The SBE meeting 2021's Book of Abstracts

Edited by the SBE meeting 2021's organizing committe

June, 2021

DOI: 10.5281/zenodo.5109989

II Virtual Meeting of Systematics, Biogeography, and Evolution: The Research of Biodiversity and the Diversity of Researchers

www.sbemeeting.com

June 19–23, 2021

Time Zone: UTC-4

DOI: 10.5281/zenodo.5109989 (new version published on July 16, 2021)

About

The I Meeting of Systematics, Biogeography, and Evolution (SBE) occurred from July 28 to July 30, 2020. The theme of the first meeting was *A Joint Effort in the Coronavirtual Era* (see `https://sbemeeting.weebly.com/`).

This abstracts book contains the abstracts of the second SBE meeting, from June 19 to 23, 2021. Our 2021's theme is *The Research of Biodiversity and the Diversity of Researchers.* Although the themes changed, our primary purposes remained the same.

First, to provide a high-quality international scientific meeting on systematics, biogeography, and evolution.

Second, to make the event accessible to people that could have difficulty attending other international scientific events due to financial constraints or the COVID-19 pandemic.

Third, to promote diversity and gender equality in science, technology, agronomy, mathematics, and medicine (STEAMM).

Come celebrate the richness of variety!

`www.sbemeeting.com`

Sponsors, Supporters, and Collaborators

The SBE Meeting 2021 is made possible thanks to our sponsors, supporters and collaborators.

Different poster awards were offered by:

- Asociación Paleontológica Argentina (APA, `www.apaleontologica.org.ar/`)
- Asociación Hepetológica Argentina (AHA, `http://aha.org.ar`)
- BIO+ Ciência (`biomaisciencia.com`)
- Transmitting Science (`www.transmittingscience.com`)

We thank the University of North Carolina at Charlotte (UNC Charlotte) for making the webinars on Zoom possible without costs for the participants.

The SBE Meeting 2021's Organizing Committee

Ángela Meneses
Colombian
Pontificia Universidad Javeriana

Denis Jacob Machado
Brazilian
University of North Carolina at Charlotte (UNC Charlotte)

Edgar Gamero Mora
Mexican
Universidade de São Paulo (USP)

Francisca Almeida
Brazilian
Universidad de Buenos Aires (UBA)

Gabriel Massami Izumi de Freitas
Brazilian
Universidade de São Paulo (USP)

Jairo Andrés Moreno-González
Colombian
Universidade de São Paulo (USP)

Janaína Gomes-da-Silva
Brazilian
Jardim Botânico do Rio de Janeiro

Juan Hurtado
Argentinian
Universidad de Buenos Aires (UBA)

Kary Ocaña
Peruan
Bioinformatics Laboratory (LABINFO)
National Laboratory of Scientific Computing (LNCC)

Lara Inés Baccaro
Argentinian
Instituto de Ecorregiones Andinas (INECOA) - CONICET

Lina María Caballero Villalobos
Colombian
Technische Universität München

Luz Eneida Ochoa Orrego
Colombian
Museu de Zoologia da Universidade de São Paulo (MZUSP)

Manolo Perez
Brazilian
Universidade Federal de São Carlos (UFSCar)

Maximiliano Nicolas Fabianelli
Argentinian
Universidad Nacional de Cordoba

Óscar Mahecha-J
Colombian
Zoological Division of the Nature Education Centre of the Jagiellonian University

Sofía Terán Sánchez
Colombian
Universidad de Caldas

Tiago Belintani
Brazilian
Universidade de Campinas (UNICAMP)

Yeison Vega-G
Colombian
Universidad Nacional de Colombia

Code of Conduct

The II Virtual Meeting of Systematics, Biogeography, and Evolution (also known as the SBE meeting 2021, or SBE21), is a space for socialization and scientific dialogue that promotes the advancement of the discipline and encourages inclusive participation based on gender equality in conferences and symposia. For its optimal development, everyone is asked to comply with the following code of conduct:

- Always use an appropriate and respectful vocabulary with the interlocutor. Behaviors, verbal expressions, or images that may be considered intimidating, vexatious, discriminatory, violent, abusive, derogatory, xenophobic, racist, or hate promoting against any person, religion, gender, or sexual orientation will not be tolerated, nor any other action tending to affect the dignified treatment deserved by every individual who participates in the virtual spaces of the SBE.
- Turn off microphones and cameras throughout the presentations. The only people allowed to speak are the hosts, moderators, and exhibitors. Assistants are allowed to speak during the allotted question time, at the end of each presentation.
- Respect the request of those who express their disagreement on being photographed, filmed, named, quoted, among other possible actions.
- Do not publish others' private information, such as physical or email address, without their explicit permission
- Exhibitors must review that the material they present, in any type of participation, is not offensive.
- The debate must be conducted in a formal tone and language. At no time should deliberate intimidation, ad hominem attacks, or trolling be carried out.
- The chat of the presentation platform must be used respectfully. Interactions through this chat must be kept to a minimum to facilitate the management of questions and the organization of each symposium. Attendees, as well as exhibitors, will have the opportunity to discuss and exchange ideas of greater length and complexity in the chat rooms of the Discord platform, enabled by the organization of the meeting.

Those who do not comply with this code will be warned by the organizing committee of the SBE and, given the persistence of the indicated abusive behavior, they will be excluded from the virtual common spaces temporarily or permanently, depending on the severity of the infractions, as determined by the meeting organizers.

Contents

Diversity and Inclusion in STEAMM

Why do gender, minorities, and diversity matter?

Recently, a growing number of studies are showing the lack of diversity in STEAMM. Though still on its infancy, these sources of evidence suggest that the underrepresentation of minorities results in a lack of plurality among researchers and the studies performed. This symposium aims to bring specialists and activists to discuss the challenges and obstacles that underrepresented groups in the STEAMM community face. It also intends to show that it is essential to promote diversity within STEAMM and develop strategies that include all gender and minority groups. Striving towards inclusive environments in academia and research areas is essential, as prejudice against many groups is still not adequately assessed.

June 19
9:10 AM
Inclusion

Diversity, equity, and inclusion: An everyone issue

Moreau C.S.[1*]

[1]Departments of Entomology and Ecology & Evolutionary Biology, Cornell University, New York, NY, USA. *Correspondence: corrie.moreau@cornell.edu.

For this STEM diversity and inclusion presentation Dr. Corrie Moreau will share what the data and research show regarding bias and inclusion in the sciences across many axes of diversity and why having diverse teams is good for science. She will end with some recommendations to be more inclusive and equitable as individuals and as departments and institutions and then open it up for Q&A/discussion.

June 19
10:00 AM
Inclusion

Possible paths to a more diverse and inclusive STEAMM

Diele-Viegas L.M.[1*]

[1*]Biology Department, University of Maryland, College Park, Maryland, USA.
*Correspondence: luisa.mviegas@gmail.com.

Science has a racism and cis-hetero-normative problem that needs to be addressed so gender equality can become a plausible reality. Understanding the academic representation gaps considering the intersectionality concept is paramount to promote real progress towards a more inclusive STEAMM, overcoming the fear of moral opprobrium that has prevented an honest debate about the persistence of racism and other forms of discrimination in scholarly work. In this presentation, I will present possible paths to fight the implicit and explicit bias in the academic environment and extinguish the existing systems of oppression within STEAMM fields.

June 19
10:30 AM
Inclusion

Surfacing anti-Black science and building antiracist teams

Caicedo H.[1,2*]

[1]Connection Science, Massachusetts Institute of Technology, Massachusetts, U.S.A.
[2]Corporate Sustainability and Innovation, Harvard University, Massachusetts, USA.
*Correspondence: caicedo.hugo@gmail.com.

In mid 2020, following the brutal killing of a Black man, George Floyd, by police in the United States, a myriad voices involved in the science and commercial business of biotech called for action on systemic racism in society and in science. In late June of 2020, the world's largest scientific society, the American Chemical Society, vigorously pointed out that it is abundantly clear that the lack of representation of Black people and members of other under-represented minorities in science and engineering education and employment is a symptom of systemic racism across all levels of education and professional life. As a Black man living in the United States, a professional contributing to the science and commercial business of biotech, and a police survivor myself, I was invited by the journal Nature Biotechnology to write an article covering racism in science and medicine. In this talk, I hope to raise awareness of unethical anti-Black "science" and help improve public understanding

of the causes and effects of racial inequity and exclusion in the life sciences. I also outline concrete action items that the biopharmaceutical industry and research academic institutions may consider to create equitable antiracist teams. The goal is not to point fingers but to raise awareness of multigenerational injuries, avoid historical mistakes, visibilize current social realities, and co-develop a more equitable world with a leveled playing field for all human beings.

The implicit bias and gender inequalities in science

June 19
11:35 AM
Inclusion

Oliveira L.[1,2*]

[1]Fluminense Federal Fluminense (UFF), Rio de Janeiro, Brazil. [2]University College London, London, England. [*]Correspondence: oliveira_leticia@id.uff.br.

The public will be encouraged to rethink points of view based on themes that question human behavior in the face of gender issues, such as: Why are there so few women in science and some sectors of society? Why is it important to change this scenario? Is there evidence that our behavior can be manipulated? How are these gender stereotypes constructed? What are the consequences of these stereotypes for female representation? These questions are especially relevant now, as the COVID-19 pandemic may have led to a widening of the gender and racial/ethnicity gaps. Implicit bias is a crucial component in this fight. Negative stereotypes that are socially constructed in a given culture are frequently associated with implicit bias (which is unconscious or not perceived). In the present talk, we point to scientific evidence that shows the presence of implicit bias in the academic community, contributing to strongly damaging unconscious evaluations and judgments of individuals or groups. Additionally, we suggest several actions aimed at (1) editors and reviewers of scientific journals, (2) people in positions of power within funding agencies and research institutions and (3) members of selection committees to mitigate this effect. These recommendations are based on the experience of a group of Latinx American scientists comprising Black and Latinx women, teachers and undergraduate students who participate in a “Women in Science” working group at universities in the state of Rio de Janeiro, Brazil. With this talk, we hope to contribute to reflections, actions and the development of institutional policies that enable and consolidate diversity in science and reduce disparities based on gender and race/ethnicity.

How do we move from theory to practice?

Recent research findings show that LGBTQIA+, minority ethnic groups, and women are more likely to be devalued or harassed in their working environment in STEAMM. Confronting academia's unfair realities and research in STEAMM areas call for scientists to care about more than only scientific productiveness. Structural discrimination requires diversifying and institutional transformations, providing novel insights, initiatives, and actions required to guide public policies. Such actions are necessary to promote acceptable practices that ensure equal opportunities for women, men and minority groups in the development of their scientific careers. Here, we show new inspiring scientific activities and activism initiatives towards diversity and inclusion in STEAMM

The parent in science movement in Brazil

June 23
2:00 PM
Inclusion

Staniscuaski F.[1*]

[1]Departamento de Biologia Molecular e Biotecnologia, Universidade Federal do Rio Grande do Sul, RS, Brazil. [*]Correspondence: fernanda.staniscuaski@ufrgs.br.

With the increase in female participation in the most varied professional fields, women are faced with the challenge of reconciling personal and professional life, especially with regard to motherhood. In the academic / scientific career, this situation is also encountered. The theme "motherhood and scientific career" is rarely discussed in the academic environment, and few studies have evaluated the parenthood impact on the career of scientists in Brazil. With this in mind, the Parent in Science Movement was created, with the goal of conducting in-depth studies on the real impact of the arrival of children in the lives of (a) scientists, aiming mainly to support the development of new policies to support parents in science.

Making science more inclusive for LGBTQIA+ individuals

June 23
2:50 PM
Inclusion

Weber G.[1*]

[1] Departamento de Ciências Básicas e Ambientais, Escola de Engenharia de Lorena, Universidade de São Paulo, SP, Brazil. [*]Correspondence: gabrielleweber@usp.br.

What is it like to be LGBTQIA+ in STEAMM? What are the barriers and difficulties we face on a daily basis in academia? Homophobia? Transphobia? Transmisoginy? These are just some of the many agressions we have to endure. But how can we do it better and promote a more inclusive and diverse environment? In this short talk, we review the findings of recent surveys regarding the issues and difficulties faced by LGBTQIA+ individuals in academia. We also discuss possible solutions and how can science outreach initiatives, such as Mamutes na Ciência, help to make science more diverse and inclusive.

Questioning the biological basis of sex and gender differences

June 23
3:15 PM
Inclusion

Puixeu Sala G.[1*]

[1]Institute of Science and Technology Austria, Austria. [*]Correspondence: gemma.puixeusala@ist.ac.at.

Women and men are different. And the acknowledgement and proper study of these differences is crucial for fields like biomedicine. But why do they differ? And how much? These are two critical questions that we have failed to address. In this talk, I argue that we have failed not because we haven't tried hard enough, but because we have tried too hard. Research about sex and gender is highly biased and expectation-dependent, influencing both the questions we ask and the answers we obtain. The biological "knowledge" about sex and gender thus requires a thorough reevaluation, for which I propose a change of paradigm that allows studying the biological dimension of sex and gender in human societies with a more bias-aware approach: it is all cultural unless proved otherwise. This talk is an invitation to question the reason why we conceive sex and gender the way we do; to reevaluate the sociological and biological evidence supporting the current paradigms, strongly reassuring gender binarism and inequality; and to find better ways to scientifically assess the differences between "women" and "men."

June 23
3:50 PM
Inclusion

SOL Seminars Online and ARG Plant Women: two initiatives to increase diversity in Plant Sciences

Deanna R.[1,2,3*]

[1]Instituto Multidisciplinario de Biología Vegetal, IMBIV (CONICET-UNC), Córdoba, Argentina. [2]Departamento de Ciencias Farmacéuticas, Facultad de Ciencias Químicas (FCQ, UNC), Córdoba, Argentina. [3]Department of Ecology and Evolutionary Biology, University of Colorado, Colorado, USA. [*]Correspondence: rociodeanna@gmail.com.

One of the largest advantages of digital interaction formats is inclusivity as they lower the barriers to participating. The increase of virtual meetings since the covid-19 pandemic have provided an opportunity to diversify participation across time zones and geographical space. However, the development of diverse networks and meetings requires additional efforts and commitments from the organizational committees towards that direction. During my talk, I will introduce two seminar series as experiences of ways to increase diversity in plant sciences. In the first place, Solanaceae Seminars Online are video-based weekly meetings focused on the tomato family (https://physaloidseminars.weebly.com/). This seminar series was created with the goals to encourage collaboration, aid in sharing information, and enhance research on this plant family by inviting specialists from across the world. Since its beginning in 2020, more than 250 researchers have engaged with an outstanding participation from South America, while also balancing the gender representation of speakers invited. Some outcomes include new research collaborations as well as broader awareness of the research conducted in Solanaceae. Secondly, the Argentinian (ARG) Plant Women network connects Argentinian women scientists working in plant science in the country and abroad, creating a much-needed networking space for all its members and the broader community (https://argplantwomen.weebly.com/). This group started with the aim to increase the visibility of the wealth of plant science topics and experimental approaches in which Argentinian women work, and has grown from weekly seminars to multiple activities, including open professional development webinars and outreach events to a wider audience. In sum, ARG Plant Women and SOL Seminars Online have provided a safe space for women and underrepresented scientists to share their work, build collaborations, and collectively advance their careers, as well as encouraging Spanish-speaking botanists to pursue their goals in science.

Paleobiodiversity and Evolution

As remarkably summarized by Croizat (1964), “Earth and life evolve together.” This symposium will integrate discussions of paleobiological approaches and systematic studies of related fossils and extant taxa with an interdisciplinary approach based on this premise. Our speakers will present new methodologies such as 3D modeling, geometric morphometry, and phylogenetic reconstructions. Moreover, discussions will aggregate knowledge from organism-environment interaction, paleoecology, paleobiogeography, and climate change research in paleoenvironments.

June 19
2:00 PM
Paleo

Is there evidence of the link between Triassic climatic and biotic events in western Gondwana?

Mancuso A.C.[1*], Irmis R.B.[2,3], Horn B.L.D.[4,5], Benavente C.A.[1] & Schultz C.L.[5]

[1]Instituto Argentino de Nivología, Glaciología y Ciencias Ambientales (IANIGLA), CCT-Mendoza, CONICET, Mendoza, Argentina. [2]Natural History Museum of Utah, Utah, USA. [3]Department of Geology & Geophysics, University of Utah, Utah, USA. [4]CPRM/Geological Survey of Brazil, Superintendência Regional de Porto Alegre, Rio Grande do Sul, Brazil. [5]Programa de Pós-Graduação em Geociencias, Instituto de Geociencias, Rio Grande do Sul, Brazil. [*]Correspondence: amancu@mendoza-conicet.gov.ar.

After the end-Permian mass extinction, during the Triassic, the origin and early diversification of several modern vertebrate clades occurred on land, including lissamphibians, lepidosaurs, turtles, dinosaurs, and mammaliaforms. The Triassic configuration of the supercontinent Pangea spread across the equator, combined with a high global sea level and no polar ice caps, would have had an extraordinary effect on the global climate. Therefore, the Triassic Earth was a hothouse world, with elevated atmospheric CO2 levels that intensified climate extremes. Multiple climate events occurred during this time, such as large igneous province (LIP) eruptions, including two that had a significant part to play in the mass extinctions that bracket the Triassic Period. Then, the marked dynamic Triassic climate becomes the period ideal to examine the effects of climate in the ecosystems. Notably, the Triassic western Gondwana non-marine strata bear a large number of rich fossil assemblages and paleoclimatic data, with geochronological age constraints, which span most of the Period. We compiled available geochronological-constrained paleoclimatic data from Triassic non-marine vertebrate-bearing strata to evaluate how local, regional, and global paleoclimatic changes may have influenced Triassic biota in South America and Gondwana as a whole. Fluctuating climate conditions dominated the western Gondwana Triassic. During the Early Triassic, arid to semi-arid conditions were dominant, with a marked humid seasonal fluctuation in the continental interior. Seasonal semi-arid conditions characterized the Middle Triassic, but there was a more humid seasonality than Early Triassic. Finally, the Late Triassic was dominated by seasonal sub-humid conditions with semi-arid intervals, particularly in the continental interior. The Triassic South American vertebrate fossil record shows some correspondence pattern with the paleoclimate record. However, we remark that expanding geochronologic control, with more multiproxy paleoclimate data and sampling fossil-bearing strata, is necessary to understand these trends better.

Diversification and dispersal dynamics of mammals during the Great American Biotic Interchange

June 19
2:50 PM
Paleo

Carrillo J.[1,2*]

[1]CR2P, Muséum National d'Histoire Naturelle, Paris, France. [2]Gothenburg Global Biodiversity Centre,Gothenburg, Sweden. [*]Correspondence: juan.carrillo@mnhn.fr.

When the Isthmus of Panama connected North and South America, it allowed the interchange of the previously separated faunas from two continents, resulting in a major biogeographic event in earth history. A puzzling aspect of the interchange is that North American mammals seem to have done better. The fossil record shows more mammals with North American origin in South America than vice versa, as result of the interchange. Clarifying the reasons and mechanisms behind this asymmetry is important for understanding the legacy of the interchange in the distribution of biodiversity of mammals today. In this talk, I will address the long-standing question of why the end result of the interchange was asymmetrical. New analyses of the mammal fossil record show that the main reason for the asymmetric result of the interchange is that South American mammals had proportionally more extinctions during the Pliocene (5.6 to 2.6 million years ago). In addition, recent findings of fossil faunas from northern South America suggests that dispersal dynamics during the biotic interchange were different between the tropics and temperate regions. This highlights the need to study biogeographic and ecological factors in order to better understand this important biotic event.

An overview of the tetrapod fauna from the Miocene of the Southwestern Brazilian Amazonia

June 19
3:15 PM
Paleo

Hsiou A.[1*]

[1]Paleontology Laboratory, Faculty of Philosophy,Sciences and Letters of Ribeirão (FFCLRP), University of São Paulo (USP), São Paulo, Brazil. [*]Correspondence: anniehsiou@ffclrp.usp.br.

The Cenozoic vertebrate fossil record in Brazil is rich and diversified. Most of the early Cenozoic fossils are specifically concentrated in the Paleogene deposits located in the northeast and the southeast parts of the country. On the other hand, deposits of Neogene age are mainly concentrated in the southwest of the Brazilian Amazon region, mainly represented at the Acre Basin (Miocene of the Solimões Formation). A large part of the Cenozoic tetrapod fossils is almost exclusively composed of medium to large-sized animals, such as mammals, crocodilians, turtles, and several specimens of scientific relevance are stored in various national and overseas research institutions. The investigative works have been focused on the phylogenetic relations and evolution of collected taxonomic groups, such as small mammals, amphibians, lizards, snakes, and the biostratigraphic/temporal and paleoenvironmental implications with other South American Neogene deposits. While keeping the investigation focus on tetrapods, in more general terms, is crucial improving the stratigraphic correlations of the Neogene deposits in the Acre Basin as well as the correlations

with those from other parts of the northern countries of South America (e.g., Peru and Venezuela), using relative (SALMAs - South American Mammal Ages) and absolute dating (detrital zircon) analyses. It is essential to point out that this type of geochronological framework at the Acre Basin has been insufficiently studied.

June 19
3:50 PM
Paleo

Ancient tropical extinctions contributed to the latitudinal diversity gradient

Sanchez Meseguer A.[1*]

[1]Department of Biodiversity and Conservation, Real Jardín Botánico, CSIC, Madrid, Spain. *Correspondence: asanchezmeseguer@gmail.com.

Biodiversity currently peaks at the equator and decreases towards the poles. Accumulating fossil evidence reveals that this hump-shaped latitudinal diversity gradient (LDG) has not been persistent through time but was restricted to cold climatic periods. Under warmer regimes, there was comparable species diversity across latitudes such that the LDG flattened. This evidence sets a new starting point on LDG research. Most evolutionary hypotheses published to date seek to understand why diversity did not accumulate in the Holarctic at the same levels than in the equator, e.g. as the result of higher equatorial diversification, limited dispersal, or higher Holarctic turnover, while recent fossil investigations show that, for many lineages, we rather need to explain why, how and when diversity was lost at high latitudes to shape the current LDG. Here, we propose a framework explaining the origin of the today's LDG, where its shape is mostly determined by changes in the global diversification and dispersal dynamics imposed by large-scale climatic transitions. We studied the LDG of Testudines, Crocodilia and Squamata using fossils and phylogenetic comparative methods and found the high latitudes have been a source of tropical diversity for these groups. During greenhouse periods, diversification rates were equivalent between latitudes. During the late Eocene transition to cold climates, however, we detected important levels of extinction for ancient tropical lineages distributed at high latitudes, coupled with high levels of range contractions and equator-ward dispersals. Our results further demonstrate the inclusion of fossils in macroevolutionary studies allows detecting the signal of ancient high-latitude extinctions and range extirpations, otherwise vanish from analyses based on present-day data only. Our results challenge the current consensus, which considers the evolutionary processes behind the LDG have acted constantly over time and suggest the LDG should be regarded as a time-varying biodiversity pattern.

Virtual palaeoprimatology: Assessing ecomorphological questions in extinct anthropoids using the morpho-functional toolkit

June 19
4:15 PM
Paleo

Püschel T.[1*]

[1]Institute of Cognitive and Evolutionary Anthropology, University of Oxford, Oxford, U.K. *Correspondence: thomaspuschel@gmail.com.

The overarching objective of this presentation is to understand the relationship between form and ecological function in diverse skeletal elements belonging to different primate clades using geometric morphometrics (GM), finite element analysis (FEA) and phylogenetic comparative methods (PCMs). GM provides a system for quantifying morphology; while FEA allows measuring biomechanical performance and PCMs are used to model how phenotypic traits have evolved through time. This presentation will provide different examples of how to combine these methods in palaeontological contexts. The main focus will be on the association between locomotion and morphology and how to apply this information in the anthropoid fossil record, although brief additional examples focused on the form-function relationship in dietary contexts will also be provided. Thus, it is expected to contribute to the understanding of the correlation between form and ecological function, which is not only relevant to appreciate the morphological diversity in extant species, but also because it allows us to infer past behaviours in fossil taxa.

How a sick dinosaur revealed the oldest known blood-borne parasitic infection

June 19
4:40 PM
Paleo

Ghilardi A.M.[1*]

[1]Universidade Federal do Rio Grande do Norte, Natal, RN, Brazil *Correspondence: mailto:aline.ghilardi@ufrn.b.

A strange pathology in a dinosaur bone posed a big question to a group of colleagues. What could have caused such injury to the animal? As they delve deeply into the scars of the disease, a startling discovery brought an unexpected outcome. A disease thought to be unusual for a reptile is described for the first time in histological detail, and dozens of blood parasites were found within the animal's bone. The description of the first substantiates the understanding of a disease that still affects humans and other animals today, and the discovery of the latter challenges our knowledge of fossildiagenesis and provides the first glimpse into previously unknown parasites and very familiar ecological relationships.

The New Era of Biogeography

The new era of biogeography leads us to view the distribution of species from a scale other than that involved in classical Biogeography. The methodology for formulating and testing biogeographic hypotheses is expanding to integrate various determinants of species distribution increasingly. This field invites us to grow on multidisciplinary approaches. At this symposium, by the hand of the new generation of biogeographers invited, we will hear about new topics and methods within the study of the distribution patterns of species.

June 20
9:00 AM
Biogeo

Bridging the micro and macroevolutionary levels in biogeography: different processes, similar patterns and new advances to integrate them

Sanmartín Bastida I.[1]*

[1]Real Jardin Botanico, Department of Plant Biodiversity and Conservation, Madrid, Spain. *Correspondence: isanmartin@rjb.csic.es.

Evolutionary biologists and biogeographers, in their efforts to determine which factors govern biodiversity dynamics, have used two approaches that differ primarily in the taxonomy level they focus on: microevolutionary processes (genetic drift, mutation, migration) act mostly on individuals and populations, while macroevolutionary processes (extinction, dispersal, speciation) focuses on diversification at and above species level in relation to environments and over longer time scales. These two levels are difficult to bridge because they often imply different analytical techniques (population genetics vs. phylogenetics) and data sources (multicopy DNA vs nucleotide substitutions in protein-coding genes). The advent of Next Generation Sequencing techniques has made this feasible by scaling up the numbers of genes, individuals, populations, and species sampled in a cost-effective way. Techniques like target sequencing permit to obtain large datasets of DNA sequences for hundreds or thousand of markers across different phylogenetic levels. This molecular revolution has gone in hand in hand with new advances in the development of analytical approaches, and the exponential growth of bioinformatics. In this conference, I will review these advances in the fields of machine learning and statistical phylogenetics, and show with examples how their integration with NGS molecular techniques and external sources of evidence (e.g., fossil evidence, paleoclimatic reconstructions, ecological traits) allow us to explore patterns and processes of biotic assembly at different spatio-temporal scales, from extinction and adaptation of species to climate change to population decline and demographic expansion in more recent times.

June 20
9:50 AM
Biogeo

Statistical comparison of DEC and DEC+J is statistically valid; and, a path towards more statistical sophistication and realism in phylogenetic biogeography

Matzke N.J.[1]* & Bland W.[1]

[1]School of Biological Sciences, University of Auckland, Auckland, New Zealand. *Correspondence: n.matzke@auckland.ac.nz.

Statistical model comparison has become common in historical biogeography, enabled by the R package *BioGeoBEARS*, which implements several models in a common framework, allowing models to be compared with standard likelihood-based methods of statistical model comparison. Ree and Sanmartín (2018) critiqued the comparison of Dispersal-Extinction-Cladogenesis (DEC) and a modification of it, DEC+J, which adds the process of jump dispersal at speciation. DEC+J provides highly significant improvements in model fit on most (although not all) datasets. However, we show that DEC+J fits better on datasets because the DEC model is statistically inadequate in the common situation when most species have geographic ranges of single areas; the DEC model requires long residence times of multi-area ranges, and when these are not observed, a model that does produce such data patterns, such as DEC+J, prevails. More fundamentally, statistical comparison of DEC and DEC+J produces identical log-likelihood differences to statistical comparison of two submodels of ClaSSE where extinction rates are fixed to 0. We conclude with suggestions for more statistical sophistication and realism in phylogenetic biogeography.

The origin and evolution of the Amazonian Biota

June 20
10:15 AM
Biogeo

Lohmann L.G.[1*] and Cracraft J.[2]
[1]Instituto de Biociências, Universidade de São Paulo, São Paulo, SP, Brazil. [2]American Museum of Natural History, Department of Ornithology, New York, NY, USA.
[*]Correspondence: llohmann@usp.br.

The Amazon represents one of the most iconic biodiversity hotspots on Earth, yet the exact factors that shaped its biota still remain to be understood. This study aims to characterize the spatial distributions of selected lineages of Amazonian taxa (e.g., plants, birds, butterflies, and primates) and their biogeographic histories. Our results show that many stem lineages of the modern Amazonian biota have old roots going back to the Paleogene or even the Cretaceous. However, numerous extant species of vertebrates and plants originated during Plio-Pleistocene times from stem-lineages that had their beginnings in the Miocene. The origin and evolution of much of Amazonia's diversity appears to be related to the establishment of the Amazon River drainage. A fuller understanding of the assembly of the Amazonian biota will depend on more comparable data across taxa, including increased phylogenetic sampling, as well as a deeper integration of the histories of river drainage formation and Amazonia's dynamic ecosystems.

Historical biogeography of Neotropical butterflies: Understanding how species diversity assemble over time and across regions

June 20
10:50 AM
Biogeo

Matos-Maraví P.F.[1*]
[1]Institute of Entomology, Biology Centre of the Czech Academy of Sciences, České Budějovice, South Bohemian Region, Czech Republic. [*]Correspondence: pavel.matos@entu.cas.cz.

Under an evolutionary perspective, a region's species diversity is shaped by three processes that define lineage accumulation and persistence: dispersal, speciation, and extinction. In this talk, I will revisit leading evolutionary explanations that depict the interplay, in different magnitudes, between species accumulation and persistence in one of the largest reservoirs of biodiversity on Earth. The Neotropics (the tropical region of the Americas) harbors an astonishing amount of species

diversity and endemism, including at least 40% of the global butterfly diversity. We use time-calibrated species trees of selected butterfly groups to infer rates of macroevolutionary dispersal and diversification through time and space. The temporal trends of butterfly species accumulation across Neotropical bioregions can be reconciled with patterns found in other terrestrial extant and extinct groups. Overall, several Neotropical butterfly lineages seem to have persisted over long periods of time in ancient biomes such as the Atlantic Forest, while other butterfly species might have rapidly accumulated via recent increased diversification in younger regions such as rainforests in Mesoamerica. There are still limitations for jointly inferring macroevolutionary dispersal, speciation, and extinction using extant organisms and molecular phylogenies, but the analyses of several lineages are starting to disentangle the complex and varying evolutionary dynamics across clades, space, and time in the Neotropics.

June 20
11:15 AM
Biogeo

Species fields: an evolutionary macroecology approach to study biodiversity patterns

Villalobos F.[1*]

[1]Laboratorio de Macroecología Evolutiva, Red de Biología Evolutiva, Instituto de Ecología, A.C., Xalapa, Veracruz, Mexico. [*]Correspondence: fabricio.villalobos@inecol.mx.

At both small and large spatial scales, species co-occurrence and the resulting emergent properties (e.g. species richness, phylogenetic structure) are usually studied at the level of entire assemblages, focusing on sites or regions. Alternatively, we could focus on species as our units and evaluate those emergent properties at the level of whole species' ranges (or sites). The concept of a "species field" introduces an species-level property based on the co-occurrence of other species within the range/site of a focal species. Doing so for all species within a clade (or other grouping such as native and non-native species) can inform us about the processes driving biodiversity patterns as their signature should be evident at the species level as well as the assemblage level. I'll present a few examples on the application of the 'species field' concept to the study of geographic patterns of co-occurrence using mammals and biological invasions using plants.

Following the footsteps and phylogeographic history of a highly polymorphic damselfly (Polythoridae: Odonata)

June 20
11:40 AM
Biogeo

Sanchez Herrera H.[1*]

[1]Universidad del Rosario, Bogota D.C., Colombia. [*]Correspondence: melsanc@gmail.com.

The New World Tropics has experienced a dynamic landscape across evolutionary history and harbors a high diversity of flora and fauna. While there are some studies addressing diversification in Neotropical vertebrates and plants, there is still a lack of knowledge in arthropods. Here we examine temporal and spatial diversification patterns in the damselfly family Polythoridae, which comprises seven genera with a total of 58 species distributed across much of Central and South America. I implemented biogeographical models and suggested that the Pebas and Acre Systems were significant geological events associated with the diversification of this damselfly family; while diversification in the tree shows some correlation with mountain building events, it is possible that other abiotic and biotic changes during our study period have influenced diversification as well. In particular, Neotropical Polythore damselflies who mainly live in waterfalls and that exhibit a striking wing color polymorphism across all its geographical range, showed a high diversification rate that can be explained by the late uplift of the Northern Andes. Moreover, I reconstructed the species tree for fifhteen morphospecies of Polythore damselflies using three mtDNA gene fragments (COI, ND1 and 16S). The latter suggested that the mtDNA lineages of these damselflies coalesced around the late Miocene (9 mya) consistent with the beginning of modern river system formation and the late uplift of the Andes. Moreover it revealed significant geographic structuring congruent with the current distribution of Amazon or Andes morphospecies. From each recovered supported geographical clusters in the species tree, we selected a representative lineages or group of lineages, to explore their mtDNA genetic and wing morphological (i.e. pattern,chromaticity and texture) variation across multiple populations and geographical scales within these highly polymorphic group of damselflies.

Phylogeography, a Growing Bridge

Phylogeography presents great power as a nexus discipline between macroevolution and microevolution. The speciation process and the species relationships can be evaluated from an infraspecific approach with variability in the space-time scale analyzed. This young discipline is in full growth, and new methodologies are on the rise. We will hear first-hand from researchers at the forefront in the field, making phylogeography an increasingly comprehensive science. In this symposium, you will hear about various approaches for interpreting the populations' genetic structure in space to infer the natural history of the species, its conservation implication in the face of climate change, and how the ecological variables affect the speciation process.

June 20
2:00 PM
Phylogeo

Narrowing the adaptive bridge in phylogeography: history and future of Neotropical herpetofauna in changing environments

Werneck F.P.[1*]

[1]Instituto Nacional de Pesquisas da Amazônia, Manaus, AM, Brazil. [*]Correspondence: fewerneck@gmail.com.

Integration of ecological and evolutionary approaches is essential to bridge the adaptation gap in phylogeography and address the relative roles of neutral and adaptive processes in shaping the origin, current and future distributions of species. In my talk I will present studies from my research group in which we combine mechanistic approaches based on physiological capacities with population genomic data to investigate potential impacts of historical and contemporary environmental change at natural populations of Neotropical lizards (speciation and population structure patterns, range shifts, adaptive potential and extinction risks). Our results point that dispersal and ecological divergence were important drivers of speciation and diversification patterns at historical scales. Although we recovered substantial intraspecific variation in thermal traits and adaptive genetic diversity, indicating that different populations have distinctive vulnerabilities and potentials to respond adaptively to changing climates, extreme scenarios of ongoing environmental change hamper the potential for evolutionary rescue among natural populations of lizards distributed across the Amazonia rainforest-Cerrado savanna environmental gradient. These results encourage for the importance of accounting for climate-adaptive genetic variation as clues for local environmental adaptation at the intraspecific level to better understand the phylogeographic history of species and their possible future outcomes.

June 20
2:50 PM
Phylogeo

The evolution of reproductive isolation within species: a growing bridge between phylogeography and speciation

Pinheiro F.[1*]

[1]Instituto de Biologia, Universidade Estadual de Campinas, Campinas, SP, Brazil. [*]Correspondence: biopinheiro@yahoo.com.br)] (biopinheiro@yahoo.com.br.

A particularly interesting topic in speciation research concerns the interaction between the geographic differentiation of lineages and the evolution of reproductive isolation (RI) within species. A detailed picture of phylogeographic patterns observed within species is crucial to reach this goal. According to the biological species concept, speciation can be viewed as the evolution of RI between formerly interbreeding populations. The identification of reproductive barriers between different species does not essentially correspond to the mechanisms that drive divergence during early stages of speciation, as isolation barriers could arise after speciation, by divergent selection and genetic drift. Therefore, an investigation of reproductive barriers within species can provide insight into the processes operating during the earliest stages of speciation, as the origin and fixation of genetic characters are

properties of population-level processes. In this talk I will discuss how phylogeographic data can be used to understand the first steps of speciation. Recent studies have shown incomplete reproductive barriers among lineages of the same species, despite strong genetic differentiation revealed by phylogeographic data. Barriers to gene exchange within species are often found to be asymmetric, which may be a result of the polymorphic nature of loci which are still not fixed. As expected, populations distributed over fragmented habitats show higher levels of genetic differentiation, which may translate into strong reproductive barriers due to genomic conflicts. By combining experimental and analytical approaches, such studies hold a great promise in decipher how speciation begins.

A generalist among specialists? Exploring the evolutionary consequences of climate-induced distributional shifts in the Soft-Grass Mouse (*Akodon mollis*, Cricetidae)

June 20
3:15 PM
Phylogeo

Alvarado-Serrano D.F.[1*]

[1]Biological Sciences Department, Ohio University, Columbus, Ohio, USA.
[*]Correspondence: alvarado.s@ohio.edu.

Climatic specialization in response to limited seasonality is thought to be prevalent in tropical mountains. Consequently, tropical montane species are expected to show narrow elevational ranges and greater population divergence than species in more seasonal mountains because of increased isolation and allopatric differentiation opportunities. However, this expectation is contradicted by elevation generalist species inhabiting tropical mountains, raising the question of what is different about these tropical generalist species. One possible explanation is that historical demographic changes driven by the interaction between past climatic fluctuations and species-specific traits have prevented environmental specialization in these species. Testing this hypothesis requires uncovering the spatio-temporal dynamics of populations' sizes and connectivity. In this talk, using the Soft-Grass Mouse (*Akodon mollis*) as a study system, I illustrate how this can be now accomplished thanks to the increased availability of genomic data and recent methodological advances in historical demographic inference. Extending this approach to other co-distributed species should help disentangle the influence of species traits on patterns of current patterns on genetic diversity.

June 20
3:50 PM
Phylogeo

Investigating patterns of cryptic speciation in response to environmental change in Madagascar's mouse lemurs

Yoder A.[1*]

[1]Department of Biology, University Program in Genetics & Genomics, Duke University, Durham, NC, USA. *Correspondence: anne.yoder@duke.edu.

Our understanding of the speciation process has been in constant flux since the time of Darwin, with species concepts offering philosophical mirrors of shifting theory. Whereas Darwin envisioned that speciation was initiated by natural selection within an interbreeding population — and by implication, with gene flow — the introduction of Mayr's Biological Species Concept shifted the conceptual focus to reproductive isolation resulting from geographic separation. These two views of speciation have long been considered to be fundamentally opposed, though the burgeoning field of speciation genomics has clarified the surprising extent to which species integrity can be maintained in the face of either episodic or ongoing gene flow. I will focus on Madagascar's mouse lemurs (genus *Microcebus*) as an emerging system for studying the process of "speciation with gene flow." These endemic primates occur across all habitats throughout Madagascar, and though genetic data reveal deep evolutionary divergence among the named species, they are morphologically cryptic. At present, the ecological and geographic forces driving this species radiation are unknown. My talk address current understanding of mouse lemur species diversity and also present data from new and ongoing studies of lineage diversification across an ecological and geographic spectrum in Madagascar. Using a combination of whole-genome sequencing and RADseq analysis we have found that patterns of speciation in mouse lemurs range from cases of complete reproductive isolation in sympatry, on one end of the speciation spectrum, to incipient population divergence within a single species on the other. We have also identified examples of intermediate levels of lineage diversification finding that effective population size, both past and present, can have enormous impacts on inferred patterns of gene flow and incomplete lineage sorting. In summary, there is no question that mouse lemurs are extraordinarily diverse, and with the benefit of genomic data and powerful statistical tools, we are entering a new phase of increased understanding of the patterns and processes that are shaping species diversity in these cryptic primates.

Patterns of genetic diversity and phylogeography in aridland rodents of Argentina

June 20
4:15 PM
Phylogeo

Ojeda A.[1*]

[1]Grupo de Investigaciones de la Biodiversidad (GIB), IADIZA-CCT Mendoza-CONICET, San Martín, Mendoza. Argentina,. [*]Correspondence: aguoje@gmail.com.

The genetic structure observed in various taxa can be explained, in part, as a biotic response to past climatic and geological changes. In this sense, phylogeography seeks to interpret intra and interspecific genetic diversity patterns, combining a geographic and phylogenetic framework to understand the historical demography and population structure. In this presentation I discuss the results of ongoing phylogeographic, and phylogenetic studies aimed to elucidate the evolutionary relationships of different lineages of Caviomorph and Cricetid Andean and lowland desert rodents. To evaluate phylogenetic relationships and the geographic distribution of genetic variation, mitochondrial DNA sequences (COI, Cit b, Control region) were analyzed in individuals from different populations throughout their distribution. Genetic distances were calculated, and phylogenetic analyses based on Maximum Likelihood were performed. Some species showed deep divergences, accompanied by an important geographic structuring, and genetically differentiated intraspecific lineages; while other species display a low molecular divergence but were accompanied by morphological and cytogenetic differences. The patterns of genetic divergence in some of the studied species suggest the presence of a complex of cryptic species, where local populations have been diverging in relative isolation for long periods of time, while others suggest a recent speciation event. Phylogeographic approaches are increasingly used in taxonomy and conservation, as they provide evidence for the delimitation of species and the detection of potential management units, which have implications for their genetics conservation.

Phylogeography: the outcome of organism-environment interactions recorded in DNA.

June 20
4:15 PM
Phylogeo

Crawford A.[1*]

[1]. Department of Biological Sciences, Universidad de los Andes, Bogotá, Colombia.[*]Correspondence: andrew@dna.ac.

Phylogeography uses population genetic and phylogenetic tools to infer the history of geographic distributions of genealogical lineages. This field is very successful at resolving historical events such as isolation, migration, and demographic fluctuations. Meanwhile, the processes behind the events are often less clear. Because the interaction of the organism with its environment is what determines the distribution and dispersal of species, organismal biology should be placed at the conceptual center of phylogeographic studies. In today's talk I first summarize previous work on Central American frogs where we introduced the term 'trait-based phylogeography' in order to establish that organismal biology can indeed predict phylogeographic structure.

Bolstered by this result, my student, Carlos Jiménez, and I use the assumption that habitat preference drives phylogeographic history to then test one of the most contentious problems in Neotropical biogeography: the relative timing of the completion of the Panamanian Isthmus versus the Great American Biotic Interchange (GABI). Molecular phylogenetic analyses of 8 genera of frogs that participated in the interchange reveal a bias in the timing of dispersal across the Isthmus, such that wet forest species tended to cross earlier than their semi-arid counterparts, suggesting that wet forest preceded the open savannas on the Isthmus. Since most mammalian taxa participating in the GABI were likely savanna dwellers, these environmental changes, rather than geological changes, could have driven the timing of the GABI. Thus, including habitat in the comparative phylogeography of frogs provides a window into environmental history and, thus, reveals the ecological processes behind the GABI.

Eco-Evolutionary Dynamics and the Making of Biodiversity

One of the main questions in Biology is how diversity originated. To investigate the processes and mechanisms that lead to the great diversity of living beings, evolutionary biologists focus on the interplay between evolutionary forces and organismal ecology. Advancements in molecular genetic techniques and analytical methods have allowed the study of many groups beyond the model species with various approaches and unprecedented detail. This symposium includes a sample of some remarkable studies that use molecular data to address pivotal evolutionary questions that help us understand the making of biodiversity and its future conservation.

June 21
9:03 AM
Mol. Ecol.

Diversity in the skies: The molecular ecology of #BatSenses

Dávalos L. M.[1*]

[1]Department of Ecology and Evolution and Consortium of Inter-Disciplinary Environmental Research, Stony Brook University, Stony Brook, USA. *Correspondence: Liliana.Davalos@stonybrook.edu.

Despite their nocturnal habits, bats occupy virtually all terrestrial niches on Earth. Yet the molecular adaptations underlying this ecological diversity remain underexplored. Working with an international team for the better part of a decade, we have used amplicons, transcriptomes, hybrid probes, and more recently genomes to relate foraging and feeding ecology to sensory genes and pathways. We have found numerous, parallel instances of pseudogenization in vision and chemosensory genes, matching diversity of diet and olfactory receptors, the conservation of functional vomeronasal receptors since the K-t boundary in some lineages, and rampant preadaptation to divergent diets in sensory pathways. Our findings have upended the model of adaptation in response to ecological opportunities in the form of new diets, suggesting instead that shifts in foraging underlie much of the diversity we see today.

June 21
9:53 AM
Mol. Ecol.

Evolutionary genomics of ancient plants and their symbionts: from species to metabolites

Cibrián-Jaramillo A.[1*]

[1]Laboratorio Nacional de Genómica para la Biodiversidad (Langebio), Unidad de Genómica Avanzada, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Guanajuato, Mexico. *Correspondence: acibrian@langebio.cinvestav.mx.

Cycads are the oldest seed plants that evolved a specialized root to host endophytic bacteria that fix nitrogen and provide specialized metabolites to the cycad host. Cycads also maintain million-year old specialized associations with beetle pollinators that carry their live cycles inside cycad cones. Additionally, a single butterfly group is among the very few cycad herbivores. We investigated the taxonomic and functional diversity of endophytic bacterial communities isolated from coralloid roots, and both specialized beetles and butterflies, to search for signatures of co-evolution in bacterial communities to the cycad niche. We employed 16S iTAGs, a sub-community co-culture experimental strategy coupled with metagenomics, and whole-genome sequencing, to reveal both predominant and rare bacteria in the context of their communities. Bacteria were also characterized using phylogenomics, multiphoton excitation fluorescence microscopy and mass spectrometry. Diazotrophic plant endophytes dominated the root, while enterobacteria dominated the insect guts, each with a 'cycad taxonomic core', shared worldwide in the case of insects. Monophyly of key taxa and metabolic specialization support co-evolved symbiotic relationships, with unique biosynthetic gene clusters that direct the synthesis of mostly peptides and siderophores. Shared biosynthetic clusters appear to be horizontally transferred and co-opted among bacteria for cycad-specific functions unique to this ancient system.

Eco-evolutionary mechanistic models, deep-time paleo-reconstructions, and the origins of biodiversity

June 21
10:23 AM
Mol. Ecol.

Hagen O.[1*]

[1]German Centre for Integrative Biodiversity Research (iDiv), Halle-Jena-Leipzig, Leipzig, Germany. [*]Correspondence: oskar@hagen.bio.

Early naturalists already acknowledged interactions between ecological and evolutionary processes, as well as the roles of earth history (e.g. continental movements, orogeny and climate variations in temperature and aridity) in shaping biodiversity patterns. However, still today, the complexity of ecological, evolutionary, geological and climatological processes became evident in an increasingly fragmented scientific landscape. Recent developments in computer modelling now enable the strengthening of interdisciplinary fields, opening unprecedented scientific pathways. I present a novel general engine for eco-evolutionary simulations (gen3sis), which consists of a spatially-explicit modelling framework that enables modular implementation of multiple ecological and evolutionary processes interacting across representative spatio-temporally dynamic landscapes. I show how applications of gen3sis can shed light into long-standing enigmas of global biodiversity patterns, such as: the latitudinal diversity gradient (LDG), the pantropical diversity disparity (PDD) and the origins and life history of cold-adapted floras. Multiple reconstructed deep-time paleo-landscapes and processes (e.g. environmental filtering, biotic interactions, energetic carrying capacities, dispersal, allopatric speciation, and the evolution of stress tolerance and competitive ability) were used to simulate emergent biodiversity patterns (e.g. a, b and g diversity, past and current species ranges, and phylogenies). Comparisons of simulated patterns with literature reviews and empirical data (e.g. species ranges, phylogenies and fossils) of multiple faunas and floras provide future valuable insights on the origins of biodiversity.

Experimental evolution of adaptive divergence under varying degrees of gene flow

June 21
11:03 AM
Mol. Ecol.

Tusso T.[1,2,3*], Nieuwenhuis B.P.S.[1], Weissensteiner B.[1], Immler S.[2,3,4], Wolf J.B.W.[1,2,3]

[1]Division of Evolutionary Biology, Faculty of Biology, Ludwig-Maximilians-Universität Munich, Munich, Germany. [2]Science for Life Laboratory, Uppsala University, Uppsala, Sweden. [3]Department of Evolutionary Biology, Uppsala University, Uppsala, Sweden. [4]School of Biological Sciences, University of East Anglia, Norwich, UK. [*]Correspondence: sergio.tusso@evobio.eu.

Populations adapting to their local environment is a key evolutionary process generating biodiversity by means of natural selection. However, how adaptation can arise in the presence of gene flow remains contentious. We shed light on this question by means of a long-term experimental evolution in 132 replicate fission yeast populations. We applied disruptive ecological selection across 53 sexual(including 700 asexual) reproductive cycles controlling for four levels ofgene flow (allopatry, parapatry, local mating and sympatry). The resulting degree of adaptation to ecological conditions, the mode and strength of fitness trade-offs and the evolutionary strategy (specialist vs. generalist) shifted along the four levels of gene flow. Ecological adaptation entailed substantialchange not only in ecological selection but also in other fitness componentsincluding asexual growth and mating, which seems to constrain evolutionarytrajectories. Whole-genome re-sequencing revealed that variance in fitness was mostly attributed to standing genetic variation in the absence of gene flow,whereas new mutations, enriched in a subset of genes, contributed under conditions of gene flow. Parallelism was not restricted to single variants, but was likewise manifest at the gene level and by shared antagonistic pleiotropy across loci with opposite effect. This experiment provides a conceptual link between adaptation and population divergence. It also highlights that adaptive trajectories are heavily influenced by the interplay between gene flow, ancestral variation, and fitness and genetic correlations.

June 21
11:33 AM
Mol. Ecol.

Phylogenetic reconstruction of ancestral butterfly-plant networks

Braga M.P.[1*]

[1]Department of Biology, Washington University, St. Louis, Missouri, USA.
[*]Correspondence: mariana@wustl.edu.

Much of the theory on the evolution of species interactions derives from the study of herbivorous insects, due to their intimate association with host plants. Starting from a simplistic expectation of coespeciation, the field has been constantly moving towards models that are able to accommodate more of the observed biological complexity. In this talk, I will describe an approach we developed to learn more about the coevolution between Pieridae butterflies and their angiosperm hosts. We reconstructed ancestral ecological networks using stochastic mappings that were generated by a phylogenetic model of host-repertoire evolution. We then measured if, when, and how two ecologically important structural features of the ancestral networks (modularity and nestedness) evolved over time. These features have been previously associated with diversification processes, hence our interest on their origins. Our results demonstrate the power of combining network analysis with Bayesian inference of host-repertoire evolution to understand changes in complex species interactions over time. The approach can be easily applied to other biological systems, from parasitisms to mutualisms.

Special Symposium of UNC Charlotte's Bioinformatics Research Center

The Faculty of the Bioinformatics Research Center (BRC) at the University of North Carolina at Charlotte focus on infectious diseases including emergent viruses, durable problems like malaria, and the intersection of hosts and microbial communities.

June 21
2:04 PM
BRC

The origins of human coronaviruses

Janies D.A.[1*], Machado D.J.[1], Scott R.[1] & Guirales S.[1]

[1]Department of Bioinformatics and Genomics/ Bioinformatics Research Center, University of North Carolina at Charlotte, Charlotte, NC, USA. *Correspondence: djanies@uncc.edu.

Although SARS-CoV-2 caught the world off guard, coronavirus infection in humans is not new. The earliest papers in the scientific literature of coronavirus infection date to 1966. To clarify the origins of human coronaviruses, we performed the largest and most comprehensive evolutionary analyses of all coronaviruses. The dataset includes 2006 genomes drawn from all four genera of the subfamily *Orthocoronavirinae*: *Deltacoronavirus*, *Gammacoronavirus*, *Alphacoronavirus*, and *Betacoronavirus* (which contains the SARS and MERS clade). As these viruses contain genomes that vary in gene content, we built new annotation and sequence analysis tools to compare the genomes appropriately. Once we had the data and tools, we created an evolutionary tree to understand the interrelationships among the coronaviruses. With this tree in place, we mapped host metadata on the tree. We see the following in the results: 1) Bats have been the fundamental sources of human coronaviruses not only in the case of SARS-CoV and SARS- CoV-2 but also MERS-CoV. 2) Transmission of MERS-CoV frequently occurred among camels and humans recently after the transmission from bats. 3) We see SARS-CoV transmission among humans and civets after the bat to human transmission. This is similar to the human and mink exchanges of SARS-CoV-2 after the bat to human transmission. 4) Our study corroborates the animal host origins of other human coronaviruses, such as HCoV-NL63 (from bat hosts), HCoV-229E (from camel hosts), HCoV-HKU1 (from rodent hosts), HCoV-OC43, and HECV-4408 (from cow hosts). 5) Transmission of coronaviruses from animals to humans occurs episodically. From 1966 to 2020, the scientific community has described eight human-hosted lineages of coronaviruses. Although it is difficult to predict when a new human-hosted coronavirus could emerge, the data indicate that we should prepare for that possibility by vouchering well-identified putative host species that can be deeply sequenced for their pathogens.

June 21
2:32 PM
BRC

A breakthrough in *Plasmodium vivax* in invading human erythrocytes: how they spread in Africa?

Lo E.[1*]

[1]Department of Biological Sciences/ Bioinformatics Research Center, University of North Carolina at Charlotte, Charlotte, NC, USA. *Correspondence: Eugenia.Lo@uncc.edu.

Plasmodium vivax malaria was previously thought to be rare in Africa because of the lack of Duffy antigen/chemokine receptor expression on the surface of human erythrocytes that the pathogen uses for invasion. The proportion of Duffy negativity ranges from 99% in West African to 30-40% in East African countries. Several recent studies that showed *P. vivax* can infect Duffy-negative Africans and that they are no longer completely resistant to *P. vivax*. These studies raise serious public

health concerns of a potential spread across Africa. Here, we compare the prevalence, parasitemia, and genetic variation of *P. vivax* in Duffy negative individuals from West-Central, Southern, and East Africa, as well as to Duffy positive *P. vivax* infections collected in the same areas. We found that *P. vivax* parasite density in Duffy-negative infections is significantly lower than in Duffy-positive infections, regardless of geographical or ethic group differences. Maximum likelihood analyses of the Duffy Binding Protein sequences indicated that Duffy-negative *P. vivax* isolates were not monophyletic but occurred in multiple well-supported clades without clear geographical boundary. Our ongoing work explores the genomes and transcriptomes of the pathogen with the goal to clarify the genetic origin and invasion mechanisms of *P. vivax* in Africa. This information is critical to predicting disease spread and formulating control measures.

Untangling the microbiome and its potential functions in the cnidarian *Nematostella vectensis*

June 21
3:00 PM
BRC

Reitzel A.[1]

[1]Department of Biological Sciences/ Bioinformatics Research Center, University of North Carolina at Charlotte, Charlotte, NC, USA. *Correspondence: areitze2@uncc.edu.

A plethora of research has shown that microbiomes are important for the development and health of the animals they associate with. The functions and potential importance of the microbiome for most invertebrate species, particularly marine organisms, remain significantly understudied. Here we use lab and field experiments to identify species composing the microbiome of the estuarine anemone, *Nematostella vectensis*. Furthermore, using a combination of antibiotic treatments and inoculations with individual bacterial species we identify how bacteria impact gene expression in species-specific patterns. Our projects continue to determine how bacterial partners may shape the physiology of animals in a dynamic environment.

Uncovering molecular mechanisms that govern dinoflagellate-coral symbiosis

June 21
3:35 PM
BRC

Xiang T.[1*]

[1]Department of Biological Sciences/ Bioinformatics Research Center, University of North Carolina at Charlotte, Charlotte, NC, USA. *Correspondence: txiang@uncc.edu.

The mutualisms between unicellular dinoflagellate algae in the family Symbiodiniaceae and their cnidarian hosts, including corals and sea anemones, are essential for sustaining coral-reef ecosystems. In cnidarian-Symbiodiniaceae symbioses, algal endosymbiont population control within the host is needed to sustain a symbiotic relationship. However, the molecular mechanisms that underlie such population control are unclear. Here we show that a cnidarian host uses nitrogen limitation as a primary mechanism to control endosymbiont populations. Nitrogen acquisition and assimilation transcripts become elevated in symbiotic *Breviolum minutum*

algae as they reach high-densities within the sea anemone host *Exaiptasia pallida*. These same transcripts increase in free-living algae deprived of nitrogen. Symbiotic algae also have an elevated carbon-to-nitrogen ratio and shift metabolism towards scavenging nitrogen from purines relative to free-living algae. *Exaiptasia glutamine* synthetase and glutamate synthase transcripts concomitantly increase with the algal endosymbiont population, suggesting an increased ability of the host to assimilate ammonium. These results suggest algal growth and replication in hospite is controlled by access to nitrogen, which becomes limiting for the algae as their population within the host increases.

June 21
4:03 PM
BRC

Microfluidic mutation accumulation (μMA) and visualization tools (CDMAP/ CDVIS) to study microbial evolution

Sung W.[1*]

[1]Department of Bioinformatics and Genomics/ Bioinformatics Research Center, University of North Carolina at Charlotte, Charlotte, NC, USA. [*]Correspondence: wsung@uncc.edu.

Recent events have shown us that pathogens can have an enormous impact on the health and economy of our society. Understanding how microbes and microbial pathogens evolve is critical to understand how pathogens spread and how to develop therapeutics and countermeasures. Although mutation-accumulation (MA) experiments have provided direct measurements of the rate and spectrum of mutations in microbes, pathogens remain difficult to study under traditional MA experiments due to difficulties in cost and effort. Furthermore, it has been revealed that mutations vary depending on the type, nucleotide content, neighboring context, and position across the genome. To this extent, we have developed a microfluidic device and web visualization platform to accelerate our study of the evolutionary processes in microbes. In this talk, I will detail our work to study spatiotemporal variation in mutation rate using the context-dependent mutation analysis package and visualization software (CDMAP/CDVIS) and our development of a microfluidic mutation accumulation device (μMA) for experimental evolution in pathogens.

Operation Poo Patrol: monitoring a pandemic via wastewater at UNC Charlotte

June 21
4:31 PM
BRC

Gibas C.[1*]

[1]Department of Bioinformatics and Genomics/ Bioinformatics Research Center, University of North Carolina at Charlotte, Charlotte, NC, USA. [*]Correspondence: cgibas@uncc.edu.

The COVID-19 pandemic has been a source of ongoing challenges and presents an increased risk of illness in group environments, including jails, long-term care facilities, schools, and residential college campuses. Early reports that the SARS-CoV-2 virus was detectable in wastewater in advance of confirmed cases sparked widespread interest in wastewater-based epidemiology (WBE) as a tool for mitigation of COVID-19 outbreaks. One hypothesis was that wastewater surveillance might provide a cost-effective alternative to other more expensive approaches such as pooled and random testing of groups. Here, we report the outcomes of a wastewater surveillance pilot program at the University of North Carolina at Charlotte, a large urban university with a substantial population of students living in on-campus dormitories. In 2020-21, wastewater surveillance enabled the identification of asymptomatic COVID-19 cases that were not detected by other components of the campus monitoring program. In the context of all cluster events reported to the University community during the fall semester, wastewater-based testing events resulted in the identification of smaller clusters than were reported in other types of cluster events. Wastewater surveillance was able to detect single asymptomatic individuals in dorms with resident populations of 150–200. In spring 2021, we sequenced 567 clinical test samples accumulated during the course of the pandemic. The pilot sequencing program detected the emergence and eventual dominance of the B.1.1.7 SARS-CoV-2 strain among the UNC Charlotte community, and preliminary results of sequencing in building wastewater suggests the emergence of B.1.1.7 is detectable there during the same time frame, even when sequences obtained are partial or fragmented. While the strategy described was developed for COVID-19, it is likely to be applicable to routine monitoring outbreaks of other viruses in universities and other group-living environments.

Principles, Philosophy, and Methodology of Phylogenetic Systematics

This symposium will be welcoming talks on past and current research on phylogenetic systematics' fundamentals. Speakers will cover many of the basics (e.g., tree thinking, outgroup sampling, and data partitioning) in an accessible language. If you are new to phylogenetics or would like to discuss its fundamentals with the greatest thinkers of this field, this symposium is for you.

June 22
9:00 AM
Methods

Fifteen years of species trees: history and future of multispecies coalescent models in phylogenetics

Edwards S.V.[1*]

[1]Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, USA. *Correspondence: sedwards@fas.harvard.edu.

The distinction between gene trees and species trees is now routine in phylogenetics, and phylogenetic models employing the multispecies coalescent (MSC) and related approaches are widespread. Here I review the history of coalescent models in phylogenetics and speculate on their future. Although coalescent models with implications for phylogenetics extend much further back than fifteen years, it was really in 2006, with the introduction of "minimizing deep coalescences" by Wayne Maddison and Lacey Knowles, that the development of phylogenetic models employing the MSC began in earnest. In the next five years, a plethora of sophisticated likelihood and Bayesian models emerged and are now widely used to reconstruct the Tree of Life. As researchers increasingly scrutinized gene trees as distinct from species trees, processes other than incomplete lineage sorting reared their heads: issues of recombination, gene flow and the anomaly zone complicated and complemented the program of species tree inference. Although statistical analysis now shows that nearly all empirical data sets are better explained by models employing the MSC than by concatenation models, the community also appreciates that "pure isolatio" MSC models, without the reticulations of gene flow, are often an oversimplification of the underlying processes. I will review challenges and opportunities for MSC models and suggest that a middle ground of model complexity is still necessary as phylogenomic data sets continue to increase in size. Future work should focus on increasing the complexity and efficiency of Bayesian models, which appropriately model and co-estimate gene trees and species histories.

June 22
9:50 AM
Methods

Hidden in the dark: the importance of integrative taxonomy and museum collections in exploring cryptic biodiversity

Pozzi L.[1*]

[1]Department of Anthropology, The University of Texas at San Antonio, San Antonio, TX, USA. *Correspondence: luca.pozzi@utsa.edu.

Describing biodiversity is one of the main goals in evolutionary biology. Species are the fundamental unit of study in phylogeny, behavior, ecology, and conservation. Though critical, our understanding of how gene flow among taxa can become restricted remains incomplete. Identifying species boundaries is particularly challenging for nocturnal, elusive taxa where only subtle morphological variation is present. Traditionally, vocal signals have been used to identify species within nocturnal primates: species-specific signals often play a critical role in mate recognition and they can restrict gene flow with other species. In this talk, I will review the importance of an integrative approach to taxonomy, the methodological advances in species delimitation analyses and how these methods can be effectively applied to unveiling

and describing cryptic diversity in nocturnal primates. Finally, I will evaluate the promises and challenges of using museum collections to obtain genomic data from species that have been historically understudied in the wild.

Phylogenetic analysis of quantitative characters: the pendulum keeps swinging?

June 22
10:15 AM
Methods

Santiago A. Catalano[1,2*]

[1,2]Unidad Ejecutora Lillo (Consejo Nacional de Investigaciones Científicas y Técnicas – Fundación Miguel Lillo), Capital Department, Tucumán, Argentina. *Correspondence: sacatalano@gmail.com.

In a long-lasting crusade against the use of quantitative characters in phylogenetics, numerous and diverse issues have been raised. Common themes are the mistaken ideas that quantitative characters are "phenetic" or that they are not heritable. The last step of this story has recently come to light with the publication of a paper by Varón-González and collaborators (2020). These authors, based on simulations, concluded that quantitative characters are not suitable for phylogenetic inference. I will use the ideas presented in that study to trigger different discussions about the use of this kind of information in phylogenetics. I will show why the results obtained by those authors-—if perhaps important from a theoretical point of view—have little connection with real world analyses. As a consequence, the general idea that quantitative characters are not suitable for (real world) phylogenetic analyses is unsupported. Contrasting with this position, I propose a positive agenda that includes different lines of research that may help improve the phylogenetic analyses of quantitative data in general, and landmark configurations in particular.

Progress and challenges in multiple sequence alignment

June 22
10:50 AM
Methods

Warnow T.[1*]

[1]Department of Computer Science, University of Illinois at Urbana-Champaign, Urbana, IL, USA. *Correspondence: warnow@illinois.edu.

Multiple sequence alignment (MSA) is a basic step in many biological research problems, including phylogeny estimation and protein structure prediction. While some datasets are easy to align with good accuracy, other datasets (especially heterogeneous datasets with large numbers of sequences) can be very challenging. In this talk, I will present several methods (PASTA, UPP, and MAGUS) developed in the last few years that improve accuracy for large-scale MSA estimation, and that can scale to 1,000,000 sequences. I will also discuss the troubling differences between statistical alignment of biological and simulated datasets (Nute *et al.*, Systematic Biology 2019).

June 22
11:15 AM
Methods

Phylogenetic supregraphs

Wheeler W.C.[1*]

[1]Division of Invertebrate Zoology, American Museum of Natural History. 200 Central Park West, New York, NY 10024-5192, USA. [*]Correspondence: wheeler@amnh.org.

Phylogenetic graph structures used in empirical and theoretical analysis have expanded beyond trees to more general directed acyclic graphs including networks and forests. Several methods to reconcile multiple such graphs are presented and discussed here, extending existing consensus and supertree techniques forming a set of phylogenetic supergraph methods. These graphs can be used as the summary of analytical results, or as heuristic initial graphs for further phylogenetic analysis.

June 22
11:40 AM
Methods

Outgroup sampling in phylogenetics

Grant T.[1*]

[1]Departamento de Zoologia, Instituto de Biociências, Universidade de São Paulo, São Paulo, SP, Brazil. [*]Correspondence: taran.grant@ib.usp.br.

Outgroup sampling is a fundamental step in the design of phylogenetic analyses, independent of optimality criterion, taxonomic group, or source of evidence. Studies have demonstrated the efficient analysis of many thousands of terminals, all of which could be included in any empirical investigation, yet outgroup samples typically include only a small number of terminals. Most discussion of outgroup sampling centers on employing “correct” or “appropriate” outgroup terminals to increase “accuracy” or “reliability” by preventing “errors” such as long branch attraction and “incorrect” ingroup rooting. As an alternative, I develop a theory of outgroup sampling grounded in the logic of scientific discovery, whereby the objective is to test nested hypotheses of ingroup topology and character-state transformation as severely as possible by incorporating outgroup terminals in unconstrained, simultaneous analysis, using background knowledge to select the terminals that have the greatest chance of refuting those hypotheses. This framework provides a logical basis for selecting outgroup taxa but does not provide grounds for limiting the outgroup sample, given that, all else being equal, testability and explanatory power increase with the inclusion of additional terminals. Therefore, I propose the ancillary procedure of successively expanding the outgroup sample until ingroup hypotheses become stable (insensitive) to increased sampling, with each expansion guided by the scientific objectives of outgroup sampling. This is a heuristic procedure that does not prevent more outgroup terminals from being sampled or guarantee that ingroup hypotheses will remain insensitive to further outgroup expansion, and it has no bearing on the objective support of a given hypothesis. Nevertheless, it provides an objective, empirical basis for limiting outgroup sampling in a given research cycle. I illustrate this procedure by examining the effect of successive outgroup expansion on the relationships among the poison frog genera *Adelphobates*, *Dendrobates*, and *Oophaga*.

Current Methods and Applications of Big-Data Phylogenetics

This symposium's central goal is to foster the phylogenetic community's growth through the exchange and dissemination of new ideas for phylogenetic inference in the genomic era.

June 22
2:00 PM
Big-data

Genome-scale phylogenetics: breakthroughs and continued challenges

Dikow R.[1*]

[1]The Smithsonian Institution, Washington, DC, USA. [*]Correspondence: DikowR@si.edu.

This is an exciting time for biodiversity science – researchers can take advantage of advances in high-throughput genomic sequencing to generate large phylogenetic datasets in terms of loci and taxa. Even chromosome-level assemblies are now within reach for many taxa. While increased access to genomic technologies has been welcomed by the biodiversity community, researchers are faced with challenges as they design genome-scale phylogenetic studies. These challenges include balancing trade-offs in terms of costs, input DNA/RNA quality, and analytical power, as well as choosing appropriate analytical methods and software, and gaining access to sufficient computational resources. In this talk, I will describe approaches for dealing with analytical and computational challenges in big-data phylogenetic studies for diverse taxa.

June 22
2:50 PM
Big-data

Mammalian systematics in the age of genomics: from phylogenomics to species delineation

Delsuc F.[1*]

[1]University of Montpellier, Montpellier, France. [*]Correspondence:
Frederic.Delsuc@umontpellier.fr.

The field of mammalian systematics was essentially based on morphological characters until the birth of molecular phylogenetics. The introduction of molecular data coupled with the use of probabilistic methods of phylogenetic inference has literally revolutionized our vision of the mammalian tree. Indeed, the concatenation of a handful of nuclear genes has been sufficient to reveal four major placental clades implying an unexpectedly high level of morphological convergence. Mammalian phylogenetics then turned to phylogenomics with the sequencing of the first complete genomes. In this talk, I will briefly review the early developments of mammalian phylogenomics and the potential caveats associated with the analyses of genome-scale datasets. Using carnivores as a case study, I will then present some practical considerations on the use of the Oxford Nanopore technology for sequencing high-quality genomes using the portable MinION instrument. Finally, I will discuss the use of complete genomes for species delineation and phylogenetic inference in Carnivora.

Do It Yourself! Publishing without publishers

June 22
3:15 PM
Big-data

Scornavacca C.[1*] & Bourguet D.[1]

[1]University of Montpellier, Montpellier, France. [*]Correspondence: celine.scornavacca@umontpellier.fr.

In this talk, we will present two different examples of high-quality scientific publishing dodging publishers: a book completely handled by researchers and Peer Community In, a free recommendation process of preprints based on peer reviews. The Phylogenetics in the Genomic Era (https://hal.inria.fr/PGE/) book project has started with the unreasonable request from a well-known publisher to make us pay 20,000 euros for an open access book that we (the editors), would have had to handle from A to Z (choose the chapters, find the authors, get the contracts signed, format the manuscript etc ...). It did not seem right, so we asked the colleagues that already had shown interest in writing a chapter for our book, to trust us. They did and, with some knowledge of LaTeX, the book came to life. The Peer Community in (PCI, https://peercommunityin.org) project offers an alternative to the current system of publication - which is particularly expensive and not transparent. PCI is a non-profit scientific organization that aims to create specific communities of researchers reviewing and recommending, for free, unpublished preprints in their field (i.e. unpublished articles deposited on open online archives like arXiv.org and bioRxiv.org). Each PCI is a group of several hundred recommenders playing the role of editors who recommend such preprints based on peer-reviews to make them complete, reliable and citable articles, without the need for publication in 'traditional' journals (although the authors can submit their recommended preprints afterwards). Evaluations and recommendations by a PCI are free of charge. When a recommender decides to recommend a preprint, they write a recommendation text that is published along with all the editorial correspondence (reviews, recommender's decisions, authors' replies) by PCI. The preprint itself is not published by PCI: it remains in the preprint server where it has been posted by the authors. The first Peer Community in has been launched in 2017: Peer Community in Evolutionary Biology (PCI Evol Biol). More than 1000 recommenders have already joined PCI Evol Biol, PCI Paleontology, PCI Ecology, PCI Animal Science, PCI Zoology, PCI Mathematical and Computational Biology, PCI Archaeology, etc. We've won the 2020 LIBER award for library innovation of the European League of Research Libraries.

June 22
3:50 PM
Big-data

The evolution of prokaryotic pangenomes

McInerney J.[1*]

[1]University of Nottingham, Nottingham, United Kingdom. [*]Correspondence:
James.McInerney@nottingham.ac.uk.

Horizontal gene transfer (HGT) is one of the most important processes in prokaryote evolution. The sharing of DNA can spread neutral or beneficial genes, as well as genetic parasites across populations and communities, creating a large proportion of the variability acted on by natural selection. In this talk I highlight the role of HGT in enhancing the opportunities for conflict and cooperation within and between prokaryote genomes. I discuss how horizontally acquired genes can cooperate or conflict both with each other and with a recipient genome, resulting in signature patterns of gene co-occurrence, avoidance, and dependence. I also present tests of the hypothesis that a pangenome's accessory gene content is structured and maintained by selection. Along with co-workers, we interrogated the genomes of *Pseudomonas* isolates to search for statistically significant coincident (i.e. co-occurring/avoiding) gene patterns. We found that 86.7% of common accessory genes are involved in $\geq$1 coincident relationship. Further, genes that co-occur and/or avoid each other - but are not vertically or horizontally co-inherited - are more likely to share Gene Ontology categories, are more likely to be simultaneously transcribed, and are more likely to produce interacting proteins, than would be expected by chance. We also analysed the accessory genome of an *Escherichia coli* pangenome using a dataset consisting of 400 genomes from 20 sequence types, in order to identify genes that display significant co-occurrence or avoidance patterns with one another. We demonstrate that genes co-occur by function, and that several highly connected gene relationships are linked to mobile genetic elements. We find that genes are more likely to co-occur with, rather than avoid, another gene, suggesting that cooperation is more common than conflict in the accessory genome. This work furthers our understanding of the dynamic nature of prokaryote pangenomes and implicates both function and mobility as drivers of gene relationships. Together, these findings suggest that the accessory genome is structured into interacting sets of genes co-selected to function together within a given strain. Given the similarity of the *Pseudomonas* and *Escherichia* pangenomes with open pangenomes of other prokaryotic species, we speculate that these results are generalizable.

Developing efficient phylogenetics scientific experiments: Experiences in the Brazilian petaflopic supercomputing system

June 22
4:15 PM
Big-data

Ocaña K.[1,2,3,7*], Vasconcelos A.[1,2,3,7], Galheigo M.[2,3,5,6], Gadelha L.[2,3,4,7], Porto F.[2,3,5], Gomes A. T.[2,3,6,7] & Osthoff C.[2,3,4,7]

[1]Laboratory of Bioinformatics (LABINFO), Petrópolis, RJ, Brazil. [2]National Laboratory of Scientific Computing (LNCC), Petrópolis, RJ, Brazil. [3]Ministry of Science, Technology, and Innovation (MCTI), Brazil. [4]National HPC Center Network (CENAPAD), Brazil. [5]Data Extreme Lab (DEXL), Petrópolis, RJ, Brazil. [6]Brazilian National System for High-Performance Computing (SINAPAD), Rio de Janeiro, RJ, Brazil. [7]Santos Dumont Supercomputer (SDumont), Petrópolis, RJ, Brazil.
[*]Correspondence: karyann@lncc.br.

New paradigms in Bioinformatics and Computational Biology drive the storing, managing, and accessing of data. HPC and Big Data advances in this domain represent a vast new field of opportunities for bioinformatics researchers. The gap between processing and data access speeds causes many applications to spend a large portion of their execution on operations. In this talk, we discuss a vision and research challenges to promote efficient usage for HPC distributed phylogenetics applications. We performed a comprehensive performance evaluation of phylogenetics simulations using BEAST and RAxML on the hybrid resources of the Santos Dumont (SDumont) supercomputer to reduce memory usage and execution time. We are currently coupling artificial intelligence to our phylogenetics experiments to generate models to prototyping science gateways that lead us to better understand how automatic learning can predict computational resource's efficient use. The computational executions are carried out at Santos Dumont, the largest supercomputer in Latin America with 5.1 Petaflops and 36,472 computational cores distributed in 1,134 computational nodes. This lecture intends to discuss the main phylogenetic challenges that allow us to reflect on specialized solutions, adaptations of existing HPC technologies, and expectations for the future.

Perpetual updates for the Fish Tree of Life

June 22
4:40 PM
Big-data

Chang J.[1*]

[1]University of California, Oakland, CA, USA. [*]Correspondence: me@jonathanchang.org.

Well-sampled phylogenies are a critical resource for comparative biologists and systematicists in understanding the diversity of life. However, the construction of large phylogenies covering the diversity of a group such as ray-finned fishes is a time-consuming task requiring many manual steps. Nearly a decade ago, the PUmPER (phylogenies updated perpetually) pipeline was developed to update existing phylogenies without human intervention. Here we extend the PUmPER (phylogenies updated perpetually) pipeline to integrate novel sources of sequence data, and enable human audit, review, and correction of machine actions, to ensure accurate phylogenies that will advance understanding of biodiversity.

Phenotype Still Matters in the Genomic Era

Although the generation and use of molecular data for biological research have increased manifold during the last years, phenotypic characters continue to play an indispensable role in taxonomic and evolutionary investigations. New approaches for gathering phenotypic data, such as geometric morphometrics, confocal microscopy, and micro-computed tomography, are expanding the universe of phenotypic features. If you are interested in discussing the importance of phenotypic traits and learning about different tools being used for phenotypic characterization, come and join us at this symposium!

June 23
9:00 AM
Phenotype

Phylogenomic node instability, node support, and the role of morphology in determining the relationships among early animal lineages

Tessler M.[1,2*]

[1]Department of Biology, St. Francis College, Brooklyn, New York, USA. [2]Sackler Institute for Comparative Genomics, American Museum of Natural History, New York, NY 10024, USA. *Correspondence: mtessler@amnh.org.

Numerous fundamental relationships among organisms have yet to be established. Many critical relationships are unstable even with the mountains of nucleic acid data produced in the budding phylogenomic era. One prime example of this is the relationships at the base of the animal (Metazoa) tree, which, if firmly established, would indicate how many fundamental features evolved (e.g., neural tissues and muscle cells). Given the lack of phylogenomic stability and the importance of these relationships, my colleagues and I have been assessing the use of morphology as an addition to phylogenomic datasets. We find that even modest upweighting of the morphology often results in a shift in this sister to other Metazoa: largely Ctenophores (comb jellies) shifting to Porifera (sponges), but sometimes Placozoa. In this talk I will discuss these findings, how they change across datasets, and why you should be sceptical of nodes with supposed full levels of bootstrap or posterior probability support.

June 23
9:50 AM
Phenotype

Carcinization as a case study of evolutionary morphology

Richter S.[1*]

[1]Allgemeine and Spezielle Zoologie, Institut für Biowissenschaften, Universität Rostock, Universitätsplatz 2, 18055 Rostock, Germany. *Correspondence: stefan.richter@uni-rostock.de.

The main task of an evolutionary morphology is the causal understanding of character transformations in time. Levels of understanding include 1) Description of morphems (as usnit of description), 2) Identification of evolutionary units (character states and characters conceptualized based on morphems) (homologization), 3) Direction of transformation (based on phylogenetic hypotheses, also under consideration of the fossil record), 4) Adaptation (form, function, biological role in relation to the (paleo)environment), 5) Phylogenetic burden and material/architectural constraints. The concepts of evolutionary morphology will be exemplified using carcinization as a case study. Carcinization refers to the evolutionary transformation into a crab-like habitus, which evolved several times independently within decapod crustaceans. Descriptions of morphems are based on microcomputer-tomography and 3D reconstruction.

From development to deep time: Reconstructing the evolution of diversity with a phenomic approach

June 23
10:15 AM
Phenotype

Goswami A.[1*]

[1]Department of Life Sciences, The Natural History Museum, Cromwell Road, London SW7 5BD, UK. *Correspondence: a.goswami@nhm.ac.uk.

What processes shape organismal diversity over large time scales? Approaches to this question can focus on many different factors, from ecology and life history to environmental change and extinction. Uniting these factors in a macroevolutionary framework is typically complicated by differences in the sources, types and scale of data collected, but open access 3D datasets have transformed this field in recent years. Here, I will discuss the patterns of and influences on cranial evolution using a vast 3D phenomic dataset spanning >300 million years of evolution. While most large-scale studies of morphological evolution utilise relatively limited descriptors of morphology, surface sliding semi-landmark analysis allows for detailed quantification of complex 3D shapes, even across highly disparate taxa. We analysed morphological evolution using a dense dataset of 700-1500 landmarks and sliding semi-landmarks for over 1000 species of living and extinct limbed vertebrates. Patterns of cranial organisation are generally conserved across large clades, but clear shifts are evident, as in the evolution of birds from non-avian dinosaurs. This particular transition involves a massive bottleneck in morphology and a drop in evolutionary rates, as well as a major shift in the localisation of cranial variation from the jaw articulation to the anterior face. Differences in the relative effect sizes of developmental or ecological factors is also evident in other tetrapod groups, with habitat the dominant driver of skull evolution in frogs, but developmental strategy primary in salamanders. A unified approach to data collection allows direct comparison of disparate taxa, and demonstrates that ecology, life history, extinction events, and climate are all significant influences on cranial shape, though the magnitudes of their effects vary markedly across different vertebrate clades.

Polymorphic, cryptic or hybridizing species? The importance of phenotype in interpreting molecular patterns in a fast evolving, taxonomically complicated group of Neotropical stingrays.

June 23
10:50 AM
Phenotype

Fontenelle J.P.[1*]

[1]Institute of Forestry and Conservation, University of Toronto, Toronto, ON, Canada. *Correspondence: fontene3@gmail.com.

The increased availability of molecular datasets during the last 25 years has provided invaluable material for the investigation of evolution in different perspectives, magnitudes, scopes and study groups, leading to an “unofficial” preference of molecular-focused studies over traditional morphology-based ones. Amidst many discussions on the validity of different datasets and studies, these advances in technology allowed for more complex evolutionary questions. Instead of establishing a winner in the morphology vs. molecular debate, these studies ended up highlighting the importance of morphology in the genetics/genomics era. While we advance towards more computational power, fundamental aspects of taxonomy, systematics, evolution and ecology become increasingly necessary. What we define as an operational taxonomic unit (OTU) ends up determining the robustness and accuracy of evolutionary investigations, and phenotype plays a major role in taxonomic delimitation. Here, I present a perspective of the importance of phenotype in the interpretation of evolutionary, biogeographic and diversity patterns in a diverse group of fishes: the Neotropical freshwater stingrays (subfamily Potamotrygoninae). This phenotypically diverse group shows striking dorsal color patterns and a wide range of body sizes (from less than 25cm to more than 1m in disc size) and occupies a vast array of niches and habitats. The lack of a robust species-level phylogeny for this group aggravates the interpretation of morphology from an evolutionary perspective, and overlaps between intra and interspecific variation prove to be additional challenges. Molecular datasets provide invaluable information in cases where morphology seems to come short; however, the assessment of molecular patterns changes how morphology is interpreted a priori. I discuss the importance of proper taxonomic assessments using morphology for the significance of molecular results, and how genomic data can be meaningful for groups in which phenotypes are still not properly understood.

June 23
11:15 AM
Phenotype

Modeling morphological data and the ongoing revolution in deep-time phenotypic macroevolution

Simões T.R.[1*]

[1]Museum of Comparative Zoology & Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, USA. [*]Correspondence: tsimoes@fas.harvard.edu.

For decades, paleobiologists and evolutionary biologists interested on the evolution of the phenotype have been limited in their available toolset to quantitatively assess organismal evolution across deep timescales. However, the last decade has been revolutionized by the emergence of a new array of methodologies and models available to address big problems in macroevolution using phenotypic data. Here, I will highlight the progress that has been made using these new methods to infer evolutionary trees based on phenotypic data from living and fossil organisms and combining it with traditional sequence and genomic data. Important results include a more accurate and precise dating of the Tree of Life, new strategies to detect diversification dynamics, as well as inferring rates of phenotypic and molecular evolution across deep evolutionary time. The collection of these results is overhauling long-standing ideas from traditional evolutionary theory and paving the way for a new class of macroevolutionary models.

Virtual Poster Sessions

The following presentations were selected for our live poster sessions on Discord.

Poster Session 1: Inclusion and Paleobiodiversity

A comparative analysis of late Early Ordovician conodont diversity from Cordillera Oriental and Precordillera, Argentina

June 19
12:00 PM
Session 1

Rueda E.K.[1*] & Albanesi G.L.[1,2]

[1]Museo de Paleontología-CIGEA, Facultad de Ciencias Exactas Físicas y Naturales, Universidad Nacional de Córdoba, Córdoba, Argentina. [2]CICTERRA (CONICET-UNC), Facultad de Ciencias Exactas, Físicas y Naturales, Universidad Nacional de Córdoba, Córdoba, Argentina. [*]Correspondence: ruedaroballo@gmail.com.

Conodont diversity dynamics is driven by plate tectonics, which implies basins reconfiguration through time, as well as global sea-level, climate, and sea-water chemistry changes. Usually, only taxonomic information is considered for conodont diversity studies. However, the fossil record is affected by a number of factors, such as variations in depositional environments and tectonic events, which must be reflected to achieve representative estimates of biodiversity, mainly at local and regional scales. A comparative conodont diversity analysis between faunas from the Precordillera and the Cordillera Oriental of Argentina for the same time interval (middle Floian of Early Ordovician) reveals two patterns: (1) A significant conodont diversity from the middle part of the San Juan Formation, Precordillera, which corresponds to the *Juanognathus variabilis* Subzone of the *Oepikodus evae* Zone. This stratigraphic interval consists of carbonate rocks deposited in an open-shelf environment. About 45 species have been described from approximately 30 m stratigraphic thickness through the whole subzone. (2) The Cordillera Oriental presents low conodont diversity for the correlative interval of the *Gothodus andinus* Zone, which occurs in the middle-upper section of the Acoite Formation. A 300 m thick stratigraphic series deposited in a shallow marine setting represented by siliciclastic rocks intercalating calcarenites and calcareous coquinas that yielded about 19 species, dominated in specimen number by endemic taxa. Middle-deep ramp environments of the Precordillera are characterized by a remarkable conodont richness compared to the correlative inner shelf environments of the Cordillera Oriental. The presence of certain endemic taxa indicates either restricted environments or wide oceanic separations between different provinces. The conodont fauna of the Cordillera Oriental characterizes the Southwestern Gondwana Province of the Shallow-Sea Realm. The Precordillera conodont fauna fits the Open-Sea Realm of the Floian Stage occupied by cosmopolitan species. The high conodont diversity of the Precordillera is related to a global marine transgression allowing continuous carbonate deposition and homogeneous conodont concentrations, which favors continuous sampling with gradual changes in taxa composition. The low diversity recorded in the Cordillera Oriental could primarily be attributed to the discrete and sparse sampling allowed, although species association is practically monotonous in the different samples analyzed across the stratigraphic succession.

June 19
12:00 PM
Session 1

A first look at the gap between women and men authors in Biogeography

Guilardi M.D.[1*] & Di-Nizo C.B.[1]

[1]Laboratório de Ecologia e Evolução, Instituto Butantan, São Paulo, SP, Brazil.
[*]Correspondence: diasgmariana@gmail.com.

Scientific articles are one of the main sources for the evaluation of scientific careers, and applications for research grants or positions in universities and institutions. Although most of the scientists in Life Sciences are women (47 to 52% of the total), it is well known that female scientists publish less than males. In the field of Biogeography, the disparity between female and male authors in scientific articles has not yet been evaluated. The aim of this work is to present a preliminary analysis in journals specialized in Biogeography. Four scientific journals were selected: Diversity and Distributions, Ecography, Global Ecology and Biogeography, and Journal of Biogeography. Articles and reviews were extracted from the Web of Science portal from the period of 2015 to 2019. The authors' genders as female or male of each manuscript were determined using the online database genderize.io. Analyses were performed using R in RStudio. Data were obtained for: year of publication; title, name and gender of each author; total number of authors; scientific journal; and authors' countries of origin. A total of 2161 publications were sampled. The Diversity and Distribution journal had the largest proportion of publications with women as first author (41.53%), while Ecography showed the lowest proportion (29.20%). In manuscripts with two or more authors, the four journals had less than 25% of manuscripts with women as last author. Results showed that the higher the number of co-authors, the lower the proportion of female co-authors. Diversity and Distribution had the largest proportions of women as first authors in each year of the period, while Ecography and Journal of Biogeography were below the average of the journals in each year. Australia was the country with the highest proportion of females as first authors. These preliminary results showed that there is a gender gap in the authorship of articles in Biogeography, whether due to the position of authorship, as well as proportion and number of authors. The disparity scenario is even greater in relation to women as last author, which can be related to the underrepresentation of female researchers in senior carriers in Life Sciences. Future analyses will be performed to investigate if there is a correlation between journal impact factor and gender of the author and if the presence of female as last author influences the first author gender.

A preliminary review of the Dinosauria findings in Brazil

June 19
12:00 PM
Session 1

Paraizo N.F.[1*], Garuba C.P.[1], Bandeira K.L.N.[2], Pereira P.V.L.G.C.[3] & Pinheiro A.E.P.[2]

[1]Laboratório de Paleontologia, Faculdade de Formação de Professores, Universidade do Estado do Rio de Janeiro, Campus São Gonçalo, Rio de Janeiro, Brazil. [2] Laboratório de Sistemática e Tafonomia de Répteis Fósseis, Departamento de Geologia e Paleontologia, Museu Nacional/UFRJ, Rio de Janeiro, Brazil. [3] Laboratório de Macrofósseis do Instituto de Geociências, Universidade Federal do Rio de Janeiro Campus Fundão, Rio de Janeiro, Brazil. [*]Correspondence: natashafrias.p@gmail.com.

The dinosaur record in Brazil increased, particularly in the last decades. Although several Mesozoic outcrops were explored more than a century ago and still present a great abundance of occurrences, other formations still seem to be underestimated. The present work evaluated a brief and preliminary reevaluation of the Brazilian dinosaur record, discussing their relevance in the light of recent hypotheses dealing with dinosaur biogeography in the Mesozoic. A total of 13 formations were analyzed, corresponding to the three distinct intervals: Upper Triassic (Santa Maria and Caturrita Formations), Lower Cretaceous (Crato, Romualdo, Alcântara, Itapecuru, Rio Piranhas and Quiricó Formations), and Upper Cretaceous (Rio Paraná, Adamantina, Presidente Prudente, Ribeirão Boiadeiro and Marília Formations). In our revision, we find 36 valid species of dinosaurs known for Brazil. As already observed in previous works, the Cretaceous strata represent the most expressive both in terms of fossil record and quantity of deposits. The order Saurischia is well presented, occurring in all geological formations, while the Ornithischia presence on Caturrita Formation still under debate. Sauropodomorphs are the most outstanding in diversity, being absent on Crato, Romualdo, and Rio Paraná Formations. In order of species richness, the formation with the higher number of species to date is the Santa Maria Formation, with 7 species, followed by the Romualdo (5) and by the Adamantina (4) formations. The Caturrita, Presidente Prudente and Marília formations show 3 species accounted for each one, while Alcântara, Crato and Quiricó formations show 2 species. The less numerous formations are the Itapecuru, Rio Piranhas, Ribeirão Boiadeiro, Rio Paraná, with one species registered for each formation. The Caturrita and Santa Maria formation are the richer also in showing diversity among Theropoda and Sauropoda clades, while the Romualdo Formation, albeit has numerous species, all are from the Theropoda clade. Titanosaurs are mainly concentrated on Adamantina, Presidente Prudente, and Marília formations, which is compatible with previous work that discusses the faunal similarity among those units. The low occurrence of dinosaur species in the Crato, Itapecuru, Rio Piranhas, Rio Paraná, and Ribeirão Boiadeiro formations is still poorly understood, requiring further exploration of these units. Finally, although preliminary, the results presented here provide an overview of the dinosaur species in Brazil. Future works observing the other osteological occurrences *versus* the nominated species will

helps to understand other paleobiological information, such as possible structural patterns of those extinct assemblages.

Authorship gender representativeness in abstracts of Chondrichthyan systematics in Brazil: Where are the women?

June 19
12:00 PM
Session 1

Petean F.F.[1] & Soares K.D.A.[2*]

[1]Instituto Tecnológico de Chascomús, Consejo Nacional de Investigaciones Científicas y Técnicas, Universidad Nacional de San Martín, Buenos Aires, Argentina. [2]Departamento de Zoologia, Instituto de Biociências, Universidade de São Paulo, São Paulo, SP, Brazil.
[*]Correspondence: karlad.soares@yahoo.com.br.

Scientific events such as conferences and symposia are relevant spaces for researchers to develop themselves, ideas, and networking. Aiming to evaluate the participation and representativeness of women and men in the authorship of abstracts in ichthyological scientific events in Brazil, we surveyed studies focused on "Chondrichthyan Systematics" (ChonSyst). We analyzed events since 1995: the 12 most recent editions of the Brazilian Meeting of Ichthyology (EBI), all 10 meetings of the Brazilian Society for the Study of Elasmobranchs (SBEEL), including the international joint event Sharks International, in 2018, and the last edition of the International Symposium on Phylogeny and Classification of Neotropical Fishes (ISPCNF). In total, we analyzed 23 scientific events and 10.332 abstracts on fishes presented over the last 26 years. The abstracts were categorized according to the studied taxa (Chondrichthyes and Osteichthyes), area of knowledge (Evolution, Ecology, Physiology), and number and gender of authors. The average proportion of abstracts on Chondrichthyes in EBI and ISPCNF is 3.4%, contrasting the group diversity regarding the number of fish species (4.5% of more than 33.000 valid species) and evidencing the low proportion of studies with the group. Also, the average proportion of abstracts with Chondrichthyes within the area "Evolution" in EBI and SBEEL is 37% and, of those, only 38.8% are first-authored by women. When specifying even more the abstracts, such as those that deal with ChonSyst (morphology, taxonomy, systematics, phylogeography, biogeography, and population genetics), they represent 21.6% of all Chondrichthyan abstracts. However, women are the first authors in only 8.9% of ChonSyst abstracts, considering all presentations in each event. Our results showed a lower proportion of women presenting in scientific events, which could be associated with (1) most Chondrichthyan specimens being large and difficult to carry and send, demanding researchers to visit ichthyological collections, which is harder for women with family and children; (2) lack of women in leading roles within ChonSyst area, since only 5.7% of abstracts has women as last authors and only 2.8% as first and last authors, suggesting that women leave Academia before becoming principal investigators; (3) lack of support for women with children at scientific events. Women should be encouraged to remain researching regardless of their personal lives by being supported not only by advisors and peers but also by event organizers who could provide adequate environments to give all attendants the same opportunities.

Head shape and stress dissipation in *Pheidole* (Hymenoptera: Formicidae) workers

June 19
12:00 PM
Session 1

Klunk C.L.[1*], Argenta M.A.[2],Casadei-Ferreira A.[3], Pie M.R.[1,4]

[1]Graduate Program in Ecology and Conservation, Federal University of Paraná, Paraná, Brazil. [2] Department of Civil Construction, Federal University of Paraná, Paraná, Brazil. [3] Biodiversity and Biocomplexity Unit, Okinawa Institute of Science and Technology Graduate University, Onna, Japan. [4] Department of Zoology, Federal University of Paraná, Paraná, Brazil. [*]Correspondence: klunkcristian@gmail.com.

In some lineages of eussocial insects, the division of labor in the worker caste was accompanied by morphological specializations. The ant genus *Pheidole* shows a remarkable degree of morphological differentiation in the worker caste, where two distinct subcastes are recognizable. Minor workers are smaller and responsible for most of the colony tasks. In contrast, majors are bigger with disproportionally larger heads and are associated with specialized tasks as defense and food processing. There is a large variation in head shape in both minors and majors of *Pheidole*, which could affect how the stresses generated by the mandibular closing muscles contraction spread throughout the head. To test the role of head shape in stress dissipation in *Pheidole* workers, we run Finite Element Analysis to explore the variation in head shapes based on a previously developed morphospace of *Pheidole* minors and majors 2D heads. According to its specialized colony demands, we hypothesize that majors present head shapes and muscular arrangements that optimize the generation of higher bite forces. We vectorized head shapes based on pictures of actual specimens. We considered actual specimens representing the extremes of the two first Principal Components and mean shapes of each morphospace, totaling five head shapes for each worker subcaste. We define two types of loading conditions for each head shape to represent the contraction of the mandibular closing muscles. The first condition distributes the loads according to the muscular arrangement of majors, and the second simulates the muscular arrangement of minors. We applied one N load to each head side, and we defined displacement restrictions in the regions of mandibular articulation. Our results show that the arrangement of the mandibular closing muscles of minors tends to generate stresses that concentrate around the mandibular articulations and the laterals of the head. Loads arranged according to majors' musculature generate more evenly distributed stresses throughout the heads. In majors, the mean shape and the extremes of the PC1 show the more evenly distributed stresses, which means that those head shapes can support higher loads. Head shapes of minors tend to concentrate stresses around mandibular articulations in both loading conditions, limiting the amount of stress that those heads can support. Those stress distribution patterns highlight the influence of head shape to the mechanics of bite in ants, and also draw attention to head regions that demand cuticular reinforcement, such as cuticular rugosity and thickness.

June 19
12:00 PM
Session 1

Is there a preservational bias among Sauropodomorpha body-fossils? A studied case of sauropodomorpha osteological occurences from Brazil

Garuba C.P.[1*], Paraizo N.F.[2], Bertolossi M.L.P.[2], Bandeira K.L.N.[3] & Pinheiro A.E.P.[1*]

[1]Faculdade de Formação de Professores, Universidade do Estado do Rio de Janeiro Campus São Gonçalo, Rio de Janeiro, Brazil. [2]Laboratório de Paleontologia, Faculdade de Formação de Professores, Universidade do Estado do Rio de Janeiro Campus São Gonçalo, Rio de Janeiro, Brazil. [3]Laboratório de Sistemática e Tafonomia de Répteis Fósseis, Departamento de Geologia e Paleontologia, Museu Nacional/UFRJ, Rio de Janeiro, Brazil. [*]Correspondence: carolinapinho.g@gmail.com.

The Sauropodomorpha is the clade of predominant herbivorous dinosaurs during most of Mesozoic, especially on south landmasses. Characterized by the small head and long necks, they inhabited a range of inland and coastal environments. However, the effect of sampling biases on our reading of sauropodomorphs still remains underestimated, especially concerning the preservation of the fossil through geological time. Here, we conducted a case study searching for the preservation quality of the osteological occurrences of sauropodomorphs from Brazil. We conduced a bibliography survey searching for the brazilian dinosaur fossil-bearing formations. A excel file was created, separating the species skeleton elements by its completeness and if if has overlapping of bones We treat two categories: the presence/absence of bones (i.e., skull, cervical vertebrae, etc.) and their completeness (complete, near-complete, etc.), in order to analyze which biases are observed through this clade. In general, the caudal vertebrae, the haemal arches and the ischia are the most common sort of bones in all sauropodomorphs analyzed, present on 10 of all 19 analysed taxa. Six species comes from Upper Triassic strata (from the Caturrita and Santa Maria formations), being classified here as basal sauropodomorphs, while 4 are neosauropods from Lower Cretaceous (from the Alcantara, Itapecuru, Rio Piranhas and Quiricó formations) and 9 from Upper Cretaceous (from the Adamantina, Presidente Prudente and Marília formations). The sauropodomorph taxa of the Lower Triassic are the ones with highest completeness of bones, especially the skull and appendicular elements. Consistently with previous studies, our survey shows that the Early Cretaceous taxa have the lower completeness of bones analyzed. Also, the Triassic sauropodomorphs show more often cranial bones (as dentary) than the most recent aged taxa. Among the Upper Triassic strata, the taxa of Santa Maria Formation, the mandible, the sacral vertebrae, femora and ilia are the most common bones, while in the Caturrita Formation there are consistently postaxial elements and mainly appendicular remains, but especially pedal elements. In Upper Cretaceous formations, the Adamantina formation has no pattern of common bones, while in the Presidente Prudente formation the most often found are the cervical and dorsal vertebrae and ribs, and in the Marília formation sacral and caudal vertebrae are the most found. As in previous contributions, the preliminary results discussed here reinforce the need for quantitative methods to assess the fossil record quality through time. Hereafter, the application of other completeness metrics of previous works will help to understand the sauropodomorph associations at different taxonomic, temporal and preservational scales.

Ostracoda (Crustacea) from the deep Northeastern Atlantic as indicators of paleoceanographic changes in the last 1,5 million years

June 19
12:00 PM
Session 1

Vieira L.M.[1], Nery D.G.[1], Baumann E.[2], Heming N.M.[3], Alvarez Zarikian C.A.[4] & Brandão S.N.[1*]

[1]Biological Sciences Department, Graduate Program in Zoology (PPGZOO), State University of Santa Cruz (UESC), Bahia, Brazil. [2]Department of Geosciences, Christian-Albrechts-Universität zu Kiel, Kiel, Germany. [3]Applied Conservation Ecology Lab, Graduate Program in Ecology and Biodiversity Conservation (PPGECB), State University of Santa Cruz (UESC), Bahia, Brazil. [4]International Ocean Discovery Program, Texas A&M University, Texas, USA. [*]Correspondence: snbrandao@uesc.br.

Ostracods are microcrustaceans which show the entire body covered by a bivalved, mostly calcified carapace. They show a high diversity with over 30,000 described species, and inhabit virtually all kinds of aquatic ecosystems on Earth. Due to these calcified carapaces, which accumulate in the sediment and have a high fossilisation potential, the class Ostracoda has an extensive fossil record since the Ordovician (approx. 440 million years), and is widely used in paleoceanographical, paleoenvironmental and paleoclimatic reconstructions. The basis of these reconstructions are: (1) precise taxonomic identifications, (2) evaluations of the single taxa occurrences, and (3) analyses of assemblages present in different layers in a sedimentary record, which are representative of the biodiversity of different time periods. Thus, the analysis of the different Ostracoda assemblages can provide clues about changes that occurred in the past in time scales from decades to hundreds of millions of years. The project, where the present work is inserted, aims at reconstructing the paleoenvironmental conditions of the Alentejo Margin (NE Atlantic) in the last 1,5 million years (Middle Pleistocene to the Holocene), by analysing ostracod samples from the Site U1391 of the International Ocean Discovery Program (IODP). Herein, we aim at providing statistically supported information on ostracods living today in the Northeastern Atlantic, in order to enable precise paleoceanographical reconstructions of the Alentejo Margin, based on ostracod assemblages present in 150 samples from Site U1391. The first steps consist of revising the taxonomy of key species from the deep Northeastern Atlantic, and publishing an online identification guide for ostracod species from this region. In this respect, three species commonly recorded from the deep sea have been revised. In parallel, a detailed bibliographic survey of the extant Ostracoda faunas from the deep Atlantic is taking place and +12,000 taxa occurrences have been collated in a spreadsheet. All taxonomic and biogeographical information are being published in the World Ostracoda Database (WOD http://www.marinespecies.org/ostracoda), which is a register of the World Register of Marine Species (WoRMS), and will be openly available to future studies. Finally, we use the ostracod present-day occurrences to study the ecological preferences of the taxa abundant in the IODP U1391 samples and will use this information for the paleoceanographical reconstructions.

June 19
12:00 PM
Session 1

Paleobiogeographic affinities of the Devonian ichthyofauna from the Southern Hemisphere

Rezende J.M.P.[1,2,3*], Figueroa R.T.[4], Ponciano L.C.M.O.[3] & Gallo V.[1,2]

[1]Laboratório de Sistemática e Biogeografia, Universidade do Estado do Rio de Janeiro -LABSISBIO/UERJ, Rio de Janeiro, Brazil. [2]Programa de Pós-graduação em Ecologia e Evolução, Instituto de Biologia, Universidade do Estado do Rio de Janeiro - PPGEE/UERJ, Rio de Janeiro, Brazil. [3]Laboratório de Tafonomia e Paleoecologia Aplicadas, Universidade Federal do Estado do Rio de Janeiro - LABTAPHO/UNIRIO, Rio de Janeiro, Brazil. [4]Museum of Paleontology and Department of Earth and Environmental Sciences, University of Michigan, Michigan, USA. [*]Correspondence: jmprezende@edu.unirio.br.

The Devonian was a period of high diversification of the main jawed vertebrate lineages (placoderms, chondrichthyans, acanthodians and Osteichthyans). Its fish fossil assemblages have been known from many continental areas, though more scarcely recorded in the South American Silurian and Devonian outcrops, except for Bolivia, Venezuela and Colombia. From the Brazilian sedimentary basins, reports of fish fossils are, to date, mostly restricted to the north and northeast (Solimões, Amazonas and Parnaíba basins), with a single occurrence know to the Paraná Basin (Southern Brazil). Based on specimens collected from the Longá Formation (Upper Devonian, Parnaíba Basin), the current research was able to determine the presence of osteichthyans to this area, along with chondrichthyans and acanthodians, unknown to date. Vertebrates are significant to understand the connections that occurred during this period, thus, these new findings also bring new information regarding the paleobiogeographic affinities within the three main Devonian bioregions. The geographic position of the Parnaíba Basin is considered intermediate between the Malvinoxhosan and Colombian-West African bioregions, suggesting this area to be a mixing zone, with elements from both bioregions. Devonian vertebrate palaeozoogeography has been elaborated with scarce information available in the literature, especially from the Middle-Late Devonian. Climatic and eustatic shifts are debated as the main cause of the Early-Middle Devonian Realms collapse, and of the greatly expanded Old World Realm that persisted through Late Devonian, that established the cosmopolitism known for some taxa. The distribution observed in Early-Middle Devonian indicates an unusually abundant vertebrate fauna of chondrichthyans and acanthodians; while placoderms and osteichthyans are either very rare or even absent in the Southern hemisphere, becoming abundant in the northern hemisphere, where the chondrichthyans and acanthodians become scarcer. Following these collapses, faunal distribution pattern is noticeably changed, with more equally distribution of fish taxa, as is observed in the Upper Devonian (Famennian) specimens from the Longá Formation, with the new chondrichthyans, acanthodians and osteichthyans finding. This new data shed some light to this matter and reinstate the need for further studies regarding the Paleozoic paleobiogeography.

The importance of support networks for an inclusive, diverse and equitable STEAMM

June 19
12:00 PM
Session 1

Diele-Viegas L.M.[1,2,3*], Pareja-Mejía D.[2,3,4], Almeida T.S.[2,5], Albuquerque E.Z.[6], Falaschi R.L.[3,7,8] & Slobodian V.[3,7,8]

[1]Federal University of Alagoas, AL, Brazil. [2]Kunhã Asé Network of Women in Science, BA, Brazil. [3]Women in Zoology Network, São Paulo, SP, Brazil. [4]Graduate Program in Zoology, Universidade Estadual de Santa Cruz, BA, Brazil. [5]Programa de Pós-Graduação em Biologia Animal, Universidade Federal do Rio Grande do Sul, RS, Brazil. [6]National Museum of Natural History, Smithsonian Institution, Washington, USA. [7]Universidade Estadual de Ponta Grossa, Departamento de Biologia Estrutural, Molecular e Genética, PR, Brazil. [8]Women in Science Brazil, www.mulheresnaciencia.com.br. [*]Correspondence: luisa.mviegas@gmail.com.

Science is still an enterprise in which positions of power are mainly held by white cisgender male academics. In the last decades, the underrepresentation of women leading research projects, higher career positions, and collaborative networks have been increasingly documented worldwide. Persistent lack of self-confidence in holding leadership positions, harassment, and difficulty reconciling family and professional demands have been the main reasons reported. The leaky pipeline can starts in childhood when girls do not even envision careers in STEAMM (Science, Technology, Agronomy, Mathematics, and Medicine) and remain until adulthood, where those who were willing to pursue such careers end up giving up due to the lack of support and opportunities. Networks of women scientists in various scientific domains have become of great importance to fight this imbalance. By belonging to a group where women can relate to many of its members with shared experiences and problems, women can seek solutions together and propose actions to make science more inclusive and equitable. We believe in an intersectional perspective on these networks, where gender identity, race/ethnicity, motherhood, origin, sexuality, and disability status issues need to be considered. It is also necessary to propose various internal groups where women can exchange information and opportunities and, most importantly, offer advice and emotional support when needed. The Kunhã Asé Network of Women in Science in Brazil and the Women in Zoology Network are examples of these networks that aim to create a network of academic and emotional support for women scientists and encourage girls and women to enter STEAMM through courses and events to promote and popularize science. In addition to encouraging girls to pursue STEAMM careers, such networks act to keep women and other professionals from underrepresented groups in their academic positions and fight different types of harassment originating from unconscious gender biases. In these networks, we can find role models ("you can only be what you can see"), support, partnerships, collaborations, and professional growth. We can only change this scenario of underrepresentation if women start to occupy more positions in STEAMM where the decisions are made. These networks create possibilities for discussing the role of patriarchy, racism, the sexual division of labor in society, and science.

June 19
12:00 PM
Session 1

The non-avian Theropod record at Northeast Brazil demonstrate great potential in fossil diversity

Nobre Y.O.M[1*], Bandeira K.L.N.[2] & Costa F.R.[3]

[1]Centro de Ciências da Natureza, Universidade Federal de São Carlos, Campus Lagoa do Sino, São Paulo, Brazil. [2]Laboratório de Sistemática e Tafonomia de Répteis Fósseis, Departamento de Geologia e Paleontologia, Museu Nacional/UFRJ, Rio de Janeiro, Brazil. [3]Laboratório de Paleontologia de Vertebrados e Comportamento Animal, Centro de Ciências Naturais e Humanas, Universidade Federal do ABC, São Paulo, Brazil.
[*]Correspondence: yuri_monteiro_nobre@outlook.com.

Theropods, and particularly the non-avian ones, consist of a very diverse and well-known group of dinosaurs. In Brazil, non-avian theropods are widespread from North to South and are mainly found on Cretaceous strata. The Northeast region stands out for having a large number of species such as *Irritator chalengeri* and *Ubirajara jubatus*, as well as a great number of isolated bones. However, the completeness of the non-avian theropod record of this region has not been completely explored yet. Here we aimed at making a bibliographical survey plotting 401 osteological remains from 45 occurrences that were separated by taxonomy, collection number, preserved material, locality, basin, and age. Regarding bone elements, cranial (n=3) and post-cranial (n=57 and n=49 for axial and appendicular remains, respectively) elements were recovered, as well as teeth (n=295), for Spinosauridae, Carcharodontosauridae, Abelisauridae, Noasauridae, Coelurosauria, and Compsognathidae clades. The highlight of this survey regarding species diversity was the Spinosauridae clade, with three species formally described and 14 collection number occurrences. The geological unit with the highest number of records was the Alcântara formation (n=21, from which 16 were teeth). The Romualdo formation stands out for its 9 occurrences and 62 postcranial elements, as well as the formation that provides more cranial bones. It is also important to discuss the fossil smuggling that has been occurring for a long time in the country. This illegal activity interferes with increasing illegal exploitation in the known Lagerstätten deposits from Brazil - especially in the Araripe Basin with its exceptionally preserved materials such as *Irritator chalengeri*, *Mirischia asymmetrica*, and *Ubirajara jubatus* from the State Museum of Natural History from Karlsruhe. Also, this indirectly harms the exploration of new outcrop locations. Moreover, this survey provides additional information on the non-avian theropod record from Brazil and sheds light on the need of exploring other Brazilian regions to increase these records.

Poster Session 2: Paleobiodiversity

Brachiopod fauna from the Middle Devonian Amazonas Basin: Taxonomic and paleobiogeographic implications

June 19
5:00 PM
Session 2

Rezende J.M.P.[1,2,3*], Ponciano L.C.M.O.[3] & Gallo V.[1,2]

[1]Laboratório de Sistemática e Biogeografia, Universidade do Estado do Rio de Janeiro -LABSISBIO/UERJ, Rio de Janeiro, Brazil. [2] Programa de Pós-graduação em Ecologia e Evolução, Instituto de Biologia, Universidade do Estado do Rio de Janeiro - PPGEE/UERJ, Rio de Janeiro, Brazil. [3] Laboratório de Tafonomia e Paleoecologia Aplicadas, Universidade Federal do Estado do Rio de Janeiro - LABTAPHO/UNIRIO, Rio de Janeiro, Brazil. *Correspondence: jmprezende@edu.unirio.br.

The occurrence of Devonian fossils is well known in the Brazilian territory, widely occurring in the three most important intracratonic basins: Amazonas, Parnaíba and Paraná. The Devonian formations of the Amazonas Basin feature the highest diversity when compared to other Brazilian Devonian fauna, embracing both vertebrates and invertebrates. However, it remains the area with fewer studies when compared to other Devonian sites in Brazil, due to the outcrops of difficult access, and the poor preservation. The brachiopods are the most common element of the Amazonas Basin. The orthotetide brachiopods are represented by a single species "*Schuchertella*" *agassizi*, an abundant element, originally described for the Ererê Formation (Middle Devonian, Eifelian-Givetian), and later to the the Maecuru Formation (Lower- Middle Devonian, Emsian-Eifelian) during the second half of the nineteenth century. Specimens classified as "*Schuchertella*" *agassizi* from both formations were studied and described, and new information regarding its taxonomy and paleobiogeography could be retrieved. The Maecuru specimens, previously classified as *Schuchertella*, will be treated as *Iridistrophia* herein, however within a different species, yet to be described. From the Ererê Formation, specimens previously classified as *Schuchertella* will also be placed with a different genus, but in this case with *Xystostrophia.* Since the Ererê Formation was the first site where this species was identified and described, it will retain its name as *Xystostrophia agassizi.* The presence of the genus *Xystostrophia* in northern Brazil is important to help elucidate the paleobiogeographic affinities within the three main Devonian bioregions. The geographic position of the Amazonas Basin is considered intermediate between the Malvinoxhosan and Colombian-West African bioregions, suggesting this area to be a mixing zone, with elements from both bioregions. *Xystostrophia* is a genus originally from the Old World Realm (Eifelian) that, along with other genera like *Tropidoleptus*, reached north South America through the transgressive peak (Eifelian-Givetian) known for causing the Early-Middle Devonian Realms (Malvinoxhosan) collapse, and the greatly expanded Old World Realm that persisted through Late Devonian that established the cosmopolitism known for some taxa.

June 19
5:00 PM
Session 2

Conodont diversity analysis from the *Oepikodus evae* Biozone (Floian) at Peña Sombría section, Argentine Precordillera

Della Costa G.M.[1*] & Albanesi G.L.[2]

[1]CICTERRA (CONICET-UNC), CIGEA, Facultad de Ciencias Exactas, Físicas y Naturales, Universidad Nacional de Córdoba, Córdoba, Argentina. [2]CIGEA, Facultad de Ciencias Exactas, Físicas y Naturales, Universidad Nacional de Córdoba, Córdoba, Argentina. [*]Correspondence: gisebiodellacosta@gmail.com.

Most research on conodont diversity patterns apparently assumes that recovered species represent all species that existed in a particular stratigraphic section. Nevertheless, different causes affect the completeness of the fossil record, such as the fieldwork methodology. In the present study, a conodont species accumulation curve is constructed to evaluate sampling efficiency. Our conodont collection represents a major part of the *Oepikodus evae* Biozone at Peña Sombría section, Argentine Precordillera. Sampled rocks are interpreted to have been deposited on distal ramp marine environments. The number of recovered conodont elements is considered as an indirect measure of the sampling method. Species accumulation curve reaches an asymptote indicating that most of the species were collected, inducting us to suppose that recovered species represent the species that existed in the analyzed time interval. Fluctuations in conodont diversity are associated with shallowing and deepening patterns of the sea level. Diversity reveals higher in deep-water than in shallow-water environments. Usually, conodont diversity studies consider the number of species (richness) as the only measure of diversity. Additionally, other diversity indices are calculated here: the Shannon (H), Simpson (1-D), and Equitability (J) indices. The relationship between lithological characteristics and species diversity are analyzed. It is concluded that: (1) diversity remains fairly constant across the represented time interval; (2) species composition is constant in the different samples analyzed being characterized each one by the dominance of the species that gives name to the biozone followed by *Periodon flabellum*; (3) species abundance fluctuated in response to environmental variations. These results indicate that deep-water environments not always present high values variations of conodont diversity. The high availability of resources supplied by upwelling currents as suggested by the high abundance and dominance of few species and mid values of equitability could explain the average values of diversity observed at Peña Sombría section. However, variability in conodont diversity most likely reflects differences in the study sections, available data, taxonomic inconsistencies, or particular environmental factors. Perhaps, and most importantly, these results reflect the need for sampling improvements. While robust database of conodont diversity from different sections of the world becomes available, it may be possible to improve sea-level-related generalities through increased sampling efforts.

Morphological evolution of Clupeomorpha during Cretaceous

June 19
5:00 PM
Session 2

Rodríguez-Sánchez E.[1,2*], Alvarado-Ortega J.[2], Ornelas-García C.P.[3], Munguia-Steyer R.E.[4] & Than-Marchese B.[5]

[1]Posgrado en Ciencias Biológicas, Unidad de Posgrado, Universidad Nacional Autónoma de México (UNAM), Mexico City, Mexico. [2]Departamento de Paleontología, Instituto de Geología, Universidad Nacional Autónoma de México (UNAM), Mexico City, Mexico. [3]Colección Nacional de Peces, Instituto de Biología, Universidad Nacional Autónoma de México (UNAM), Mexico City, Mexico. [4]Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México (UNAM), Mexico City, Mexico. [5]Instituto de Ciencias Biológicas, Universidad de Ciencias y Artes de Chiapas (UNICACH), Tuxtla Gutiérrez Chiapas, Mexico. *Correspondence: ednars@ciencias.unam.mx.

The superorder Clupeomorpha consists of fishes commonly known as herrings and anchovies. This is a diverse and widely distributed (spatially and temporally) group, appearing in all environments and exhibiting a record form Lower Cretaceous to the present. Some studies indicate a potential diversification on Albian-Cenomanian limit, as occurred in other Actinopterygii groups. Therefore, we studied the morphological modification and diversification of the group throughout the Cretaceous. We performed a geometric morphometric analysis from photographs of worldwide species dated in this period, available in publications, digital public collections, and obtained directly by us from specimens housed into the Colección Nacional de Paleontología (UNAM) and the Museo de Paleontología "Eliseo Palacios Aguilera". Fifteen landmarks and 35 semilandmarks were digitalized and multivariate analyzes were performed in about 90 specimens of 40 species representative of both orders of this group, Clupeiformes and Ellimmichthyiformes. The results show a wide variation in body shapes of Clupeomorpha. Furthermore, they suggest a shape covariation with the Early and Late Cretaceous and with the species distribution to the east or west of the Tethys Sea. This indicates a morphological diversification throughout the Cretaceous which could also be influenced by the geographical distribution.

New itasuchid material (Mesoeucrocodylia, Sebecia) expands time range of the group to Late Turonian of Bauru Group (Paraná Basin, Brazil)

June 19
5:00 PM
Session 2

Pinheiro A.E.P.[1*], Silva K.F.[1], Bandeira K.L.N.[2], Pereira P.V.L.G.C.[3], Brum A.S.[2] & Simbras F.M.[4]

[1]Departamento de Ciências, Faculdade de Formação de Professores, Universidade do Estado do Rio de Janeiro Campus of São Gonçalo, Rio de Janeiro, Brazil. [2] Departamento de Geologia e Paleontologia, Museu Nacional/UFRJ, Rio de Janeiro, Brazil. [3]Departamento de Geologia, Universidade Federal do Rio de Janeiro, Campus Fundão, Rio de Janeiro, Brazil. [4]Departamento de Biologia, Universidade Federal Rural de Pernambuco, Pernambuco, Brazil. *Correspondence: andre.eduardo.pinheiro@uerj.br.

The Bauru Group is an important sedimentary sequence in Brazil which presents a prolific fossil record for archosaurs from the Upper Cretaceous, with emphasis on the great paleodiversity of mesoeucrocodylians. We report a new occurrence of this group that enhanced the knownledge of the Itasuchidae lineage. The specimen came partially inside a rock block as resulted from commercial activities in the quarry, being composed of a yellowish gray-colored muddy sandstone matrix from the top of Araçatuba Formation (Late Turonian). The original block holded a partially preserved skull with just one tooth externally visible, and two vertebrae. The block was roughly cut-off by a minning machinery, partially exposing the inner structures from the snout at the preorbital region. Due to the block shape and condition, a hand-saw was employed to level the damaged face with subsequent application of plaster to horizontally suport and protect the fossil during preparation. The opposite block side was mechanically prepared by paleontological pens to acess and expose the right lateral surface of the preserved skull and mandible. We recovered a partial snout fragment of preorbital region - FFP PG 130-R, formed by maxilla and jugal, as so a partial hemimandible formed by dentary and surangular, and four teeth (two from upper row and two from lower one). Unfortunately, the fragmentary skull preserved few diagnostic and no autapomorphic characters, but shares anatomical similarities with itasuchids as *Pepesuchus deiseae* (MN 7005-V – holotype, and MCT 1788-R) and mostly *Pepesuchus* sp. DGM 1723-R, which are: well-marked dermal ornamentation formed by circular pits and irregular grooves; the conformation of the antorbital fenestra region; and dentition formed by round-sectioned and conidont teeth with fine and low apicobasal ridges, with both mesial and posterior crenulated carinae (false-ziphodonthy). Once FFP PG 130-R was found at the top of Araçatuba Formation, formed by sequences from prodeltaic complex in a marginal lacustrine paleoenvironment, it increases the temporal distribution of the Itasuchidae group, from the Late Turonian to Early Maastrichtian. Besides, draws back the emergence for the group to Turonian, being itasuchids found in three from the four *Crocodylifomes Assemblage Zones* recently proposed to Bauru Group (CAZ 1, 3 and 4); only still missing to lower and mid strata of Adamantina Formation. This study brings new information about this longevous and endemic but still poorly known brazilian neocretacic mesoeucrocodylian.

June 19
5:00 PM
Session 2

New record of fossil Anura (Batrachia: Lissamphibia) from the Miocene of El Salvador

Barcelos L.A.[1*], Muniz F.P.[1], Molina M.A.[2] & Molina M.A.[1]

[1]Laboratório de Paleontologia, Universidade de São Paulo, Ribeirão Preto, Brazil.
[2]Museo de Historia Natural de El Salvador, San Salvador, El Salvador. [*]Correspondence: lbarcelos@usp.br.

Anura is the most speciose clade of Lissamphibia, with nearly 88 percent of the living species diversity. Although, its fossil record is, comparatively, exiguous. The Anura fossil record for Central America is marked by few specimens recovered in Mexico, Honduras and Antilles. Besides that, there is only one Anura specimen recovered in El Salvador, *Rana sickenbergi* Seiffert from the Miocene Pliocene of

Río Sisímico. Here we present the second record of Anura from the Miocene of Torola Valley, El Salvador. The fossil material is housed at the Museo de Historia Natural de El Salvador and is included in two sedimentary rocks. The material was CT-Scanned in a medical facility and the obtained images were segmented in Avizo software, helping the recognition of several remains included the rock matrix. Nearly all elements are disarticulated and dissociated from the neighboring bones, although they are almost certainly attributable to a single individual. Our preliminary study allows the recognition of several bone remains (synapomorphies of Anura marked with asterisks). The material is composed of skull elements (i.e. sutured frontoparietals, prootic, occipital, and nasals, maxilla with teeth, quadratojugal, and free squamosal), and postcranial elements (i.e. two presacral vertebrae, humeri, fused radioulna*, fused scapula and clavicle, phalanges, sutured ilia, ischia and pubis, femur, fused tibiofibula*, and fused astragali-calcanea*). This new record shed light into the poorly known paleodiversity of Anura in the Central America. As next steps, we intend to describe, phylogenetic allocate the fossil material, and hypothesize on its significance for the paleobiogeography of Anura species in Central America. Funding: FAPESP 2019/24466-5, and 2019/14153-0.

Protocol improvement for determining the luminescence sensitivity of quartz and feldspar in fine-grained sediments

June 19
5:00 PM
Session 2

Melo D.B.[1*]

[1]Institute of Marine Sciences, Federal University of São Paulo, Santos, Brazil.
[*]Correspondence: dayane.melo@unifesp.br.

Paleoclimatology is the study of climatic variations throughout the Earth's history, starting from the analysis and interpretation of natural traces that could describe the climate in the past. Among the best natural files of these variations are the marine cores, which store information about salinity, surface temperature, intensity of ocean currents and even continental precipitation, using chemical components and microscopic fossils. In addition to the analyzes enshrined in the literature, a new indicator of paleoprecipitation was recently discovered based on the sensitivity to luminescence of quartz and feldspar grains. LOE (Optically Stimulated Luminescence) and TL (Thermoluminescence) applied to marine core sediments, were used successfully in two marine cores collected near the mouth of the Parnaíba River (GL1248 and GeoB1602-1), allowing the assessment of precipitation changes in the Brazilian semi-arid region over the past 120 thousand years. In this sense, the present work seeks to improve the already existing protocols for reading luminescence sensitivity. The samples were tested with different reading temperatures of the LOE signal (125°C and 20°C - room temperature) and with different preparation procedures: Crude samples (with organic matter and carbonate) x Processed samples (without organic matter and carbonate) . The samples were submitted to photo-emptying of the signal emitted by the feldspar through the infrared LED and the quartz by the blue LED, followed by a new dose of radiation to read the LOE signal. The results were compared with data previously obtained from the GeoB1602-1 core. Through this work, it is concluded that both LOE tests (125°C x 20°C) and with different preparation (processed sample x raw sample), proved to be compatible with those previously established, which suggests the possible adoption of a simplified protocol with raw samples at room temperature, which will facilitate the diffusion of the method, as it makes the process simpler and less costly.

June 19
5:00 PM
Session 2

Temporal evolution (1984-2020) of Praia do Leste (Iguape/SP, Brazil) and the exposure of the blue whale fossil (*Balaenoptera musculus*)

Spanghero N.F.[1,2*] & Buchmann F.S.[2]

[1]Programa de Pós-graduação em Biodiversidade de Ambientes Costeiros, Instituto de Biociências, Universidade Estadual Paulista, São Vicente, São Paulo, Brasil. [2] Laboratório de Estratigrafia e Paleontologia, Instituto de Biociências, Universidade Estadual Paulista, São Vicente, São Paulo, Brasil. [*]Correspondence: sg_nata@msn.com

In 2012, a blue whale fossil (*Balaenoptera musculus*) surfaced in Praia do Leste, Iguape-Brazil. This area is made up of microtidal coastal strands. The presence of river mouths can change the patterns of erosion and deposition on adjacent beaches, in addition to influencing the supply of sediment to the surrounding coastline. This study aims to describe the recent events that allowed the fossil to emerge and its evolution. Geo-referenced satellite images with a time series from 1984 to 2020 and photographs obtained with UAV (Unmanned Aerial Vehicle) were used. The coast lines were delimited through a vectorization process made in the *ArcGIS Pro* software, and the *Digital Shoreline Analysis System* (*DSAS*) package was used to compare the time series. The following statistical parameters were calculated: LRR (Linear Regression Rate), NSM (Net Shoreline Movement), EPR (End Point Rate) and SCE (Shoreline Change Envelope). Between 1984 and 2001 there was an accretion of 12.5 meters/year in Praia do Leste; Between 2001 and 2020, coastal erosion occurs, averaging 32.47 meters/year. The sediment supply from Ilha Comprida and Jureia beaches, which are parallel to the study area, are also influenced by the presence of river mouths. Due to the effect of a hydraulic jetty, the increase in length of the Ilha Comprida spit follows the direction of the coastal drift and the point of the Jureia follows the opposite behavior of the beach. Current erosion has exposed the fossil on the beach, showing erosion and progradation cycles with direct influence from the Ribeira de Iguape river.

The first complete titanosaurian femur from the Presidente Prudente Formation (Bauru Group, Paraná Basin): preliminary morphology and systematics affinities

June 19
5:00 PM
Session 2

Bertolossi M.L.P.[1*], Bandeira K.L.N.[2], Silva K.F.[1], Pereira P.V.L.G.C.[3] & Pinheiro A.E.P.[1]

[1]Laboratório de Paleontologia, Faculdade de Formação de Professores, Universidade do Estado do Rio de Janeiro Campus São Gonçalo, Rio de Janeiro, Brazil. [2] Laboratório de Sistemática e Tafonomia de Répteis Fósseis, Departamento de Geologia e Paleontologia, Museu Nacional/UFRJ, Rio de Janeiro, Brazil. [3] Laboratório de Macrofósseis do Instituto de Geociências, Universidade Federal do Rio de Janeiro Campus Fundão, Rio de Janeiro, Brazil. [*]Correspondence: malu.peres@gmail.com.

The femora are one of the most frequently appendicular remain recovered for titanosaurs, at least in South America. Despite this, the Brazilian titanosaur femora are quite rare, since only three to ten species of Brazilian titanosaurs present it, and other four femora attributed to Lithostrotia indet are known, where mostly are fragmentary or incomplete. Here we described a new titanosaurian femur, FFP PG 112-R, collected in outcrops of the Presidente Prudente Formation, in Alfredo Marcondes municipality (São Paulo state) during fieldwork in 2019. Albeit not the first occurrence, FFP PG 112-R stands out for being the most complete for the unit, having only the femoral head slightly eroded. Curiously a tree stem growed through inside the the element shaft causing a large crack along the diaphysis, but that not affected. FFP PG 112-R is a medium-sized femur with 115 cm at length. The proximal epiphysis has 33 centimetres and the distal end has 31.9 centimetres wide. Compared to other titanosaur species of South America, such as *Saltasaurus loricatus*, the femoral head of FFP PG 112-R is slightly elevated and medially shifted. The greater trochanter is relatively well pronounced. The abductor crest is well developed laterally and is restricted to the medial portion of the shaft. The fourth trochanter is developed and proximally positioned when compared to other South American species, as in *Arrudatitan* and *Uberabatitan*. As in other titanosaurs, the distal condyles are dorsomedially beveled. We investigated the phylogenetic relationships of FFP PG 112-R within Titanosauria using a dataset (115 taxa, 50 as ingroup and 435 characters) and performing a "New Technology Search," where searches employed "Sectorial Search", "Ratchet", "Drift," and "Tree Fusing". The resultant trees as the starting topologies for a "Traditional Search", using Tree Bisection-Reconstruction, and using equal weighting of characters. Our preliminary phylogenetic analysis resulted in 275 MLTs showing a well-resolved topology of 1854 steps (CI = 0.306/ RI = 0.602). FFP PG 112-R was retrieved as the sister taxon of a clade composed of two other Brazilian titanosaurs (*Arrudatitan* + *Adamantisaurus*). Regarding the hindlimb stance, the morphological features of FFP PG 112-R previously indicate this specimen could has a comparatively narrower gait compared with other Brazilians titanosaurs femora previously reported, as in *Arrudatitan* and *Uberabatitan*. Future studies will evaluate other associated axial elements (under preparation at the time) to help the systematic position of this specimen, besides other paleobiological questions.

June 19
5:00 PM
Session 2

The "World Ostracoda Database" as a solid base for evolutive, biodiversity and (paleo)biogeography studies

Nery D.G.[1], Vieira L.M.[1] & Brandão S.N.[1*]

[1]Biological Sciences Department, Graduate Program in Zoology (PPGZOO), State University of Santa Cruz (UESC), Bahia, Brazil. [*]Correspondence: snbrandao@uesc.br.

Ostracods are microcrustaceans, which inhabit all kinds of aquatic ecosystems and also humid areas of tropical forests. The mostly calcified carapace of these tiny creatures show a high fossilisation potential, which guarantees to this group one of the most extensive fossil records among all animals. Ostracoda are the single metazoan group to have left a very diverse and abundant fossil record from all kinds of aquatic ecosystems and from most of the Phanerozoic (440 million years). Other abundant and geologically long lasting microfossils are mostly unicelular eucariots, pollen, and plant and fungi spores. While other animal groups have either temporally or ecologically restricted fossil records, or rarely left abundant assemblages. Therefore ostracods constitute a rare opportunity of investigating Phanerozoic metazoan evolution and biogeography in "real time", by looking at their morphologies, diversities and geographical distributions in the fossil record. Herein, we present an ambitious and long lasting project, which aims at capturing and openly publishing all available information on the taxonomy, taxonomic diversity, paleobiogeography, "(neo)biogeography", genetics, ecology and morphology of ostracods. Usually long lengths of time are spent by scientists simply gathering published information, and worse the information one scientist have gathered usually goes lost after the project is finished. Therefore, by providing a platform where all kinds of information on ostracods can be shared with other scientists and can also be constantly updated, opens a new era of research where scientists built on previous efforts instead of spending a long time doing again and again what others have already done. The ultimate aim is to enable evolutive, phylogenetical, phylogeographical and biogeographical analyses based on taxa that live/lived from the Ordovician to the present. Since its inception in 2013, the World Ostracoda Database (WOD, http://www.marinespecies.org/ostracoda/index.php) grew substantially, and has now 54,452 taxa, including 45,297 species, 3,679 genera and 209 families, organised in a tree following a published classification. Still considering the taxonomy, users can also access the proposed synonymies for every taxa and the currently accepted (genus) combination for each species. Over 22,000 citations of publications are available in the portal as well as pdfs of +5,000 publications can be accessed either directly (if open access) or through request (if there is restrictive copyright). Further kinds of data being currently collated are georeferenced occurrence data and ecological and morphological traits, e.g., body size (in mm and in size classes), habitat (plankton, benthic), feeding type (filter feeder, deposit feeder…), mobility (mobile or sessile), larval and juvenile development... Although still quite incomplete in some aspects, WOD has already proven valuable, since it has been cited in almost 100 publications on a wide range of topics, like taxonomy, macroecology, biogeography, paleoceanography, autoecology, evolution... and will probably prove to be even more useful in the future, when more data will be available in the database.

Were recent Pleistocene climate changes responsible for the extinction of Gomphoterids (Mammalia, Proboscidea) in South America?

June 19
5:00 PM
Session 2

Cruz E.N.S.[1*], Faurby S.[2] & Sawaya R.J.[1]

[1]Universidade Federal do ABC (UFABC), São Paulo, Brazil. [2]University of Gothenburg, Gothenburg, Sweden. [*]Correspondence: evelynnathaliascruz@gmail.com.

The emergence of the isthmus of Panama allowed the exchange of biotas between North and South America, including two species of proboscideans. Those species dispersed from North America and expanded their geographic distributions across the South American continent during the Pleistocene. *Cuvieronius hyodon* likely have used the Andean region as its dispersal route, whereas *Notiomastodon platensis* probably have dispersed by the Amazonian Craton. Both species went extinct about nine thousand years ago due to the climate variability of the last thousands of years, according to some hypotheses. We aim to map and document the geographic distribution records as well as to identify climatically suitable areas for both species across South America. We test the hypothesis that the climatic changes of the last 120,000 years were one of the possible factors related to the extinction of gomphotherids. We also explore the possible routes of dispersal of those species in South America. Our inferences were based on paleoclimate models of the Last Interglacial (120 thousand years before the present - tybp), the Last Glacial Maximum (22 tybp), and the mid-Holocene (8 tybp). Four bioclimatic variables were included as predictors in species distribution models (Bio2, Bio 6, Bio7, and Bio19), as they have been related to geographic distributions of living elephant species according to previous studies. Although both species were probably extinct before the mid-Holocene, climate should have been still favorable for the permanence of both species in South America, as extensive areas within their estimated geographic range were identified as suitable areas by our models. We then reject the hypothesis that recent Pleistocene climate changes would be the main factor responsible for the extinction of Gomphotherid species in South America.

Poster Session 3: Biogeography

June 20
12:00 PM
Session 3

Beta diversity along climate and distance gradients: are mites of agroecosystems responsive?

Antunes T.J.[1*] & Nuvoloni F.M.[1]

[1]Universidade Federal do Sul da Bahia, Porto Seguro, Bahia, Brazil. [*]Correspondence: taina.j_antunes@hotmail.com.

Agroecosystems are noteworthy more homogeneous habitat than natural ecosystems. Although they may harbor a variety of arthropod species, their intrinsic characteristics and high level of anthropization do not allow the establishment of a complex and perennial biological community. Historically, eco evolutive and biogeographic studies have not been considering those ecosystems as suitable models to test their hypothesis and predictions. In this context, understanding processes that lead to the species colonization and establishment of a resident biological community are still unclear and challenging. Based on the beta diversity partitioning approach, we aimed to test whether beta diversity (βSOR) and its components (turnover βSIM, and nestedness βNES) vary in function of climatic and distance gradients, using mite communities associated with rubber trees (*Hevea brasiliensis* Muell Arg. - Euphorbiaceae) as model. The study relies on a database of mites occurrence on rubber trees (Acari Collection of DZSJRP - UNESP São José do Rio Preto, SP) from 55 sites, 9 states and several biomes in Brazil, varying from 2.6S to 24.5S and 39.16W to 67.87W. The relationship between species composition and beta diversity components with macroclimatic (from WorldClim) and geographic data (latitude/longitude) were evaluated based on variance partitioning and multivariate analysis. Our results pointed out that the species composition varied among sites (R2= 0,28, F= 4,93, $p<0{,}001$) and accordingly to the biomes (R2= 0,19, F= 5,66, $p<0{,}001$) (PERMANOVA). We also found out that geographic distance is the main predictor of beta diversity (βSOR) (R2= 0.383; F= 460.7; $p<0.001$) and their components (βSIM: R2= 0.370; F= 436; $p<0.001$; βNES: R2= 0.008; F= 6.994; p=0.001), although climatic gradient also drives βSOR (R2= 0.203; F= 189.7; $p<0.001$) and βSIM (R2= 0.146; F= 127.8; $p<0.001$). Considering that our study is framed in the regional (or biogeographic) scale (distances >106m), turnover component (βSIM) plays the main role of beta diversity among mite communities, being geographical distance its main predictor. In conclusion our study sheds a light about the importance of agroecosystems as a new and viable study model to test the effect of environmental gradients and processes modulating the biological communities in biogeographic scales.

Biogeography of Peracarida (Crustacea) associated with macroalgae: from local to global patterns

June 20
12:00 PM
Session 3

Iwasa-Arai T.[1,2,*], Siqueira S.G.L.[1], Segadilha J.L.[3], Leite F.P.P.[1]

[1]Departamento de Biologia Animal, Instituto de Biologia, Universidade Estadual de Campinas, Campinas 13083 862, SP, Brazil. [2]Programa de Pós-Graduação em Biologia Animal, Instituto de Biologia, Universidade Estadual de Campinas, Campinas 13083-862, SP, Brazil. [3] Laboratório de Carcinologia, Departamento de Invertebrados, Museu Nacional/UFRJ, Rio de Janeiro 20940-040, RJ, Brazil. [*]Correspondence: araitammy@gmail.com.

The distinctive evolutionary histories of oceanic islands and their high endemicity caused by isolation provide insights into global macroecological processes. These volcanic islands arose from the ocean bottom without life, and singular dispersal events shape the islands' diversity. The island of Trindade is located about 1160 km off the coast of the state of Espírito Santo, Brazil, in the tropical southwestern Atlantic, and the low richness of Peracarida agrees with the isolation of the island. The superorder Peracarida is one of the most endemic taxon among the marine invertebrate fauna, and it showed a high endemicity rate of 45% in Trindade, higher than other Crustacea taxa previously reported for the island. Based on the endemic species of tanaid *Synapseudes isis*, the phylogenetic analysis of this shallow water genus associated with macroalgae was inferred by cladistic methods based on 22 morphological characters. The biogeographical events and ancestors' distribution areas were analyzed from *Synapseudes* phylogenetic tree topology through the Bayesian Binary MCMC analysis (BBM), which suggested an Indo-Pacific origin for the genus, supporting the proposal of an Indo-Pacific 'center of origin'. Six species presented the current distribution within the realm of Indo-Pacific and Indian Ocean, followed by three species distributed on the Mediterranean, the Caribbean and Gulf of Mexico, and Offshore South Atlantic, suggesting multiple dispersal to other ocean realms.

Comparative analyses of habitat-suitability models and good old Rabinowitz's rarities classification in conservation biogeography of gymnosperms

June 20
12:00 PM
Session 3

Quiroga M.P.[1*] & Souto C. P.[1]

[1]INIBIOMA/CONICET, Universidad Nacional del Comahue, Bariloche, Río Negro, Argentina. [*]Correspondence: paulaquiroga@comahue-conicet.gob.ar.

Biodiversity hotspots of the planet harbor 77% of all endemic plant species, have high levels of species richness, endemism and threats. High species diversity in these hotspots is often attributed to an accumulation of narrow-ranged species via high speciation rates and/or preservation of species over time, via low extinction rates, in such a way that they often host ancient and young species. Patagonian Temperate Forest (PTF) is a biodiversity hotspot, but over the past centuries, it has been over-exploited, fragmented and replaced with exotic species plantations, and lately also threatened by climate change. Also, many of its species are considered rarities, included in the IUCN red list, therefore, conservation actions are in need.

We studied nine gymnosperm species endemics to the PTF. Our aim is to better understand patterns of niche overlap of key dominant elements of the forest, complementing traditional approaches to biodiversity conservation. Combining vegetation databases, we extracted 3024 occurrence data, we deployed ecological niche models, and classified species according to Rabinowitz's type of rarity. We then compared the extent and overlap of their niches and considered types of rarity in a spatial ecological context. Finally, we overlapped ENM and protected areas. We generated ENMs for 9 Patagonian gymnosperms and found that most niches overlap, and only one species displayed a unique niche. Surprisingly, we found that three species have divergent suitability of habitats across the landscape. We showed that as rarer a species is as smaller niche volume tends to be and that there are two unprotected suitable areas for key species of the PTF. We observed that protected areas are needed in Chile, in the northern-central coast to conserve gymnosperms' niches in the PTF. Our approach of overlapping habitat suitability of multiple species, and types of rarity highlight that there are conservation gaps in the PTF. Suggesting that integrating ENM, niche overlap and estimation of levels of rarity, can be a handy tool to identify potential areas for conservation planning of biodiversity hotspots.

June 20
12:00 PM
Session 3

Contrasting diversification patterns in "sky islands": a comparative approach in Cambessedesieae (Melastomataceae) from *campo rupestre* and *campo de altitude*

Bochorny T.[1*], Bacci L.F.[2], Reginato M.[2], Vasconcelos T.N.C.[3], Michelangeli F.A.[4],& Goldenberg R.[5]

[1]Universidade Estadual de Campinas, Campinas, São Paulo, Brazil. [2]Universidade Federal do Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil. [3]University of Arkansas, Fayetteville, Arkansas, USA. [4]New York Botanical Garden, New York, New York, USA. [5]Universidade Federal do Paraná, Curitiba, Paraná, Brazil.
[*]Correspondence: tbochorny@gmail.com.

The *campo rupestre* and the *campo de altitude* are two highly diverse vegetations types that characterize montane areas in eastern South America. These systems are associated with landscapes of different geological histories and are inserted within different phytogeographic domains and biomes. It is unclear, however, whether lineages with distribution in both areas also present different diversification dynamics and patterns of climatic niche evolution. Here we aim to answer this question by analyzing the biogeographical history, climatic niche evolution and diversification dynamics of Cambessedesieae (Melastomataceae), a clade with high endemism in both *campo rupestre* and campo de altitude. We select a time-calibrated phylogenetic tree alongside with carefully curated distribution points of Cambessedesieae to estimate ancestral ranges and contrast diversification dynamics and climatic regimes in lineages distributed in both areas. We use models of biogeography (BioGeoBEARS), diversification (BAMM, GeoSSE) and trait-evolution (l1ou). Our results show that Cambessedesieae is a relatively old clade in comparison to other lineages of similar distribution, with early diversification dated to the late-Eocene (37 Mya). An initial split between lineages mainly endemic to *campo rupestre* and campo de altitude happened earlier in the clade's evolutionary history. Surprisingly, both clades share the same diversification dynamics and similar climatic niche evolution. Shifts in climatic regimes occurred only near the present, they are not associated with changes in diversification rates and they are mainly restricted to the genus *Huberia*. Overall, we show that montane areas with different geological histories and inserted within different biomes can impact the diversification of endemic lineages in a similar way.

Days of the future past: The climatic niche evolution for species of Brachycephalidae in the South American Atlantic Forest

June 20
12:00 PM
Session 3

Brasil-Godinho M.[1*], Almeida-Silva D.[1], Barcelos L.A.[2], Verdade V.K.[2] & Sawaya R.J.[3]

[1]Programa de Pós-Graduação em Evolução e Diversidade, Universidade Federal do ABC, Brazil. [2]Programa de Pós-Graduação em Biologia Comparada, Universidade de São Paulo, Brazil. [3]Centro de Ciências Naturais e Humanas, Universidade Federal do ABC, Brazil. [*]Correspondence: marcela.brasil@ufabc.edu.br.

Climatic niche of species is the set of climatic conditions in the areas where it occurs. The range of climatic variation that the species can tolerate over time would help understanding the species' resilience under scenarios of climate change, a major threat to biodiversity nowadays. Herein, we explore the temporal conservation of climatic niche and its range in Brachycephalidae, an anuran family distributed along the coast of South American, mainly in Atlantic Forest (AF). We ran and dated a molecular-based phylogeny by a Bayesian multispecies coalescent method. We estimated ancestral climatic niche and its range under Brownian-Motion (BM, implying that niche was not under selection, or under a strong selection in a randomly varying environment) and Ornstein-Uhlenbeck (OU, implying the occurrence of stabilizing selection acting on the niche) models. For this approach, we used volume and centroid values from minimum-volume ellipsoids performed in Niche Analyst for each Brachycephalidae species. We considered that the volume and the centroid values represent the range and niche specificity of a species, respectively. Virtual niche was produced by the most frequent variables to identify climate refugia for the endemic amphibians in AF: Isothermality (Bio 3), Max Temperature of Warmest Month (Bio 5), and Precipitation of Warmest Quarter (Bio 18). Our main results were coincident under BM and OU models, showing genus-level variability in niche and niche volume conservation. Furthermore, the two estimated variables were independent: niches can be more similar between sister species while their volumes are not, and vice-versa. Hence, suitability to environment under a climate change scenario is a complex issue and it is much more accurate if considered within the phylogenetic context of species. Besides encouraging the discussion about the probable environmental parameters a given lineage could tolerate in a climate change scenario by the recognition of environmental suitability of each clade, our approach could improve knowledge about paleoenvironment of species, a major issue in paleontology.

June 20
12:00 PM
Session 3

Neotropical montane butterflies: a historical perspective on diversity patterns

Gueratto P.E.[1*], Magaldi L.M.[1], Silva-Brandão K.L.[1], Sobral-Souza T.[2] & Freitas A.V.L.[1]

[1]Universidade Estadual de Campinas, Campinas, São Paulo, Brazil. [2]Universidade Federal do Mato Grosso, Cuiabá, Mato Grosso, Brazil. [*]Correspondence: patyegueratto@gmail.com.

Integrating the different faces of Biogeography and Macroecology, this work investigates how historical and contemporary climatic conditions and biogeographical processes shape patterns of diversity in montane areas in the Neotropical region. For this purpose, it was used tools of ecological niche modeling and historical biogeography and butterflies of the genus *Actinote* as a study model. The genus *Actinote* Hubner, 1819 (Nymphalidae: Heliconiinae: Acraeini) has 38 species currently described that are widely distributed in South and Central America, occupying mainly areas of the Atlantic Forest and the northern Andes. Potential distributions were predicted for the current, Mid-Holocene (6ka) and Last Glacial Maximum (21ka) climatic scenarios using ensemble approach. Event-based models (DEC) were used to infer the ancestral distribution of the group. The preliminary results suggest that the ancestral distribution of *Actinote* comprises an area now dominated by the Atlantic Forest. Thus, the posterior colonization of the Andean possibly occurred through events of dispersion. Based on this, it was explored whether the expansion of the occurrences areas of the species may be related to climatic events. The following hypotheses were tested: a) the distribution of species in the group is related to environmental variables, such as temperature and precipitation, b) Areas of greater climatic stability predict greater richness, and c) in periods with higher temperatures (like the present), there was a retraction of the richest areas, which remained only in mountainous regions, while in colder periods, these areas expanded, with a connection between the different mountainous massifs of the Atlantic Forest, and also between the Atlantic Forest and the Andean region.

Niche conservatism among continental species of the Philisca (Anyphaenidae) spiders

June 20
12:00 PM
Session 3

Pacheco M.P.[1*] & Soto E.M.[1]

[1]Departamento de Ecología, Genética y Evolución, IEGEBA (CONICET-UBA), Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Ciudad Universitaria, Pabellón II (C1428 EHA), Buenos Aires, Argentina. [*]Correspondence: piapacheco262@gmail.com.

Philisca (Anyphaenidae) spiders inhabit the Valdivian forest ecoregion. The genus is constituted by fourteen species (eight continental, distributed along the Andes mountain range in both Chile and Argentina, and nine endemic to Robinson Crusoe island) that are divided into two clades with clear morphological differences. The genus has been studied in recent years, however the potential areas where the species could be found and the variables that could determine those distributions were not analyzed. That is why habitat suitability models were developed and evaluated for seven continental species of the genus *Philisca* and after that, niche conservatism tests were carried out between the selected models for each species. The georeferenced data of each species were obtained from the collections of the Argentine Museum of Natural Sciences "Bernardino Rivadavia" (MACN) and the California Academy of Sciences (CASENT). Before the analyzes, the database was reviewed in search of duplicate data and those whose georeferencing has been determined doubtful, in order not to consider them in the study. The nineteen environmental variables analyzed were obtained from ecoClimate. Those uncorrelated variables were selected from the analysis of the variance inflation factor (VIF) using R. Habitat suitability models (training percent: 30%, 100 replicates) were developed for each species considering different combinations of "features" and "regularization multipliers" using MaxEnt. The best model for each species was selected using the AICc and AUC. Niche conservatism was evaluated using ENMTools for the calculation of the Schoener (D) and Warren (I) index, and their subsequent comparison with the values of a null distribution generated by permutations (100). Preliminary results show that niches between species inside each clade were conserved but, niches among both clades of *Philisca* were not. Mean annual temperature would play an important role in determining the distributions of spiders of the genus *Philisca*. However, there would be different secondary environmental factors that determine the microenvironments occupied by the different species.

Predicting biogeographical responses of marine phytoplankton to climate change using ecological niche modeling

June 20
12:00 PM
Session 3

Edullantes B.[1,2*], Low-Decarie E.[3], Steinke M.[2] & Cameron T.[2]

[1]Department of Biology and Environmental Science, College of Science, University of Philippines Cebu, Lahug, Cebu, Philippines. [2]School of Life Sciences, University of Essex, Wivenhoe Park, Colchester, Essex, United Kingdom. [3]Astronauts, Life Sciences and Space Medicine, Canadian Space Agency, 6767 Route de l'Aéroport Saint-Hubert, QC, Canada J3Y. [*]Correspondence: bedullantes@up.edu.ph.

The warming of the climate is likely affecting the distribution and diversity of marine phytoplankton in time and space. However, our current understanding on the ecological responses of non-toxic and toxic marine phytoplankton to future climate scenarios is still limited. In this study, correlative and mechanistic ecological niche modeling were applied to examine the effect of climate change on non-toxic and toxic phytoplankton species. In correlative ENM, the species occurrence data of marine phytoplankton species were collected from various databases and linked to environmental data to forecast the habitat suitability of a species using maximum entropy (Maxent) method. In mechanistic ENM, the thermal performance curves of selected marine phytoplankton species were obtained from literature and used to establish a causal relationship between species distribution and temperature. Both the correlative and mechanistic ENMs were projected into the present and future climate scenarios, which were then compared to provide a better insight on the ecological responses of non-toxic and toxic phytoplankton to climate change. The findings reveal future shifts in the latitudinal range and habitat suitability of most marine phytoplankton species. Furthermore, the results show changes in the phytoplankton community structure and the relative composition of toxic species in future climate scenarios. The warming temperature may likely exceed the physiological limits of marine phytoplankton species. These species must avoid the extreme temperatures or else they are at risk of thermal danger. Also, these species must either adapt or migrate to new favourable habitats to survive, otherwise, their extinction is inevitable. The findings of this study advance our current predictive understanding on the ecological responses of marine phytoplankton to climate change.

June 20
12:00 PM
Session 3

Predicting the occurrence of four *Dynamena* species (Cnidaria, Hydrozoa)

Silva P.K.R.[1*] & Oliveira O.M.P.[1]

[1]Universidade Federal do ABC, São Paulo, Brazil. [*]Correspondence: paula.keshia@ufabc.edu.br.

The hydroids are the main components of zoobenthos. They are voracious generalists eating a variety of prey acting in local diversity, energy link between planktonic and benthic environments. Events of hydroids bioinvasion are mainly caused by human activities once they break the species' boundaries (e.g. larvae or medusae in ballast water or setting on ship hulls). With the ability of setting on several kinds of natural and artificial substrates, these animals can occupy open niches and, consequently, modify local communities' structure. With that in mind the present study aims to verify the potential occurrence areas (with or without previous records) of some hydroid species. To achieve this, we combined OBIS (Ocean Biodiversity Information System) database, and new distributional information on these species. In a second step, we validated all occurrence points and taxonomic names using Google Earth and following WORMS (World Register of Marine Species), respectively, and then we removed all duplicated data and sampling bias. After that, we elaborated models using the SDM (Species Distribution Models) package in R software with three methods (Generalized Linear Models, Generalized Additive Models,

and Random Forest). We modeled four species of *Dynamena* genus (*D. crisioides*, *D. disticha*, *D. pumila*, and *D. quadridentata*) using only temperature and salinity as predictor variables. In general lines, the models using GLM for all Dynamena species had the worst results for AUC – ROC curve (Area Under the Curve - Receiver Operating Characteristics) score among 0.51 to 0.67. While for the remaining methods, the lowest AUC score obtained was 0.70. Finally, we elaborated consensus maps from all methods. *Dynamena pumila* showed possible distribution restricted to latitudes close to 50º in both hemispheres. While the *D. crisioides*, *D. disticha* and *D. quadridentata* showed a possible occurrence in a large range in the equator. Maps produced will be of great help for monitoring species bioinvasion.

Spix's Macaw back to nature: is there a safe place to return despite climate change?

June 20
12:00 PM
Session 3

Gomides S.C.[1*], Machado T.M.[1], Evangelista-Vale J.C.[2], Martins-Oliveira A.T.[3], Pires-Oliveira J.C.[3], Muller A.O.[3], Rosa L.B.[4], Santos-Silva D.L.[3] & Eisenlohr P.V.[5]

[1]Universidade Federal do Oeste do Pará, Oriximiná, Pará, Brazil. [2]Universidade de Brasília, Brasília, Distrito Federal, Brazil. [3]Universidade do Estado de Mato Grosso, Nova Xavantina, Mato Grosso, Brazil. [4]Universidade Federal de Mato Grosso, Cuiabá, Mato Grosso, Brazil. [5]Universidade do Estado de Mato Grosso, Alta Floresta, Mato Grosso, Brazil. [*]Correspondence: samuelbio@hotmail.com.

Cyanopsitta spixii (Ararinha-azul or Spix's Macaw) is extinct in the wild since 2000, but the few existing individuals rised in captivity will participate in a reintroduction project within the species' original distribution area, in the Caatinga domain (Brazil). The project is challenging because of the limited data available on the ecology of the species in its natural environment and the occurrence records for this bird are old and inaccurate. In support of this reintroduction project, we evaluated the potential effects of climate change on environmental suitability for the 14 plant species most commonly used by *C. spixii*. These species are key elements for the long-term re-establishment of this bird in the wild. Understanding how the distribution of these plants can vary in the region over time is fundamental to the bird's conservation policy. We produced models of environmental suitability based on 19 bioclimatic variables and 10 physical soil and topography variables. Climate projections were created for the present and the year 2070 with an optimistic (SSP2-4.5) and a pessimistic (SSP5-8.5) climate scenario. The results indicate that both future climate scenarios foresee a reduction in area of environmental suitability for the plant species most used by *C. spixii*. The area of environmental suitability where the 14 plant species occur simultaneously in the Caatinga domain will suffer a reduction of between 33% (SSP2-4.5) and 63% (SSP5-8.5). In addition to climate change, other potential threats to the preservation of *C. spixii* include hunting, habitat alteration, wind farms, and the lack of corridors between protected areas. The maintenance of *C. spixii* will essentially depend on programs for the recovery of degraded areas, especially riparian forests, and the preservation of already existing natural areas. The Caatinga domain is very threatened by habitat loss and, for the success of this

reintroduction project, the parties involved must act in protecting both the species and the environments and resources it uses.

Poster Session 4: Phylogeography

An integrative approach for species delimitation in a species complex of *Eryngium* (Apiaceae) endemic to Chile

June 20
5:00 PM
Session 4

Padin A.L.[1,*] & Calviño C.I. [1,**]

[1]Instituto de Investigaciones en Biodiversidad y Medioambiente (INIBIOMA),
Universidad Nacional del Comahue-CONICET, Bariloche, Río Negro, Argentina.
Correspondence: [*]arianapadin@comahue-conicet.gob.ar and
[**]ccalvino@comahue-conicet.gob.ar.

Species delimitation impacts on most fields of biology, including biogeography, phylogenetics, ecology and conservation. Species complexes include phylogenetically closely related species whose boundaries are unclear, posing enormous challenges for species delimitation. The *Eryngium anomalum* species complex comprises a group of annual herbs that are found along coastal areas of central-northern Chile. Based on current taxonomy this complex includes two species that are morphologically very similar. Recent phylogenetic studies estimated that the species complex is monophyletic, however, the species that comprise it probably are not, casting doubts on their limits. Moreover, based on qualitative characteristics of the fruits, we recognized different morphotypes, suggesting the presence of an additional new species within the complex. In this study, we tested the hypothesis that the *Eryngium anomalum* complex comprises three species (not two) through an integrative taxonomic approach using morphological, geographic distribution, climatic, and molecular data. For that, we analyzed quantitative morphological characters and climatic variables using uni- and multivariate statistics on 181 individuals from herbarium specimens of the *Eryngium anomalum* species complex. We also analyzed their geographic and altitudinal distributions using georeferenced localities indicated on the specimen labels. In addition, we tested hypothesis of species delimitation based on chloroplast and nuclear DNA sequence data from eight regions using two Bayesian coalescent-based methods: Bayes factors (BF) and Bayesian phylogenetics and phylogeography (BPP) estimation. The different lines of evidence examined, i.e. morphology, climatic niche, altitudinal and geographical distribution, and genetic, support the recognition of three different species within the *Eryngium anomalum* complex. The integrative approach followed in this study allowed robust hypotheses of species limits within a species complex. In turn, this grants solid grounds for future studies or policies on conservation, biogeography, ecology, and many others.

June 20
5:00 PM
Session 4

Demographic processes, refugia and dispersal routes within the sigmodontine rodent assemblage from South American Pampas during the Pleistocene

Ortiz N.O.[1*], Pinotti J.D.[1], Trimarchi L.I.[1], Gardenal N.C.[1,3], González-Ittig R.E.[1,3] & Rivera P.C.[1,2]

[1] Instituto de Diversidad y Ecología Animal (IDEA CONICET-UNC), Córdoba, Argentina. [2]Universidad Nacional de Chilecito, Chilecito, Argentina. [3]Cátedra de Genética de Poblaciones y Evolución, FCEFyN, UNC, Córdoba, Argentina.
[*]Correspondence: natalia_ortiz05@hotmail.com.

The geographical distribution of a taxon is the result of the interaction among geological, environmental and ecological processes in a space-time dimension. Theoretically, co-distributed species should have congruent phylogeographic patterns as a result of being subject to common environmental and geological changes. However, these patterns may be affected by ecological differences among the species, such as dispersal abilities and food or habitat preferences, and by the possible instability of the assemblage itself through time. South America presents one of the most extended subtropical-temperate grasslands in the world, the Pampas. In the Pleistocene, this biome would have experienced expansions over forest areas during cold and generally dry (glacial) periods and retractions during warm and generally humid (interglacial) climates. The sigmodontine rodents inhabiting the Pampas are one of the best known rodent assemblages in South America, being a good study model to analyze the impact of the Pleistocene climate changes in the evolutionary history of the region through comparative phylogeography. We studied the phylogeographic patterns of seven rodent species inhabiting the Pampas; our aims were to evaluate the concordance of phylogeographic patterns among them, assess if they experienced congruent demographic changes, estimate the time in which this demographic change occurred, and infer if the dispersal routes are shared among them. Four of the seven species evidenced recent demographic expansion. However, no temporal synchrony was observed since *Oligoryzomys nigripes* and *Oxymycterus nasutus* experienced a population increase about 250,000 years ago, whereas for *Calomys musculinus* and *Oligoryzomys flavescens* it was about 125,000-100,000 years ago. We observed three common centers of origin for the species populations, which would have acted as grassland refugia where species would have developed isolated lineages. The reconstruction of lineage dispersal showed common dispersion routes for all of the species, following the grassland expansion to North, West and South. Our results support the idea that recent glacial cycles had a more moderate impact in South America because of its latitude and continentality, and that open biomes such as grasslands would have been more stable in comparison with tropical forests. In this context, ecological differences could have gained a greater prominence, producing a more complex scenario, like the one observed in the present study.

Genetic structure and diversity of a bat with unexpectedly fragmented populations, *Natalus mexicanus* (Chiroptera: Natalidae)

June 20
5:00 PM
Session 4

López-Wilchis R.[1], Méndez-Rodríguez A.[1], Juste J.[2], Serrato Díaz A.[3], Rodríguez-Gómez F.[4] & Guevara-Chumacero L.M.[1,*]

[1] Departamento de Biología, Universidad Autónoma Metropolitana-Iztapalapa, Ciudad de Mexico, Mexico. [2]Estación Biológica de Doñana, C.S.I.C., Sevilla, España. [3]Departamento de Hidrobiología, Universidad Autónoma Metropolitana-Iztapalapa, Ciudad deMexico, Mexico. [4]Departamento de Ciencias Computacionales, Centro Universitario de Ciencias Exactas e Ingenierías, Universidad de Guadalajara, Guadalajara, Jalisco, Mexico. [*]Correspondence: lmgc@xanum.uam.mx.

Recent historical and anthropogenic changes in the landscape causing habitat fragmentation can disrupt the connectivity of wild populations and pose a threat to the genetic diversity of multiple species. This study investigated the effect of habitat fragmentation on the structure and genetic diversity of the Mexican greater funnel-eared bat (*Natalus mexicanus*) throughout its distribution range in Mexico, whose natural habitat has decreased dramatically in recent years. Genetic structure and diversity were measured using the HVII hypervariable domain of the mitochondrial control region and ten nuclear microsatellite loci, to analyze historical and contemporary information, respectively. The mitochondrial and nuclear results pointed to a differential genetic structuring, derived mainly from philopatry in females. Our results also showed that genetic diversity was historically high and currently moderate; additionally, the contemporary gene flow between groups observed was null. These findings confirm that the effects of habitat fragmentation have started to be expressed in populations and that forest loss is already building barriers to contemporary gene flow. Gene flow is a process essential to ensure that the genetic diversity of *N. mexicanus* populations (and probably of many other forest species) distributed in Mexico is preserved in the long term by maintaining forest connectivity between locations.

Hybridization between two species of bats (Chiroptera: Mormoopidae) in Central America

June 20
5:00 PM
Session 4

Méndez-Rodríguez A. [1,*], Juste J.[2,3], Centeno-Cuadros A.[4], Rodríguez-Gómez F.[5], Serrato Díaz A.[6], García-Mudarra J.L.[2], Guevara-Chumacero L.M.[1] & López-Wilchis R.[1]

[1] Departamento de Biología, Universidad Autónoma Metropolitana Iztapalapa, Ciudad de México, Mexico. [2] Estación Biológica de Doñana, C.S.I.C., Sevilla, Spain. [3]CIBER de Epidemiología y Salud Pública, CIBERESP, Madrid, Spain. [4]Universidad de Cádiz Facultad de Ciencias del Mar y Ambientales, Biomedicina, Biotecnología y Salud Pública. Cádiz, Spain. [5]Departamento de Ciencias Computacionales, Centro Universitario de Ciencias Exactas e Ingenierías, Universidad de Guadalajara, Mexico. [6] Departamento de Hidrobiología, Universidad Autónoma Metropolitana Iztapalapa, Ciudad de México, Mexico. [*]Correspondence: aline_mera@hotmail.com.

The evolutionary and genetic relationships between two sister species of nacked-backed bats (*Pteronotus fulvus* and *P. gymnonotus*). Traditionally differentiated by their forearm size, individuals with intermediate size have been found in sympatric populations in Southern Mexico. Considering the above, in this study we are determined if there is genetic flow between these species, as well as if the intermediate morphotypes correspond to the hybrid individuals. We used a mitochondrial DNA marker (COI), and various nuclear DNA consisting of two introns (PRKCL and STAT5A), the Recombination Activator gene 2, and 13 microsatellites. These markers have been studied in sympatric and allopatric populations of the two species, inside and outside their distribution in Mexico and also near to *P. davyi* distribution range, another species closely related. The comparative genetic study confirmed the validity of these three lineages at a specific level (*P. fulvus*, *P. gymnonotus* and *P. davyi*), but showed discordance between the evolutionary hypotheses produced by the nuclear and mitochondrial markers. We found that the discordance between markers is related to a mitochondrial capture from of *P. fulvus* in the populations of *P. gymnonotus*. This Introgression was verified in all individuals of *P. gymnonotus* throughout the sympatric distribution (Mexico Nicaragua) and it related to the population expansion/retraction pulses, in association with changes in the distribution of forests during the Quaternary climatic cycles. The microsatellites analysis showed current genetic contacts between the two species in sympatry, with 1.5-3.01% of the total samples identified as hybrids. No relationship was found between hybridization and the individuals with intermediate morphotypes in Southern Mexico. These results confirm the need to use with caution both, forearm size and external characters, for field identification of *P. fulvus*, *P. gymnonotus* and *P. davyi* and the use of mitochondrial DNA for their distinction in the laboratory.

June 20
5:00 PM
Session 4

Low genetic diversity and high genetic structure in the Endangered Lima Leaf-Toed Gecko *Phyllodactyllus sentosus* revealed by Genome-wide SNP data

Arana A.[1,*], Esteves J.F.[1], Ramirez J.L.[1] & Pérez J.[1]

[1] Facultad de Ciencias Biológicas, Universidad Nacional Mayorde San Marcos, Lima, Lima, Perú. *Correspondence: alejandra.arana@unmsm.edu.pe.

The loss and fragmentation of natural habitats due to urbanization is a major threat to biodiversity. The Lima leaf-toed gecko *Phyllodactylus sentosus* is an endemic species of Peru, considered Critically Endangered, with few known localities of occurrence within Lima City which are mainly in archaeological areas known as "huacas." Using information obtained through Genotyping-by Sequencing, this study aimed to analyze the genetic diversity and population genetic structure of this species. A total of 52 individuals were sampled from 13 localities along Lima City and we obtained 313k loci with at least one SNP after filtering the data using ipyrad. To measure genetic diversity within populations we used 2 different indexes: Expected Heterozygosity (He) and Nucleotide Diversity (π). Our results showed low levels of genetic diversity in all populations, Expected Heterozygosity ranged from 0.0406 in the Tambo Inga population to 0.134 in the Huaca Pucllana population and Nucleotide Diversity ranged from 0.0812 in the Tambo Inga population to 0.145 in the Cerro Mulería population. Through PCA and DAPC, three groups were recovered corresponding to the populations of the huacas Mateo Salado, Pucllana, and San Marcos/Parque de Las Leyendas. Population genetic structure was also analyzed using the software STRUCTURE (admixture model) and we identified the most probable number of genetic groups by Evanno's method. The STRUCTURE analysis shows four genetic groups analyzing an unlinked data set of 3373 SNPs (without missing data) and six genetic groups analyzing an unlinked data set of 15 816 SNPs. Results show that lower-density populations have lower levels of genetic diversity, except for two huacas (Cerro Mulería and Cerro La Milla), which showed greater Nucleotide Diversity levels than the Mateo Salado population which holds a relatively big population. We also found high differentiation between populations indicating that urbanization and the consequent modification of the habitat of this species represent barriers to gene flow among the populations that are sheltered in the huacas of Lima.

Multilocus phylogeography of the endemic andendangered angular angelshark (*Squatina guggenheim*)in the Southwest Atlantic Ocean

June 20
5:00 PM
Session 4

Bunholi I.V.[1,2*], Ferrette B.L.S.[1,3], Domingues R.R.[1], Rotundo M.M.[4], Cuevas J.M.[5,6], García M.[5], Gómez S.[5], Freitas R.H.A.[7], Oliveira C.[2], Foresti F.[2] & Mendonça F.F.[1]

[1]Universidade Federal de São Paulo (UNIFESP), Santos, SP, Brasil. [2]Universidade Estadual Paulista Júlio de Mesquita Filho (UNESP), Botucatu, SP, Brasil. [3]Universidade Santa Cecília (UNISANTA), Santos, SP, Brasil. [4]Acervo Zoológico, Universidade Santa Cecília (UNISANTA), Santos, SP, Brasil. [5]Universidad Nacional de La Plata, La Plata, Argentina. [6]Wildlife Conservation Society de Argentina, Argentina. [7]Universidade Federal de Santa Catarina (UFSC), Florianópolis, SC, Brasil.
[*]Correspondence: ivasconcellos@sycamores.indstate.edu.

The angular angelshark (*Squatina guggenheim*) is a coastal endangered angel shark and one of the major bycatch victims. Despite major concerns about this species, little is known about its evolutionary connectivity among its whole geographic distribution. In this study, genetic connectivity, phylogeographic patterns, and demographic history of the angular angelshark were assessed for 122 individuals across Southwest Atlantic Ocean regions based on a multilocus mitochondrial DNA approach (control region [CR], cytochrome b [CytB], and cytochrome c oxidase I [COI]) in order to provide genetic information from genetic markers with distinct evolutionary times. The concatenated mitochondrial dataset was used to access overall genetic diversity indices as well as in each geographic region. Pairwise ϕST and hierarchical AMOVA analyzes were applied to test the null hypothesis of panmixia and then a gene flow analysis was incorporated to understand whether population divergence has been accompanied by gene flow. Additionally, the phylogeographic pattern was also investigated through the phylogenetic correlation among haplotypes and demographic analyzes using Bayesian inferences. The angular angelshark showed high levels of haplotype diversity (hCR-CytB-COI = 0.838 ± 0.033) and low nucleotide diversity (πCR-CytB-COI = 0.0017 ± 0.0009), with distinct genetic diversity patterns among populations. Although signs of stepping-stone gene flow were observed, a strong and statistically significant genetic structure into at least four populations was detected ($\phi ST = 0.23$, $p < 0.05$), which matches with the species' biological traits as well with the oceanographic particularities of the Southwest Atlantic Ocean. The phylogenetic analysis revealed the presence of two matrilineal lineages that diverged during the peak-warmth interglacial of the early Pliocene, showing the influence of temperature in its dispersal pattern. Contrasting demographic patterns were detected among populations, in which only South-southwest Atlantic populations showed signs of population expansion after intense climatic and sea-level oscillations of the Pleistocene period. Despite the existence of connectivity among regions, our results suggest that conservation plans should be carried out following the uniqueness of each population.

June 20
5:00 PM
Session 4

Phylogeographic history of the butterfly *Heliconius erato phyllis* (Lepidoptera: Nymphalidae: Heliconiini) in the Atlantic Forest

Machado P.A.[1,*], Silva-Brandão K.L.[1,2], Seraphim N.P.[3], Ramos R.R.[1] & Freitas A.V.L.[1,4]

[1]Instituto de Biologia, Universidade Estadual de Campinas, Campinas, SP, Brasil. [2]Centro de Ciências Naturais e Humanas, Universidade Federal do ABC, Santo André, SP, Brasil. [3]Instituto Federal de Educação Ciência e Tecnologia de São Paulo, Campus Campinas, SP, Brasil. [4]Museu de Zoologia, Instituto de Biologia, Universidade Estadual de Campinas, Campinas, SP, Brasil. [*]Correspondence: patyavelino95@gmail.com.

The Atlantic Forest (AF) is one of the most threatened biomes in the world, characterized by high biodiversity and high levels of endemism. Phylogeographic studies in this biome can contribute to understanding key questions about AF species distribution and their relation to its geological history. Butterflies have long contributed to our understanding of evolutionary and ecological patterns and the genus *Heliconius* is an ideal model taxon for such studies. Among all known species in the genus, *Heliconius erato phyllis* is one of the subspecies with the broadest distribution, occurring throughout all the AF and in the adjacent Cerrado, Caatinga and Chaco biomes. Considering the high habitat heterogeneity through the AF and the wide distribution of *H. erato phyllis*, this butterfly is an ideal organism for studies on its genetic population structure, and the results can provide insights for better understand the role of climatic and geological events in the evolutionary history of this Biome. In the present study we used data from mtDNA COI sequences of 378 individuals from 68 localities on the AF and neighbor biomes. The results showed that *H. erato phyllis* populations are highly structured (Fst = 0.34, $p < 0.001$), and with a significant correlation between genetic and geographic distances (Mantel test, r = 0.322, $p < 0.001$). The haplotype network indicated three major haplogroups, which are associated with three different regions within the AF: 1) Northeast, 2) Southeast, and 3) Southern. This geographical pattern was explained by climatic variables related mainly to temperature. These results suggest that climatic barriers likely contributed to the observed genetic structure of *H. erato phyllis.*

Phylogeography of *Colpomenia sinuosa* (Ectocarpales, Phaeophyceae) in Brazil

June 20
5:00 PM
Session 4

Martins N.T.[1*], Cassano V.[1] & Gurgel C.F.D.[2]

[1]Universidade de São Paulo, Instituto de Biociências, Departamento de Botânica, São Paulo, SP, Brazil. [2]Universidade Federal de Santa Catarina, Centro de Ciências Biológicas, Departamento de Botânica, Florianópolis, SC, Brazil. [*]Correspondence: tavaresmartins.nuno@gmail.com.

Colpomenia sinuosa is a cosmopolitan marine brown macroalgal species-complex, therefore a great candidate for evolutionary studies in the marine environment. Since 2009, three distinct phylogenetic lineages, subdivided into eight subgroups, have been identified within *C. sinuosa* worldwide collections. Yet, world sampling remains limited and spotty. Molecular data from Brazilian *C. sinuosa* collections have been limited to 10 specimens from a single locality. However, *C. sinuosa* populations occur along the entire Brazilian coast. Consequently, knowledge on population genetic diversity and phylogeographic structure along the Brazilian coast are absent. Barriers to gene flow play a pivotal role in the dynamics of population genetics promoting genetic isolation, differentiation, being inexorably associated with the development and maintenance of phylogeographic structure. The identification of phylogeographic structure provides subsidies for the management of natural genetic resources, aiding in the recognition of areas of conservation interest. Several geographic and oceanographic processes located along the Brazilian coast have been proposed as barriers to gene flow. We performed a phylogeographic analysis of *C. sinuosa* populations along its entire distribution in Brazil. The highly variable mitochondrial-encoded *cox*3 marker was sequenced for 148 individuals collected at 12 localities. Our results identified two genetically distinct population groups (north vs. south) separated by the Vitória-Trindade seamount chain (20.5° S). Genetic diversity in northern populations are 14.6 and 15.5 times greater than the southern populations in terms of haplotype and nucleotide diversity, respectively. Within the northern populations, the Bahia state holds the largest genetic diversity, most likely due to a local refugium-effect during recent geological time. The southern populations' lower genetic diversity and lack of internal genetic sub-structure suggest past demographic bottlenecks followed by recent colonization from northern haplotypes. Our results do not indicate recent introductions of foreign haplotypes in Brazil, and reinforce the crucial importance of the Vitória-Trindade seamount chain driving marine evolution in the Southwestern Atlantic Ocean.

June 20
5:00 PM
Session 4

Phylogeography of the Neotropical species *Paralucilia fulvinota* Bigot (Diptera, Calliphoridae) based on mitochondrial COI sequences

Madeira-Ott T.[1;*], Marinho M.A.T.[2] & Thyssen P.J.[1]

[1]Campinas University, Campinas, São Paulo, Brazil. [2]Federal University of Pelotas, Pelotas, RS, Brazil. [*]Correspondence: madeira.t@outlook.com.

Paralucilia (Diptera, Calliphoridae) is a genus of neotropical blowflies that has presented several taxonomic conflicts. Among the reasons are the high morphological homogeneity between species and the polymorphism between individuals of the same species. This study aims to investigate the phylogeography of the species *Paralucilia fulvinota* (Bigot, 1877). 55 sequences of a fragment of the mitochondrial COI gene were obtained from *P. fulvinota* specimens, using molecular techniques and from the BOLD System database. The genetic diversity of the 12 investigated populations (3 - Brazil; 1 - Colombia; 5 - Costa Rica; 3 - Ecuador) was obtained using the DNAsp v.6 software. The historical phylogeography of the populations was inferred through two analyzes: construction of a haplotype network, performed in the PopART software, and the reconstruction of ancestral areas of distribution, performed in the RASP 4.2 software. The phylogenetic tree used in the reconstruction of ancestral areas was obtained by the Bayesian inference method, reconstructed in BEAST v.2 software. For the reconstruction of ancestral areas, we considered the division of the Neotropical region proposed by Morrone (2014). The analyzes of genetic diversity showed high global haplotypic diversity among the studied populations (0.899 ± 0.022), with the Ecuador-Pichincha population showing the greatest diversity (0.938 ± 0.026). 16 haplotypes were recovered, ranging from 1-14 between populations, the majority of which are associated with geography. The reconstruction analysis of the ancestral area indicated a greater probability that the ancestor of *P. fulvinota* belonged to the Pacific dominion. The specimens were grouped into three main clades, the majority of which were associated with a geographic region. The ancestral areas recovered for each of these groups were Pacific, Boreal Brazilian and Parana dominion. This study demonstrated that *P. fulvinota* has a well-defined genetic structure, having the Pacific dominion as the probable area of origin, and later diversification into three Neotropical domains.

June 20
5:00 PM
Session 4

Phylogeography of *Nothofagus dombeyi* reflects past geological and climatic changes in southern South America

Mathiasen P.[1*], Fasanella M.[1], Diaz D.G.[1], Juri G[2], Hasbún R[3] & Premoli A.C[1]

[1]Instituto de Investigaciones en Biodiversidad y Medioambiente (INIBIOMA-CONICET COMAHUE). Bariloche, Río Negro, Argentina. [2]Instituto de Investigaciones en Recursos Naturales, Agroecología y Desarrollo Rural (IRNAD CONICET-UNRN). El Bolsón, Río Negro, Argentina. [3]Laboratorio de Epigenética Vegetal, Departamento de Silvicultura, Facultad de Ciencias Forestales, Universidad de Concepción, Chile. [*]Correspondence: pmathiasen@gmail.com.

The southern tip of South America has a long and complex geological history, which begun with the breakup of Gondwana and was followed by global sea level rises, tectonic processes such as mountain building and volcanism, glaciations, and the associated climatic changes. The ancient flora of South America evolved under these changing environments. As a result, lineage diversification of long-lived woody taxa, such as *Nothofagus*, will reflect the effects of the Paleogene paleogeography of Patagonia and more recent climatic oscillations of the Neogene. The objective was to evaluate the phylogeographic patterns of *Nothofagus dombeyi* combining geological evidence from marine sedimentary basins, Andean orogeny, and climatology with phylogenetic and statistical analyses. A total of 203 individuals along the entire range of distribution of the species were sampled and analyzed by sequencing three non-coding regions of the chloroplast DNA. We found 24 chloroplast DNA haplotypes across the range. The phylogenetic tree and the haplotype network yielded three strongly differentiated lineages that were latitudinally structured (AMOVA PhiST1-2=0.692, PhiST1-3=0.928, PhiST2-3=0.904). Two phylogeographic breaks were observed at 39°S and 42°S. The groups identified by BAPS and the PCA analysis were in agreement with the three lineages. Lineage divergence was concordant with ancient geological events that took place during Eocene to Miocene epochs, while haplotype diversification within lineages was driven by more recent climatic changes during the Pliocene. Middle-range Lineage 2 was the most polymorphic (67.11%), holding 15 of the 24 haplotypes, showing that marine transgressions (late Middle Miocene, Late Miocene, and Early Pliocene) could favor the great genetic diversity. These ages have been assigned recently to Chilean formations near the Pacific coast and across the Chilean Central Depression.

Poster Session 5: Molecular Ecology

Are there genetic biases for showy males? A revaluation of the theory by the lizards' perspective

June 21
12:00 PM
Session 5

Luzete J.[1,*] & Klaczko J.[1]

[1]Laboratory of Comparative Vertebrate Anatomy, Department of Physiological Sciences,
Institute of Biological Sciences, University of Brasilia, Brasilia, DF, 70910-900, Brazil.
[*]Correspondence: juluzete@gmail.com.

The evolution of extremely extravagant males in animals, especially the propensity of some groups to the evolution of ornaments, has intrigued evolutionary biologists for a long time. Newly arisen and rare alleles encoding male secondary sexual traits are usually vulnerable to loss by genetic drift, however, the sex chromosome system can reduce the probability of loss by random processes. Reeve and Pfennig (2003) suggest that animals with a ZW system are more prone to the evolution of elevated sexual dimorphism and propose a relationship between the sex chromosome system and sexual dimorphism in animals, with male ornaments evolving in response to the genetic system. Although they corrected for the non-independence of data due to shared evolutionary history, they do not incorporate a phylogenetic hypothesis. Thus, we revaluated their theory in lizards—which is diverse in both sex chromosome system and sexual dimorphism—using comparative phylogenetic methods and including more species in the analysis. We transformed the sex chromosome system in an ordinal scale ranked according to the relative strength of selection on a rare allele encoding a male ornament, following Reeve and Pfennig (2003). This scale varies between 4 (a heteromorphic ZZW system) and -4 (a heteromorphic XXY system). We estimated the degree of sexual dimorphism by scoring the number of traits unique to males reported in descriptions of external morphology and sexual size dimorphism. We calculated the phylogenetic signal for the sexual chromosome and sexual dimorphism scores using Pagel's λ and Blomberg's K. Then, we performed a PGLS between the two variables using a BM model of evolution and an OU model incorporating the λ value. We found a significant and high phylogenetic signal for the sex chromosome score for both λ and K. The sexual dimorphism score was also significant for both λ and K but much lower than the sex chromosome score. The PGLS using a BM model of evolution found a significant and positive relationship between both variables. In contrast, the PGLS using an OU model of evolution showed no relationship between the two variables and had a better fit. In lizards, showy males have evolved frequently in many lineages that share a XY system, suggesting that the theory proposed by Reeve and Pfennig might not be the only process involved in the evolution of male ornaments.

Does sponge have a growth zone? Some (ongoing) molecular and *in situ* inferences

June 21
12:00 PM
Session 5

Cajado B.[1,*], Nunes da Fonseca R.[2], Riesgo A.[3] & Lanna E.[1]

[1]Universidade Federal da Bahia, Salvador, Bahia, Brazil. [2]Universidade Federal do Rio de Janeiro, Macaé, Rio de Janeiro, Brazil. [3]Museo Nacional de Ciencias Naturales de Madrid, Madrid, Spain. [*]Correspondence: cajadobruno96@gmail.com.

Although sponges (Porifera) are considered to have a complex molecular repertoire, they have a quite simple body plan. Regional specializations, such as a growth zone, are usually observed in the body of many modular invertebrates. However, this characteristic is considered absent in sponges - which are considered to have undetermined growth. But, are sponges that simple? Understanding whether body regionalization is present in sponges is important to comprehend the evolution of the body plans in metazoans. Here, we are investigating this issue by comparing the transcriptome of different regions of the body of the sponge *Cladocroce caelum* (Haplosclerida). We used RNAseq analysis to obtain the transcripts of two regions of the sponge: proximal (with developed aquiferous system modules) and distal regions (the supposed growth zone). This species was chosen as model-species due to its morphology: it has reptant branches, positive relationship between size and number of oscula, and it does not have oscula at the distal region, indicating a preferred growth zone. The transcriptome was assembled *de novo* using Trinity. We obtained 167,551,552 reads from eight fragments, comprising 140,614 transcripts, and 51,150 of which had an annotation. We found that 99% of the transcripts of *C. caelum* were recovered for Eukarya and 94% of its predicted genes are found in Metazoa. All the sponges' characteristic genes involved in reproduction and stem cells, besides Hedgehog, Wnt, JAK/STAT, RTK, nuclear receptors (NR), TGF-beta and Notch-Delta signalling pathways were expressed in both regions. However, 60 transcripts were significantly differentially expressed between the two regions (39 transcripts were upregulated at the distal region, while 21 were upregulated at the proximal one). Among these genes, Frizzled-2 (a receptor related to the Wnt pathway) was expressed differently at the distal region. In addition to the transcriptome analyses, we followed the growth of 37 specimens *in situ*. These observations indicated that the growth is carried out preferentially at the proximal region (28.2% in length vs. 12.8% in width). The gene expression profile of the two regions is only slightly different, but, apparently, can indicate some regionalization in the sponge body. Our results indicate that despite the differences in the morphology of sponges compared to other invertebrates, these animals can share specialized zones of their body to grow.

June 21
12:00 PM
Session 5

Floral evolution and Bee avoidance in *Mutisia* L.f. (Mutisieae, Asteraceae)

Monge M.[1,2,*], Felix T.H.A.[1], Reginato M.[3], Moreira-Muñoz A.[4], Nakajima J.[1] & Brito V.L.G.[1]

[1]Universidade Federal de Uberlândia, Uberlândia, Minas Gerais, Brazil. [2]Universidade Estadual de Campinas, Campinas, São Paulo, Brazil. [3]Universidade Federal do Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil. [4]Pontificia Universidad Católica de Valparaíso, Valparaíso, Chile. *Correspondence: marcelomonge@gmail.com.

The morphological variation of floral traits were selected for fitting different types of interactions, such as pollinator attraction or antagonists misleading. These traits include floral morphology, size, color, and they produce complex signals which are decoded differently by each visiting group due the variation in their cognitive abilities. It is expected a strong selection pressure for highly exclusive communication channels that advertise the effective pollinators and avoid less effective interactors. The bee avoidance hypothesis states that “hummingbirds flowers” prevent the access to the resources by bees. One prediction of it is that flowers with narrow and long tubes will avoid nectar robbing by bees and keep these resources available only to hummingbirds; and red (yellow and orange) flowers will be less visible to bees, not attracting these pollinators. *Mutisia* is a South American genus of vines and shrubs with ca. 60 species. The capitula of *Mutisia* is remarkable, it is big, and has long ray-colored flowers. Several species of *Mutisia* have red, orange or yellow flowers, called in the literature as hummingbird-coloured “flowers” and some of them are indeed visited by hummingbirds. In this sense, we aim to investigate the presence of niche exclusiveness for hummingbird pollination in *Mutisia*. We used the most complete phylogenetic tree of *Mutisia* and coded the color of the flowers and measured its floral traits. We conducted comparative analysis of ancestral trait reconstructions, phylogenetic signal, and evolutionary correlations. We found the ancestral reconstructions of traits related to hummingbird pollination in *Mutisia* have different tempo and mode of evolution. Our results support the bee avoidance hypothesis in *Mutisia*, with traits being more restricted than others. These results show a complex pollinator driven evolutionary scenario with niche exclusiveness for hummingbird pollination based on bee avoidance.

June 21
12:00 PM
Session 5

Gains and losses of anemochory in the daisy family

Costas S.M.[1,*], Baranzelli M.C.[1], Giaquinta A.[1] & Cocucci A.A.[1,]

[1]Instituto Multidisciplinario de Biología Vegetal (CONICET-UNC), Córdoba, Córdoba, Argentina. *Correspondence: scostas@imbiv.unc.edu.ar.

Dispersal of individuals far from progenitors is a key life cycle process which entails benefits and costs that might result in adaptations and eventually promote speciation. However, owing to the difficulty to estimate the dispersion ability in speciose plant lineages, our knowledge on the role of this key process in evolution remains limited. One of the most widespread dispersal modes in Angiosperms and

supposedly predominant among daisies is the use of wind as a seed vector (anemochory). It has been reported that around 70% of the daisy family carry on the dispersal units, presumably structures associated with anemochory such as setose pappi (modified calyxes) and wings. A number of functional parameters have been studied on these traits and it appears that morphological variation within them is correlated with wind dispersal ability. An important role has been given to the pappus in diversification of the daisy family and anemochory possibly has a significant bearing in the ecological and evolutionary success of the family. However, to the best of our knowledge no comparative studies have been carried out on the evolution of dispersal in the family. A comparative study appears opportune since knowledge of the relationships among daisy species is now very robust, at least at tribe level. Thus, the present study aimed to estimate dispersion ability and to assess the role of the papus in the evolution of the dispersal in the family. The published knowledge on the morpho-functional association of dispersal units among a subset of daisy species representative of the whole family allowed us through predictive models to extrapolate dispersion ability to a larger set of species included in the latest published phylogeny. Subsequently, we reconstructed character evolution of wind dispersal and wind dispersal ability as discrete and continuous characters, respectively. Finally, we reconstructed the evolution of morphological pappus characters not utilized in the estimation of dispersion ability to explore for possible associations with dispersal mode. We found multiple events of reduction and loss of wind dispersal ability, mainly concentrated in the tribes Anthemideae, Arcotideae and Heliantheae. In addition, several more restricted losses also occur across the family. Finally we found evolutionary associations between pappus morphology and dispersion mode. In conclusion, we suggest that pappus morphology could play an important role in the evolution of dispersal in the daisy family and that constraints in the evolution of the dispersion probably exist due to changes in the pappus traits. Future work should concentrate in identifying drivers of such transitions in pappus traits.

Livestock can affect the evolutionary potential of native plant species in Monte Desert

June 21
12:00 PM
Session 5

Jaume D.F.[1,*], Pelliza Y.I.[1], Tadey M.[1] & Souto C.P.[1]
[1]Lab. ECOTONO, INIBIOMA, CONICET, Bariloche, Río Negro, Argentina.
[*]Correspondence: daiana.jaume@gmail.com.

Understanding how anthropogenic disturbances affect genetic, ecological and evolutionary processes aids the development of sustainable management and conservation strategies, particularly in drylands threatened by desertification. Introduction of domestic livestock in natural areas of arid environments affects the dynamics and stability of plant communities with unpredictable evolutionary consequences. We hypothesize that livestock grazing exert selective pressures, negatively affecting genetic diversity and fitness of consumed plants, and also of their offspring. We predict lower genetic diversity (heterozygosity and allelic diversity) and fitness (reproductive success and seedling vigor) in rangelands with high stocking levels

(HSL) compared to those with low stocking level (LSL), in both parental and offspring generations. We collected foliage and seeds of *Atriplex lampa*, a dominant consumed bush of the Patagonian Monte Desert, from two rangelands with HSL and LSL, measuring fitness (height and diameter, % reproductive branches, seed weight and viable seed proportion). We sowed seeds under common garden conditions and evaluated offspring vigor as height and branch number. We calculated standard population genetic parameters using microsatellite markers. As expected, we detected significantly lower genetic diversity in rangelands with HSL ($He = 0.354$ and $Ad = 0.251$) compared to those with LSL ($He = 0.441$ and $Ad = 0.291$) (all $p < 0.05$). Fitness parameters and vigor were negatively associated with browsing (all $p < 0.05$). Regarding reproductive success, viable seed proportion was lower at LSL (77.2%) than at HSL (85.8%), $p = 0.017$. Although, HSL seeds weight (1.200 mg) was lower than in LSL (1.300 mg), $p = 0.06$. Furthermore, allelic diversity was associated with seed weight ($\beta = 0.173$), and offspring branch number ($\beta = 10.977$, $p \leq 0.06$). Parental individual heterozygosity was positively associated with plant cover (p =0.01), suggesting natural revegetation may be compromised. Endogamy was high in both rangelands and generations ($Fis \geq 0.326$), while only parental generation at HSL exhibited a significant excess of heterozygosity, indicating a recent genetic bottleneck. Our results show that domestic livestock cause genetic diversity loss between generations in a highly consumed desert shrub. With parental and offspring generations showing high levels of inbreeding. Also, livestock reduced plant fitness and vigor, even with unexpectedly viable seed proportions. Unmanaged grazing seriously affects dryland vegetation sustainability, creating a disturbance that threatens plant evolutionary potential. Highlighting the importance of considering preserving genetic diversity across generations not only to protect the evolutionary potential of the species but also to protect the ecological services of the system by the development of sustainable management and conservation strategies.

June 21
12:00 PM
Session 5

Molecular evolution of genes related to antioxidant response in cetaceans

Selleghin-Veiga G.[1], Freitas L.[1], de Souza É.M.S.[1], Silva F.A.[1], Magpali L.[1] & Nery M.F.[1,*]

[1]State University of Campinas (UNICAMP), Campinas, São Paulo, Brazil.
[*]Correspondence: mariananery@gmail.com.

Cetaceans are a lineage of aquatic mammals completely dependent on the aquatic environment and share many specific adaptations related to living underwater. Here we focused on the ischemia and reperfusion of peripheral tissues, a consequence of vasoconstriction, which are part of the strategies to cope with hypoxia during apnea diving. Reperfusion leads to the production of ROS (reactive oxygen species) by many pathways resulting in oxidative damage. Previous studies showed that cetaceans do not suffer from this issue, mainly due to their antioxidant enzymes. In this study, we aimed to investigate the molecular evolution of known antioxidant enzyme genes such as CAT, GPX3, GSR, PRDX1, PRDX3, SOD1, as well as the production of ROS, by XDH gene. We used the rate of nonsynonymous (dN) to synonymous (dS) substitutions (ω = dN/dS) in the codeML program from the PAML and HyPhy packages to identify adaptive molecular evolution on these genes focusing on cetaceans. We obtained at least 61 mammalian sequences of the main representative mammalian groups, including 16 cetacean species. As some previous studies indicate, our analysis showed that the genes GPX3, GSR, PRDX1, PRDX3 and SOD1 are positively selected in cetaceans, with GPX3 and PRDX1 showing significant differences of ω values between Mysticeti and Odontoceti. We identified 23 and 1 sites evolving under positive selection in PRDX1 and SOD1 respectively, with some sites at positions close to the active site of the protein, suggesting a possible change in functional activity. We also found strong episodic selection in the GSR gene in a specific clade of Odontoceti, which demands more investigation. Further, we will perform analyses of the physicochemical properties of amino acid sites found to be evolving under positive selection and we will employ the same methodological framework to study antioxidants in pinnipeds and other semi-aquatic mammalian species to investigate for a possible convergent evolution.

New records of parasitism of the "Fuller's rose weevil" *Naupactus cervinus* (Coleoptera, Curculionidae) in Argentina

June 21
12:00 PM
Session 5

Fernandez Goya L.[1,*], Cabrio V.[2], Confalonieri V.A.[1], Lanteri A.A.[3] & Rodriguero M.S.[1]

[1]Departamento de Ecología, Genética y Evolución, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires,- IEGEBA (CONICET-UBA), Buenos Aires, Argentina. [2]Universidad Nacional del Noroeste de la Provincia de Buenos Aires (UNNOBA), Pergamino, Buenos Aires, Argentina. [3]División Entomología, Museo de La Plata, Facultad de Ciencias Naturales y Museo, Universidad Nacional de La Plata, CONICET, Buenos Aires, Argentina. [*]Correspondence: luciaf.goya@ege.fcen.uba.ar.

Naupactus cervinus is an invasive species native to South America and distributed throughout the world. It is considered a pest of citrus in several countries because of root herbivory. Also, eggs on fruit have been a quarantine barrier for exports of citrus and kiwifruit to markets in East Asia. Study of natural parasitoids of this weevil is important in order to develop possible biological control strategies. We studied two parasitoids found in adult females of *N. cervinus* collected in Entre Ríos province, Argentina. DNA was extracted and the mitochondrial COI gene was amplified and sequenced. *Wolbachia* infection was diagnosed through PCR and characterized through MLST genotyping. BLAST analysis suggested one of the parasitoids was 85-91% similar to several Braconidae (order Hymenoptera).The other parasitoid shared a 93-97% identity with the COI sequences of several Tachinidae (order Diptera). Then, for each parasitoid we performed a family-level analysis by retrieving sequences of several related genera from GenBank and BOLD databases. MRMODELTEST v.2.4 was used to establish the best fit model of nucleotide substitution and MRBAYES v.3.2.7a was used to perform Bayesian inference. We also compared COI genetic distances between our samples and putative congeneric species by pairwise comparisons using MEGA v.6, thus testing whether our genus-level identification was compatible in terms of genetic variability. The hymenopteran parasitoid fell within the genus *Microctonus* with high nodal support. A previous study by Rodriguero *et al.* (2014) first reported a *Micronoctus* sp. parasitoid for *N. cervinus* but the species herein studied would be different from the former. Until present, none of them could be identified based on COI gene sequences (they do not match with those of known species), or by morphology of the larvae (we did not obtain adult specimens of the parasitoid). This wasp was infected with the wNau5 strain, the same present in *N. cervinus*. This enforces the ongoing hypothesis that parasitoids are vehicles for *Wolbachia* horizontal transmission. The other parasitoid here reported belongs to the genus *Oestrophasia* within the family Tachinidae. The Tachinids gather several endoparasitoids of insects, and *Oestrophasia* is associated with some Neotropical broad-nosed weevils, e.g. *Oestrophasia sabroskyi* in *Artipus floridanus*. Until present we could not identify the species associated with N. cervinus. In this case, the parasitoid was not infected with *Wolbachia*.

June 21
12:00 PM
Session 5

Pollen flower classification: an evolutionary perspective

Melo L.R.F.[1,*], Vasconcelos T.N.C.[2] & Brito, V.L.G.[3]

[1]Postgraduate Program in Ecology and Conservation of Natural Resources - Institute of Biology, Universidade Federal de Uberlândia, Uberlândia, Minas Gerais, Brazil.
[2]Biological Sciences Department, University of Arkansas, Fayetteville, Arkansas, USA.
[3]Institute of Biology, Universidade Federal de Uberlândia, Uberlândia, Minas Gerais, Brazil. [*]Correspondence: lilian.melo@ufu.br.

"Pollen flower" is a term coined by Vogel in 1978 to describe flowers that present pollen as the only resource available for pollinators. Currently, it is estimated that over twenty thousand species of flowering plants present "pollen flowers". These flowers present a series of adaptations, especially in the male reproductive system, related to their close interaction with pollinators, mainly bees. In these flowers, pollen has a dual function, because it is important for both feeding the bees and for the plant's reproductive success. According to Vogel, there are three types of pollen flowers: Magnolian, Papaver and Solanum. In this work, we aim to understand if the floral types created by Vogel are enough to classify the entire diversity of pollen flowers in angiosperms or if it is necessary to create a new classification including more traits and considering more species. First, a review was made of all flowering plant families following the APG IV and considering the five traits listed by Vogel: number of stamens, floral visitors, anther dehiscence, pollen release and visitor behavior. Second, an analysis of ancestral character reconstruction was performed to map how many times pollen flowers appeared in the evolutionary history of angiosperms. Third, a morphospace analysis was performed using the original traits described by Vogel to check how the species are grouped using a Nonmetric Multidimensional Scaling (NMDS). This analysis was then repeated including new traits (e.g., petal's position, stamen dimorphism, single flower or inflorescence, "buzz pollination + longitudinal anthers", fixation of anthers) and contrasted with the first analysis. Pollen flowers were identified in 71 of the 420 families recognized in the APG IV. Next, we expanded the pollen flower categorization to all species reviewed and use the morphospace comparison to see if the original categorization proposed by Vogel was sufficient or not. We believe that by including new traits, species will be grouped differently because Vogel's classification did not consider important floral traits that had been little studied or were not known at the time. Given the increasing in knowledge on plants' biodiversity and their relationship with pollinators, a reclassification of "pollen flowers" is necessary for a better understanding of both their ecology and evolutionary history.

Replaying life's tape: determinism in Pantropical ant-plant mutualisms

June 21
12:00 PM
Session 5

Probst R.S.[1,*] & Longino J.T.[1]

[1]School of Biological Sciences, University of Utah, Salt Lake City, UT, United States.
[*]Correspondence: probstrodolfo@gmail.com.

Natural selection can promote repeatable outcomes in evolution, contributing to the idea of evolutionary determinism in different biological systems. Obligatory ant-plant symbiotic interactions have evolved multiple times and involve a wide array of both ant and plant partners. The subfamily Formicinae comprises a major clade of ants, with around 3000 species globally distributed. Among that clade, several genera are dominant components in most terrestrial ecosystems. Also, within that subfamily, there are instances of arboreal lineages engaged in unique symbiotic associations with understory plants. Those lineages are distributed throughout different biogeographical boundaries, with plant-ants found pantropically. By taking advantage of an available dataset of enriched ultraconserved elements (UCEs), we applied phylogenomic analyses to understand the tempo and mode of the evolution of ant-plant mutualisms within Formicinae. Mapping of the mutualistic lineages revealed that formicine genera involved in highly symbiotic relationships with plants evolved at least three times independently in the rainforests from the African, Indomalayan, and Neotropical regions. Moreover, those distant-related lineages share an impressive phenotypic similarity, with their natural histories extensively overlapping. Interestingly, our diversification analyses using BAMM showed that the evolution of ant-plant symbioses does not correspond to quick shifts in diversification rates for those formicine lineages. Finally, our divergence timing analyses estimated the age of those independent evolutions of obligatory associations to be young (between 2-15 Ma) and highly concurrent. Taking it all together, we suggest that obligatory ant-plant symbiotic interactions in a major clade of ants are remarkable and relatively recent cases of extreme convergent evolution.

June 21
12:00 PM
Session 5

Why tropical plants can have small genomes? Genome size evolution in Cactaceae is shaped by geographically structured polyploidy

Rodrigez P.E.[1], Ameida E.[1], Costa L.[1], Amorim B.S.[2], Guignard M.S.[3], Carvalho-Sobrinho J.[4], Sader M.A.[1,*], Lopes S.[5], Mota L.[5], Loureiro J.[5], Leitch I.J.[3] & Souza G.[1,*]

[1]Laboratório de Citogenética e Evolução Vegetal, Universidade Federal de Pernambuco, Brasil. [2]Museu da Amazônia, MUSA, 69099-415 Manaus, Amazonas, Brazil. [3]Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3AB, UK [4]Laboratory of Plant Cytogenetics, Department of Biology, Federal Rural University of Pernambuco, Recife, Brazil.[5]Centre for Functional Ecology, Department of Life Sciences, University of Coimbra, Calçada Martim de Freitas, 3000-456 Coimbra, Portugal. [*]Correspondence: lgrsouza@hotmail.com.

Genome size (GS) displays a broad variation across land plants. Although it is considered to be influenced by selection pressures depending on different environmental conditions and life-history strategies, the underlying drivers of GS variation across lineages remain elusive. Latitude gradients of GS tend to show contrasting patterns among different plant groups, sampling and statistical approaches. A recent analysis suggested that niche conservatism in dry environments may be associated with bigger GS increase at higher latitudes. However, it is not clear how the extreme ecological conditions in these dry environments might play a role in driving GS evolution. We investigated GS evolution in the dry-climate specialized family Cactaceae, aiming to explore the relationship between GS and latitude as well as a range of cytogenetic and climatic variables. We used flow cytometry to generate original GS data for *Melocactus* and *Pereskia* species which together with GSs compiled from previous publications, resulted in data for 344 species belonging in 63 genera, including representatives in all the main Cactaceae lineages. 1C-values varied 14.31-fold, with high variability of GS was observed at the genus level for representatives of the Cactoideae II and Opuntioideae clades. Our comparative analysis revealed that these clades contain most of the Cactaceae polyploids that have been identified. Molecular clock analysis revealed that the Opuntoideae polyploid lineages are older than those in Cactoideae II, which is correlated with low monoploid GS (1Cx) values in the Opuntioideae paleopolyploids. A positive correlation was observed between 1C-values and latitude, with a tendency for species with larger genomes to occur more frequently at higher latitudes, associated to higher levels of polyploidy (up to 22x) in temperate regions. In contrast, the 1Cx vs. latitude relationship showed the complete opposite result, with a decrease in monoploid GS at higher latitudes, indicating that in the temperate regions the polyploids (mainly of Opuntioideae) have smaller amounts of DNA per monoploid chromosome set. Surprisingly, correlations between tested environmental variables and GS in the Cactaceae seem to be, in general, low. We believe that endoreduplication, such as in the epidermis, can enable diploid plants to physiologically act as a polyploid in certain tissues, masking the correlations between GS and temperature/ precipitation traits. Our data suggest that polyploidy (associated with processes such as gene duplication, asexual reproduction, nucleotype effects etc.), have played a role in contributing to the geographic distribution and diversification of Cactaceae lineages.

Poster Session 6: Bioinformatics and Molecular Ecology

June 21
5:00 PM
Session 6

Classification of dengue virus serotype 4 in biological groups using reverse immunodynamics

Villabona-Arenas L.S.[1*], Villabona-Arenas C.J.[2] & Lourenço J.[3]

[1]Industrial University of Santander, Bucaramanga, Colombia. [2]The Centre for the Mathematical Modelling of Infectious Diseases, London School of Hygiene & Tropical Medicine, London, England. [3]University of Oxford, Oxford, England. [*]Correspondence: LIZ.VILLABONA2@correo.uis.edu.co.

Identifying antigenic variation is a cornerstone of vaccine development as differences in antigenicity might lead to immune evasion. Dengue virus (DENV) serotypes are classified into genotypes that are delimited using genetic thresholds. However, it is currently unclear if these thresholds reflect differences in antigenicity. To identify signatures of antigenic variation between genotypes, we applied computational reverse immunodynamics methods that allow us to identify combinations of genetic loci that can be tested as potential targets of immune selection allowing us to classify virus variants into antigenic groups. For this, we collated 341 publicly available DENV-4 genomic sequences representing genotypes I and II that were sampled from 23 countries between 1953 and 2017. We quantified the association of alleles between pairs of loci using indexes from information theory, population genetics, and phylogenetics under the biological assumptions of the multilocus strain theory of host-pathogen systems. Among 5,740,966 possible combinations of loci across the DENV-4 genome, we identified 49 loci with a total of 131 combinations with a high degree of genetic discordance which is not likely due to common ancestry. These pairs of loci broadly recover the two genotypes and also show some additional degree of partitioning for genotype I, which appeared to have been exported to the American continent from Asia where it became the predominant combination of alleles. The majority of these loci (43 of 49) have been described as part of DENV epitopes in the literature, but six of them represent new candidate targets of immunity. We demonstrated that reverse immunodynamics can provide unique insights into the spatio-temporal patterns of DENV evolution. It further provides indirect evidence that DENV-4 genotypes might be antigenically discordant groups. We identified loci that can be potential targets of interest for vaccine development.

Comparative genomics scientific workflow for finding drug targets in protozoan neglected tropical diseases

June 21
5:00 PM
Session 6

Terra R.S.[1*] & Ocaña K.[1]

[1]National Laboratory for Scientific Computing, Petrópolis, RJ, Brazil. [*]Correspondence: rafaelst@lncc.br.

This work describes using a comparative genomics scientific workflow to find drug targets in protozoan-based neglected tropical diseases. To achieve this, we searched for specific cysteine proteases in the genomes of the protozoans, vectors and hosts found in online databases and created a scientific workflow to find possible drug targets including an analytical search in the literature for interpretation of the plausibility and supporting evidence of our results. The in silico workflow for comparative genomics conceptually was constructed to search for differences in pathogen/vector/host genomes that may be exploited for drug targeting. A workflow,in short, is like a computer relay race with each program running and then passing the resulting data to the next with each program (or racer) performing a function (i.e.,finding, eliminating, comparing) to get our target information. We applied the workflow to neglected tropical diseases isolating a biological component of interest,in this case, cysteine proteases (often involved in several essential life activities of organisms) in the genomes of the protozoans, vectors and hosts (downloaded from GOLD, MEROPS and PFAM online databases). To target a specific cysteine protease to cause an interruption in an essential function in the protozoan without interrupting the physiology of the vector, we identified cysteine proteases present in theprotozoan and absent or distant from those in their host. Our main conclusions are: Firstly, our work identified 9 novel cysteine proteases that show promise for drug targeting in several different neglected tropical diseases. Secondly, as mentioned above, our methodology can be applied to any biological component in which an online database is available. As such, it serves as a model for drug target search in comparative genomics experiments. Thirdly, and most importantly, the text and investigation is focused and directed towards non-computer experts (i.e.,researchers) and follows a series of steps, explanations for not only conducting this type of experiment, and also the analysis and interpretation of the results.

Diversification of *Prochilodus* in the eastern Brazilian Shield: Evidence from complete mitochondrial genomes (Teleostei, Prochilodontidae)

June 21
5:00 PM
Session 6

Santos R.P.[1,2,*], Melo B.F.[3], Yazbeck G.M.[2], Oliveira R.S.[4], Hilário H.[1], Prosdocimi F.[5] & Carvalho D.C.[1]

[1]Laboratório de Genética da Conservação, Programa de Pós-Graduação em Biologia dos Vertebrados, Pontifícia Universidade Católica de Minas Gerais, Belo Horizonte, MG, Brazil. [2]Laboratório de Recursos Genéticos, Programa de Pós-Graduação em Ecologia, Universidade Federal de São João del-Rei, São João del-Rei, MG, Brazil. [3]Departamento de Biologia Estrutural e Funcional, Instituto de Biociências, Universidade Estadual Paulista, Botucatu, SP, Brazil. [4]Programa de Pós-Graduação em Ciência da Computação, Universidade Federal de São João del-Rei, São João del-Rei, MG, Brazil;

[5]Laboratório de Genômica e Biodiversidade, Instituto de Bioquímica Médica Leopoldo de Meis, Universidade Federal do Rio de Janeiro, Rio de Janeiro, RJ, Brazil.
*Correspondence: rosianepsantos@ufsj.edu.br.

The Neotropical fish genus *Prochilodus* includes five species occurring in the main drainages of the eastern Brazilian Shield: *P. argenteus*, *P. costatus*, *P. lineatus*, *P. harttii*, and *P. vimboides*. Multi and single locus phylogenies have questioned the monophyly of *P. costatus* and *P. lineatus*, and the biogeographic history of these species in the Brazilian Shield has never been explored. We characterized new mitogenomes for these species to reconstruct their evolutionary history, estimated the timing of *Prochilodus* cladogenesis, and discussed the implications of past geologic events on species diversification. The phylogeny supports the monophyly of both *P. costatus* and *P. lineatus*, and indicates a Miocene divergence of *P. vimboides*, much earlier than subsequent species diversification. The Early Pleistocene split of *P. argenteus* and *P. harttii* (2.1 million years ago—MYA) is hypothesized to be related to recent Quaternary re-activations of the Rio Araçuaí Fault that promoted river captures between the eastern tributaries of the São Francisco basin and the upper Rio Jequitinhonha in the Serra do Espinhaço mountain range. The time- calibrated phylogeny also indicated a subsequent split of *P. costatus* and *P. lineatus* (1.1 MYA) likely due to Quaternary activities of the Upper Rio São Francisco crustal discontinuity and Estrela Fault that catalyzed river captures between the upper Rio São Francisco and the Rio Grande of the Paraná basin in the Serra da Canastra mountain range. These results provide a temporal context for the diversification of Prochilodus and bring new insights to further study the historical biogeography of other riverine fish groups along the upland basins of the eastern Brazilian Shield.

June 21
5:00 PM
Session 6

Genetic identification and labeling of fish: DNA Barcoding in the detection of mistakes, fraud, and environmental crimes

de Oliveira V.[1*]

[1]Universidade Federal de São Paulo, Santos, SP, Brazil. *Correspondence: vitoria.oliveira@unifesp.br.

Fish consumption has grown rapidly in recent years, due to its high nutritional value and increased production and commercialization. With the increase in demand for fishing resources, they become more scarce and economically valuable, motivating the adoption of commercial strategies that are not always correct. In this scenario, it is common cases as labels have incomplete and even misleading information. Several studies on mislabeling show the ecological and economic consequences, and even harm to consumer health. Consequently, it has become of paramount importance as identifications of food items at the species level. However, the processing of organisms results in a loss of many taxonomic characters that would make identifications based on morphological characters possible. Thus, thepresent study aims at genetic identification, using DNA barcoding with the COI gene(cytochrome oxidase I), in fresh, salted, frozen, and canned fish available to consumers in supermarkets in the city of Santos (São Paulo, Brazil). The data from these evaluations indicate that in 26% of the analyzed samples, incorrect labeling occurred and 20% of the companies were not following the marketing rules imposed by the ordinance. We unveiled the situation of the commercialization of the fish in Santos given the identification of misleading labels, we indicate a necessity for trade supervision. And the standardization of nomenclatures provide greater transparency in marketing.

Genomics of cycads' coralloid-root bacterial microbiome suggests adaptation from bacterial symbionts allowing holobiont to thrive in contrasting environments

June 21
5:00 PM
Session 6

Garfias-Gallegos D.[1], Cibrián-Jaramillo A.[1,*] & Barona-Gómez F.[1]

[1]Laboratorio Nacional de Genómica para la Biodiversidad, CINVESTAV, Carretera Irapuato-León No. Km 9.6, León-Irapuato, Irapuato, Guanajuato, 36824, México.
[*]Correspondence: acibrian@langebio.cinvestav.mx.

The relationships between eukaryotes and prokaryotes have played a pivotal role in the evolution of macrobes. Cycads are an ancient lineage of gymnosperms distributed in a myriad of environments around the globe. These plants develop a special organ called coralloid root where symbiotic bacteria thrive and which is considered a key trait for its survival. This bacterial microbiome can perform diverse processes for the plant by diverse metabolic functions encoded in their genomes as biosynthetic gene clusters (BGCs). BGC diversity is related to chemical-structural variations of their molecular products, resulting in different biological activities that can serve as adaptations for the holobiont. We chose *Dioon edule* as a model to search for the relationship between the environmental differences where cycads thrive (soil type and pH), and the coralloid root microbiome's genomic diversity (BGCs) across two contrasting environments. Using a culture-independent methodology, we found that Nostoc populations dominate over other bacterial lineages, contrary to previous observations. Differences in nitrogenase GCs and siderophore BGCs among the two environments suggest metabolic adaptation from the microbiome to the respective soil characteristics. Moreover, signatures of selection found in the dN/dS ratio point that differences in the BGCs genomic sequence can be the result of positive selection acting on critical parts of the cluster. A terrestrial-symbiotic Nostoc lineage comparison suggests that these changes in dN/dS ratio are not balanced by genetic drift, expected in obligate symbionts. Together, this evidence confirms the main role that bacterial populations have to help cycads in coping with the environment and holobioint adaptation to different niches.

June 21
5:00 PM
Session 6

Identification and functional annotation of hypothetical proteins of the *Bifidobacterium breve* genome

Santos R.S.[1], Freire R.B.M.[1], Alves J.T.C.[2], Veras A.A.O.[3] & Sá P.H.C.G.[1*]

[1] Federal Rural University of Amazonia (UFRA) Campus Tomé-Açu, Tomé-Açu, Pará, Brazil. [2] Pará State University (UEPA) Campus Marabá, Marabá, Pará, Brazil. [3] Federal University of Pará (CAMTUC-UFPA) Campus Tucuruí, Tucuruí, Pará, Brazil. [*]Correspondence: pablogomesdesa@gmail.com.

In recent years, the application of high-throughput sequencing has generated an increase in the genomes available in the databases. Because of this, there was also an increase in hypothetical proteins deposited. Functional identification of these proteins can lead to a better understanding of the biological processes and molecular functions that they can perform. Functional annotation can also lead to discoveries related to more recent structures and assist in the identification of new functions in target organisms of interest, such as Bifidobacterium breve, which represents a common member of the intestinal microbiota and its presence has been associated with the well-being of the host. Thus, this work aimed to perform the functional annotation of hypothetical proteins from the genome of Bifidobacterium breve strain DSM 20213 = JCM 1192. The reference genome used in this work is available in the public database (NCBI NZ_AP012324.1). The hypothetical proteins were extracted using the Artemis software v18.1.0. For functional annotation, the following were used: CDART and SMART to search for conserved domains; The CD-Search tool, which combines models based on multiple sequence alignments; And the ProtoNet software, which provides automatic hierarchical classification of protein sequences. Proteins were identified that are directly related to molecular functions, biological processes, and membrane components. A total of 273 hypothetical protein sequences were analyzed, among which, 28 presented significant results, and of these we can mention the BBBR_RS05180 sequence, which is involved in the direction of cells during hematopoiesis, also participating in biological processes such as the development of the nervous system. Another interesting sequence was BBBR_RS06455, which has the molecular function of selectively and not covalently interacting with peptidoglycan, in addition to participating in the immune response against potential internal or invasive threats. This work demonstrated the possibility of identifying functions for proteins that had no annotated function.

June 21
5:00 PM
Session 6

Phylogenomics and chloroplast genome evolutionary dynamics of Myrteae tribe

Carvalho L.R.[1,3], Nunes R.[1,3,4*], Targueta C.P.[2,3,4], Braga-Ferreira R.S.[1,3,4] & Telles M.P.C.[1,3,4]

[1]PPG em Genética e Biologia Molecular – Universidade Federal de Goiás. [2]PPG em Biotecnologia e Biodiversidade – Rede Pró-Centro-Oeste – Universidade Federal de Goiás. [3]Laboratório de Genética & Biologia Molecular – LGBio – Universidade Federal de Goiás. [4]Instituto Nacional de Ciência e Tecnologia – Ecologia, Evolução e Conservação da Biodiversidade (INCT - EECBio). [*]Correspondence: rhewter@ufg.br.

Myrteae is the most diverse tribe in Mytaceae family with many species of ecological or economic importance. However, some Myrteae species have not yet been included in molecular systematics studies. This is the case of the species *Eugenia klotzschiana*. Therefore, we assembled the *E. klotzschiana* chloroplast genome and, along with 44 others previously published Myrtales chloroplast genomes, we tested four different approaches to evaluate the phylogenetic reconstruction. We also mapped in the phylogeny events of loss and gain of genes in chloroplast genomes of the Myrteae tribe. *Eugenia klotzschiana* chloroplast genome was sequenced in Illumina MiSeq (600 cycles), assembled using NOVOPlasty and annotated using CHLOROBOX platform. Phylogenetic analysis were performed using two datasets: one containing standard phylogenetic gene markers (rbcL and matK) and the other containing 77 protein-coding sequences (CDS). These two datasets were used to reconstruct phylogenies using Bayesian (BI) and Maximum Likelihood (ML) methods, performed using MrBayes and MEGA, respectively. The best fit base substitution model used was "GRT+I+G" calculated on jModelTest. Consensus phylogenies were edited using Figtree. To verify the evolutionary dynamics of the Myrteae tribe, we compared six species available at NCBI: *Eugenia brasiliensis*, *Eugenia selloi*, *Eugenia uniflora*, *Eugenia piryformis*, *Plinia trunciflora* and *Rhodomyrtus tomentosa*. We observed that, regardless of the phylogenetic reconstruction method (BI or ML), the use of only standard marker genes generated phylogenies with a greater number of uncertainties, with some low consistency node values and some polytomies. Using the 77 CDS, we obtained the same tree topology for both BI and ML. The phylogeny that showed the best support values for the nodes was used to map losses and gains of genes in the chloroplast genomes of the six species Myrteae tribe. We observed events of loss of the trnG UCC and trnS-CGA genes, loss of introns, such as in petB, petD and rpl16 and the presence of pseudogenes between the species in Myrteae tribe. The results generated demonstrate that, in *Eugenia* for the intragender relations, the use of a larger number of regions can generate higher values of node reliability in phylogenetic analysis and that mapping genomic characteristics in phylogenies can be an advantage to evaluate the evolution of gain and loss of genes in chloroplast genomes. We also well-placed, for the first time, *E. klotzschiana* in a molecular phylogeny resolving its relationships.

Retrotransposition of genes in the B chromosome of *Psalidodon paranae* (Teleostei, Characiformes)

June 21
5:00 PM
Session 6

Lasmar L.F.[1,*], Silva D.M.Z.A.[1], Vidal M.R.[1], Oliveira C.[1] & Foresti F.[1]

[1]São Paulo State University - UNESP, Botucatu, São Paulo, Brazil. [*]Correspondence: lucas.lasmar@unesp.br.

Several eukaryotes have additional genomic elements called B chromosomes, which carry redundant genetic information already present in standard A chromosomes. For a long time, these elements were considered inert and were classified as intragenomic parasites. However, in the last years several protein coding genes were detected in these elements, among which some are actively expressed. The fish genus

Psalidodon harbors a great diversity of these elements, which were extensively investigated by classical cytogenetic methods. Recently, with the use of high throughput NGS methods, it was discovered that the B chromosome of *P. paranae* harbors several protein-coding genes, among which some are incomplete, pointing to the existence of pseudogenes copies on this chromosome. Thus, the present study aimed to investigate the structure of these genes on this B chromosome to check what class of pseudogenes they are. For this, we sequenced the genome and transcriptome of 0B and 1B individuals of *P. paranae* by Illumina. We then assembled the transcriptome of *P. paranae* to get the coding sequences using the Trinity software. Then, we mapped the genomic reads of 0B and 1B individuals to these coding sequences using the ssaha2 software. Curiously, several 1B reads mapped on the exon-exon junctions of five putative pseudogenes (cia30, g2e3, numa1, sbno2 and simc1), while 0B reads only mapped in the regions within exons. These results show that 1B individuals harbor genomic sequences in which the introns are lost, indicating the occurrence of retrotransposition processes, and that these sequences are present on the B chromosome, since they are exclusive of the 1B individuals. Previous studies have reported the presence of single retroinserted genes in B chromosomes, but here we present for the first time an evidence of several genes retrotransposed to the B chromosomes of a given species. These findings open the possibility of investigating the structure of these retrogenes with more advanced methods, such as the assembly of genomes at chromosome level.

The first chloroplast genome sequence of *Serjania erecta* Raldk. and comparative analysis within Sapindaceae plastomes

June 21
5:00 PM
Session 6

Corvalan L.C.J.[1], Targueta C. P.[1,2], Braga-Ferreira R. dos S.B.[1,3], Diniz-filho J.A.F.[1], Telles M.P. de C.[1,4] & Nunes R.[1,3*]

[1]PPG em Genética e Biologia Molecular – Universidade Federal de Goiás, Goiânia, Goiás, Brasil. [2]PPG em Biotecnologia e Biodiversidade – Rede Pró-Centro-Oeste – Universidade Federal de Goiás. [3]Instituto Nacional de Ciência e Tecnologia – Ecologia, Evolução e Conservação da Biodiversidade (INCT - EECBio). [4]Pontifícia Universidade Católica de Goiás, Goiânia, Goiás, Brasil. [*]Correspondence: rhewter@ufg.br.

Serjania is a genus from the Sapindaceae family that presents around 208 species. Some of them are described as having medicinal properties. This is the case of the species Serjania erecta. Despite its medicinal importance, little is known about its genetic and evolutionary aspects. Also, the phylogeny of the genus *Serjania* is still poorly resolved and has many uncertainties. Therefore, we sequenced and annotated the chloroplast genome of *S. erecta*, the first for the genus *Serjania*, and used it in a comparative analysis with other plastomas of the Sapindaceae family. We extracted DNA from leaves using the CTAB protocol and sequenced using Illumina MiSeq. The chloroplast genome of *S. erec*ta was assembled using NOVOPlasty v3.2 and annotated using CHLOROBOX platform. We used the following species for comparative analysis: *Acer buergerianum, Aesculus wangii, Dimocarpus longan, Dipteronia dyeriana, Dodonaea viscosa, Eurycorymbus cavaleriei, Koelreuteria* *paniculata, Litchi chinensis, Pometia tomentosa, Sapindus mukorossi, Xanthoceras sorbifolium.* We also reconstructed a plastome-based phylogeny involving 16 species of Sapindaceae and 7 other species as outgroups. We aligned the protein-coding genes using Mafft, to concatenate the alignments was performed in the Sequence Matrix and filtered alignment using GBlocks. The phylogeny was reconstructed using the IQ-TREE program with 1000 replicates. The chloroplast genome of *S. erecta* has a size of 159,297 bp, a quadripartite structure with two regions of single copy, the small single copy (SSC) and large single copy (LSC), divided by two inverted repeat regions (IRa and IRb). We identified a total of 132 genes and 2 pseudogenes (infA and ycf1), 87 of which are protein-coding genes, 37 tRNAs and 8 rRNAs. Among the genomes evaluated in the comparative analysis, the size ranged from 163,258 bp (*K. paniculata*) and 155,871 bp (*A. wangii*) and the number of genes between 132 (subfamilies Sapindoideae and Xanthoceratoideae) and 128 (*A. buergerianum* and *A. wangii*). The genes rpl22, rps3, rps19 are duplicated in the subfamily Sapindoideae which increased the size of the IRs in this group. In addition, the rps2 gene is pseudogenized in the subfamilies Hippocastanoideae and Xanthoceratoideae. The phylogenetic tree had well supported nodes within Sapindaceae and *Serjania* formed a clade with *Sapindus*, *Litchi*, *Dimocarpus*, and *Pometia* genera. The results obtained in this study provide the assembly and annotation of the chloroplast genome of *S. erecta*, the first annotation of a species of the genus. It also provides an idea of how chloroplast genomes evolved in the Sapindaceae family.

The mitochondrial genome of holoparasites of the family Balanophoraceae has been severely impacted by horizontal gene transfer

June 21
5:00 PM
Session 6

Roulet M.E.[1,*], Ceriotti L.F.[1,2] & Sanchez-Puerta M.V.[1,2]

[1]IBAM, Universidad Nacional de Cuyo, CONICET, Facultad de Ciencias Agrarias, Almirante Brown 500, M5528AHB Chacras de Coria, Mendoza, Argentina. [2]Facultad de Ciencias Exactas y Naturales, Universidad Nacional de Cuyo, Padre Jorge Contreras 1300, M5502JMA Mendoza, Argentina. [*]Correspondence: meroulet@mendoza-conicet.gob.ar.

Plant vascular connections established in a host-parasite relationship allow the passage of water, nutrients, and nucleic acids. This intimate contact promotes the exchange of genetic information between unrelated species, a process named Horizontal Gene Transfer (HGT). Plant mitochondrial genomes (mtDNAs) are frequently impacted by HGT. We deciphered the mtDNA of the holoparasitic angiosperm *Lophophytum leandri* (Balanophoraceae). This plant grows in Argentina, parasitizing roots of the mimosoid legume *Parapiptadenia rigida* (Fabaceae). The *L. leandri* mtDNA is 806,114 bp long and has a multichromosomal structure consisting of 50 circular chromosomes (5-72 kb in length). This multipartite genome was recently described in the relatives *L. mirabile* and *Ombrophytum subterraneum*. Similarity searches revealed 46.37% of shared regions between the mtDNA of *L. mirabile* and *L. leandri*. The *L. leandri* mtDNA carries 3 ribosomal RNA genes, 6 transfer RNA genes, and 35 protein-coding genes that represent 7.25% of the genome and are distributed across 23 chromosomes. The remaining 27 chromosomes are devoid of any identifiable coding region. Comprehensive phylogenetic analyses showed that L. leandri harbors 5 foreign and 15 chimeric mitochondrial protein-coding genes as a result of HGT from its legume hosts. To unveil the overall impact of HGT in the *L. leandri* mtDNA, we performed BLASTn searches against angiosperm mtDNAs. The *L. leandri* mtDNA presents 48.3% foreign sequences acquired from legumes and 31.9% native DNA, while 19.6% remains undetermined, as it is not similar to any other angiosperm mtDNA. The availability of the *L. leandri* mtDNA permitted a genus-wide evolutionary assessment. The analyses uncovered the presence of 19 chimeric genes in *L. mirabile*, representing almost half (43.18%) of the protein-coding genes. Besides, we found evidence for ancient HGT events in which foreign mitochondrial genes or regions were acquired before the divergence of *L. mirabile* and *L. leandri.*

Poster Session 7: Phylogenetic Methods and Biogeography

Accuracy of phylogenetic inference from quantitative traits under parsimony

June 22
12:00 PM
Session 7

Tagliacollo V.A.[1,*], Pinna M.[1] & Datovo A.[1]

[1]Museu de Zoologia da Universidade de São Paulo, São Paulo, SP, Brazil.
[*]Correspondence: vatagliacollo@gmail.com.

Quantitative traits constitute an important source of evolutionary information often overlooked in cladistic studies. These data can be analyzed without subjective discretization, thus avoiding biased choices in delimiting categorical character states. However, the ability of continuous characters in correctly inferring species relationships is still incompletely understood, especially when matrices are analyzed under parsimony. This study evaluates the overall accuracy of phylogenetic inferences from continuous traits using simulations under three continuous-time processes and subsequent analyses of parsimony in TNT with Equal Weighting (EW) and Implied Weighting (IW) schemes with multiple k values (1-10). We generated 100 trees to simulate 1,500 matrices including 26 terminals and 100 continuous characters evolving along branch lengths under Brownian-Motion (BM), Ornstein-Uhlenbeck (OR) and Early-Burst (EB) models with various parameters. Comparisons of cladogram reconstruction accuracy using Robinson-Foulds distances (RF) reveals that matrices of continuous traits analyzed by parsimony carry evolutionary signals sufficient to infer species relationships. The overall accuracy of cladogram reconstructions is significantly higher from character matrices simulated with the BM model, regardless of the sigma2 rate parameter. Implementation of IW with any k value did not substantially interfere in tree inferences across all simulations. Continuous traits show higher accuracy to resolve relationships of internodes closer to the terminals, when compared to those more deeply located. Our simulations provide controlled tests of the effectiveness of quantitative traits in tree inferences by parsimony and highlight the importance of model adequacy in estimating shallow nodes in phylogenetic trees.

Evolutionary analysis of the heart ventricle of Characiformes and Siluriformes (Teleostei: Otophysi) by stochastic character mapping

June 22
12:00 PM
Session 7

Gardinal M.V.B.[1,*], Roxo F.[1,2], Dal-Pai-Silva M.[2], & Benine R.C.[1]

[1]Institute of Biosciences of UNESP, Department of Biosciences, Plant Biology, Parasitology and Zoology, Botucatu Campus. [2]Institute of Biosciences of UNESP, Department of Structural and Functional, Botucatu, São Paulo, Brazil Campus.
[*]Correspondence: mario.buzete@unesp.br.

The teleost heart is composed of six anatomical components arranged in series. Among them, the ventricle stands out for presenting considerable morphological variations related to its external anatomy, myocardial arrangements (i.e., myoarchitecture), and coronary vessel distribution. One of the ventricle classification systems considers the presence or absence of a compact external layer in the myocardium, its thickness, and the penetration level of the coronary vessels, which allows grouping the ventricle into four main types (I – IV). Although this classification is a tool that, at some level, enables inferences about the evolution of ventricular morphology in teleosts, no analysis using comparative phylogenetic methods has been carried out so far. Thus, the present study represents the first attempt to apply comparative phylogenetic methods on the ventricular traits to understand its evolution in neotropical lineages of Characiformes and Siluriformes. For this purpose, it were mapped the ventricular traits on a phylogeny proposed with Ultra Conserved Elements of DNA (UCEs) by SIMMAP software to provide a relevant historical framework on ventricular evolution. We used 11 species of Characiformes and nine species of Siluriformes, and anatomical and histological techniques described the morphological traits. All Characiformes studied presented a pyramidal ventricle, mixed myocardium, and coronary vessels restricted to the compact layer (Type II ventricle). This morphology was well-preserved in Characoidei taxa showing different phylogenetic position and occurred independently of the swimming habit. In Siluriformes, the ventricular anatomy was rounded in all species, but the myoarchitecture and vascularization were variable. Overall, our morphological observations and SIMMAP results strongly suggest the pyramidal type II ventricle as the ancestor condition in the clade (Characoidei + Siluriformes). We suggest that since the split of these groups at 100Ma, the Characoidei lineage would maintain the ancestral ventricular morphology and their active lifestyle in lotic environments. On the other hand, Siluriformes widespread worldwide increased the range of lifestyles and, consequently, the possible forms of myocardium arrangements and vascularization in the ventricle.

June 22
12:00 PM
Session 7

Integrative dataset enlightens systematic of Epyrinae (Hymenoptera, Bethylidae)

Colombo W.D.[1,*], Tribull C.M.[2], Waichert C.[3] & Azevedo C.O.[1]

[1]Universidade Federal do Espírito Santo, Vitória, Espírito Santo, Brazil. [2]Farmingdale State College, Farmingdale, New York, USA. [3]Universidade Vila Velha, Vila Velha, Espírito Santo, Brazil. [*]Correspondence: wesleycolombo@gmail.com.

Epyrinae are one of the most speciose subfamilies in Bethylidae (commonly known as the flat wasps). A total evidence phylogeny of Epyrinae is reconstructed by using Bayesian inference with the genes 18S ribosomal 1 (RNA18S1), 28S ribosomal 1 (RNA28S1), mitochondrially encoded 16S rRNA (MT-RNR2), mitochondrially encoded cytochrome c oxidase I (MT-CO1), and mitochondrially encoded cytochrome b (MT-CYB), along with 232 morphological characters. This is the first phylogenetic study to examine all 42 epyrine genera, including junior and senior synonyms and extinct taxa. In total, this study considered 195 terminal taxa, with 175 as ingroup taxa and 20 as outgroup. The resulting total evidence tree recovered *Anisepyris*, *Bakeriella*, *Calyozina*, *Chlorepyris*, *Disepyris*, *Laelius*, and *Trachepyris*

as monophyletic, whereas *Formosiepyris*, *Epyris*, and *Holepyris* were not. Our results uncovered two new genera and revalidated six genera, with five of them junior synonyms of *Epyris* and one of *Holepyris*. Sixteen new synonyms of genera are also proposed. In addition, the most broadly used diagnostic character, the mesoscutum-mesoscutellar suture, was mapped onto the morphological parsimony implied weighted tree and shown to be homologous within the lineages. We provide a checklist of all species of Epyrinae, analyzed via direct observation of the type, illustrations, or literature. Finally, we split Epyrinae into 17 genera, allocating 962 species within the subfamily.

Phylogenetic analysis of Foot-and-mouth disease in Mar Chiquita- Argentina

June 22
12:00 PM
Session 7

Lozano L.C.[1*], Cabanne G.S.[2], Aznar N.[3], Marcos A.[4] & König G.A.[1]
[1]Instituto de Agrobiotecnologia y Biologia Molecular (IABIMO) INTA-CONICET, Castelar, Buenos Aires, Argentina. [2]Museo Argentino De Ciencias Naturales "Bernardino Rivadavia"-CONICET, CABA, Buenos Aires, Argentina. [3]Instituto de Patobiologia INTA-CONICET, Castelar, Buenos Aires, Argentina. [4]Servicio Nacional de Sanidad Animal y Calidad Agroalimentaria (SENASA), CABA, Buenos Aires, Argentina. [*]Correspondence: Lozano.laura@inta.gob.ar.

Foot-and-mouth disease is a highly contagious disease that affects cloven-hoofed animals. There are seven serotypes distributed around the world and it produces high economic losses. Its causal agent is a picornavirus of approximately 8500b, single chain, member of the aphthovirus family. In some areas of the world, this disease is endemic. Nevetheless, in South America, most countries are free (applying vaccination or not) of it. At present, Argentina is considered a free zone. However, in 2001, the country was the focus of an important epidemic that left data and samples available for subsequent epidemiological analysis. The objective of this work is to propose possible routes of virus transmission in a district of the Province of Buenos Aires (Mar Chiquita), Argentina. Epidemiologically representative field samples were selected from 21 farms located in the Mar Chiquita district, which had a positive diagnosis by PCR and serology for a particular virus strain (A/Argentina/2001). In the NSB4OIE biosafety SENASA laboratory, the samples were inactivated with Trizol® and transferred to the Institute of Agrobiotechnology and Molecular Biology (IABIMO) for subsequent RNA extraction and synthesis of cDNA. Later, all genome was amplified by PCR with high fidelity enzymes and the amplicons were sequenced by the Sanger technique. Based on the generated sequences, different analyzes were carried out through networks and phylogenetic trees using methodologies such as maximum likelihood and parsimony. Finally, the results were compared with epidemiological analyzes and possible hypotheses about routes of viral transmission were proposed. Firstly, we observed that the population with the highest prevalence of the disease was animals whose ages ranged between 1 and 2 years. In a context of coincidence among the phylogenetic analyses, it was possible to observe the formation of three local transmission clusters inside the Mar Chiquita district. Finally, it was possible to identify the existence of long geographical distances between pairs of very similar sequences. We can conclude that the

Mar Chiquita district had at least three independent introduction routes. Furthermore, the route of contagion through aerosols would not be the main spread route of the virus among cattle herds. Alternatively, due to the low correlation between geographic and genetic distances, a virus dispersal of the virus by non-replicating vectors is proposed, for example, by machinery, water, and human transport.

June 22
12:00 PM
Session 7

Phylogeny of the species of the genus *Celtis* (Cannabaceae) of southern South America: morphological and molecular evidence

Chamorro D.C.[1,2,*], Mogni V.Y.[1], Zamengo H.B.[3], Oakley L.J.[1], Ortiz J.P.[2] & Prado D.E.[1,2]

[1]Cátedra de Botánica, Facultad de Ciencias Agrarias, UNR, Zavalla, Santa Fe, Argentina. [2]IICAR (Instituto de Investigaciones en Ciencias Agrarias de Rosario), CONICET (Consejo Nacional de Investigaciones Científicas y Técnicas), Facultad de Ciencias Agrarias, UNR, Zavalla, Santa Fe, Argentina. [3]Escola Nacional de Botânica Tropical, Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Rio de Janeiro, Brasil.
[*]Correspondence: chamorro@iicar-conicet.gob.ar.

The genus *Celtis* (Cannabaceae) comprises around 70 temperate to tropical woody species, commonly known as hackberries. In southern South America it is represented by around ten taxa (all belonging to the subgenus *Mertensia* Planch.) restricted to the Domain of Neotropical Seasonally Dry Forests, and the subtropical Chaco and Espinal biogeographical regions. The latter species present significant inter- and intraspecific morphological variability and similarity that has generated widespread taxonomic confusions. This work aimed was to study the phylogeny of some species of the genus *Celtis*, with morphological characters and DNA sequences combined, as well as the main morphological features to improve taxonomic circumscriptions. Twenty-nine specimens representing seven taxa of *Celtis* and five outgroup accessions were included. Twenty vegetative and reproductive morphological characters were selected based on previous works. The nuclear FA16180b marker was amplified and sequenced. The sequences were aligned using Mega 6.06, through ClustalW v1.8. The data were analyzed under the parsimony optimality criterion using the program TNT. This group of *Celtis* species resulted as monophyletic, although there is no clear resolution between these taxa. Nevertheless, six species of southern South America Celtis are recognized. As regards *C. pallida* (with its two varieties), a polytomy of specimens was observed; however, it differentiates clearly from the rest of the species. Meanwhile, *C. tala*, *C. chichape* and *C. clausseniana* do not form a clade but are visibly separated from the rest of the species. A defined clade formed by *C. serratissima* and *C. spinosissima* differentiates from the rest. The characters that have the greater correspondence with the formed groups were: growth habit, type of spines, type of styles, type of foliar margin, indument of the foliar veins and, pyrene ornamentation. Except for the hygrophilous *C. chichape*, the other five species are confined to well-defined biogeographical regions, thus coinciding with its distribution in the phylogenetic tree.

Taxonomy and complete plastid genome of the genus *Etlingera* (Zingiberaceae) including a remarkable new endemic species

June 22
12:00 PM
Session 7

Naive M.A.K.[1,2,3,*], Demayo C.G.[3] & Yu W.-B.[1,4]

[1]Center for Integrative Conservation, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Mengla, China. [2]University of Chinese Academy of Sciences, Beijing, China. [3]Department of Biological Sciences, College of Science and Mathematics, Mindanao State University-Iligan Institute of Technology, Lanao del Norte, Philippines. [4]Southeast Asia Biodiversity Research Institute, Chinese Academy of Science, Yezin, Nay Pyi Taw 05282, Myanmar. *Correspondence: arciinaive19@gmail.com.

Zingiberaceae are well known for their medicinal and economic significance across the world yet remained poorly known and studied and unfortunately considered one of the most threatened plant families in the Philippines. Such is the case for the genus *Etlingera*, where its taxonomy and nomenclature are much disputed particularly for several species in the archipelago that have been studied very little for over a century. Here, we report the seven newly sequenced *Etlingera* plastomes obtained through genome skimming using next generation sequencing. All plastomes displayed a typical quadripartite structure and their size ranges from 163,615–164,641 bp which encoded 113 different genes (80 protein-coding, 30 tRNA, and four rRNA genes) with 36.1% GC content. Gene content, gene order, and GC content were highly similar among these genomes. The maximum likelihood tree of the seven *Etlingera* within the family showed that plastomes can be used as a super-barcode to identify *Etlingera* spp. and provides an important reference and solid foundation in the establishment of species identification and phylogeny of Zingiberaceae. In addition, recent fieldwork in Mindanao resulted in the discovery of a new species (*Etlingera dostseiana* Naive, Demayo & Alejandro) and a new species record (*E. pilosa* A.D.Poulsen & Docot).

What's the matter with the Fire-Eye Tetra *Moenkhausia sanctaefilomenae*? Unraveling the upper Paraná River basin diversity, Southeastern Brazil

June 22
12:00 PM
Session 7

Reia L.[1,*], Oliveira C.[1] & Benine R.C.[1]

[1]Instituto de Biociências de Botucatu, Universidade Estadual Paulista, Botucatu, São Paulo, Brazil. *Correspondence: laisreia@yahoo.com.br.

The genus *Moenkhausia* comprises 98 species and belongs to the hyperdiverse family Characidae, a group of freshwater fishes widely distributed in the Neotropical Region. Although *Moenkhausia* cannot be asserted as monophyletic, a subgroup of four species is inferred as so based on their distinctive color pattern, named *Moenkhausia oligolepis* group. This group comprises the popular Fire-Eye Tetra *Moenkhausia sanctaefilomenae* known from the Parnaíba, São Francisco, Tocantins, and upper Paraná river basins, and the remarkably similar species *M. oligolepis*, known from coastal rivers of Guyana and Mearim, Amazon, Orinoco, and Paraguay River basins; *Moenkhausia australis*, from the La Plata River basin and upper Madeira River basin (Amazon basin); and *M. forestii*, from the upper Paraná, Paraguay, and upper Madeira River basins. These species are well diagnosable except for populations from the upper rio Paraná, commonly identified as *M. sanctaefilomenae*, that present features of both *M. australis* and *M. sanctaefilomenae* (from Parnaíba River, its type locality), raising doubts on the limits of these species. Therefore, our main goal was to determine if samples from the upper rio Paraná are genetically closer to *M. australis* or to *M. sanctaefilomenae.* For this, we ran a maximum likelihood analysis using sequences of the gene cytochrome oxidase subunit I (COI) of nine species of *Moenkhausia*, including all species of the *Moenkhausia oligolepis* group, and putatively close-related species. Our results showed that samples from the upper rio Paraná are genetically closer to *M. australis*, whereas the lineages of *M. sanctaefilomenae* from Parnaíba and São Francisco river basins clustered with *M. oligolepis.* Therefore, we conclude that *M. sanctaefilomenae* is restricted to the Parnaíba and São Francisco river basins, with only *M. australis* and *M. forestii* occuring in the upper rio Paraná basin.

Poster Session 8: Phylogenomics, Biogeography, and Phylogeography

A phylogenetic network-based experiment for the identification of reticulation events in Brazilian Dengue

June 22
5:00 PM
Session 8

Terra R.S.[1], Carvalho D.[2], Osthoff C.[1], Garcia-Zapata M.[3] & Ocaña K.[1*]

[1]National Laboratory for Scientific Computing, Petrópolis, Rio de Janeiro, Brazil. [2]Federal Centre for Engineering Studies and Technological Education, Rio de Janeiro, Brazil. [3]Federal University of Goiás (UFG), Goiânia, Brazil. [*]Correspondence: rafaelst@lncc.br.

The tropical climate makes Brazil susceptible to the cocirculation of different arboviruses, such as Dengue (DENV), Chikungunya (CHIKV), Zika (ZIKV), and SARS-CoV-2. Given its large population, Brazil had 2,241,974 cases of Dengue in 2019, 70% of the total reported, and more than half of all deaths from this disease. To date, there is no effective vaccine or specific antiviral therapy for dengue. The four DENV antigenically related types are known to be genetically distinct from each other, and each one has genetic variations classified as subtypes or genotypes. DENV-2 was the most prevalent serotype in several outbreaks in the Americas, followed in sequence by DENV-3, DENV-1, and DENV-4. Phylogenetic networks can exhibit evolutionary and reticulated events observed in viruses due to the high diversity mediated by a high mutation rate and frequent homologous recombination, leading to antiretroviral resistance and immune evasion. This study aims to investigate the presence of reticulation events of complete genomes of DENV serotypes present in Brazil through the analysis of phylogenetic networks. We downloaded complete DENV genomes of Brazil from GenBank with keywords "(complete genome dengue virus type 1) AND brazil". GenBank searches returned 50, 67, 87, and 58 genomes for DENV-1 to DENV-4, respectively. After this initial search, we selected genomes with "human" as host, reducing our data to 39, 58, 77, and 57 genomes. After preliminary computational tests for processing phylogenetic networks, we decided to reduce the number of genomes to 12, 8, 6, and 7 genomes for DENV-1 to 4, using CD-HIT with a threshold of 0.99. The sets of viral dengue genes we analyzed were annotated through the FLAVi pipeline. The initial search for recombination in dengue virus was conducted using parsimony analysis in PhyloNet Version 3.8.2 and maximum pseudo-likelihood in PhyloNetworks. All maximum likelihood trees used here were constructed with the test version 8 of RAxML. Our parsimony and likelihood analyses provide evidence for networked evolution among dengue viruses of two possible hybridization events. However, previous studies from the viral envelope (E) gene observed evidence of recombination in DENV-1 and no good evidence for recombination in the other dengue serotypes or genes. The method described here is actually a simplification of one in which all gene sequences in each dengue data set are used and where two different tree topologies are fitted for identifying each possible breakpoint.

June 22
5:00 PM
Session 8

Finding subtleties: DNA barcoding of two orchid bees from the viridis group

Feitosa-Santos D.C.[1*], Frantine-Silva W.[2], Kotelok-Diniz T.[3], Sofia S.H.[3] & Augusto S.C.[1]

[1]Federal University of Uberlândia, Uberlândia, Minas Gerais, Brasil. [2]State University of Northern of Rio de Janeiro, Campos dos Goytacazes, Rio de Janeiro, Brasil. [3]State University of Londrina, Londrina, Paraná, Brasil. [*]Correspondence: danilocrisfs@gmail.com.

The Euglossini tribe contains approximately 240 species distributed in five genera, including *Euglossa* that holds 54% of the described species. In this species matrix, few are the cases such as the one seen in *Euglossa azurea* and *Euglossa viridis.* This pair of species are morphologically similar to each other, with a diffuse distribution pattern throughout the Amazon Forest, Atlantic Forest, and Brazilian Savanna (Cerrado). Considering the relationship of these bees and their habitat, as well as their truncated taxonomic history, we tested the hypothesis of *E. azurea* and *E. viridis* constituting distinct taxonomic entities. We analyzed 627 bp of the mitochondrial gene cytochrome c oxidase I (COI) from 7 and 6 individuals of each species and other 4 COI sequences from closely related species available in the GenBank. We evaluate the genetic distances based on the Kimura-2-parameter (K2P), observing the distance patterns found for the *Euglossini* species as a baseline parameter. Our findings pointed out a significant difference between *E. azurea* e *E. viridis* species, indicating that specimens from Cerrado belong to *E. azurea* and samples from the Atlantic Forest *Euglossa* cf. *viridis.* This study contributes to the correct recognition of the taxonomic status of these species in the Cerrado region of Triângulo Mineiro and provides important pieces of information about biogeography of Euglossine bees in Brazilian savanna that help in the development of future conservation strategies for these bees.

June 22
5:00 PM
Session 8

Modeling a workflow for the construction of phylogenetic networks in the high performance computing environment

Terra R.S.[1*], Osthoff C.[1], Ocaña K.[1] & Carvalho D.[2]

[1]National Laboratory for Scientific Computing, Petrópolis, Rio de Janeiro, Brazil. [2]Federal Centre for Engineering Studies and Technological Education, Rio de Janeiro, Brazil[*]Correspondence: rafaelst@lncc.br.

Phylogeny refers to the evolutionary history and relationship between biological lineages related by common descent. Phylogeny term also embodies the methodology of reconstructing these relationships. In viral phylogeny, deep insight into virus evolution, metabolic aspects of virus life cycles, and interactions with hosts are required for reconstructing parameters of major evolutionary events that promoted the virus origin and spread. Virus phylogeny can be inferred using genomes or distinct genes under standard assumption in phylogenomics. The condition of each analyzed data set has a uniform phylogeny may be violated due evolved mechanisms of genetic

exchange (homologous recombination) between closely related viruses. In phylogenetics, recombination may be revealed through incongruence of trees in regions of genomes with occurrence of recombination. Reticulate evolution refers to the origination of lineages through the complete or partial merging of ancestor lineages. Networks may be used to represent lineage independence events in non-treelike phylogenetic processes. In terms of information through reticulate evolution, genetic recombination entails the splitting and rejoining of two unrelated or distantly related DNA to form a new DNA. As the recombinant sequence is a merger of two evolutionary histories, such a process cannot be modeled by trees. Instead, a phylogenetic network representation of a recombination event is needed. The methodology for reconstructing networks is still in development. Here we explore two methods for reconstructing unrooted phylogenetic networks, PhyloNetworks and Phylonet, which employ computationally expensive and time consuming algorithms. The construction of phylogenetic networks follows a coordinated processing flow of data sets analyzed and processed by the coordinated execution of a set of different programs, packages, libraries or pipelines, called workflow activities. In view of the complexity in modeling network experiments, the present work introduces a workflow for phylogenetic network analyses coupled to be executed in High-Performance Computing (HPC) environments. The workflow aims to integrate well-established software, pipelines and scripts, implementing a challenging task since these tools do not consistently profit from the HPC environment, leading to an increase in the expected makespan and idle computing resources. At first, we draw a straightforward workflow without optimization to create phylogenetic networks aiming to observe the performance of the employed tools. Parsl -a scalable parallel programming library for Python- was used to orchestrate the flow activities. This integration shows overperformed result executions of the workflow, also with better management of HPC resources, enabling us to scale our phylogenetic studies.

Native and foreign proteins conform the OXPHOS complexes of *Lophophytum mirabile* (Balanophoraceae)

June 22
5:00 PM
Session 8

Gatica-Soria L.M.[1*], Ceriotti L.F.[1] & Sanchez-Puerta M.V.[1,2]
[1]IBAM-CONICET, Facultad de Ciencias Agrarias (UNCUYO), Chacras de Coria, Mendoza, Argentina. [2]Facultad de Ciencias Exactas y Naturales (UNCUYO), Ciudad de Mendoza, Mendoza, Argentina. [*]Correspondence: leogatica1018@gmail.com.

The intimate contact between the holoparasitic plant *Lophophytum mirabile* (Balanophoraceae) and its host plant (Mimosoideae, Fabaceae) facilitates the exchange of genetic information, increasing the frequency of horizontal gene transfer (HGT). *Lophophytum* has revealed the unprecedented acquisition of a large number of mitochondrial genes from its legume host that replaced the native homologs. These foreign genes are functional and encode proteins that form multi-subunit enzyme complexes together with proteins of nuclear origin. For all these reasons, *Lophophytum* is an interesting model to study the evolution of multiprotein complexes in the mitochondria, the impact of HGT in the nuclear genome, and its co-evolution with the mitochondrial genome. Given the presence of foreign mitochondrial proteins in

Lophophytum, it is proposed that nuclear genes that encode proteins involved in these complexes are also foreign, minimizing the incompatibilities in the assembly and functioning of these multiprotein complexes. Multiple alignments were generated from nucleotide sequences of 25 angiosperms to infer the phylogenetic relationships of 75 nuclear genes (obtained from the *Lophophytum* transcriptome) involved the oxidative phosphorylation system (OXPHOS) of *Lophophytum*. Maximum likelihood phylogenetic analyses were ran with RAxML 8.2.11 using GTRGAMMA models along with 1,000 rapid bootstrapping pseudo-replicates. To examine gene conversion events within genes we used Geneconv. Based on these results, we infer that 74 subunits are native and one is foreign (SDH3) as a result of HGT from mimosoid hosts. These results reflect that the OXPHOS of *Lophophytum* is exceptional due to the presence of foreign (mostly encoded in the mitochondrial genome) and native (mostly encoded in the nuclear genome) subunits, generating new questions about the evolution and physiology of this parasitic plant. It is possible that the interactions between native and foreign proteins do not generate incompatibilities in the assembly and functioning of OXPHOS due to the low rate of evolution of mitochondrial genes in angiosperms. In contrast, the higher divergence among angiosperm nuclear genes would cause a negative effect on OXPHOS activity if foreign genes replace the native homologs.

June 22
5:00 PM
Session 8

Phylogenomics of Hemidontidae (Ostariophysi: Characiformes)

Nogueira A.F.[1*], Oliveira C.[2], Langeani F.[3] & Netto-Ferreira A.L.[4]
[1]Universidade Federal do Pará and Museu Paraense Emílio Goeldi, Belém, PA, Brazil.
[2]Universidade Estadual Paulista “Júlio de Mesquita Filho”, Botucatu, SP, Brazil.
[3]Universidade Estadual Paulista “Júlio de Mesquita Filho”, São José do Rio Preto, SP, Brazil. [4]Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil.
[*]Correspondence: acacio.freitas89@gmail.com.

The South American characiform family Hemiodontidae comprises five genera and 33 species. The family lacks comprehensive phylogenetic hypotheses resolving its monophyly and most of its intra-familial relationships. The few studies that addressed these questions exhibited a narrow taxon sampling and/or used single-locus markers. Even so, well-known morphological traits in some members of the family have been used to propose interrelationships among taxa. Therefore, here we used ultraconserved elements (UCEs) to provide the first molecular phylogenetic hypothesis for hemiodontids encompassing all its genera and most species (26 out of 33). We surveyed a total of 1,286,841 base pairs (bp) and 2,508 UCE loci with mean locus size of 513 bp (range = 100–1,577). We generated matrices of 70% and 90% UCEs completeness to explore the role of missing data on phylogenetic reconstruction. Phylogenetic inferences were based on maximum likelihood, Bayesian and species tree analyses on both complementary matrices. We used nine species from related characiform families as outgroups. In all phylogenetic methods on both complementary matrices we recovered the monophyly of Hemiodontidae, as well as the genera *Argonectes* and *Bivibranchia*, with maximum statistical support.

The genera *Anodus* and *Hemiodus* were not monophyletic because *Anodus elongatus* was sister to the monotypic *Micromischodus* instead of *A. orinocensis*, and *H. immaculatus* did not form a clade with its other congeners, but was sister to the *Anodus* and *Micromischodus* clade. Conversely, all remaining species of *Hemiodus* were placed together into a monophyletic group, where they were arranged into four major subclades. The sequence of diversification in the family is summarised as: (*Bivibranchia* + (*Argonectes* ((*H. immaculatus* + *Anodus* + *Micromischodus*) + *Hemiodus* clade))), in discordance with the morphological classification that placed all genera monophyletic and resolved the family as: ((*Anodus* + *Micromischodus*) + (*Hemiodus* + (*Argonectes* + *Bivibranchia*))). Considering all this, we propose the synonymization of *Micromischodus* and *Hemiodus immaculatus* to *Anodus.* Our results showed some concordance with mitochondrial studies of hemiodontids, especially in intra-generic relationships and recognition of undescribed species. We discussed putative origins and evolution of conspicuous morphological traits of the family and cast light on future solutions for the non-monophyletic genera considering the use of shared derived morphological characters.

Phylogeny, morphology, and biogeography of *Myrcia* sect. *Aguava* (Myrtaceae)

June 22
5:00 PM
Session 8

Lima D.F.[1*], Goldenberg R.[2] & Lucas E.[3]

[1]Universidade Federal de Santa Catarina, Florianópolis, Santa Catarina, Brazil. [2]Universidade Federal do Paraná, Curitiba, Paraná, Brazil. [3]Royal Botanic Gardens, Kew, UK. [*]Correspondence: duaneflima@gmail.com.

Myrcia (Myrtaceae) is a large Neotropical genus, including ca. 800 species currently divided into nine sections. *Myrcia* sect. *Aguava* is one of most complex groups of *Myrcia* due its extensive distribution range, from the Caribbean to southern Brazil and Paraguay, and high levels of morphological variation in some species, notably the taxonomically tense *M. guianensis* (Aubl.) DC. Plastome sequences obtained through genome skimming were generated for some species of *M.* sect. *Aguava* and were combined with five DNA regions of additional species to increase taxonomic coverage. Molecular-phylogenetic analyses were conducted using maximum likelihood. Divergence times using a Bayesian approach and historical biogeography using ancestral range probabilities were also estimated. Our results confirm the efficiency of combining NGS and Sanger data for recovering robust phylogenetic trees. *Myrcia* sect. *Aguava* is monophyletic, comprising 32 species with exclusively trilocular ovaries, but has no apparent relationship with other trilocular groups of *Myrcia.* Species with bilocular ovaries that were thought to belong to *M.* sect. *Aguava* emerge within *M.* sect. *Aulomyrcia. Myrcia* sect. *Aguava* is also characterized by the leaves with raised adaxial midveins, symmetrical inflorescences, flowers with free calyx lobes, and glabrous staminal rings. Three lineages that correspond to species distributions are observed within *M.* sect. *Aguava.* Multiple accessions of *Myrcia guianensis* reveal this species as polyphyletic and emphasize the geographical structure of the group. *Myrcia* sect. *Aguava* has a probable origin in the Cerrado region during mid-Miocene, with subsequent late Miocene migrations to the Atlantic Forest, Amazon, and Caribbean, indicating transitions from open to forested areas that are less common in the Neotropics. The lineages that persisted in the Cerrado diversified only more recently, near the border of Miocene/Pliocene. A group of species also colonized the northern Atlantic Forest, highlighting the southern/northern biogeographic and floristic partition of this biome. Results presented here are the basis for a complete taxonomic revision of the complex *Myrcia* sect. *Aguava.*

June 22
5:00 PM
Session 8

Predictive comparative phylogeography in the east-west division of Cerrado taxa

Silva L.M.D.[1*], Bonatelli I.A.S.[2] & Moraes E.M.[1]

[1]Universidade Federal de São Carlos, Sorocaba, São Paulo, Brazil. [2]Universidade Federal de São Paulo, Diadema, São Paulo, Brazil. [*]Correspondence: luana.deoclecio@estudante.ufscar.br.

The Brazilian Cerrado is the second largest biome in South America and is the most diverse savanna in the world. Some taxa sampled to date show a congruent phylogeographic break along the Central Brazilian Plateau, with lineages separated in two groups, east and west. Our objectives were to investigate temporal patterns of diversification of co-distributed taxa across this phylogeographic break and to identify biotic and abiotic characteristics that are predictors of this divergence. We assemble published mitochondrial and chloroplastidial DNA data from 21 phylogeographic studies performed in the Cerrado, including 12 animal species and nine plants widely distributed across the central region of the biome. We used a maximumlikelihood analysis to identify the presence or absence of east-west phylogeographic structure, then estimated lineages divergence times using Bayesian Dating. We tested for synchronous diversification of three co-distributed taxon-pairs (two lizards and one frog) sharing the eastwest structure using Bayesian analysis of shared evolutionary events. Finally, we used a Random Forest classification approach over a matrix of biotic, climatic and geographic variables, to investigate the possible predictors variables of this structure. A deep split into east-west lineages was revealed in six cases: *S. hirtipupa* (insect), *P. acuticostris* (lizard), *N. meridionalis* (lizard), *H. lundii* (frog), *B. coccolobifolia*, and *P. aurisetus* complex (plants). We infer that frog and lizard east-west populations diverged by one or multiple MiocenePliocene events, while plant and insect genetic structure were structured by Pleistocene events. Our results supported one pulse of synchronous diversification within *H. lundii* and *P. acuticostris* in the early Pliocene, while lineages of *N. meridionalis* were diverged asynchronously in late Miocene. Our Random Forest classifiers were not accurate, with prediction accuracy between 60% and 62% depending on the number of instances used. The diversification processes on this phylogeographic break cannot be restricted to a particular time interval or mechanism. Taxa that share the east-west structure in the Cerrado show idiosyncratic population histories, linked to a succession of geological and climatic events in the biome.

Temporally and spatially decoupled evolution of mimicry in Neotropical butterflies

June 22
5:00 PM
Session 8

Kozak K.M.[*,1], Rastas P.[2] , Figueiredo C.[3], Perez Martins A.[4], Baur B.H.[5], Salazar C. [6], Pieczarka J.[3], Ready J.[3] & Owen McMillan W.[1]

[1]Smithsonian Tropical Research Institute, Ancón, Panama. [2]Institute of Biotechnology, University of Helsinki, Finland. [3]Instituto de Ciências Biológicas, Universidade Federal do Pará, Belém, Brazil. [4]Department of Biology, McGill University, Montreal, Canada. [5]Departamento de Biologia, Universidad de los Andes, Mérida, Venezuela. [6]Universidad del Rosario, Bogotá, Colombia. [*]Correspondence: evoecogen@gmail.com

How do complex adaptive phenotypes of mimetic taxa arise and diversify in dynamic physical environments? The butterflies *Heliconius erato* and *H. melpomene* may provide an answer, through a natural experiment in rapid intraspecific diversification and repeated interspecific convergence. Across the Neotropics the two species mimic each other, and yet diverged into a dazzling patchwork of 29 aposematic wing patterns. To what extent have the two radiations coevolved, is one of them the model for the other, and how were they shaped by the dynamic environments of the Neotropics? We leverage phased whole genome re-sequencing data from 400 butterflies in 25 races of each species, sampled densely across the Neotropics, with emphasis on previously unexplored diversity in the Brazilian Amazonia. We apply statistical cartography (tess3R, EEMS), phylogeography (BEAST2, TreeMix) and demographic analyses of haplotypes (MSMC2). *Heliconius erato* has diversified for millions of years in the valleys of Andes and Central America, followed by a recent invasion of the Amazon basin, leading to rapid emergence of the most complex phenotypes from a surprisingly uniform genomic background. In contrast, the mimic *H. melpomene* shows a distinct pattern of steady dispersal, with deep differentiation between the Upper, and Lower Amazonia populations separated by major rivers. In both species, demographic analyses show a staggering diversity of histories and complex patterns of connectivity. Although *H. erato* is generally older, in the Amazon basin *H. melpomene* is the model for mimicry. Our research reveals the surprising temporally and spatially decoupled nature of co-evolution in a highly selected trait.

The complete mitochondrial genome of the Honduran white bat *Ectophylla alba* (Allen, 1982) (Chiroptera: Phyllostomidae)

June 22
5:00 PM
Session 8

Vivas-Toro I.[1*], Ortega J.[1] & Baeza J.A.[2,3,4]

[1]Laboratorio de Bioconservación y Manejo, Departamento de Zoología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Department of Biological Sciences, Clemson University, Clemson, SC, USA. [3]Smithsonian Marine Station at Fort Pierce, Fort Pierce, FL, USA. [4]Departamento de Biología Marina, Facultad de Ciencias del Mar, Universidad Católica del Norte, Coquimbo, Chile. [*]Correspondence: isavivas94@gmail.com.

The Honduran white bat, *Ectophylla alba** (Allen, 1982), is one of eight species belonging to the family Phyllostomidae that exclusively roosts in tents. Due to its restricted distribution, habitat specificity, and diet requirements, *E. alba* has been strongly affected by habitat loss and fragmentation during the last decade. In this study, we developed the first genomic resource for this species; we assembled and analyzed the complete mitochondrial genome of *E. alba* in detail. It was assembled de novo, based on Illumina paired-end sequencing, using a seed-extend algorithm. The mitogenome of *E. alba* is 16,664 bp in length and is comprised of 13 protein coding genes (PCGs), 2 ribosomal RNA genes, 22 transfer RNA genes (tRNAs), and a putative Control Region (CR) 1,232 bp in length. Gene arrangement in the mitochondrial chromosome of *E. alba* is identical to that reported before in other species of co-familiar bats. All PCGs are under purifying selection, with atp8 experiencing the least selective pressure. In all PCGs, codons ending with adenine are preferred over others ending in thymine and cytosine. All tRNAs exhibit a cloverleaf secondary structure except tRNA-Serine 1 which lacks the DHU stem. The CR of *E. alba* exhibits three domains commonly described in other mammals, including bats; i. extended terminal associated sequences (ETAS), central, and conserved sequence block (CSB). A maximum likelihood phylogenetic reconstruction of the family Phyllostomidae based on all 13 mitochondrial PCGs confirms the monophyletic status of the subfamily Sternodermatinae and indicates the close relationship between *E. alba* and the genus *Artibeus.* This is the first genomic resource developed for *E. alba* and represents the first step to improving our understanding of the genomic underpinnings involved in the evolution of specialization as well as acclimatization and adaptation to local and global changes of specialist bats.

June 22
5:00 PM
Session 8

Time and direction of dispersal events of Triatominae (Insecta: Hemiptera) between biomes in the New World

de la Barrera Cardozo M.[1*], Rabinovich J. E.[2] & Löwenberg-Neto P.[1]
[1]Universidade Federal da Integração Latino-Americana – UNILA, Foz do Iguaçu, Paraná, Brasil. [2]Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina.
[*]Correspondence: marina.cardozo@aluno.unila.edu.br.

The Triatominae (kissing bugs) is the only subfamily of the Reduviidae (Hemiptera: Heteroptera) whose members feed on vertebrate blood, and all 177 known species are potential Chagas disease vectors. This subfamily originated in northern South America or Central America between 45 and 30 million years ago [Ma]. New world species of Triatominae inhabit a variety of tropical, subtropical and temperate environments. Their distribution extends from the southern United States to Patagonia. We aimed to describe how the Triatominae species have historically assembled in the different New World biomes by dispersal events. Dispersal events (area expansions) were inferred by dispersal–extinction–cladogenesis model. We analyzed species geographic distribution from the DataTri, a dataset of American triatomine species, and the most recent time-calibrated molecular phylogeny (63 species). Terrestrial biomes were assumed as biogeographic units, including Andean and Nearctic regions (12 units). Six dispersal constraints matrixes were tested for the best-fit model:

1) unrestricted routes; 2) cis-climatic routes (seasonality); 3) cis-climatic routes (humidity); 4) trans-climatic routes (seasonality); 5) trans-climatic routes (humidity); and 6) neotropical landscape evolution (temporally-stratified). For the best-fit model, we quantified the direction and frequency of dispersals through time in absolute numbers and in relation to the number of lineages (LTT). The best-fit model was the 'neotropical landscape evolution', which inferred 127 events of dispersals, 22% of which were trans-climatic events regarding seasonality and 35% were trans-climatic regarding humidity. The direction of the dispersals was strongly asymmetric: the 'Cerrado and Chaco' (CEC) biome was the primary source of lineages (57% of the dispersal events) for all other regions except the 'West indies' (WIN) and 'Nearctic' (NEA) region. The main sink for these CEC dispersals (23%) was the 'Atlantic Forest' (ATF), whereas the 'Amazon' (AMA) was the primary global sink (17%). The relative frequencies of dispersal plot was marked by five phases: the early peak of the frequency (40–35 Ma), a valley of almost null frequencies (35–30 Ma), the greatest peak of dispersal frequencies (30–25 Ma), a relative low frequencies valley (20–10 Ma), and a final peak of dispersal frequencies (10–5 Ma). Our results support that the historical narrative of the Triatominae was temporally and spatially correlated with the main geological events and biome evolution in the Neotropics. Further, dispersal events were episodic through time (three peaks and two valleys), and the 'Cerrado and Chaco' area was the primary source of Triatominae lineages.

Poster Session 9: Phenomics

Allometry, sexual selection, and evolutionary lines of least resistance shaped the evolution of exaggerated sexual traits within the genus *Tyrannus*

June 23
12:00 PM
Session 9

Fasanelli M.N.[1,*], Milla Carmona P.S.[2,3], Soto I.M.[1,2] & Tuero D.T.[1]

[1]Instituto de Ecología, Genética y Evolución de Buenos Aires (IEGEBA-CONICET), DEGE, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Buenos Aires, Argentina. [2]Laboratorio de Biología Integral de Sistemas Evolutivos. DEGE, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Buenos Aires, Argentina. [3]Laboratorio de Ecosistemas Marinos Fósiles, Instituto de Estudios Andinos Don Pablo Groeber (CONICET-UBA), Buenos Aires, Argentina. [*]Correspondence: fasanellimartin@gmail.com.

The direction and magnitude of evolutionary change not only depend on change driving processes (e.g., selection) but also on the genetic architecture underlying, making intraspecific variation a key factor to evolution increasing or impeding response to selection. Here we study the genus *Tyrannus* as a model for examining the conditions and drivers that facilitate the repeated evolution of exaggerated, secondary sexual traits in the face of significant functional limitations, with particular focus on the role of phenotypic trait covariation. The clade includes two deep-fork-tailed species, the Scissor-tailed (*T. forficatus*) and Fork-tailed (*T. savana*) flycatchers. Both show extremely elongated and functionally-constraining long feathers that independently diverged from the rest of the genus. We then focused on the roles of allometry, sexual selection, and their interaction on the diversification of tail morphology in *Tyrannus.* Historically, birds' tails have been understood as mere flight devices, tackling the phenomenon of exaggerated traits mainly from a 'selection' angle. That way, the origin of this trait was regarded either as the result of natural (adaptive) selection or, more prominently, sexual selection. Instead, we approached the issue from a 'structuralist' perspective, isolating and assessing different types (or axes) of morphological variation (interspecific and intraspecific –e.g., sexual dimorphism and allometric variation–). As a main result of this study, both sexual dimorphism and allometric variation of the deep-forked species aligned with the between-species maximum variation axis of 'ordinary'- tailed species. Therefore, we present evidence of amplified divergence via the cooption and reorientation of allometric shape variation feeding a sexual selection process that repeatedly drove morphology along a historically favoured direction of cladogenetic evolution.

Comprehensive phenotypic analysis supports the monophyly of stromateiform fishes (Teleostei: Percomorphacea)

June 23
12:00 PM
Session 9

Pastana M.N.L.[1,2], Johnson G.D.[2] & Datovo A.[1,*]

[1]Museu de Zoologia, Universidade de São Paulo, São Paulo, SP, Brazil. [2]National Museum of Natural History, Smithsonian Institution, Washington, DC, USA.
[*]Correspondence: adatovo@usp.br.

Percomorphs comprise a massive fraction of the extant fish diversity, including over half of all known ray-finned fishes and about one-fourth of the living vertebrates. Among the dozen percomorph orders, Stromateiformes encompasses 77 extant species distributed in 16 genera and six families. Stromateiform monophyly has never been explicitly tested on morphological grounds, and molecular analyses have recurrently rejected it. We performed a comprehensive phenotype-based phylogenetic revision of Stromateiformes, sampling all its valid genera and all percomorph families previously aligned with the order by morphological and molecular studies. Our final dataset comprised 66 taxa representing 46 acanthopterygian families and 207 characters (19 quantitative and 188 qualitative). Investigated phenotypic systems included osteology, myology, desmology, squamation, laterosensory system, viscerae, external morphology, and behavior. A sensitivity analysis of 11 different implied-weighted parsimony schemes was implemented. Each scheme used a k value in which the fit of a character with an average amount of homoplasy (under equal weights) equaled 50-90% of the fit of a homoplasy-free character. All analyses resolved Stromateiformes as monophyletic, supported by seven unequivocal synapomorphies. The final topology positioned Amarsipidae as the sister group of the remaining stromateiforms. Centrolophidae was polyphyletic, with three genera grouped into an early branching clade and the other four placed as successive sister taxa to a lineage containing all remaining stromateiform families. Each of these families was monophyletic, with Nomeidae and Stromateidae appearing as successive sister groups to the clade Tetragonuridae + Ariommatidae. Contrary to the molecular phylogenies, our analysis indicated that the two most singular morphological novelties of stromateiforms evolved only once: the intradermal canal system of the trunk appeared at the base of Stromateiformes, and the pharyngeal sac in the node formed by non-amarsipid stromateiforms. Notably, the monophyly of these two clades is retained even when all characters related to the intradermal canals and pharyngeal sac are excluded from the matrix. Congruences and conflicts of the present hypothesis with molecular classifications and past morphological analyses are critically discussed.

June 23
12:00 PM
Session 9

Fluctuating asymmetry as a tool for assessing development stability on small mammals from the Argentine agroecosystem

Martini G.A.[1,*], Coda J.A.[1] & Priotto J.W.[1]

[1]Grupo de Investigación en Ecología Poblacional y Comportamental (GIEPCO), Instituto de Ciencias de la Tierra, Biodiversidad y Ambiente (ICBIA), UNRC CONICET, Río Cuarto, Córdoba, Argentina. [*]Correspondence: gastonmartini@hotmail.com.

Evolutionary biologists have not paid as extensive attention to nongenetic components of variation as they have done to genetic variation of phenotypic traits. Generally, nongenetic components are grouped in categories such as the "environmental variation". However, they differ in both their origin and biological significance. Individuals experience different environmental conditions resulting in phenotypic plasticity. Therefore, it is necessary to consider the developmental system and how it produces variation in phenotypic traits. Developmental instability (DI) results from random variation during development, which produces deviations in each developing structure from expected for both genotype and environment. Fluctuating asymmetry (FA), defined as small random deviations of perfect bilateral symmetry, has been suggested as a good DI estimator. Recently, agricultural activity has increased, being one of the key causes of habitat destruction and subsequent biodiversity loss. Thus, we evaluated the effect of agricultural intensification through local and landscape variables on DI (skulls and mandibles) of individuals of three rodent species. Landscape variables were recorded: area perimeter ratio (PA) and habitat diversity index. The local variable was vegetation volume (Vv) of habitat edge. We used individuals housed in the UNRC-Mammal Collection caught during 2016 in the central-Argentine agroecosystem. Type I and II landmarks were digitized in 2D images. Asymmetric components (size and shape) were extracted using geometric morphometrics. For the analysis, GLM were generated, using the AIC-Criterion to select them. No associations between explanatory variables and FA were found in *Akodon azarae* and *Calomys musculinus* skulls. A negative association of FA with PA and Vv was observed in *C. venustus* skull. No associations with the explanatory variables were found for any of the species' mandibles. The study shows a disparity in morphological responses, depending on whether the skull or the mandible is analyzed. The results are discussed based on the degree of habitat requirements of the species.

Geographic variation of skull shape in *Caluromys philander* (Didelphimorphia, Didelphidae)

June 23
12:00 PM
Session 9

Damasceno E.M.[1,*], Bandeira I.[2] & Astúa D.[1]

[1]Universidade Federal de Pernambuco, Recife, Pernambuco, Brazil. [2]Universidade Federal Rural de Pernambuco, Recife, Pernambuco, Brazil. [*]Correspondence: elismarinad@gmail.com.

The bare-tailed woolly opossum (*Caluromys philander* Linnaeus, 1758) is a didelphid marsupial (Didelphidae, Didelphinae) with a wide distribution range in South America. Across its distribution, *C. philander* can be found in different types of biomes such as the Atlantic Forest, the Amazon Forest, and the Brazilian Cerrado. There are four subspecies of *C. philander* currently described in the literature, based on external characters, such as size and fur color. The goal of this research is to assess how the skull morphology of these animals differs according to the different localities and biomes they are found in. We used geometric morphometrics to quantify skull shape and subsequently analyze morphological variation according to distribution. Skulls of 316 specimens were observed (130 males, 132 females, and 54 of unknown sex) in three different views: dorsal, ventral, and lateral. We digitized 28, 22, and 28 landmarks on the dorsal, lateral, and ventral views, respectively, using TPSDig2. We used MorphoJ software to run all multivariate comparative analysis and ggplot package in R software to generate the graphs. The specimens were grouped into 13 localities using geographical proximity and/or biome as criteria. The results from our CVA analyses of the dorsal view show differences between three main clusters of populations. One cluster comprises populations from southeastern Brazil; the second cluster has populations from Cerrado, Guiana, Madeira/Tapajós, and Amazonian rivers, along with animals from Southern Venezuela. The third cluster is formed by specimens collected north of the Orinoco River, in Venezuela and Trinidad and Tobago. Animals North of São Francisco River, from Northeastern Brazil seem to be in a transition state between the southeastern population and Amazonian populations. Analyses on the other views of the skull differentiate the southeastern Brazil population, but overlap the two that are on different sides of the Orinoco River. Our analyses suggest that *C. philander* consists of three taxonomic units, instead of four, that are well defined by geographic distribution and morphological characters. We can also conclude that both the Orinoco and the São Francisco rivers act as geographical barriers for this species.

Geometric morphometrics of the mite *Laelaps mazzai* associated with different species of the sigmodontine rodent *Calomys* in Argentina

June 23
12:00 PM
Session 9

Espinoza-Carniglia M.[1,*], Pardiñas U.F.J.[2] & Lareschi M.[1]

[1]Laboratorio de Ectoparásitos, Centro de Estudios Parasitológicos y de Vectores (CEPAVE) (CONICET-UNLP), La Plata, Buenos Aires, Argentina. [2]Instituto de Diversidad y Evolución Austral (IDEAus-CONICET), Puerto Madryn, Chubut, Argentina. [*]Correspondence: marioespinozac@cepave.edu.ar.

Calomys (Rodentia, Cricetidae) is one of the most widespread genera of Neotropical sigmodontine fauna. Pelage coloration, body size, and external appearance vary greatly among species and sometimes among populations of the same species. In Argentina, *Calomys* is represented by at least 7 species, some of them having wide distribution ranges (e.g., *C. laucha*, *C. musculinus*) and zoonotic importance. Previous records associate the mite *Laelaps mazzai* (Mesostigmata, Laelapidae) with *C. laucha* and *C. musculinus* in Argentina, with *C. callosus* in Brazil, and with *C. hummelincki* in Venezuela. *Laelaps mazzai* is traditionally recognized by a hypertrichous dorsal shield, but its morphology and taxonomic status have been poorly studied. Although other laelapids have been proposed as species-specific, there is no data to support if this is the condition of *L. mazzai*. Here we explore the morphological variation of dorsal and ventral shields of females of *L. mazzai* in samples obtained from 5 species of *Calomys* from 13 localities of Argentina to evaluate if they are or not species-specific. We take photographs of 57 *L. mazzai* from *C. callosus* (n = 20), *C. callidus* (n = 15), *C. laucha* (n = 8), *C. venustus* (n = 9) and *C. musculinus* (n = 5). We positioned 64 landmarks in setae insertions and pores from dorsal shield (DS) and 16 landmarks in ventral shields [sternal (SS), metasternal (MS) and genitoventral (GS)] with the tpsDig2 software. Shape variations were analyzed with a Canonical Variate Analysis in MorphoJ. Differences were showed with Procrustes distances and p-values are calculated with 100000 permutations. Results show that there are five different morphotypes of *Laelaps mazzai* related each by one to their host species. Further studies are needed to clarify if the detected morphological variation can be interpreted as indicative of a complex of species under the current concept of *L. mazzai.*

June 23
12:00 PM
Session 9

MicroCT, birds and brains: insights on the endocranial morphology of Tyrannides (Aves, Australaves)

Demmel Ferreira M.M.[1,*], Degrange F.J.[1] & Tirao G.A.[2]

[1]Centro de Investigaciones en Ciencias de la Tierra (CICTERRA), UNC, CONICET, Av. Vélez Sarsfield 1611, X5016GCA, Córdoba, Córdoba, Argentina. [2]Instituto de Física Enrique Gaviola (IFEG), UNC, CONICET, Córdoba, Córdoba, Argentina.
[*]Correspondence: manudemmel@gmail.com.

The infraorder Tyrannides or New World suboscines (Aves, Passeriformes) include one of the greatest endemic vertebrate radiations of South America with more than 1200 species. Although its ecology has been well studied, little is known about its endocranial morphology. This work aims to explore the endocranial morphology of the Tyrannides, in an attempt to establish morphological differences between the different families and their relationship with macroevolutionary aspects. Fifteen skulls of adult Furnariidae and Tyrannidae were CT scanned and 3D models of the endocast were generated. Phylogenetically corrected regression analysis shows that only one furnariid (Syndactyla rufospuerciliata) has a brain volume larger than expected for their body mass, whereas the rest of the furnarids and all tyranids have smaller brains. All species have an airencephalic type of brain. The telencephalon of Furnariidae and Tyrannidae is wider than longer (except for *Coryphistera alaudina* and *Agriornis montanus*, respectively). In all the species studied here, the eminentiae sagittales correspond to type A (i.e., rostrally placed). These structures are extensive and elongated. The bulbus olfactorius is short and small in both families. The hypophysis is oriented perpendicularly to the horizontal semi-circular canal of the inner ear. The optic lobes of furnarids are laterocaudally partially overlapped by the telencephalic hemispheres, but in tyrannids this condition is not that noticeable. When observed in lateral view, the optic lobes are placed rostrally; equally developed in both families. The cerebellum is elongated with a marked and variable number of folia in all species. In furnarids, this structure has a sub-rectangular shape. Among tyrannids, the shape of the cerebellum is variable: in some species is squarer and in others is rhomboidal. The medulla oblongata of Furnariidae has an elongated aspect, whereas in Tyrannidae is globose and it is in most cases as long as wide. The mean hearing ranges vary greatly in both families, ranging from 2899.20 Hz to 3567.61 Hz in furnarids, and from 2996.93 Hz to 3228.29 Hz in tyrannids. Phylogenetical signal is poor in all of the features measured in the endocraniums (brain volume, Wulsts, optic lobe and olfactory ratio, width over height of cerebellum, and telencephalic hemispheres). These preliminary results provide key information that contributes to a better understanding of Tyranni radiation, and subsequently to the evolution of the largest order of birds, the Passeriformes.

New data on bird's nest fungi (Nidulariaceae, Basidiomycota) from Bahia, Brazil

June 23
12:00 PM
Session 9

Fermiano R.R.[1,*] & Silva B.D.B.[1]

[1]Universidade Federal da Bahia, Salvador, Bahia, Brazil. [*]Correspondence: rafaelrf313@gmail.com.

The Nidulariaceae family is commonly known as the bird's nest fungi. Nidulariaceae includes five genera: *Crucibulum*, *Cyathus*, *Mycocalia*, *Nidula*, and *Nidularia*. *Cyathus* is characterized mainly by the basidiome in the form of a cone or inverted bell, with small internal structures (peridioles), resembling small bird's nests with eggs inside, an analogy that gave its family name. In total, 154 species have been described in the World, 31 of them recorded in Brazil. *Cyathus* has a great importance in nutrient cycling in vegetable organic matter, such as branches, trunks, leaves, fruits, or even herbivore manure. Many species produce antibacterial, antifungal, antioxidant, and anticancer substances. Considering the relevance of these fungi, this work aimed to study the diversity of the genus *Cyathus* in the state of Bahia. Collections were carried out in the municipalities of Salvador, Elísio Medrado, Santa Teresinha, and Mucugê. Morphological and molecular studies were carried out. For macro and microscopic analysis of the basidiomata, the usual methodology for gasteroids was followed. Macroscopic observations included characters such as: basidiome shape, internal and external plication and shape and type of peridioles cortex, and the color of each of these structures. Microscopic analyzes consisted of mounting slides to determine the spores' morphology. The identified specimens were registered in the Herbarium Alexandre Leal Costa of UFBA. The ITS and nucLSU regions were amplified. The combined data set was analyzed under parsimony and Bayesian inference. Thirteen species of the *Cyathus* were identified: *Cyathus* sp. nov. is proposed as a new species. Its diagnostic features include single-layered cortex, peridioles angular, and elipsoide basidiosporos measuring 15–21 × 11–13 μm (L = 17.95; W = 12.20 μm, Qm = 1.5). *Cyathus discoideus* is recorded for the first time in Latin America; *C. costatus*, and *C. minimus* represent the first records for Brazil; *C. morelensis* and *C. stercoreus* are registered for the first time for northeastern Brazil; *C. earlei*, *C. hortensis*, *C. intermedius* and *C. triplex* are new occurrences for the state of Bahia; while *C. limbatus*, *C. montagnei* and *C. striatus* represent the second occurrences for Bahia. The results obtained so far have great relevance for Brazilian mycology, especially for the state of Bahia.

June 23
12:00 PM
Session 9

Phylogenetic and biogeographical analysis of Rhodaliidae (Cnidaria, Siphonophorae)

Oliveira O.M.P.[1,*], Nishiyama E.Y.[1] & Cieni D.[1]

[1]Laboratory of Gelatinous Zooplankton, Federal University of ABC, São Paulo, Brazil.
[*]Correspondence: otto.oliveira@ufabc.edu.br.

Rhodaliids are epibenthic siphonophores, living near the bottom in a great range of depths, from the shelf to bathyal regions. Differently from the other siphonophores, with planktonic or pleustonic habits and worldwide distribution, each rhodaliid species is found in restricted areas along the ocean floor. To determine the family relationships and trace back the distribution of the internal lineages, we performed a phylogenetic analysis, including all fifteen species of the family and three other siphonophore species as outgroup, considering 28 morphological characters. Our results support the monophyly of the family and genera. The consensus topology was confronted with the map of species distribution. As a result, we attested that the older lineage (genus *Archangelopsis*, with two species) presents a distribution restricted to the Indo-Pacific Ocean. Other lineages also present restricted distributions (e.g. genus *Angelopsis*, two species in the North Atlantic; genus *Tridensa*, two species, both in Celebes Sea). Whereas, the genus *Stephalia* presented their three species apart from themselves (*S. bathyphysa* off New Zealand, *S. corona* in Northeastern Atlantic, and *S. dilata* in Equatorial and North Eastern Pacific). Although, the absence of genetic data limited the possibility of establishing a molecular clock to determine the age of the lineages, we believe that most of the distribution patterns can be explained by the plate tectonics and consequent changes in the ocean floor since the initial split of Pangea. However, this hypothesis needs to be tested with additional studies.

Phylogenetic relationships and morphological evolution of threadfins (Actinopterygii: Perciformes: Polynemidae)

June 23
12:00 PM
Session 9

Presti P.[1,2*] & Datovo A.[2]

[1]Instituto de Biociências da Universidade de São Paulo, São Paulo, SP, Brazil. [2]Museu de Zoologia da Universidade de São Paulo, São Paulo, SP, Brazil. *Correspondence: ppresti@usp.br.

Threadfins compose the Polynemidae, a family of primarily marine fishes with eight genera and 42 extant species. The phylogenetic position of polynemids within Percomorphacea, as well as their intrafamilial relationships, are poorly understood. Little osteological and almost no myological information for threadfins are documented in the literature. The most remarkable feature of polynemids is their pectoral fin divided into a dorsal lobe, which retains the morphology of a typical fin, and a ventral portion modified into elongate tactile filaments. Most muscles involved in such an intricate structure are completely subdivided into two major segments, each serving a distinct division of the pectoral fin. These findings, along with comparisons with outgroup taxa, indicate the necessity of a novel terminology for the pectoral muscles. Even more surprising is the discovery of gustatory components in the massive nerves that run along the pectoral filaments, indicating that these structures have not only tactile but also tasting functions. The *adductor mandibulae* complex of polynemids exhibits unique features among percomorphaceans, such as the *promalaris* entirely lateral to all other muscle sections. Myological data supports the hypothesis of a sister-group relationship between polynemids and sciaenids, and several new synapomorphies derived from the muscular system are advanced for the family. A phylogenetic analysis of all valid polynemid genera based on 166 morphological characters and 24 terminals resulted in a fully resolved new hypothesis of relationships. Thirty-three synapomorphies support the monophyly of the family, which is divided into two major lineages, one containing only two genera and the other grouping all remaining taxa. All genera were resolved monophyletic except *Polydactylus.* This study was funded by the São Paulo Research Foundation (FAPESP

Preliminary assessment of shape variation in the skull and mandible of mouse opossums, genus *Marmosa* (Didelphimorphia, Didelphidae)

June 23
12:00 PM
Session 9

Maia P.F.A.[1,*] & Astúa D.[1]

[1]Universidade Federal de Pernambuco, Recife, Pernambuco, Brazil. *Correspondence: paula.maia@ufpe.br.

Mouse opossums of the genus *Marmosa* Gray, 1821 are currently divided in five subgenera. With 25 species, *Marmosa* can be considered the most species-rich genus of didelphid opossums. Recent advances in phylogeny and taxonomy are revealing a group more diverse than initially thought. However, a comprehensive quantitative analysis of cranial and mandibular shape variation within *Marmosa* has not been

conducted. Here we provide initial results of the diversity and variation observed within the genus and related it to the current phylogenetic knowledge. To do so, we used images of the dorsal view of the cranium (432 specimens) and lateral view of the mandible (445 specimens) of 12 species, where we placed 35 and 19 landmarks, respectively. Landmark configurations went through a Generalized Procrustes Alignment and resulting shape variables were analyzed through Principal Component Analyses. An independent phylogenetic hypothesis was also used to generate a phylomorphospace and test for phylogenetic signal. All analyses were conducted in MorphoJ. Overall, there is considerable overlapping among most species, indicating little interspecific shape variation . We also found a significant phylogenetic signal for both the cranium and mandible ($p=0.0384$ and $p= 0.0060$, respectively). The most divergent species in cranium phylomorphospace are *Marmosa tyleriana* (with wider nasal bones and narrower zygomatic arches) and *M. lepida* (with a more globose braincase and shorter nasal bones), whereas most other species show a conservative or convergent cranial shape. In contrast, *Marmosa rubra* and *M. xerophila* converge in their more robust mandibles, and *M. tyleriana* remains the most distinctive in mandible shape, with a narrower mandible. These preliminary results will be completed with the inclusion of additional species of *Marmosa*. This will help to understand better the morphological diversification of the genus.

In Video Presentations

The following abstracts were selected as videos that were posted on the SBE meeting's YouTube channel:

`https://www.youtube.com/channel/UCgGlkPp4jCoZoatnG2--RJA`

Scan me:

Video only
YouTube

An unexplored anatomical complex: evolution of the musculature associated with fins in Gymnotiformes (Teleostei: Ostariophysi)

Peixoto L.A.W.[1*] & Datovo A.[1]
[1]Museu de Zoologia da Universidade de São Paulo, São Paulo, SP, Brazil.
[*]Correspondence: luizwp@yahoo.com.br.

Skeletal musculature is among the most important anatomical complexes of vertebrates. However, this source of information is barely explored in most groups of bony fishes, with knowledge usually limited to brief anatomical descriptions in a few species. That is the case in one of the most important lineages of freshwater fishes, the neotropical electric eels (Gymnotiformes). Following the usual trend of studies with teleosts, most morphology-based phylogenies of gymnotiforms have an inordinate emphasis on osteology, leaving other relevant anatomical systems unexplored. The present study attempts to fill this gap by analyzing the pectoral- and anal-fin musculature of Gymnotiformes from a phylogenetic perspective. All results from the descriptive analyzes were tested within a cladistic paradigm. A detailed comparative study comprising 83 species of Gymnotiformes identified 25 new myological characters from these fin muscles which were concatenated with a larger phenotypic matrix including characters from several different sources. After parsimony analysis, about 23 new myological synapomorphies were recovered for all major lineages in the Gymnotiformes. Our efforts bring light to new synapomorphies for different level within Gymnotiformes phylogeny, as follow: (1) the arrector dorsalis secundarium located medially to the coracoid, (2) the inclinatores anales higher than one and a half of each anal-fin rays, and (3) the absence of the infracarinalis are three conditions found only in Gymnotiformes among ostariophysians. Further, the abductor profundus extending dorsally at its origin on the process of the coracoid, being visible in lateral view, is a synapomorphy for Eigenmanniinae. Results indicate that characters from myology can significantly improve both support and resolution of important components of phylogenetic hypotheses.

Video only
YouTube

Bryophyte species richness along a precipitation gradient outlined by six Colombian paramos

Moreno-Gaona D.A.[1,*], Berdugo M.B.[2] & Morales-Puentes M.E.[1]
[1]Universidad Pedagógica y Tecnológica de Colombia, Tunja, Boyacá, Colombia. [2] University of Marburg, Marburg, Hessen, Germany. [*]Correspondence: diego.moreno@uptc.edu.co.

About half of the paramo areas of the world occur in Colombia. There, the Boyaca Department hosts paramos differing in the amount of rain they receive, potentially composing a moisture gradient. To assess the effects of varying precipitation on bryophyte diversity, we estimated several alpha diversity parameters for mosses and liverworts in six paramo complexes of the Colombian Andes within the Boyaca Department and coupled these diversity estimates to the WorldClim modelled bioclimatic variable Annual Precipitation (BIO12) to test for the correlation between alpha diversity and precipitation along the moisture gradient. The exploration of 4461

species occurrence records from herbaria collections and from grey literature (i.e., undergrad and graduate thesis as well as technical reports inventorying bryophyte diversity) indicated that the studied Paramos, representing a fifth of the paramo areas in Colombia, host 35% of the bryophyte species recorded for the country, 341 moss and 248 liverwort species. The modelled climate data indicated that the six studied paramos composed a precipitation gradient ranging between 850 and 1900 mm of annual precipitation. Four of the paramos grouped toward the dry end of the gradient, Cocuy, Iguaque – Merchan, Rabanal – Rio Bogota, and Guantiva – La Rusia. The paramo with annual precipitation of 1500 mm (TBM: Tota-Bijagual-Mamapacha), above the mean precipitation value along the gradient, hosted the higher number of bryophyte species (370, 215 moss and 155 liverwort species). On the other hand, the paramos located in both extremes of the precipitation gradient hosted lower number of species: in Cocuy (850 mm) 134 bryophyte species (104 moss and 30 liverwort species) and in Pisba (1900 mm) 126 bryophyte species (91 moss and 35 liverwort species). There was more moss than liverwort species richness in all paramos, but Iguaque – Merchan. Because the interpolation and extrapolation analyses indicated that our methodological approach corresponded to an equally-complete sample among the studied paramos, we concluded that bryophyte species richness exhibits a hump shape distribution along the studied precipitation gradient. The dataset that we compiled can inform conservation initiatives if used to identify species-rich and beta-diverse areas. Identifying such areas may improve our ability to protect these fascinating and unique ecosystems from anthropic pressure emerging from farming and mining activities.

Cytogenetic study in species of the subfamily Stethaprioninae, Characidae

Video only
YouTube

Soares L.B.[1,*], Paim F.G.[1], Foresti F.[1] & Oliveira C.[1]

[1]Instituto de Biociências, Botucatu, São Paulo, Brazil. [*]Correspondence: leticia.b.soares@unesp.br.

It is estimated that there are 5,160 species of Neotropical freshwater fishes with 69 described families, which represents one third of the planet's freshwater fishes. Within these families, the family Characidae with 1,211 species, the largest family of Neotropical fishes. It is divided into four groups: subfamily Spintherobolinae, without cytogenetic information so far; Stevardiinae, Clade B (Cheirodontinae and Characinae, for example) and the subfamily Stethaprioninae with cytogenetic information. What draws attention to the latter group is the presence of a large metacentric pair not found in the species of the other two lineages. Thus, the aim of this study was to test cytogenetic markers for this large metacentric pair, to better understand its evolution within Stethaprioninae. Muscle tissue and fin cells from *Hollandychthys multifasciatus* and *Hyphessobrycon boulengeri* were isolated and maintained at 27.5°C, 5% CO_2, in complete medium (DMEM + fetal bovine serum + antibiotics + antimycotics) until reaching confluence and peaked at a ratio of 1 : 2. These cells from different passages were used to obtain metaphasic chromosomes and, later, the chromosomes were subjected to cytogenetic techniques

(Giemsa, C-Band, Ag-NOR - Nucleol Organizing Regions and fluorescent in situ hybridization (FISH) with probes obtained via PCR). The diploid number of both species is 2n = 50 chromosomes, with a difference in the karyotype formula, for *H. multifasciatus* with 8M + 10SM + 32ST, and *H. boulengeri* with 6M + 8SM + 36A, with both species presenting large metacentric as the first pair. The constitutive heterochromatin in the large metacentric pair was located in the terminal region of both arms and in the pericentromeric region for *H. multifasciatu*s, while in *H. boulengeri* it was not possible to observe markings for this pair. NORs are also not located in this first metacentric pair, but in other chromosomes. For FISH experiments, only the 5S DNAr probes are located in the first metacentric pair of H. multifasciatus in the pericentromeric region. The other probes (18S DNAr, U1 and U2 RNAsn) were unable to provide signals in this first metacentric pair, but could be observed in other chromosomal pairs for both species. For a better understanding of the evolution of this large metacentric pair, additional cytogenetic information for Spintherobolinae is necessary to affirm whether this metacentric pair is exclusive to Stethaprioninae, as well as obtaining whole chromosome probes to study the sharing of sequences between species of the family.

Video only
YouTube

Current knowledge and importance of the *Ramaria* Fr. ex Bonord. (1851) in Mexico

González-Ávila A.[1], Ramiro Martínez-González C.R.[2], Santiago-Alvarado M.[1] & Espinosa D.[1]*

[1]Facultad de Estudios Superiores Zaragoza, Universidad Nacional Autónoma de México, Batalla del 5 de mayo s/n, Ejército de Oriente, Iztapalapa, CP 09230, Ciudad de México, México. [2]Instituto de Horticultura, Posgrado en Biotecnología Agrícola, Universidad Autónoma Chapingo, Chapingo, México. *Correspondence: dnespinosao@gmail.com.

The genera *Ramaria* is characterized by having basidiomas branched with a choraloid appearance; spores are brown in different shades and ornate. About 500 species are known in the world, the forests of western North America are considered the world center of diversity of this genera. Traditionally, four subgenera are recognized (*Echinoramaria*, *Laeticolora*, *Lentoramaria*, and *Ramaria*), distinguishable by the arrangement of the branches, consistency, habitat, type of ornamentation in the spores, and characteristics of the hyphae. This study presents the current knowledge and importance of this taxon in Mexico. Herbarium records, published works, institutional databases, and personal collections in Mexico show that this genus is represented in the country by 64 species, which chiefly inhabit temperate montane forests. Traditionally, more than half of the species have a nutritional value among the different ethnic groups that inhabit Mexico. It is also known that many of the species are ectomycorrhizal. In comparison to other groups of Basidiomycota, there is little taxonomic knowledge about the species of this genus, due chiefly to the lack of specialists in the group. Conservation of the species of the genus is important for maintaining the delicate balance of temperate Mexican forests, mainly coniferous ones, which require an association with fungi for their survival. The distribution data of the studied specimens were considered to carry out a biogeographic analysis that made it possible to determine areas rich in species, for which a 1° x 1 ° latitude and longitude grid system was used and using the Biodiverse software. The richest areas in species were found in the Tras-Mexicana Volcanic Belt, mainly in the states of Tlaxcala and Estado de México. In addition to a phylogenetic analysis of the Mexican species.

Discovering the biogeographical path before it is lost: A case of study based on the Amphibians from southern India

Video only
YouTube

Hegde A.A. [1*], Dinesh K.P.[2] & Kadadevaru G.G.[1]

[1]Breeding behaviour and Bioacoustics Lab, Department of Zoology, Karnatak University, Dharwad, karnataka, India. [2] Zoological Survey of India (ZSI), Western Regional Centre (WRC), Pune, Maharashtra India. [*]Correspondence: amithegdevargasara@gmail.com.

The Indian' Western Ghats continuous mountain ranges are considered to be one of the global biodiversity hotspots, and also known for high amphibian endemicity on the west coast of peninsular India. On the other hand, the Eastern Ghats represents a discontinuous mountain range close to the East coast of peninsular India that is characterized by a lower amphibian diversity and endemicity. Around 250 species of amphibians are known from the Western Ghats, of which more than 90% are endemic to this region, whereas 27 species are known from the Eastern Ghats. The most recently described species from the Eastern Ghats was *Minervarya kalinga*, which is distributed at an elevation between 600 to 1200 a.s.l. Northeast India is also one of the centers for amphibian diversity and endemicity and as the Eastern Ghats lies between the Western Ghats and the north-eastern Indian region, We hypothesize that the Eastern Ghats could have acted as a ‘land connection’ for the exchange of biota between these two biogeographic regions, To understand distribution and patterns of the amphibians, we used primary data through multiple nocturnal surveys in and around Southern India, observations were made, in several microhabitats in different seasons. Specimen collections were made, natural history information were collected and for molecular studies, 16S rRNA gene sequences generated in the present studies were combined with those from previous studies for analysis. After the morphometric measurements, morphometric variables and Principal Component Analysis (PCA) were performed in *Minervarya kalinga* and secondary literature used for other amphibians (e.g. Anura, Apoda) which are support this hypothesis. *Indosylvirana sreeni* which is thought to be endemic to the southern Western Ghats found in the Eastern Ghats and *Gegenophis orientalis* from the Eastern Ghats is the ancestor clade of all the diverse *Gegenophis* caecilians found in the Western Ghats. *Icthyophis bombayensis* is thought to be endemic to the Western Ghats found in the Eastern Ghats. Higher elevated mountains with forest and freshwater bodies in the Eastern Ghats might have facilitated the dispersal of amphibians across northeastern India and the Western Ghats, for example, a study about the phylogeographic pattern of *M. kalinga* from the Mahendragiri hills of the Eastern Ghats to the Sirsi region of the Western Ghats, will permit to corroborate our hypothesis. Moreover, It is expected that population studies in *M. kalinga* on the region, permitted to validate them as subspecies based on morphological variations due to geographical variations intraspecifics.

Video only
YouTube

Distribution of mites (Mesostigmata: Laelapinae) associated with species of *Oligoryzomys* (Rodentia: Cricetidae) in a geographical gradient

Savchenko E.[1*], Melis M.[1] & Lareschi M.[1]

[1]Centro de Estudios Parasitológicos y de Vectores (CONICET-UNLP), La Plata/Buenos Aires, Argentina. [*]Correspondence: ekaterina@cepave.edu.ar.

Laelapin mites are common parasites of cricetid rodents and worldwide distributed. A comprehensive knowledge of the distribution of both host and mite is needed, especially when factors and patterns of distribution are studied to evaluate variation in the composition and structure of biological communities across space and/or over time. Although the distribution of the *Oligoryzomys* species (also known as pygmy rice rats) is broadly known, their associations with laelapids mites are scarce or null for some areas in Argentina. In the present study, we report new records of laelapid mites associated with *Oligoryzomys flavescens* and *O. nigripes*, obtained during collections carried out for more than a decade in 35 localities situated between 25 to 35 degrees South and from 53 to 58 degrees West in Argentina. We found the same parasitic assemblage of the laelapids species *Androlaelaps fahrenholzi*, *Gigantolaelaps wolffsohni*, *Mysolaelaps microspinosus* and a new, yet not described species from the genus *Laelaps*, independent from sympatric or allopatric distribution of the rodent, its geographical position, or the host species itself. Solely the species *Mysolaelaps parvispinosus* was restricted to the northeastern and was absent in the central part of the area, even when both rodents were present. In contrast, the species *Laelaps schatzi* was unique in association with *O. flavescens*, while *Laelaps paulistanensis* was exclusive to *O. nigripes*, regardless of locality. The results support that species reflect the distribution of each host and together with known reports of Brazil and Uruguay, also almost the whole registered distribution of the rodent(s). The exception showed by *M. parvispinosus* could be more associated with the geographical gradient. Hence, the majority of the reported mites showed a wide distribution in Argentina, some extending more than 1,500 km. This indicates a strong host-mite association and a deep coevolutionary history, especially for the *Laelaps paulistanensis*, *L. schatzi* and their correspondent rodent species.

Do neotropical lineages from *Coprinopsis* have higher diversification rates?

Video only
YouTube

Schünemann B.L.B.[1*], Reginato M.[1], & Silveira R.M.B.[1]

[1]Federal University of Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil
[*]Correspondence:barbarabotura@hotmail.com.

Coprinoid fungi is a saprophytic group mushroom known to have the autolysis of the pileus and hymenophore as part of the sporulation process. *Coprinopsis* P. Karst. (Psathyrellaceae, Basidiomycota) is the major coprinoid genera, with ca. 160 species. Most of the species were described from Europe, and just a few studies have been developed in the Neotropics. Furthermore, the diversification dynamics in within the family is largely unknown, despite studies showing that an increase in diversification rates was detected in the crown of Psathyrellaceae. In this study, we aim to estimate and compare the diversification rates of coprinoid lineages from *Coprinopsis*, including neotropical lineages for the first time. We used ultrametric dated phylogenys, including 196 sequences of *Coprinopsis* from nITS region constructed from GenBank sequences. Phylogenetic uncertainty was accounted for (350 samples from the posterior were used). To test our hypothesis that Neotropical lineages present higher diversification rates, we built eight BiSSE (Binary State Speciation and Extinction) models: 1) zero variation, 2) speciation variable, 3) extinction variable, 4) speciation and extinction variable, 5) transition variable, 6) speciation constant, 7) extinction constant and 8) all rates variable, using diversitree package in the R software. The best-fit model was selected based on the smaller mean of AIC, and significance was assessed with a T test. Our results showed that the best model to explain the diversification dynamics of *Coprinopsis* is the extinction constant with speciation and transition rates variable (AIC mean = 0.94), followed by the model of speciation constant with extinction and transition rates variable (AIC mean = 1.15). The lineages from different regions have significant differences in diversification rates (state 0 (other regions) mean± sd= -0.024 ± 0.033, state 1 (neotropics) = 0.31 ± 0.39, $t = -14.454$, $df = 349$, $p < 0.001$). The neotropical lineages have a highest rate of speciation and smaller rates of extinction, resulting in the higher rate of diversification. We also estimated dispersal rates from one region to another, and our results showed that dispersals to the Neotropical region are more frequent (mean 0.532 ± 0.195), than the opposite (mean 0.018 ± 0.017). We can conclude that Coprinopsis lineages have different diversification rates depending on the region, and the neotropics lineages have higher rates.

Video only
YouTube

Evolution of ploidy in amphibians recovered from phylogenetic reconstruction

Silva C.M.[1*], Almeida-Silva D.[1], Barcelos L.A.[1,2] & Verdade V.K.[1]
[1]Universidade Federal do ABC, São Bernardo do Campo, São Paulo, Brazil.
[2]Laboratório de Paleontologia, Universidade de São Paulo, Ribeirão Preto, São Paulo, Brazil. *Correspondence: cecilia.silva@aluno.ufabc.edu.br.

Phenotypic variation leads to differential fitness and enables natural selection to operate among individuals cohabiting. In a broader sense, the environment plays the role of a filter for biodiversity, becoming responsible in a large extent for the speciation process. Also, phenotype emerges as a balance between genotype and the environmental mediation, and this interaction may lead to different responses according to the context. Due to this scenario, diverse phenotypes may be expressed from the possible genotype combinations. Therefore, in general lines, the more genotypic variability, the wider are phenotypic possibilities, resulting in biodiversity as far as we know. Polyploidization events would be advantageous by increasing genotypic variation, when not disrupting or impeding developmental routes. Duplicating the whole genome content leads to an increase in mutation rates and provides a buffer for harmful recessive alleles or deleterious mutations, by producing gene redundancy. In fact, occurrence of polyploidization is being assigned as an enhancer to species diversification among eukaryotes (e.g. angiosperms). Although less common in Metazoa, many cases of polyploidy are recognized in Anura, particularly in groups of early diversification. Once anurans have the greatest diversity of occupied ecological niches among terrestrial vertebrates, this early occurrence of polyploidy may have played an important role in the group diversification. To address this issue we performed an ancestral state estimation for polyploidization in a phylogeny with 1405 amphibian species. For our analysis, we use the larger phylogenetic dated tree available and we compiled ploidy information in the literature. Our approach also allowed the verification on how these events are distributed along the phylogeny of Anura, and to compare this frequency with other Lissamphibia. Ancestral state estimation was performed in a maximum likelihood framework, under an equal rates model. Our findings do not argue in favor of a polyploidization event in the most recent common ancestor of Anura, but suggest occasional events occurring across the phylogeny in highly diverse groups. The polyploidization scenario for Pipoidea recovered in our analysis, for instance, is congruent with the paleodiversification known for this clade (i.e. more than 40 extinct species described). Moreover, these events are much more frequent in Anura than among other amphibians. Thereafter, we calculated D statistics, the suitable metric of phylogenetic signal for binary characters, resulting in a clumped pattern. In short, the comprehension of the evolution of amphibian polyploidy evokes additional factors, to be discussed from this phylogenetic framework.

Genic content indicates a common ancestry for two B chromosome variants in *Psalidodon fasciatus* (Cuvier 1819) (Characiformes, Characidae).

Video only
YouTube

Vidal, M.R.[1*], Silva, D.M.Z.A.[1], Lasmar, L.F.[1], Oliveira, C.[1], Foresti, F.[1]

[1]São Paulo State University - UNESP, Botucatu, São Paulo, Brazil. [*]Correspondence: mateus.vidal@unesp.br.

B chromosomes are additional genomic elements found in many eukaryotes. The fish genus *Psalidodon* displays a wide diversity of these elements, and the species *P. fasciatus* has at least four B chromosome variants, of which the two large metacentric elements are of interest for this study. The BfMa variant found in individuals of Alambari river population (Piratininga, São Paulo) presents interspersed heterochromatic blocks, while the BfMb variant identified in individuals of Araras stream population (Araras, São Paulo) presents a whole heterochromatic nature. Thus, the present study aimed to compare genic composition of BfMa and BfMb variants in *Psalidodon fasciatus* to test a possible common origin, being this kind of analysis employed for the first time in the comparison of two different B chromosome variants in the same species. The classical cytogenetic analysis performed to identify presence of B chromosomes included cytological preparations of metaphasic chromosomes and use of C-banding technique. For genic content analysis, qPCR assays were performed using primers designed in a previous study for the large metacentric B chromosome of the congeneric species *P. paranae*. A total of 12 genes were analyzed using the autosomal single-copy gene hprt as reference. Relative quantification of copy number was performed using the $2^{-\Delta Ct}$ method. Statistical analyzes were performed using two-group comparisons by the Gardner-Altman estimation plot method. The qPCR analysis showed that 10 genes have a higher abundance in 1B individuals, and among those, six genes were present in both variants. Moreover, each variant also presented two exclusive genes, and two tested genes were not found in any variant. Our data showed a high gene content similarity between the two B chromosome variants of *P. fasciatus.* As previously reported, the large metacentric B chromosome of *P. paranae*, *Psalidodon scabripinnis*, *Psalidodon bockmanni*, and *P. fasciatus* originated about 4 mya ago from a common ancestor. However, the high similarity in BfMa and BfMb gene content cannot be parsimoniously explained by chance or independent origin. It is highly likely that both variants originated in a common ancestor and then later diversified. In conclusion, despite its common origin, different B chromosomes found in the same species are able to diversify at the point of changing their gene content or lose regions to which congeneric primers were designed to bind. These findings open new perspectives in B chromosome research, and the usage of high-throughput NGS sequencing technologies will allow us analyze the full content of these chromosomes.

Video only
YouTube

Intra-specific phylogeny of the native Patagonian grass *Festuca pallescens*

Guidalevich V.[1*], Azpilicueta M.M.[1], López A.[1], Marchelli P.[1*]

[1]Instituto de Investigaciones Forestales y Agropecuarias Bariloche (IFAB INTA Bariloche-CONICET), San Carlos de Bariloche, Río Negro, Argentina. *Correspondence: guidalevich.veronica@inta.gob.ar.

Drylands constitute the largest terrestrial biomes, highly sensitive to climate change and desertification, and known for their environmental heterogeneity. Widely distributed species are usually adapted to these heterogeneous environments characterized by climatic gradients which promote the expression of phenotypic variability and hybridization processes. The Patagonian native grass *Festuca pallescens* has a broad geographic distribution, occurring at highly diverse environments. Because of the broad phenotypic plasticity of this species, it can be hard to identify individuals on the field, particularly in extreme suboptimal habitats where repeated exposure to stressful conditions might enhance phenotypic variation or local adaptations. In addition, its ecological niche partly overlaps with other native grasses like *Festuca argentina* and *F. gracillima*, which also show morphological variability. Given the scarce information about the genetic variation of *F. pallescens*, and the possible hybridization and speciation processes at suboptimal conditions, the objective of this study was to reconstruct the phylogenetic relationships between populations of this forage grass. We included the sympatric species *F. argentina* and *F. gracillima*, as well as other fescues of the genus. A total of 20 populations along the distribution range of the species, which encompasses around 1.800 km of Patagonia, were sampled. Sequences from the ITS region, which allows phylogenetic reconstructions, were obtained and complemented with sequences of the chloroplast marker *trnL-F*. Sequences of species from other regions were retrieved from NCBI. The variation detected with these two markers allowed us to identify four variants with a clear geographic distribution. Edge populations were distinctly different from most of the populations noticing a northern, a north-eastern and two southern variants. From these, the north-eastern variant resembles *F. argentina*, and the southern variant was closely related with *F. gracillima*. These results constitute the first reconstruction of Patagonian fescues phylogeny and highlight the relevance of suboptimal regions for possible speciation and hybridization processes.

Molecular and taxonomic evidence unmasking hidden species diversity in the genus *Acrobrycon* (Characiformes: Characidae)

Video only
YouTube

Briñoccoli Y.F.[1,*], Bogan S.[2], Arcila D.[3], Rosso J.J.[4,6], Mabragaña E.[4,6], Delpiani M.S.[4,6], Díaz de Astarloa J.M.[4,6] & Cardoso J.P.[5,6]

[1]Laboratorio de Ictiofisiología y Acuicultura, Instituto Tecnológico Chascomús, Universidad Nacional de San Martin. Chascomús, Buenos Aires, Argentina. [2]Fundación de Historia Natural "Félix de Azara", Centro de Ciencias Naturales, Ambientales y Antropológicas. Universidad Maimónides. Buenos Aires, Argentina. [3]Sam Noble Oklahoma Museum of Natural History and Department of Biology, University of Oklahoma. Norman, Oklahoma, USA. [4]Grupo de Biotaxonomía Morfológica y Molecular de Peces, Instituto de Investigaciones Marinas y Costeras (IIMyC), Facultad de Ciencias Exactas y Naturales, Universidad Nacional de Mar del Plata. Mar del Plata, Buenos Aires, Argentina. [5]Laboratorio de Sistemática y Biología Evolutiva, Facultad de Ciencias Naturales y Museo, Universidad Nacional de La Plata. La Plata, Buenos Aires, Argentina. [6]Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), Buenos Aires, Argentina, Godoy Cruz 2290, CABA, Argentina. [*]Correspondence: ybrinoccoli@gmail.com.

Patterns of fish diversity in the Neotropics are still poorly understood and mostly limited to higher taxonomic levels (e.g., order or family level). Here, we conducted a review of the neotropical genus *Acrobrycon* distributed from the western Amazon Basin to the northwestern region of the La Plata Basin. A previous morphological study synonymized the two traditional recognized species in the genus, *A. ipanquianus*, distributed from the western portion of the Amazon River to the northwest region of the La Plata River Basin, and *A. tarijae*, described from the Lipeo River in Bolivia. We revisited in 24 individuals this result by collecting additional morphometric, meristic, and genetic data (COI mitochondrial gene), and three important processes of geographic isolation in La Plata River Basin were collected. Our results revealed a more complex history of diversification and geographic distribution across *Acrobrycon* species than previously suspected. We present new evidence that leads us to reconsider the validity of *A. tarijae* formerly synonymous of *A. ipanquianus*, which are distinguished by the number of vertebrae (37-39 vs. 41-42), pleural ribs (12-13 vs 14), and unbranched rays (v-vi vs. ii-iii) in the anal fin, respectively. Our genetic result, indicated two major genetic clusters of *A. tarijae*: the first group consisted of specimens from the Bermejo, Pilcomayo, Itiyuro and Juramento River Basins (northern Argentina), and the second group is composed of specimens from the southernmost basins, such as the Salí River in Tucumán and the Quinto River in the province of San Luis separating these groups at the genetic level by 1.87%. This result suggests that the genetic structure may be a consequence of the geographical distance that separates the two groups and the type of basin. Our results also provided evidence of a range expansion of *A. tarijae* to the Quinto River, this being the only record known for this province and the southernmost known for this species.

Video only
YouTube

Molecular identification of Neotropical fish species of the genus *Piabucus* Oken 1817 (Characiformes, Iguanodectidae)

Ribeiro-Silva L.R.[1,*], Melo B.F.[1], Foresti F.[1] & Oliveira C.[1]

[1]Department of Structural and Functional Biology, Biocience Institute, Botucatu, SP, Brazil. *Correspondence: lrr.silva@unesp.br.

Iguanodectidae is the eighth most diverse family of Neotropical Characiformes, despite being represented by only three genera, *Bryconops* Kner 1858, *Iguanodectes* Cope 1872 and *Piabucus* Oken 1817. The species of the family are distributed across the Amazon, Orinoco, Essequibo, São Francisco and Paraná-Paraguay basins, in the coastal rivers in Venezuela, Guyana, and northeastern Brazil, with *Piabucus melanostoma* being the only species of Iguanodectidae found in the Paraguay River basin, including the Pantanal. The genus *Piabucus* is distinguished from *Bryconops* and *Iguanodectes* by the presence of a long pectoral fin, almost reaching the origin of the pelvic fin and a well-developed pectoral keel, elongated body, multicuspidated teeth, united gill membranes free of the isthmus, posterior end of the maxilla extending to the eye, origin of the dorsal fin usually posterior to the middle of the body and relatively long anal fin. The genus *Piabucus* has only three valid species: *Piabucus caudomaculatus* Vari, 1977, *Piabucus dentatus* (Koelreuter, 1763) and *Piabucus melanostoma* Holmberg, 1891. To date, there are no inclusive genetic studies that test relationships within the genus *Piabucus* and there are no published taxonomic reviews for *Piabucus.* Therefore, the aim of the present study was to use, through molecular tools, to evaluate the possible existence of new species within the genus *Piabucus*, using the cytochrome c oxidase subunit I (COI) DNA barcode technique, associated with delimitation methods of species. The methods performed in the present study demonstrated substantial intraspecific variation in both groups, separating the species of *Piabucus* into five different possible strains. Genetic distance values of mtDNA COI sequences indicated high values with intraspecific variation between groups, *Piabucus melanostoma* Poconé, MT (24.7%), *Piabucus melanostoma* Cáceres, MT (25.8%), *Piabucus dentatus* Waini river (25.3 %), *Piabucus dentatus* Mana river (24.7%) and *Piabucus caudomaculatus* Solimões river (24.9%), these results show possible species not yet described within the genus *Piabucus.*

Video only
YouTube

Morphology of jewel beetles ovipositor and the evolution of leaf-mining habit in Tracheini (Coleoptera, Buprestidae, Agrilinae)

Migliore L.J.[1,*]

[1]Museu de Zoologia da Universidade de São Paulo, Av. Nazaré, 481 – Ipiranga, 04263-000, São Paulo, SP, Brazil. *Correspondence: lmigliore@usp.br.

Agrilinae is one of the most representative and most diverse of the six subfamilies of the family Buprestidae. It includes exclusively endophyte species, divided into four tribes roughly classified according to the eating habit of the larvae, such as xylophages (Agrilini and Coraebini), stem miners of herbaceous plants (Aphanisticini),

and leaf miners (Tracheini). The phylogenetic relationships among the twelve leaf-mining genera currently included in the tribe Tracheini and the relationship among Agrilinae tribes are not well resolved. It is supposed that Tracheini is not monophyletic and the larval leaf- mining habit has multiple origins inside Agrilinae. The subtribe Rhaeboscelidina (Agrilini), was established especially based on the particular presence of four styli in the ovipositor, as opposed to the usual pair found in Buprestidae. Up to now, the study of the female genitalia has been quite overlooked in Buprestidae. However, the investigations about this structure proved to be useful in taxonomic and systematic studies. The presence of an extra pair of styli in the ovipositor had not been mentioned in any group beyond Rhaeboscelidina, currently including *Rhaeboscelis* Chevrolat, 1838, *Paragrilus* Saunders, 1871 and *Velutia* Kerremans, 1900. This type of ovipositor represents a characteristic unique not only in Buprestidae, but also within Coleoptera. Authors from the 20th century have already pointed out the remarkable morphological similarities between members of Rhaeboscelidina (Agrilini) and the Leiopleurina (Tracheini), without considering the study of their ovipositor. The most recent phylogenetic study has recovered such subtribes as closely related. During a systematic study of Tracheini, aiming to investigate the evolution of the leaf-mining behavior, the female genitalia and ovipositor of Agrilinae species were thoroughly explored. It was found the double-paired styli in species of Leiopleurina genera, *Leiopleura* Deyrolle, 1864 and *Callimicra* Deyrolle, 1864. The presence of ovipositor with four styli in these two genera of Leiopleurina suggests that the ovipositor of these species is highly derived and evidence that probably, Leiopleurina and Rhaeboscelidina form a monophyletic grouping, corroborating the similarity pointed out by previous authors. Also, the inclusion of female genitalia characters can help to elucidate the origin and evolution of leaf-mining species, since the study of this structure has proved to be useful in systematics.

Multilocus phylogeny and historical biogeography of *Hypostomus* shed light on the processes of fish diversification in La Plata Basin

Video only
YouTube

Cardoso Y.P.[1,4*], Jardim de Queiroz, L.[2,4], Bahechar I.A.[2], Posadas P.E.[1] & Montoya-Burgos J.I.[2,3]

[1]Laboratorio de Sistemática y Biología Evolutiva, Facultad de Ciencias Naturales y Museo, Universidad Nacional de La Plata, Consejo Nacional de Investigaciones Científicas y Técnicas, Paseo del Bosque S/N, B1900FWA, La Plata, Buenos Aires, Argentina. [2] Department of Genetics and Evolution, University of Geneva, 30 quai Ernest Ansermet, 1211 Geneva 4, Switzerland. [3] Institute of Genetics and Genomics in Geneva (IGE3), University of Geneva, Geneva, Switzerland. [4] These authors contributed equally. [*]Correspondence: yamilapcardoso@gmail.com.

Distribution history of the widespread Neotropical genus *Hypostomus* was studied to shed light on the processes that shaped species diversity. We inferred a calibrated phylogeny, ancestral habitat preference, ancestral areas distribution, and the history of dispersal and vicariance events of this genus. The phylogenetic and distribution analyses indicated that *Hypostomus* species inhabiting La Plata Basin do not form a monophyletic clade, suggesting that several unrelated ancestral species colonized this basin in the Miocene. Dispersal to other rivers of La Plata Basin started about 8 Mya, followed by habitat shifts and an increased rate of cladogenesis. Amazonian *Hypostomus* species colonized La Plata Basin several times in the Middle Miocene, probably via the Upper Paraná and the Paraguay rivers that acted as dispersal corridors. During the Miocene, La Plata Basin experienced marine incursions, and geomorphological and climatic changes that reconfigured its drainage pattern, driving dispersal and diversification of *Hypostomus.* The Miocene marine incursion was a strong barrier and its retraction triggered *Hypostomus* dispersal, increased speciation rate and ecological diversification. The timing of hydrogeological changes in La Plata Basin coincides well with *Hypostomus* cladogenetic events, indicating that the history of this basin has acted on the diversification of its biota.

Video only
YouTube

Phylogenetics of the Atlantic reef-building coral *Favia* spp. (Scleractinia, Mussidae)

Adam C.L.[1,*], Toonen R.J.[2], Carlon D.B.[3] & Barbeitos M.S.[1]

[1] Universidade Federal do Paraná, Curitiba, Paraná, Brasil. [2] Hawai'i Institute of Marine Biology, Manoa, Hawai'i, USA. [3] Bowdoin College, Brunswick, Maine, USA.
[*]Correspondence: carolinaladam@gmail.com.

The skeletal traits traditionally applied in the taxonomy of reef-building corals are known to carry high levels of morphological variation. Genomic data showed that many of the traditional Scleractinian families are not monophyletic. At lower taxonomic levels there is extensive debate on the validity of multiple coral species, exemplified by the two Atlantic mussids *Favia fragum* and *F. gravida.* The two species display overlap in their diagnostic morphological characters, leading some researchers to suggest that the latter is an ecomorph of the former. Nonetheless, they have an allopatric distribution and evidence of genetic differentiation based on nuclear and molecular markers. *F. gravida* occurs in the South Atlantic and *F. fragum*mostly in the Caribbean, but they are listed as a single species in the IUCNRed List with a distribution that covers the range of both species. To assess the molecular support for the current taxonomy of the Atlantic *Favia*, we employed RAD-seq discovered markers (single nucleotide polymorphisms - SNPs). Using bioinformatics tools, we also recovered a significant number of ultraconserved elements (UCEs) using a previously published bait set targeting Hexacorallia loci. In both SNP and UCE datasets the two species were recovered as reciprocally monophyletic in our phylogenetic reconstructions, regardless of the varying levels of missing data and matrix completeness. A clade comprised of exclusively Brazilian samples was recovered with high branch support values in all datasets, and the Ascension Island specimen was recovered as a distinct lineage within the *F. gravida* clade. Our results demonstrate the need to re-evaluate the threat status of Atlantic *Favia* in the IUCN's Red List, adding *F. gravida* as a separate species whose distribution range does not overlap with *F. fragum.* Furthermore, we have shown that it is possible to retrieve capture-based UCE loci from RAD-seq generated data given a suitable bait set.

Phylogeny and phylogeography based on the complete coding sequences of the viral matrix protein Z of haemorrhagic fever Mammarenaviruses in South America

Video only
YouTube

García R.S.L.G[1*]

[1]Brazilian Army Institute for Chemical, Biological, Radiological and Nuclear Defense (IDQBRN), Brazilian Army Technological Center (CTEx), Rio de Janeiro, RJ, Brazil.
[*]Correspondence: garcia.romulo@eb.mil.br.

Many mammarenavirus are the etiologic agents of viral haemorrhagic fever disease and coexist in eight South America countries (Argentina, Bolivia, Brazil, Colombia, French Guiana, Paraguay, Peru and Venezuela). In this work, phylogeographic reconstructions of 96 sequences of mammarenavirus were performed. All RNA L nucleotide sequences corresponding to the Z protein from mammarenaviruses were acquired in the comprehensive GenBank® genetic database to compose the necessary dataset for phylogeography analysis. Sequences were processed through NGPhylogeny workflow and the geographical regions of each viral isolate from hosts were retrieved through GeoBoost2 for further observation of fifteen viral haemorrhagic fever mammarenaviruses distribution patterns for Allpahuayo mammarenavirus (ALLV), Argentinian mammarenavirus which is also known as Junin mammarenavirus (ARGV), Apore mammarenavirus (APOV), Brazilian mammarenavirus which is also known as Sabia mammarenavirus (SABV), Cali mammarenavirus which is also known as Pichinde mammarenavirus (CALV), Chapare mammarenavirus (CHAV), Cupixi mammarenavirus (CUPV), Flexal mammarenavirus (FLEV), Guanarito mammarenavirus (GUAV), Latino mammarenavirus (LATV), Lymphocytic choriomeningitis mammarenavirus (LCHV), Machupo mammarenavirus (MACV), Oliveros mammarenavirus (OLIV), Paraguayan mammarenavirus (PARV), Pirital mammarenavirus (PIRV), Serra do navio mammarenavirus, also known as Amapari mammarenavirus (AMAV) and Xapuri mammarenavirus (XAPV). Phylogeographic analysis was performed only with sequences that have complete information on the date and place of collection. The multiple alignments of the selected sequences were performed using MAFFT version 7.4701, Alignment Curation was performed using BMGE version 1.12 and Tree inference was performed using FastTree version 2.1.11., all of them using the multi platform NGPhylogeny followed by phylogenetic tree performed with Interactive Tree Of Life program version 6. The geographical data was generated by GeoBoost2 and plotted on a map to visualize the global distribution routes of the mammarenavirus through GeoJSON. Group 1, mainly formed by LCHV strains, has not been noticed out from Argentina and Bolivia. Group 2, mainly formed by ARGV, CALV, CUPV, SABV, PIRV, ALLV and MACV strains has been noticed across Argentina, Bolivia, Brazil, Peru and Venezuela, being the bigger group in presence. Bolivia, Brazil, Paraguay and Venezuela have Group 3, mainly formed by PIRV, FLEV and LATV strains and Group 4, mainly formed by SABV, ARGV, MACV, AMAV and GUAV strains. Both

Group 3 and Group 4 has not been noticed outside from Bolivia,Brazil, Paraguay and Venezuela in this study.

Video only
YouTube

Phylogeny of the enigmatic knifefish *Tembeassu* (Gymnotiformes: Apteronotidae), with description of a new species from the upper Rio Paraná basin, Brazil

Peixoto L.A.W.[1,*], Campos-da-Paz R.[2], Menezes N.A.[1], de Santana C.D.[3] & Datovo A.[1]

[1]Museu de Zoologia da Universidade de São Paulo, São Paulo, SP, Brazil. [2]Universidade Federal do Estado do Rio de Janeiro, Centro de Ciências Biológicas e da Saúde, Instituto de Biociências, Rio de Janeiro, RJ, Brazil. [3]National Museum of Natural History, Smithsonian Institution, Washington, DC,USA. [*]Correspondence: luizwp@yahoo.com.br.

The electric knifefish genus *Tembeassu* was originally described to include a single species from the Rio Paraná basin, Brazil. The genus was diagnosed solely by the presence of an enlarged fleshy lateral lobe and a tooth patch at the anterior portion of the oral cavity roof. The single species, *Tembeassu marauna*, was recently redescribed and, based on data from X-ray microcomputed tomography (μCT scan), the taxon was phylogenetically positioned in a polytomy at the base of the Apteronotidae. Detailed examination of gymnotiform material deposited at the fish collection at the Museu de Zoologia da Universidade de São Paulo (MZUSP) revealed a set of apteronotid specimens collected in a cofferdam at Ilha Solteira (Paraná river basin), near to the type-locality of *T. marauna*, and Araguari River, a tributary of the Paranaiba River, Brazil. These specimens share several morphological characters with *T. marauna*, but is distinguished from the congener by other features such as the absence of tooth patch at the anterior portion of the oral cavity roof; the external corner of the mouth slightly surpassing the vertical through posterior margin of the posterior nares; and a set of measurements and counts. All attempts of extraction and amplification of DNA from the formalin-fixed specimens of both species of *Tembeassu* were unsuccessful so that only morphological data for the genus were coded. Morphological data from *Tembeassu*, as well as new morphological characters, were incorporated into the total-evidence matrix recently published composed of 168 terminal taxa and 5504 characters, being 227 from morphology and 5277 from three nuclear (RAG1, RAG2, Zic) and three mitochondrial markers (16S, COI, and CytB). The total evidence analysis aimed to include the largest amount of evidence possible to infer the phylogenetic position of the genus within Apteronotidae. The combined matrix was analyzed under Bayesian inference and the morphological partition alone under the parsimony optimality criterion. Preliminary results recover *Tembeassu* as a monophyletic linage. The genus was resolved as the sister group of Apteronotini in the total-evidence analysis and as sister to the clade *Megadontognathus* + *Apteronotus s. s.* based solely on the morphology dataset.

Rediscovering *Cearanthes* Ravenna (Amaryllidaceae): a monotypic genus from the Brazilian Caatinga on the brink of extinction

Video only
YouTube

Campos-Rocha A.[1,*], Dutilh J.H.A.[1], Messias P.A.[2], Castro A.S.F.[3] & Meerow A.W.[4]

[1]Universidade Estadual de Campinas, Campinas, São Paulo, Brazil. [2]Universidade Federal de São Carlos, Sorocaba, Brazil. [3]Movimento Pró-Árvore, Fortaleza, Ceará, Brazil. [4]Arizona State University, Arizona, USA. [*]Correspondence: camposrocha@hotmail.com.

Cearanthes Ravenna was described as a monotypic genus based on a single specimen, which was collected in the early 1970s, consisting of only two inflorescences and very limited information on its distribution and habitat. Ravenna (2000) suggested that *Cearanthes* should belong to the tribe Griffinieae, and is possibly related to the genus *Griffinia* Ker Gawl., although its phylogenetic position had never been tested. There is no subsequent record of the occurrence of *Cearanthes*, which came to be ignored or considered a doubtful taxon. Here we report its rediscovery almost fifty years after its first and single record, with four remaining populations located in the Serra da Ibiapaba, the border between the Brazilian states of Ceará and Piauí. Fresh DNA material collected provides an opportunity to rigorously test its position among South American Amaryllidaceae in a broad phylogenetic context. Next generation sequence capture recovered coding regions from hundreds of low copy nuclear genes and 75-90% of the entire plastome for phylogenetic reconstruction. Previously, a hypothesis with the nuclear marker ITS was elaborated, revealing strong support for *Cearanthes* as sister genus to *Griffinia*. Its rediscovery revealed that its original description was incomplete and partially incorrect, and had ignored its main diagnostic features. As part of our ongoing taxonomic revision of Griffinieae, we also present a corrected and improved description of the genus *Cearanthes* and its type species, *C. fuscoviolacea*, plus a detailed illustration and previously unpublished in vivo photos of the species. Additionally, comments are provided on its geographic distribution and conservation status, and the major pressures and threats affecting their populations are carefully examined. With an AOO of 16 km2 and EOO of 250 km2, *C. fuscoviolacea* is considered endangered (EN) based on International Union for Conservation of Nature (IUCN) sub-criteria B1ab(i, ii, iii, v)+2ab(i, ii, iii, v) due to the low number of known records (<5) and continuous decline of EOO, AOO, and habitat quality. The rediscovery of *C. fuscoviolacea*, a taxon with unique morphological and ecological features among Griffinieae, contributes to ongoing studies on the tribe, enabling a better understanding of its evolutionary history.

Video only
YouTube

The complete mitochondrial genome of the Honduran white bat *Ectophylla alba* (Allen, 1982) (Chiroptera: Phyllostomidae)

Vivas-Toro I.[1,*], Ortega J.[1] & Baeza J.A.[2,3,4]

[1]Laboratorio de Bioconservación y Manejo, Departamento de Zoología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, CDMX, México. [2]Department of Biological Sciences, Clemson University, Clemson, SC, USA. [3]Smithsonian Marine Station at Fort Pierce, Fort Pierce, FL, USA. [4]Departamento de Biología Marina, Facultad de Ciencias del Mar, Universidad Católica del Norte, Coquimbo, Chile. [*]Correspondence: isavivas94@gmail.com.

The Honduran white bat, *Ectophylla alba* (Allen, 1982), is one of eight species belonging to the family Phyllostomidae that exclusively roosts in tents. Due to its restricted distribution, habitat specificity, and diet requirements, *E. alba* has been strongly affected by habitat loss and fragmentation during the last decade. In this study, we developed the first genomic resource for this species; we assembled and analyzed the complete mitochondrial genome of *E. alba* in detail. It was assembled *de novo*, based on Illumina paired-end sequencing, using a seed-extend algorithm. The mitogenome of *E. alba* is 16,664 bp in length and is comprised of 13 protein coding genes (PCGs), 2 ribosomal RNA genes, 22 transfer RNA genes (tRNAs), and a putative Control Region (CR) 1,232 bp in length. Gene arrangement in the mitochondrial chromosome of *E. alba* is identical to that reported before in other species of co-familiar bats. All PCGs are under purifying selection, with atp8 experiencing the least selective pressure. In all PCGs, codons ending with adenine are preferred over others ending in thymine and cytosine. All tRNAs exhibit a cloverleaf secondary structure except tRNA-Serine 1 which lacks the DHU stem. The CR of *E. alba* exhibits three domains commonly described in other mammals, including bats; i. extended terminal associated sequences (ETAS), central, and conserved sequence block (CSB). A maximum likelihood phylogenetic reconstruction of the family Phyllostomidae based on all 13 mitochondrial PCGs confirms the monophyletic status of the subfamily Sternodermatinae and indicates the close relationship between *E. alba* and the genus *Artibeus*. This is the first genomic resource developed for *E. alba* and represents the first step to improving our understanding of the genomic underpinnings involved in the evolution of specialization as well as acclimatization and adaptation to local and global changes of specialist bats.

The kids are growing up so fast (are they?). What drives body size variation in species whose tadpoles grow in lotic versus lentic water?

Video only
YouTube

Rama T.R.[1,*], Almeida-Silva D.[1] & Verdade V.K.[1]
[1]1Universidade Federal do ABC, São Bernardo do Campo, São Paulo, Brasil.
[*]Correspondence: r.rama@aluno.ufabc.edu.br.

Species that have wider phenotypic ranges may have a selective advantage when facing a given selective pressure in unstable and heterogeneous environments. The phenotypic plasticity can be verified in different aspects of the biology of a species, and is more important when affecting morphology in groups that present a complex life cycle. In these groups, morphological and ecological characteristics vary substantially over the ontogeny, with very different niches occupied by larvae and adults. Anurans are the most illustrative example of this scenario among terrestrial vertebrates. Recent findings evidenced that the relation between larval and adult body size, for instance, varies along the phylogeny of the group. However, a comprehensive mechanism driving plasticity in relation to body size is still in debate. In the case of aquatic tadpoles, the relation between competition (intra- and interspecific) and predation seems to play a fundamental role in the scene. This relation affects foraging time and amount of feeding, acting on the balance between growth and developmental rates of tadpoles. Here we argue that energy from resources is prioritized differently between species whose tadpoles develop in lentic or lotic environments. As such, we expect to find different growth versus developmental rates among tadpoles using one or another of these water bodies, and also different actors promoting variation in larval size between species that use both types of water bodies for reproduction and specialists using either lotic or lentic water for reproduction. To test our hypothesis we measured the total length of tadpoles in the initial developmental stages of four species (*Scinax fuscovarius*, associated with lentic environment, *Hylodes asper* associated with lotic environment and *Bokermannohyla hylax* and *Rhinella* cf. *ornata* which both reproduce and develop in both environments). We also collected data from biotic and abiotic variables from the water bodies studied. Unexpectedly, the results of multiple regression models suggest that the same variables (canopy closure and dissolved oxygen) explain larval size variation in both lentic and lotic environments. However, it is clear that the same factors trigger different responses among species with reproduction associated with lotic or with lentic water, versus more generalist species that use both kinds of environments. Canopy closure and dissolved oxygen seem to positively affect size in *H. asper* and *S. fuscovarius*, whereas negatively affect it in *B. hylax* and *R.* cf. *ornata.* Our results add an important contribution to discuss how autecology and natural history modulate larval size evolution in Anuran.

Author Index