone on an island: The reassessment of an enigmatic species of Handmaiden Moth (Lepidoptera, Erebidae) endemic to Mauritius. *Zoologica Scripta*, 50: 752–768.

30. Md Jahir Rayhan, Gisella DePiazza, Jacob Bethin, David Plotkin, Shashank R. Pathour, Bert Foquet, and Akito Y. Kawahara
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A CRISPR-based rapid identification approach for Tomato Pinworm, *Tuta absoluta* (Meyrick, 1917)

Tuta absoluta is a rapidly spreading pest, ravaging tomatoes and related crops worldwide. As part of a cryptic species complex, accurate identification is crucial but hindered by time-consuming, morphology-based methods that require expert validation. To address this, we aim to develop a CRISPR-based rapid identification tool for precise and field-deployable species diagnosis. Our approach focuses on targeting a highly conserved genetic region that remains stable across *T. absoluta* populations. Comparative genomic analyses have identified several potential molecular markers for species delineation. Once an optimal marker is validated, CRISPR-based detection will be rigorously tested to ensure high specificity and efficiency. This research will lead to a potentially innovative tool for scalable, real-time pest monitoring, transforming agricultural pest control in the future.

31. Anisha Sapkota* and Sajan KC
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Revision of *Pholisora* (Scudder, 1872) (Lepidoptera: Hesperiidae)

The genus *Pholisora* (Scudder, 1872), a group of North American spread-wing skippers, has undergone significant taxonomic revisions due to morphological and ecological overlap with related genera *Staphylus* and *Bolla*. Currently, five species are recognized, but uncertainties persist, including the validity of *P. crestar* and the placement of *P. litus*. Conflicting molecular phylogenies further complicate relationships: mtDNA places *P. catullus* as sister to (*P. albicirrus* + (*P. crestar* + *P. mejicanus*)), while Z chromosome analyses support *P. mejicanus* as sister to (*P. albicirrus* + (*P. crestar* + *P. catullus*)). To resolve these discrepancies, we examined 1,800 museum specimens to construct a cladistic tree based on detailed morphology, including study of genitalia. Our results align with Z chromosome phylogeny, which is also supported by distributional evidence. We provide redescriptions, updated distribution records, and dichotomous keys, advancing *Pholisora* systematics and supporting conservation efforts for the imperiled *P. crestar*.

32. Vaughn M. Shirey, Jayme Lewthwaite¹, Ann Marie Gawel², Laura Melissa Guzman³, and Matthew Williamson⁴

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MGCL, FLMNH, UF, Gainesville, FL

¹Carleton University, ²American Museum of Natural History, ³Cornell University, ⁴Boise State University

Tracking scientific integrity and influence with regard to Endangered Species Act rulemaking and lepidopteran conservation in the United States

Signed into law in 1973, the U.S. Endangered Species Act (ESA) is a hallmark conservation law, and several butterflies were among the first listed species. Throughout its history and recent years, the ESA has faced numerous legal challenges, and listing decisions have not gone without scientific controversy. Tracking the history of scientific integrity and influence, especially with the increasing and recent changes to the role of the U.S. Executive Branch in rulemaking, will be necessary for understanding how the federal conservation landscape is shifting for lepidopterans well into the future. Here, I present the results of two projects in which we used web mining and artificial intelligence to survey the state of invertebrate conservation under the ESA, and profiled spheres of influence in rulemaking for lepidopterans. We found that the southeastern United States, according to U.S. Fish and Wildlife, is a hotspot of threats and threatened invertebrate species, and a few key figures emerged as Lepidoptera conservation “influencers” in the U.S. Together, these results provide a historical roadmap for where we’ve been and guideposts for where we need to go to effectively conserve butterflies and moths while maintaining scientific integrity in governance.

Related publications:

V.M. Shirey, J.M.M. Lewthwaite, A.M. Gawel, and L.M. Guzman. In press. “50 Years of Invertebrate Conservation Under the United States Endangered Species Act—History and Threats to Species.” *Frontiers in Conservation Science*.

V.M. Shirey and M.A. Williamson. In prep. “Comprehensive Peer-reviewed Bibliographic Data Used to Support United States Endangered Species Act Rulemaking.”

33. Jeffrey R. Slotten

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MGCL Research Associate, Gainesville, FL

Tribute to Howard David Baggett, founder of the Southern Lepidopterists' Society

Howard David Baggett passed away at the age of 76 on July 27, 2024. I will present a brief synopsis of his life and contributions.

34. Andrei Sourakov, Jing Zhang, Qian Cong, and Nick V. Grishin
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MGCL, FLMNH, UF, Gainesville, FL

Bella Moth updates

In my talk I am going to give a quick update related to research on the Bella Moth. Following a series of chemical ecology and wing pattern studies conducted at the University of Florida, a new collaboration has emerged with the University of Texas that has focused on the underlying genetics. Genomes of 100 *Utetheisa ornatrix* specimens from the McGuire Center's collection were analyzed by my Texas colleagues to understand the population structure of this variable species. By sequencing a variety of phenotypes and analyzing their genomes, we identified two candidate genes that play a role in determining color and pattern differences between *bella* and *ornatrix* phenotypes. By comparing the reference genome of *U. ornatrix* with genomes of other Arctiinae, unique gene duplications were identified which may be associated with detoxification of alkaloids from the moth's hostplants, *Crotalaria*. Sequencing 50 additional specimens of related taxa from our collection allowed reconstruction of the evolutionary history of the genus *Utetheisa* and better understanding of the role of hostplant switches in the evolution of this lineage.

35. Sarah R. Steele Cabrera*, Michael Belitz, Thomas C. Emmel, Emily S. Khazan, Matthew J. Standridge, Kristin Rossetti, Jaret C. Daniels
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MGCL, FLMNH, UF, Gainesville, FL

Long-term population dynamics of the endangered Schaus' swallowtail butterfly are influenced by hurricane-mediated disturbance

Effective species conservation requires understanding of an organism's population dynamics and natural history, but long-term data are challenging to collect and maintain. As a result, conservation management decisions are frequently made using short-term data, which are insufficient to accurately assess population trends in most species. For less-studied taxa, including most invertebrates, inadequate understanding of life and natural history also impedes conservation efforts. Long-term studies are highly valuable for improving conservation decisions for target species, as they serve as a model for other understudied species. We use mark-recapture data collected over 36 years to examine weather drivers of population patterns for an endangered butterfly, Schaus' swallowtail (*Heraclides ponceana*), and to enhance our understanding of its natural history. We show that the population size of Schaus' swallowtail was highly variable, ranging from under 100 to over 10,000 individuals. Population size is influenced by wind events and population size in the previous year. Population size was lower immediately following high wind events, but was positively influenced by high wind events four years prior, with notable population increases following tropical cyclone events. This study reveals the potentially beneficial role of hurricane-mediated disturbance on Schaus' swallowtail populations, potentially due to increased treefall gaps and the resulting shifts in plant communities. This remarkable data set represents one of the

longest-term studies on a tropical insect and highlights the need for further study of tropical cyclone disturbance on insect populations.

36. Olivia L. van der Vlugt*, Anastasia Baluk Garavaglia*, Md Jahir Rayhan, Lauren Eccles, Whitney Stoppel, Bert Foquet, and Akito Y. Kawahara
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An in-depth study of lepidopteran silk glands

Silk is a unique biomaterial which is used by humans in the textile industry, but also in engineering components and medical applications. Caterpillars in the order Lepidoptera use silk in many different ways, including cocoon generation, protection from predators, communication, and dispersal. To better understand how this variety of silk is produced, we generated nanoCT scanning data for a large number of lepidopteran taxa to investigate the size and structure of the silk glands. We will show the structure of these glands, and have measured the volume and length of the silk glands for each of these taxa. Finally, we will discuss how these variables relate to their phylogenetic placement and the amount of silk they spin.

37. Rachel L. Walsh*, R. Keating Godfrey, Yi-Ming Weng, Paul B. Frandsen, Jaret C. Daniels, and Akito Y. Kawahara
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MGCL, FLMNH, UF, Gainesville, FL

New high-quality genome for the imperiled Loammi skipper butterfly (*Atrytonopsis loammi*: Hesperiidae)

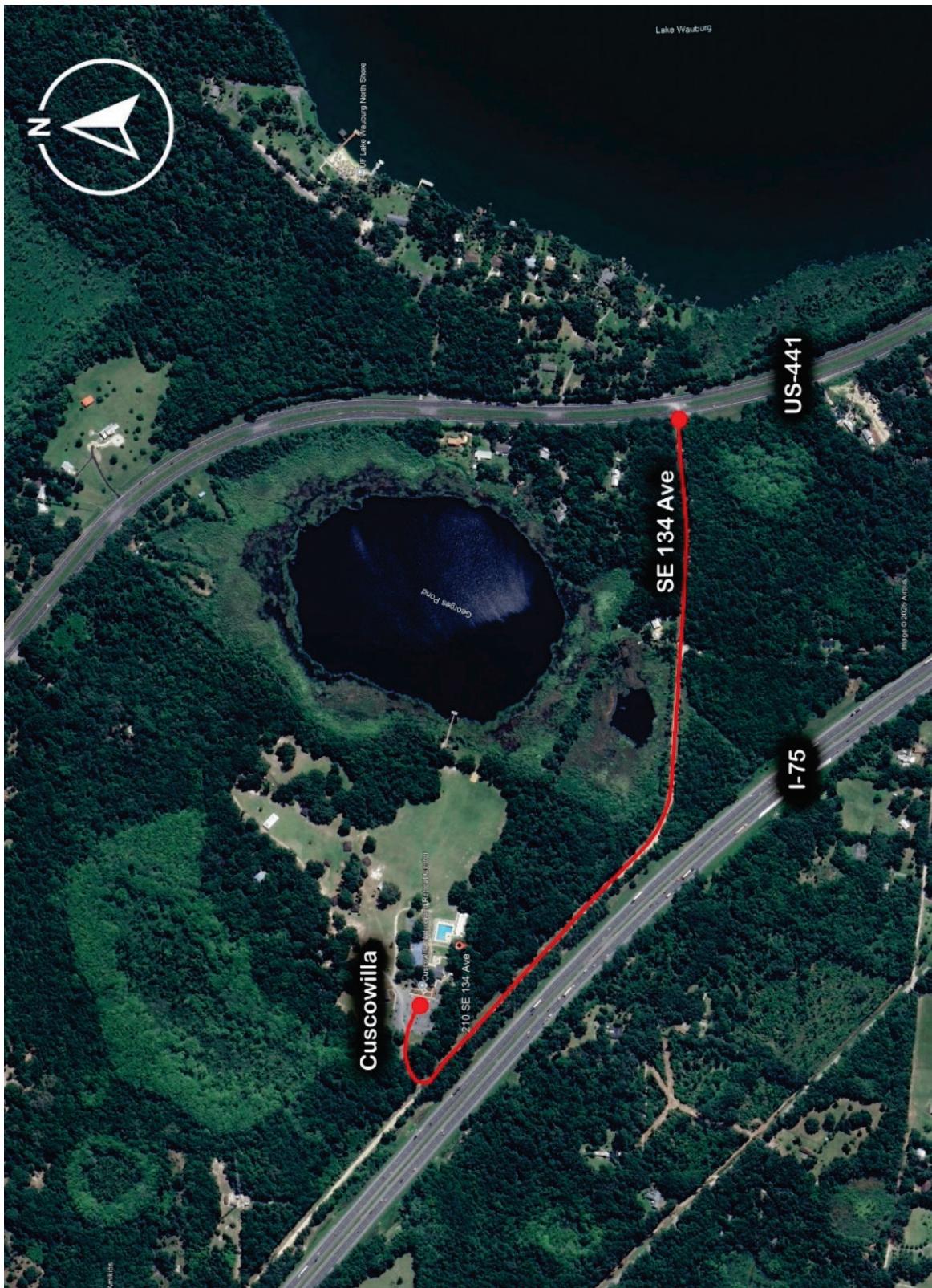
The Loammi skipper (*Atrytonopsis loammi*: Hesperiidae) is an imperiled, host-specialist grass skipper (Hesperiinae) that occurs in fire-dependent prairies in Florida. While most *Atrytonopsis* are univoltine, including the closely related *Atrytonopsis hianna*, *A. loammi* is bivoltine. Despite this ecological distinction and morphological differences, some authors consider *A. loammi* to be a subspecies of the more widespread but allopatric *A. hianna*. Taxonomic uncertainty combined with imperiled status and lack of genetic studies make *A. loammi* an important subject for genomic research. Here we report a high-quality genome produced using PacBio HiFi sequencing. Future work will annotate genes that may be associated with habitat preference and climate sensitivity. The genomic data produced in this study will fill critical knowledge gaps, aiding future work and informing conservation efforts for this species.

38. Keith R. Willmott
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New Neotropical butterfly species are where you find them

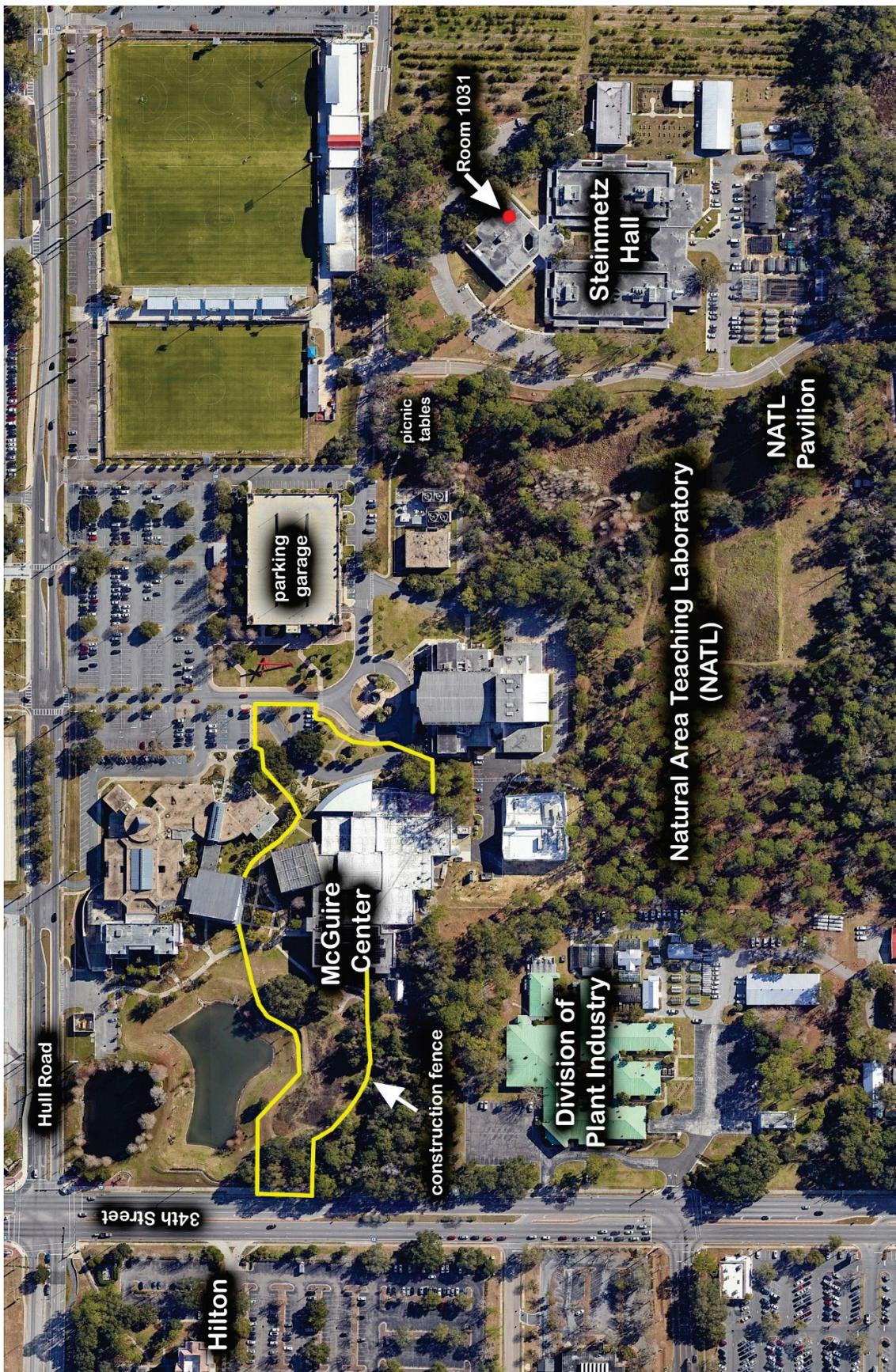
The Neotropical butterfly fauna continues to surprise with its seemingly endless diversity and complexity. Taxonomic work at the *coalface* of cryptic species complexes continues to uncover hidden species, and expeditions to remote regions often result in spectacular finds, yet new discoveries also continue to be made in the most unexpected places. Classically dull, usually monotonous satyrine lineages demand multiple character sources, multiple specimens, new

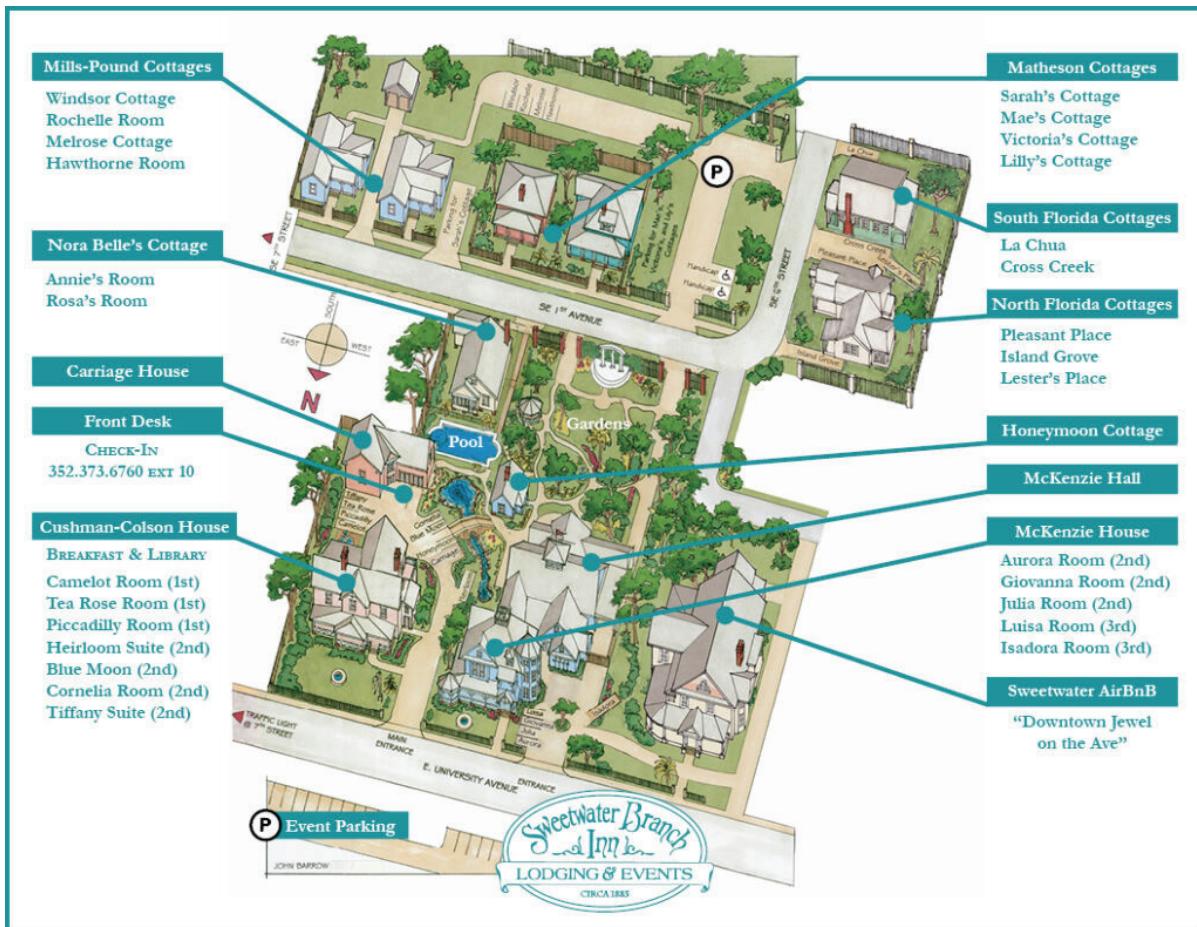
data, and a focus on what were thought to be well-known taxa. Mercurial metalmarks require understanding, patience, and perseverance over decades. One might think that big, bold brassolines and conspicuous *Adelpha* should be well-understood, but they too contain mysteries to be unraveled, and Andean cloud forests prove to be hiding-places for even the most colorful butterflies. I discuss my recent and ongoing taxonomic research with collaborators on diverse Neotropical butterfly groups.



Cuscowilla Nature & Retreat Center
210 SE 134 Ave., Micanopy, FL 32667

Cultural Plaza & Vicinity





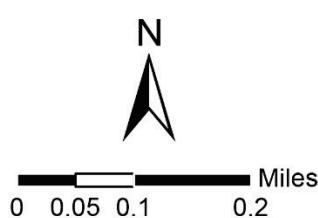
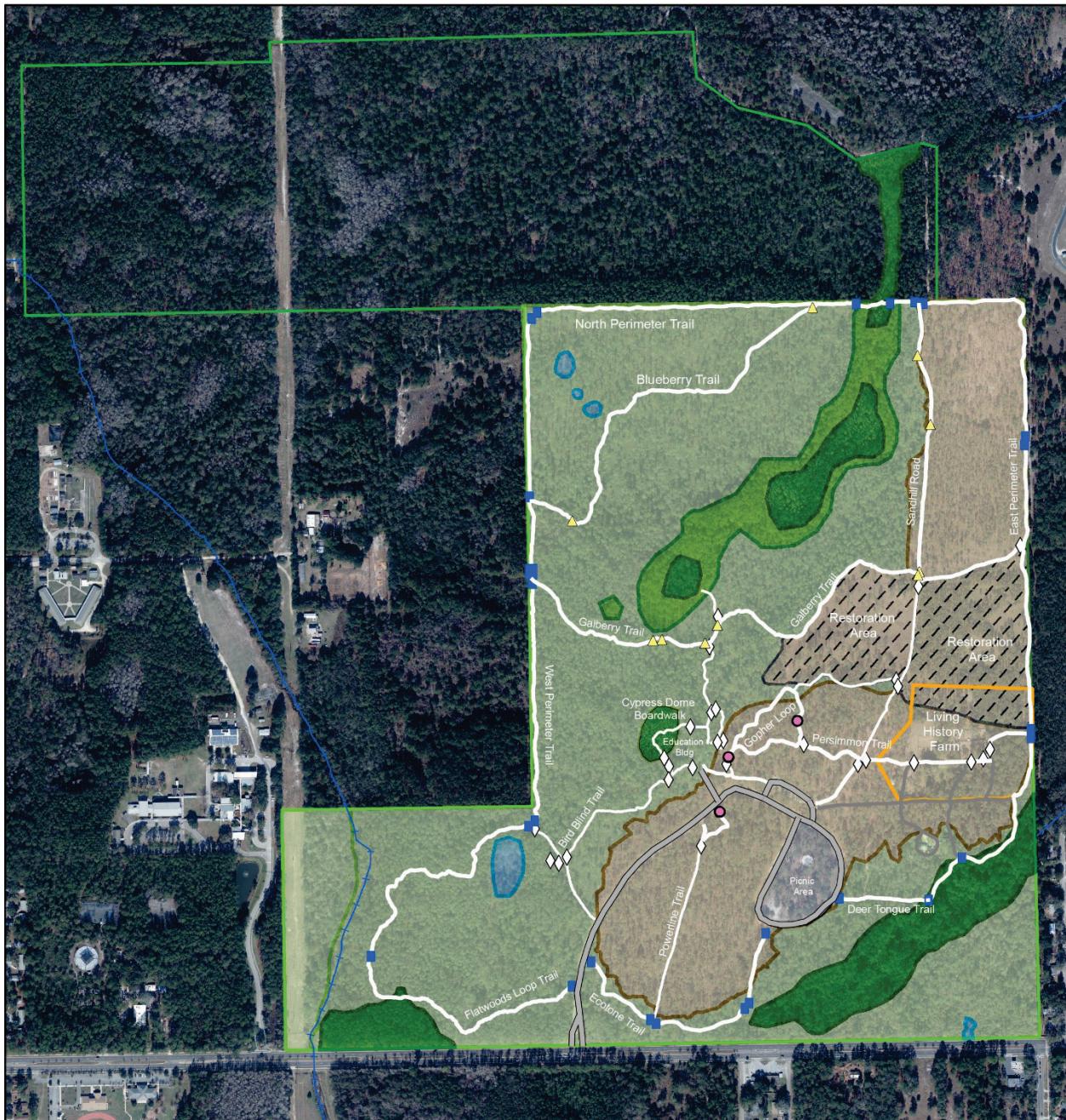
Sweetwater Branch Inn

625 E. University Ave., Gainesville, FL 32601

Event parking for the banquet is available north of University Avenue (see map above).

Morningside Nature Center

3540 East University Ave., Gainesville, FL 32601



Natural Communities	
Basin Swamp	Farm Boundary
Depression Marsh	Nature Park Boundary
Dome Swamp	Creeks
Developed	Paved Roads
Mesic Flatwoods	
Restoration Area	
Sandhill	
Wet Flatwoods	

●	Pink Loop (.25 miles)
◇	White Trail (connector)
■	Blue Loop (3 miles)
▲	Yellow Loop (1.5 miles)
—	Closed to Public