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PLENARY TALKS

P1

Biotic changes on Chimborazo, the cradle of plant biogeography

Naia Morueta-Holme, University of Copenhagen

The legacy and works of Alexander von Humboldt not only constitute the foundation of biogeography, but also the (probably) oldest dataset on elevation ranges of plant taxa. In this talk, we travel back to the cradle of plant geography both in the literal and figurative sense. I present the results of a 2012 resurvey of Chimborazo, finding strong upward shifts in the vegetation, and discuss some of the challenges and potentials of using historical datasets for documenting biotic responses to global environmental change. We also explore Humboldt's pioneering insights on the broad-scale patterns of nature and relevance to biogeography. I highlight a few ways in which our understanding of the world has remained much the same as Humboldt's, and views that have changed drastically thanks to new theories, data, and methods. Finally, I argue that his holistic approach and view that "everything is interconnected" remains ever so important both to the field and for addressing global challenges of the Anthropocene.

P2

Hybridization fuels adaptive radiation of cichlid fishes

Joana Meier, University of Cambridge; Ole Seehausen, University of Bern and EAWAG, Switzerland

Lake Victoria in East Africa was colonized by five different lineages of cichlid fishes. One of them diversified into 500 species, whereas the others did not even speciate once. This is highly replicated among all major lakes in the Lake Victoria Region, whereby always the same lineage diversified in each lake forming so-called adaptive radiations. With genomic and phylogenetic methods, we found that this one lineage is able to diversify rapidly because it is of hybrid origin between two divergent cichlid lineages from different drainage systems. The large genetic variation resulting from the combined gene pools of the two ancestral lineages, facilitated rapid diversification. Even though Lake Victoria is only 15,000 years old, this lineage diversified into 500 species ranging from algae scrapers, molluscivores, and zooplanktivores to large predators. We show that these species really evolved in only 15,000 years in the lake through selection on pre-existing variation that was generated through the hybridization event at the origin of the species group. Similarly, in the African Lake Mweru, we discovered multiple adaptive radiations of cichlid fishes. We found that all of them evolved from hybrid ancestry between two or more ancestral lineages from different drainage systems that came into contact during a river capture event about 1 million years ago. Also in this system the large genetic variation generated during the hybridization event facilitated rapid diversification. We propose that hybridization may be key to rapid diversification in general.

PLENARY TALKS (CONT'D)

P3

The Origin of Elevational Replacements in Neotropical Birds: Uncovering the Roots of Humboldt's Elevational Zonation

Daniel Cadena, Universidad de los Andes

Tropical mountains are biodiversity hotspots. In particular, mountains in the Neotropics exhibit remarkable beta diversity reflecting species turnover along elevational gradients. Elevational replacements of species have been known since early surveys of the tropics as evidenced by work by Alexander von Humboldt on the geography of plants, but data on how such replacements arise are scarce, limiting our understanding of mechanisms underlying patterns of diversity. I will present data from recent studies in which collaborators and I evaluated hypotheses posed to account for the origin of elevational replacements in Neotropical birds including the Henicorhina leucophrys complex (Troglodytidae) and the genus Scytalopus (Rhinocryptidae), two groups with limited dispersal abilities but broad geographic ranges in tropical mountains. Using phylogeographic data for H. leucophrys and a robust molecular phylogeny for Scytalopus, we found that most cases of elevational replacements involve populations or species not closely related to each other. These results, as well as our research on other clades, suggest that replacements of species along elevational gradients result primarily from secondary contact following allopatric speciation and not via parapatric speciation along mountain slopes. Our study suggests that accumulation of species diversity in montane environments reflects colonization processes as opposed to in situ divergence even in dispersal-limited animals.

P4

Del viaje de Humboldt a los viajes del Instituto Humboldt: 200 años de exploraciones en biodiversidad

Brigitte Baptiste, Instituto de Investigación de Recursos Biológicos Alexander von Humboldt

Cuando el mundo entero parece estar suficientemente explorado y sus ecosistemas caracterizados, invocamos la labor de Alexander von Humboldt en Colombia y en América en general como fuente de inspiración para entender las cualidades de la biodiversidad en el contexto social contemporáneo. La vigencia de las observaciones y sobre todo, del enfoque interpretativo que orientó el trabajo del científico, llevó hace 25 años a la creación y operación del Instituto que lleva su nombre en Colombia, y al desarrollo de toda una política de expediciones y síntesis del conocimiento que hoy se presenta con una perspectiva de relevancia crítica para la toma de decisiones y la orientación de la gestión ambiental en el país. Desde la articulación académica de las colecciones biológicas y sistemas de información para el acceso libre a los datos de biodiversidad, pasando por la producción de herramientas interpretativas para su manejo por actores públicos y privados, llegamos a las propuestas más recientes de acuerdos de gobernanza territorial y construcción de un modelo de transiciones a la sostenibilidad basado en la incorporación de consideraciones de biodiversidad en todos los sectores y actividades sociales y económicas del país.

P5

The importance of species inventories to decipher diversification patterns on islands: lessons from Madagascar's amphibians and reptiles

Miguel Vences, Technische Universität Braunschweig

Madagascar is home to a fascinating herpetofauna characterized by high species richness and, especially, by an extreme degree of endemism. All of Madagascar's 355 described and probably over 300 undescribed amphibian species, and over 90% of all reptile species, are endemic to the island. Molecular timetree analyses suggest that the majority of these and other vertebrate clades colonized the island by overseas rafting, mostly from Africa, resulting in opportunities for diversification spread over time. Those colonizers that succeeded adapting to rainforest conditions were most successful in terms of species numbers. Analyzing spatial patterns of richness and endemism using generalized linear spatial models furthermore suggests that a mix of factors, such as montane refugia, river barriers and ecotones were responsible for the diversification, with different groups of vertebrates differing in the relative influence of these mechanisms. Examples from numerous newly discovered miniaturized frog and chameleon species, microendemic to tiny patches of habitat, demonstrate the importance of intrinsic traits such as body size for the diversification potential of animal clades. New perspectives to further elucidate these patterns come from phylogenomic approaches that hold promise to provide more robust phylogenetic reconstructions even of fast-radiating groups, and to more efficiently delimit species. However, our ongoing work in this intriguing system exemplifies that a real understanding of the diversity and evolution of tropical faunas is only possible after assembling baseline data sets through "Humboldtian" field exploration of species diversity and natural history.

P6

Imbabura and Chimborazo: two geodetic landmarks at the dawn of biogeography

Alberto Gomez, Instituto de Genética Humana - Pontificia Universidad Javeriana - Bogotá, Colombia

This work describes findings of Francisco José de Caldas and Alexander von Humboldt on their respective "Leveling of the plants" and "Geography of the plants", as they were written by each explorer in 1803. These primary texts allow to support a simultaneous emergence and evolution of the concept of biogeography in the mind of Caldas since 1796 in New Granada. In particular, the drawing entitled "Leveling 30 species of plants, on the western view of Imbabura, mountain near Ibarra, by FJ de Caldas", is presented and compared with Alexander von Humboldt's "Tableau physique" and its corresponding text entitled " Essai sur la géographie des plantes près de l'équateur "

Successive documentary evidence indicates that Caldas's phytogeographic drawing on Imbabura would have been conceived at least a year and a half before its physical execution in the second semester of 1803, and sustains both the simultaneity and the implicit and explicit differences of pioneering approaches of Caldas and Humboldt to biogeography.

SPECIAL TALKS

ST1

Can we realize the vision of Alexander von Humboldt's "Kosmos" in the 21st century?

Susanne Fritz, Senckenberg Biodiversity and Climate Research Centre (BiK-F), Germany

Alexander von Humboldt transcended scientific disciplines when he proposed a holistic view of nature with humans integrated in an interconnected Earth system. Revisiting this vision now, 250 years after his birth, provides a fresh perspective on urgent scientific and societal challenges. Although future ecosystem functioning and human quality of life are threatened at a planetary scale, interdisciplinary approaches to provide scientific knowledge for transformative change are largely lacking. I introduce a conceptual framework called "geobiodiversity research" that follows Humboldt by transcending the geosciences, biosciences, and social ecology. For example, integrating the geo- and biosciences can significantly improve our understanding of how biodiversity is generated and maintained; I will illustrate this with a case study from mountain biogeography, investigating the effects of palaeotopographic and palaeoenvironmental change on the diversity of large terrestrial mammals in Turkey since the Miocene (approximately 23 million years ago). Geobiodiversity research uses this kind of interdisciplinary integration, aiming to identify and quantify the dynamic geological, climatic, evolutionary, ecological, and social-ecological processes that affect biological diversity within the changing Earth system, as well as the effects of biodiversity on other system components. Through combining current understanding of the Earth system, biodiversity, and human well-being, geobiodiversity research will realize Humboldt's vision and provide a coherent scientific basis for transformation towards a sustainable future.

ST2

Diversification of Frogs in a Dynamic Environment

Andrew Crawford, Universidad de los Andes, Bogota, Columbia

A major focus of biogeography is understanding the causal factors that explain the spatial patterns of biodiversity and the current distribution of species. The primary formation of species is a key component of the origin of local and regional biodiversity. The physical division of an ancestral species by vicariance is one of the simplest and widely applicable models for speciation. The historical emphasis on vicariance re-enforced a logical but unnecessary emphasis on the appearance of topographic or 'physical' barriers as drivers of vicariant species. Alexander von Humboldt replaced an antiquated vision of the world as a static landscape with our current understanding that the environment is wildly dynamic over ecological and evolutionary time. Here I explore the role of the environment as a driver of diversification by revisiting classic cases of vicariance as well as dispersal caused by geological changes and ask if environmental variation could explain well-known biodiversity patterns as well or better. Using three case studies of comparative phylogeography of frogs developed by students in my lab group, I first ask if environmental variation can explain genetic divergence using a technique I dubbed trait-based phylogeography. Second, I explore whether environmental variation could predict genetic divergence in species that participated in the Great American Biotic Interchange. Finally, I discuss a re-analysis of divergence in lowland tetrapods across the Northern Andes through a collaboration between geneticists and a leading geologist, and the results suggest indeed a lesser role for orogeny and a greater role for environmental variation in explaining divergence. Given Humboldt's great insight that global habitats are dynamic, we should not be surprised to find that the primary divergence of populations and species is less likely tied to mountains and rivers and more often tied to the environment.

SYMPOSIA

Symposium 1: Geology and climate change as drivers of biodiversity and evolutionary processes in the Andes-Amazonian system

Organized by Carina Hoorn & Hanna Tuomisto

S1-1

The tectonic evolution of the Northern Andes

Cristian Vallejo, Escuela Politécnica Nacional; Brian Horton, University of Texas at Austin; Richard Spikings, University of Geneva; Sarah George, University of Texas at Austin

The Northern Andes are considered to have formed during multiple, continent-ocean interactions since the Triassic. In contrast to the central Andes, the northern Andes have experienced less shortening, and are relatively narrow. In the Andes of Ecuador, distinct events can be documented in the sedimentary record that evolved in response to the growth of the Andes. In this contribution, we review the growth of the Ecuadorian Andes using compositional, geochronological, thermochronological data from the i) Jurassic-Present retro-arc foreland basin (Oriente and Subandean zone), ii) Late Cretaceous-Paleogene sedimentary basins and arcs of the Western Cordillera and Costa that precede, and post-date the collision of the Caribbean Plateau, and iii) other post-collisional Neogene sedimentary rocks that crop-out in the flat forearc (Costa).

Our results provide new depositional age constraints and provenance information for the geological evolution of the Northern Andes. Variable sedimentary sources through time reflect a fluctuating system characterized by: (1) Triassic extensional basin genesis with synrift clastic accumulations and formation of S-type batholiths; (2) Westward migrations of the Jurassic volcanism and extensional sag deposits, with localized subsidence; (3) a phase of shallow marine deposits accumulated during the Cretaceous; (4) the onset of Andean shortening in the latest Cretaceous in response of the collision of the Caribbean Plateau; and (e) progressive eastward advance of the fold-thrust belt and related foreland basin system since the Paleogene.

S1-2

Leaf-wax lipid biomarker paleoaltimetry and eco-hydrologic evolution of the south-central Andean Plateau (Puna)

Alexander Rohrmann, Universität Potsdam; Andreas Mulch, Senckenberg Research Institute; Heiko Pingel, Universität Potsdam; Manfred Strecker, Universität Potsdam; Dirk Sachse, German Research Centre for Geosciences; Ricardo N. Alonso, Universidad de Salta

The growth of the Andean Plateau is one of the main controlling factors of present-day′s South American climate and hydrological state and has played a major role in the evolution of species on 106 yr timescales. Yet, information about the timing of uplift and ensuing variability of climatic, hydrologic, and ecologic conditions are sparse. Reconstructions of topographic growth of mountain belts increasingly rely on leaf-wax hydrogen isotope data (δDwax), a paleo-hydrology proxy obtained from organic material in sedimentary rocks. We present a multi-isotope record of hydrogen (δDwax), carbon (δ13Cwax) and oxygen (δ18Ocarb) on a well-dated sedimentary section from the 4-km-high Andean Plateau (Pastos Grandes Basin, 24°38' S, 66°40' W) and compare this record to an intermontane basin record (Angastaco Basin, 25°41' S, 66°04' W) in the E Cordillera to decipher patterns of eco-hydrological changes during topographic growth. We show that over the last 9 Myr the eastern plateau margin experienced: (a) variable influx of moisture and related changes in eco-hydrologic conditions related to the onset of the South American Low-Level-Jet starting at 7.6 Ma; and (b) relative surface uplift (0.8 km/Myr) of the plateau basin on the order of 2 km between 9-4 Ma and later uplift of the intermonate basin after 5 Ma to its present-day elevation. The timing of uplift contradicts earlier findings that most of the southern Puna had attained its high-elevation as early as 38 Ma. Instead, we conclude that basins in the west attained elevation earlier, whereas basins farther east reached higher elevations later on.

S1-3

Neogene climate, vegetation, and elevation history of the Central Andean Plateau

Camila Martinez Aguillon, Cornell University; Carlos Jaramillo, Smithsonian Tropical Research Institute; Alex Correa-Metrio, Universidad Nacional Autónoma de México; William Crepet, Cornell University; Jorge Moreno, Smithsonian Tropical Research Institute; Angélica Aliaga, Museo de Historia Natural de Lima; Federico Moreno, University of Rochester; Mauricio Ibañez-Mejia, University of Rochester; Mark Bush, Florida Institute of Technology

A rapid surface uplift of approximately 2500 m occurred in the northern part of the Central Andean Plateau (CAP) during the Neogene. Understanding the impact of this event on climate and biota is fundamental to predict the effects of future rapid climate change on regional biomes. We investigated the fossil record from the Neogene of this region (pollen, leaves, fruits, wood). Our estimations suggest that compared with modern CAP, regional precipitation was higher during the early Pliocene when the area was near modern elevations, and was even wetter during the late Miocene, when the cordillera was around ~1700 m.a.s.l. By the early Pliocene there existed a Puna-like ecosystem with a higher abundance of ferns than today, and a late Miocene montane ecosystem without modern analogs.

S1-4

The elevational dance of the Andean high mountain biome in the Pleistocene arena

Suzette Flantua, University of Bergen; Renske Onstein, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig ; Aaron O'Dea, Smithsonian Tropical Research Institute; Henry Hooghiemstra, University of Amsterdam; Catalina Giraldo-Pastrana, IBED, UvA; Rotterdam University of Applied Sciences

The high elevation Andean alpine grasslands (páramos) became established after Andean uplift and expanded due to climate cooling in the Pleistocene. Rapid global changes in temperature drove major shifts in the elevation of the páramo ecosystem. During warm interglacials, the complex topography of the Andes created a plethora of small mountaintop-bound páramo islands, while during cold glacial periods, páramo elevations dropped and the ecosystem covered much of the Andean slopes above 2000 m, causing previously isolated islands to merge into larger páramo complexes. Using a 1 million years-long pollen record we modelled elevational fluctuations to reveal the complex connecting and disconnecting dynamic history of páramos. Our findings show that temporal patterns of connectedness of páramo varied greatly among the different mountain ranges of the Northern Andes, producing individual 'mountain fingerprints', with cordillera-specific implications for evolutionary trees. Some mountain ranges lost their páramo biome in each interglacial, meaning that in each glacial, páramo had to recolonise from scratch. Other páramos persisted in island archipelagos, becoming connected during extreme cold glacial periods only, whereas other mountains ranges experienced greater connectivity even during mild cooling. In all mountain ranges, our data demonstrate that the present-day status of extreme páramo isolations is historically a rare configuration - accounting for a small proportion of the history of the páramo. Here we highlight the important, but neglected role of the history of spatial and temporal connectivity of alpine ecosystems, coined as the 'flickering connectivity system', as a driver of ecological change and mountain biodiversity.

S1-5
Amazonian plant species distributions mapped by satellite

Hanna Tuomisto, University of Turku; Jasper Van doninck, University of Turku; Mirkka Jones, Aalto University School of Science; Gabriela Zuquim, University of Turku; Kalle Ruokolainen, University of Turku; Gabriel Moulatlet, IKIAM; Anders Sirén, University of Turku; Glenda Cárdenas Ramírez, University of Turku; Samuli Lehtonen, University of Turku

Species distribution models (SDMs) have a variety of applications in ecology, biogeography and conservation biology. Since they can be used to generalise information about species occurrences across unvisited areas, SDMs can be especially useful in poorly known areas, such as Amazonia. Unfortunately, the scarceness of field data affects not only species occurrence information but also leads to low spatial and thematic accuracy in the environmental maps that are needed to model habitat suitability. Remote sensing data are a promising but under-utilised source of information about spatial patterns in the environment. We have recently produced a Landsat TM/ETM+ image composite that covers all Amazonia, and it has proved very useful as an environmental layer for predicting understory plant species turnover patterns across Amazonia. In this presentation, we will explore to what degree the Landsat composite can improve the accuracy of SDMs in relation to models based on climatic data only, and if the resulting SDMs can be considered reliable enough to be used in practical applications.

S1-6
Explosive radiations of the Asteraceae in the Andes: a history of climate change, geology, isolation and reconnexion

Mauricio Diazgranados, Royal Botanic Gardens, Kew

The Andes is the largest, widest and highest mountain range in the world. Some of the driest and wettest places on earth are found in these mountains, which cover an impressive variety of climates, soils, geologic formations and landscapes. From the biological point of view, they are extremely diverse, holding several centres of independent radiations, such as the Tropical Andes, considered the world's most biodiverse hotspot. There are about 50,000 plant species (~50% endemic) along the Andes, with striking differences in terms of biogeographic patterns and radiations. Can these patterns be explained by the influence of abiotic factors? The family Asteraceae is an excellent model to investigate this: with 3,000-3,500 Andean species, with both ancestral and recent origins, the family exhibits multiple centres of radiation and high level of endemism across the Andes. Based on georeferenced records and phylogenetic reconstructions, this work identifies the main patterns of richness, species turnover and endemism of the Asteraceae throughout the Andes, as well as the potential explanations for its diversification. Particular attention is paid to the most speciated groups, e.g. Espeletiinae, Diplostephium, Baccharis, Senecionae and Mutisia, identifying radiation patterns of different lineages within the family. Results suggest that the influence of the Late Pliocene - Pleistocene glaciations and the geological changes triggered the radiations in the Northern Andes, with more complex explanations for the Southern clades. Besides contributing to understanding the potential causes of the observed biogeographic patterns, findings could be used to identify regional Asteraceae hotspots, to inform conservation strategies. [Symposium: Geology and Climate Change - Andes-Amazonian System]

S1-7
Topography, erosion, and biodiversification in continental freshwaters

James Albert, University Louisiana Lafayette; Pedro Val, Universidade Federal de Ouro Preto; Nathan Lyons, Tulane University; Nicole Gasparini , Tulane University; Ying Reinfelder, Rutgers University; Jane Willenbring, University of California San Diego

Biodiversity patterns are widely-known to covary with gradients of habitat size, productivity, temperature, geographic distance and isolation, yet the macroevolutionary processes that drive biodiversification (i.e. speciation, dispersal, and extinction) remain poorly understood at continental scales. Theory predicts that river capture potentially affects all these parameters and thereby promotes diversification in freshwater taxa. Here we assess correlations between species density and basin-wide topographic metrics (elevation, average relief, slope, drainage area), hydrologic metrics (discharge, runoff, total suspended sediment, sediment yield), and environmental metrics (average rainfall and air temperature). Our results show: 1) correlations vary with latitude and elevation; 2) correlations with topographic relief only if rainfall is statistically accounted for, but not for large basins (>10,000 km2), 4) positive correlations with habitat area and erosion rates in tropical and lowland basins, but not extra-tropical or upland basins; and 5) highest species densities at intermediate levels of sediment yield. Isolated measures of topography and erosion are poor predictors of freshwater fish species richness at the basin scale, and more local complexity governs the dynamics of species macroevolution driven by river capture. These measures are spatially and temporally coarse, integrating landscape processes over many scales, thereby masking the effects of river capture within large watersheds. Further, river capture is a transient landscape evolution event, and species density is predicted to rise most rapidly when a landscape is near the peak of topographic transience. We illustrate these effects using the SpeciesEvolver module in Landlab, to model transient increases in species richness associated with river capture.

S1-8

Bird diversification and the evolution of Amazonian landscapes

Camila Ribas, Instituto Nacional de Pesquisas da Amazônia

Amazonia comprises an intricate mosaic of diverse types of forest formations, flooded environments and open vegetation. Increased knowledge about the distribution of Amazonian species has led to the recognition of complex biogeographic patterns, and their confrontation with information on the geological and climatic history of the region has generated several general hypotheses dedicated to explain the origin of the biological diversity. Two main abiotic drivers have guided these hypotheses: the uplift of the Andes and its influence on the evolution and reconfiguration of the drainage system, and climatic oscillations due to glacial cycles during the Quaternary. Here we will discuss how recent developments on comparative studies of birds associated to the different Amazonian habitats have been collaborating to understand how strong has been the relationship between landscape evolution and biological diversification in Amazonia. This has been accomplished by testing specific predictions associated to the geological history of the different environments using genomic data of bird populations associated to these distinct environments. The results show that several different histories are superimposed in Amazonia, each of them collaborating to distinct portions of its large diversity and responding differently to geological and climatic history. Although general congruence remains elusive, there is strong evidence of an important role for Earth history in driving biological diversification and thus generating the current patterns of diversity.

Symposium 2: Architects of Variation: How climate and physiology shape patterns of biodiversity

Organized by Alisha Shah & Cameron Ghalambor

S2-1

From Humboldt to Janzen; How latitude and mountains generate biodiversity

Cameron Ghalambor, Colorado State University; Alisha Shah, University of Montana

Alexander vonHumboldt first recognized the latitudinal gradient in species diversity over 200 years ago, yet the mechanisms underlying this fundamental ecological pattern remain unresolved and controversial. The fundamental problem relates to linking latitudinal variation in the environment to the processes that lead to the evolution of reproductive isolation and species formation. Dan Janzen's climate variability hypothesis stands out as one of the few explanations for how reduced seasonality of temperature in the tropics could drive the evolution of physiological tolerance, dispersal, and speciation. While these ideas are increasingly being tested in terrestrial and aquatic organisms, we have relatively little understanding on how thermal regimes, physiology, dispersal patterns, and speciation change across latitude and elevation. I will review the state of knowledge on this topic and point out areas of research in need of further study.

S2-2

Climate Variability and Thermal Tolerance in Aquatic Insects: Can they Stand the Heat?

Alisha Shah, University of Montana

Alexander von Humboldt was one of the first scientists to relate latitudinal variation in climate to global differences in biodiversity. Since then, climate variability has been implicated in shaping the thermal breadths and therefore geographic distributions of animals. In 1967, Daniel Janzen extended the 'climate variability hypothesis' to include elevation gradients. He posited that the seasonal temperature variation experienced across temperate mountains should favor the evolution of species with broad thermal tolerances, greater dispersal ability, and therefore, wider elevation range sizes. On the other hand, tropical mountain species that typically experience stable year-round temperatures, should evolve narrower thermal tolerances. These species should be physiologically restricted to narrow elevation ranges because they would encounter suboptimal temperatures if they move to either higher or lower elevation. Few studies have tested this hypothesis using standardized methods, and to our knowledge no studies have examined thermal tolerance patterns in aquatic systems, where fluctuations in temperature are reduced relative to air. Here, we measured thermal tolerance in a number of aquatic insects from streams in the temperate Rocky Mountains and the tropical Andes. For nearly all of the thermal tolerance traits measured, we found that temperate aquatic insects from the Rockies have broader tolerances compared to their tropical Andean relatives. Thus, our results support the predictions made by Humboldt and Janzen, and indicate that climate variability may play an important role in shaping the thermal breadths of aquatic insects. Importantly, our work suggests that lowland tropical aquatic insects are the most vulnerable to climate change.

S2-3
Stretched to the limits: field investigations to examine the predictive power of critical temperatures for understanding range shifts in amphibians

Alessandro Catenazzi, Florida International University

Thermal critical limits are useful traits to understand species distributions and vulnerability to climate change. The common assumption that geographic ranges reflect species′ physiological tolerances relies on the hypothesis that operating over a broad range of temperatures has high physiological costs, thus promoting adaptation to local thermal conditions. Among commonly used thermal traits, the critical thermal maximum or CTmax measures the temperature at which animals lose motor control. The ease and convenience of measuring CTmax, however, may lead to its overuse as a predictive metric. Some caveats of CTmax include the potential to have high phenotypic plasticity, and poor understanding of mechanisms tying loss of motor control to individual fitness. Over the past decade, we examined the thermal physiology of amphibians, a globally imperiled group of vertebrates. We found that CTmax of tropical frogs exhibit phenotypic plasticity and low phylogenetic signal, and that montane species can quickly acclimate their CTmax when translocated to lower elevations. Furthermore, body temperatures of field-active amphibians suggest they will be unlikely to experience CTmax in the near future, and that populations which live closest to their CTmax are the least likely to have declined over the last two decades. Furthermore, field experiments indicate that temperature limits of traits closely linked to fitness often are much lower than CTmax, undermining the usefulness of CTmax to predict species vulnerability to climate change. Invited participant of the Architects of Variation symposium.

S2-4
Effects of temperature variation along elevational gradients in the Andes: the case of a poison frog

Monica Paez-Vacas, Universidad Tecnologica Indoamerica; Marine Banse, Université Libre de Bruxelles (ULB) / Vrije Universiteit Brussel (VUB); Chris Funk, Colorado State University

Although geographic isolation is a main force in differentiation of several montane groups, divergent selection can also drive diversification along elevation gradients. The greater seasonal uniformity in tropical mountains could lead to the evolution of narrow thermal tolerance in organisms inhabiting these areas. Therefore, they would show limited reduced dispersal along elevation, which could lead to greater genetic divergence between populations, enhanced speciation, and greater species turnover along elevation gradients. We explored the role of temperature as a force of divergent selection leading to local adaptation in thermal tolerance and performance, across elevational gradients in a poison frog species, Epipedobates anthonyi, in Southern Ecuador. We measured the thermal limits (CTMAX and CTMIN), and growth thermal performance of tadpoles along two elevational gradients (200 – 1700 m). We also tested if tadpoles could shift their thermal limits in response to exposure to different temperatures (20 °C, 24 °C, and 28 °C). Overall, we found that CTMIN was lower at higher elevations, suggesting that elevational variation in temperature causes divergent selection on this thermal trait across elevations. We found differences between the two elevational gradients in thermal growth performance, but not across elevations. All populations shifted their thermal tolerances for CTMAX and CTMIN, according to the treatment, demonstrating phenotypic plasticity in thermal limits. Overall, differences in CTMIN among high, mid, and low elevation populations were maintained despite plastic responses to treatment temperature. These results demonstrate that low temperature acts as a selective force along elevation, even when populations show acclimation abilities

S2-5

Can plant thermal tolerance evolve under climate change? A comparison of central and edge populations

Rachel Wooliver, North Carolina State University; Seema Sheth, North Carolina State University

Under climate change, temperatures are rising and becoming more variable. A major question is whether the abilities of populations to adapt to such changes vary across species' geographic ranges. While mean increases in temperature should drive evolution of population-level trait means, increased variation in temperatures should drive evolution of trait plasticity within populations. We tested these predictions using a resurrection study of the perennial, riparian herb Mimulus (Erythranthe) cardinalis, whose range extends from central Oregon, USA, to northern Baja California, Mexico. Populations across the species' range have experienced marked increases in mean temperatures and temperature anomalies in the past decade. We grew ancestor (2010) and descendant (2017) propagules from two northern edge, two central, and two southern edge populations in growth chambers across a gradient of seven temperatures. We then compared thermal performance curves between ancestors and descendants of each population. Increased thermal optima from ancestors to descendants would indicate adaptive evolution of a population-level trait mean. Increased thermal tolerance breadths from ancestors to descendants would indicate adaptive evolution of a type of plasticity called phenotypic buffering, wherein organisms are able to maintain a functional phenotype in stressful environments. Importantly, we expect that the magnitude of evolutionary shifts in these thermal performance curve parameters is predicted by temporal variation in temperature experienced by each population. Results of this study have important implications for understanding how range position can shape plant evolutionary responses to global change. (Invited to present in Architects of Variation symposium)

Island Biogeography of the Anthropocene

Organized by Gonzalo Rivas-Torres & Jaime Chaves

S3-1

Common Denominators of Adaptive Radiation on Islands

Rosemary Gillespie, University of California Berkeley

Adaptive radiation plays a fundamental role in understanding the evolutionary process. However, the concept has provoked tremendous controversy, with disagreements linked to the very different systems being examined. Here I compare disparate adaptive radiations, from plants to insects and vertebrates and remote islands to lakes, to understand common denominators. Radiations differ considerably in the mechanisms of speciation between members of the radiation, depending on the interplay between selection imposed by the external environment and the evolution of intrinsic incompatibilities arising during speciation. Introgression also may play a role in species differentiation, and hybridization between divergent lineages may generate adaptive novelties via recombination. Moreover, for lineages in whichdivergent selection between environments may play a dominant role, diversity increases with the degree of environmental specialization. In contrast, for lineages that become isolated without any shift in environment or associated divergent selection, secondary sympatry will lead to direct interaction between close relatives and, given genetic incompatibility, ecological divergence through character displacement. The conclusion is that adaptive radiation is produced by multiple processes, with differences dictated largely by whether the drivers tend to be external to the radiation (mostly the environment) or internal (interactions among members of the radiation). Adaptive radiations will only be useful for understanding evolutionary phenomena if we make these distinctions in comparing processes across lineages.

S3-2

Isolation, Fragmentation, and Plant Endemism in the tropical Andes

Jens Mutke, University of Bonn; Tim Böhnert, Nees Institute for Biodiversity of Plants; Maximilian Weigend, Nees Institute for Biodiversity of Plants

The tropical Andes are one of the major centers of global biodiversity, housing an estimated 50,000 plant species. The rugged and dissected topography of the Andes results in high geodiversity and strong climatic gradients – leading to often small and isolated patches of different vegetation types. We study the patterns of small range, micro-endemic plant species of habitats across different elevations in the Amotape-Huancabamba Zone (AHZ) of southern Ecuador and northern Peru. Many of the species investigated are currently restricted to isolated remnants of natural vegetation, experiencing further fragmentation of their distribution by land use and climate change, and, e.g., fire events. We compiled large distribution datasets for the entire Andes: 645,000 records from GBIF (3,850 genera) and >10,000 more reliable records (12 genera) compiled and verified directly by the respective taxonomists. We use these data with bioclimatic models and data on land cover change to assess the degree of natural isolation and increasing human-induced fragmentation of plant populations and communities. Habitat fragmentation is rapidly increasing and there is a strong overall decrease of forest cover, especially in the very poorly studied relic forests at the western Andean slopes of the AHZ. Here, the small overall size of individual forest fragments and the extremely narrow distributions of individual taxa are likely to contribute to a dramatically increased extinction risk

S3-3

Disease Ecology of Galapagos Birds and their Parasites.

Patricia Parker, University of Missouri - St. Louis and Saint Louis Zoo

In 2001, we launched a collaborative effort to screen Galapagos endemic, introduced, and domestic birds for their parasites and pathogens. The primary institutional partners are the Charles Darwin Foundation, the Galapagos National Park, the University of Missouri – St. Louis, and the Saint Louis Zoo, in recent years adding the Agency for Biosecurity Galapagos. Since then, our teams have worked on all major islands of the archipelago, examining and sampling more than 20,000 individuals of 26 endemic bird species, including systematic surveys of marine birds throughout their ranges, such as penguins, flightless cormorants, the three species of boobies, both frigatebird species, and surveys of terrestrial birds on multiple or all islands of their ranges, including the Galapagos hawk, mockingbirds, finches, warblers and flycatchers. We have used genetic and phylogeographic approaches to estimate colonization times for many species and to estimate current population structure. Each of these parameters is important for understanding the ecology of pathogens acting in a community that is structured by island, by time of each species in residence, and by opportunities for gene flow and disease transmission among islands over time, as well as changing host-parasite relationships. The lists grow for pathogens that accompanied their colonizing host lineage, as well as those that arrived on one colonist and jumped to another resident species, along with those that are the most recent arrivals associated with human travel and traffic. Current work will add the dynamics of gut microbiomes to our understanding of disease threats to Galapagos birds.

S3-4

Ecological and biogeographic patterns of the Scalesia (Asteraceae) endemic genus in Galapagos

Gonzalo Rivas-Torres, Universidad San Francisco de Quito; Juan Guevara, Universidad de las Américas 1791362845001; Jaime Chaves, Universidad San Francisco de Quito; Ross McCauley, Fort Lewis College; Leo Zurita, Universidad San Francisco de Quito; Cas Verbeek, University of Amsterdam

The Galapagos Islands are recognized for recording species and biological processes unique to the planet. However, the ecological factors that explain the differential distribution of endemic plants in this archipelago are still scarce. Therefore, this work presents for the first time the distribution patterns and the current ecological niche classification of all the species of the endemic Scalesia (Asteraceae) plant Genus. Although this Genus, of similar biological importance to Darwin's iconic finches, has 15 species described and distributed on 11 islands, studies that describe their ecology and biogeographic patterns are relatively non-existent. Using ~1000 records obtained from herbarium and drone collections and from ~100 plots located throughout the archipelago, spatially explicit classification and analyses methods were used to describe the ecological niche, range size, distribution and endemism patterns of all

the species of this group. As a result, we know now that 12 Scalesia species are endemic to only one or two islands, can be very restricted to particular ecological niches, with narrow distributions and pressing threats like co-occurring introduced plant competitors.

The results of this research not only fill a significant gap of information regarding the ecology and distribution of arguably the most important plant group in this world-known Heritage Site, but also serve to 1.replicate this methodology in other similar groups, 2.provide basis for phylogeographical studies and for; 3.help taking appropriate managerial decisions by local authorities, particularly to implement efficient regulations that protect these unique species from latent threats such as invasive species and climate change.

Symposium 4: Diversity patterns along latitudinal and environmental gradients across the Andes

Organized by Francisco Cuesta, Carolina Tovar & Priscilla Muriel

S4-1

Thermal niche traits of tropical high-elevation plant species and communities and their vulnerability to global warming along a 4000 km latitudinal gradient in the Andes

Francisco Cuesta, Universidad de las Américas Carolina Tovar, Royal Botanic Gardens, Kew; Luis Llambí, ICAE-Universidad de los Andes; William Gosling, University of Amsterdam; Stephan Halloy, Ministry for Primary Industries; Julieta Carilla, IER-Universidad Nacional de Tucumán - CONICET; Priscilla Muriel, Pontificia Universidad Católica del Ecuador; Rosa Meneses, La Paz Herbarium, Universidad Mayor de San Andrés; Stephan Beck, La Paz Herbarium, Universidad Mayor de San Andrés; Carmen Ulloa, Science & Conservation Division, Missouri Botanical Garden; Nikolay Aguirre, National University at Loja; Wouter Buytaert, Imperial College London; Harald Pauli, Austrian Academy of Sciences, Institute for Interdisciplinary Mountain Research

Here we test the Climate Variability Hypothesis (CVH), postulating that reduced seasonal temperature variation selects for narrower thermal tolerances of species, along latitudinal and elevation gradients, in order to assess the vulnerability of alpine plant species to climate change effects. For 505 vascular plant species from alpine communities on 49 mountain summits, temperature data were extracted from a total of 29,627 geo-referenced occurrences. Species thermal niche traits (TNTs) were estimated using bootstrapping for: minimum temperature, optimum (mean) temperature, and breadth (maximum-minimum) during the growing season. Plant community scores were estimated using the weighted average of the TNTs of their constituent species, and vulnerability to global warming was assessed for both species and communities.

Species with ranges restricted to near the equator had narrower niche breadth than those with broader latitudinal distributions. Plant communities found on Andean summits reflected the species patterns by exhibiting a significant positive relationship between community niche breadth scores and latitude and a negative one between community mean and minimum temperature scores and altitude; the community niche breath, however, did not change along the elevation gradient. The strongest loss of thermal tolerance under 1.5 °C warming scenario is expected for alpine species restricted to equatorial latitudes, thus these species were classified as the most vulnerable ones. Our results confirm the CVH for plant communities across a latitudinal gradient throughout the tropical Andes and, thus, should be considered as important components in assessments of vulnerability plant diversity to the impacts of climate warming.

S4-2

Effects of experimental climate warming and nutrient addition on plant community and productivity in tropical mountain grasslands

Sisimac Duchicela, University of Texas at Austin-Department of Geography and the Environment; Francisco Cuesta, Universidad de las Américas 1791362845001; Priscilla Muriel, Pontificia Universidad Católica del Ecuador; Esteban Pinto, Consortium for the Sustainable Development of the Andean Ecoregion; Ricardo Jaramillo, Escuela de Ciencias Biológicas, Pontificia Universidad Católica del Ecuador; Andrea Terán, Fundación Jambato; Carolina Tovar, Royal Botanic Gardens, Kew

Anthropogenic stressors, specifically changes in mean annual air temperature, are causing major shifts in tropical alpine ecosystems. To determine the trajectory of these shifts in the Andes, it is important to continuously evaluate the ecosystem under scenarios of anthropogenic change, including how these stressors will interact. To assess short-term ecosystem changes in the Andean páramo we established monitoring sites in the Yanacocha Reserve, 15km northwest of Quito, Ecuador. Five monitoring blocks were installed in July 2012 at an altitude of 4,200 m.a.s.l. Twenty open-top chambers (OTC, to raise 1.5 °C of air and soil temperature) and six herbivore exclusion areas, to control for limited herbivory in the OTCs, were installed randomly in plots among the five blocks. The monitoring included assessing the effects of the following variables through time: aboveground biomass, plant community diversity, and litter and vegetation coverage. We used mixed effects models to compare these variables among the OTC, herbivore exclusion, and control plots. Then we used a SIMPER analysis to test the similarity of the vegetation community between the treated and control plots. This experiment showed a significant difference in species richness between the OTCs and the control. Additionally, there were differences in percent vegetation cover of certain species between the treatments, for example, grasses that are more inclined to dominate in areas with mid to frequent disturbances decreased in dominance, while shrubby vegetation increased.

S4-3

Patterns and causes of elevational diversity gradients in soil protists

Leonardo Fernandez, Centro de Investigación en Recursos Naturales y Sustentabilidad (CIRENYS), Universidad Bernardo O'Higgins; Loreto Hernández, Universidad Bernardo O'Higgins; Ulises Mosqueira, Universidad Bernardo O'Higgins

Ancestral adaptations to warm environmental conditions drive the biogeographical and macroecological patterns of numerous multicellular organisms. Recent evidence suggests that this niche conservatism may also be shaping broad-scale diversity patterns of soil unicellular organisms, although empirical evidence is limited only to Acidobacteria and testate amoebae. Herein, we tested the predictions of this hypothesis in five soil protist groups (Bacillariophyta, Cercomonadida, Ciliophora, Euglyphida and Kinetoplastida) plus an artificial group combining all these taxa, along a humid but increasingly cold elevational gradient in the Chilean Andes. We found support for the predictions of this hypothesis in all protist groups, including decreasing diversity and increasing geographical ranges towards high and cold elevations; correlations between diversity and temperature; communities phylogenetically structured by competition and habitat filtering at sites with optimal and suboptimal thermal conditions, respectively; and beta diversity patterns characterized by phylogenetic turnover among communities. Mid-domain null models confirmed that these findings were not the result of stochastic processes. Our results therefore suggested that soil protists exhibit evolutionary constraints to temperature, probably linked to an ancestral adaptation to warm climates, which limit their survival in exceedingly cold sites. This niche conservatism might explain why temperature often emerges as one of the most important environmental variables to predict the spatial distribution of soil protist diversity over broad spatial scales, including latitudinal and elevational gradients.

S4-4

New biotic communities, ecosystems and landscapes from climate and glacier change in the high tropical Andes: an integrated perspective

Luis Llambí, ICAE-Universidad de los Andes; Francisco Cuesta, Universidad de las Américas 1791362845001; Christian Huggel, University of Zurich; Fabian Drenkhan, University of Zurich; William Gosling, University of Amsterdam; Priscilla Muriel, Pontificia Universidad Católica del Ecuador; Ricardo Jaramillo, Escuela de Ciencias Biológicas, Pontificia Universidad Católica del Ecuador; Carolina Tovar, Royal Botanic Gardens, Kew; Manuel Peralvo, CONDESAN; Andres Avella, Instituto Alexander von Humboldt; Liz Johanna Díaz, IDEAM

The high tropical Andes are rapidly changing due to climate change, leading to strong biotic community, ecosystem, and landscape transformations. While a wealth of glacier, water, and ecosystem research exists, an integrated perspective on the drivers and processes of glacier, landscape, and biota dynamics is currently missing. Here, we present an interdisciplinary review that analyzes past, current, and future evidence on climate and glacier driven changes in landscape, ecosystem and biota at different spatial scales. We first review documented glacier changes and analyze projected future glacier shrinkage until 2100 for two case studies. The effects of climate and glacier change on high Andean biota are then examined based on chronosequence and diachronic studies of vegetation dynamics. The review indicates major twenty-first century landscape transformations with important socioecological implications which can be grouped into (i) formation of new lakes and drying of existing lakes as glaciers recede, (ii) alteration of hydrological dynamics in glacier-fed streams and high Andean wetlands, resulting in community composition changes, (iii) upward shifts of species and formation of new communities in deglaciated forefronts,(iv) potential loss of wetland ecosystems, and (v) eventual loss of alpine biota. We advocate strengthening an interdisciplinary research and monitoring agenda with a strong policy formulation link that enables enhanced cross-sectorial cooperation and knowledge sharing, capacity building, and a more active participation of both government agencies and social organizations. We illustrate the approach through the ongoing development of a proposal for integrated monitoring of high Andean ecosystems in Colombia.

S4-5

In the footsteps of Humboldt and Whymper— The importance of historical data in present-day climate change assesments in the Andes

Priscilla Muriel, Pontificia Universidad Católica del Ecuador; Pierre Moret, CNRS; Olivier Dangles, Centre d'Ecologie Fonctionnelle et Evolutive, UMR 5175, CNRS, Université de Montpellier; Ricardo Jaramillo, Escuela de Ciencias Biológicas, Pontificia Universidad Católica del Ecuador

Developing tools for monitoring the effects of global warming in high tropical mountain ecosystems is a major challenge for the coming years. The comparison between historical and recent surveys has contributed significantly to the assessment of global warming ecological effects on different organisms in temperate regions. However, for the Ecuadorian Andes, current empirical data to track species range shifts are still insufficient, in addition most historical accounts do not contain precise information related to species identity, geographical location or ecological attributes, and don´t cover different taxonomic groups simultaneously. Two noteworthy exceptions are the works related to the expeditions of Alexander von Humboldt (1769–1859) and Edward Whymper (1840–1911). Humboldt's Tableau Physique (1807) is by far the oldest existing dataset on plant altitudinal ranges for tropical mountain vegetation, and despite problems of interpretation it represents a unique source to assess vegetation shift in response to climate change. The accounts of Whymper's expedition to Ecuador (1879/80) provide important information about different taxonomic groups (plants and arthropods) at high elevations, with high topographic precision and completed with photographs. We present these two case studies in which historical and present data have been combined to evaluate the effects of global warming in high-Andean ecosystems, emphasizing that the use of historical information is not straightforward, and that partnership between historian and ecologists is needed to tease out the intermeshing and discrepancies of past and present biodiversity records.

S4-6

Endemism and diversity of caddisflies (Trichoptera) in an Andean elevation gradient

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Aquatic insects from Trichoptera order are extremely diverse in species number as well as in their trophic roles. However, in the Neotropics their distribution and diversity patterns are unknow, including endemic species restricted to tropical mountain systems. Recent studies on tropical mountains have shown high levels of endemism of aquatic insects, but the incidence of environmental filters that explain such patterns have not been addressed quantitatively. Given the relevance of understanding Trichoptera spatial diversity patterns to prioritize conservation areas for freshwater diversity as well as base information to predict changes in aquatic communities facing global environmental changes, our aim was to assess species distribution and assemblages of caddisflies (Trichoptera) in an elevational gradient, from 600 to 3600 m asl in the western versant of the Tropical Andes in Ecuador in which we had long continuous climate data with hourly resolution. We used light traps in 7 localities in this gradient. Each locality was sampled 3 times during 2 hours each time. All the specimens collected were identified to species or morphospecies. Our results showed a significant increase in species number with decreasing altitude. There was a significant shift in community composition at the species and genus level at 1000 m asl. Minimum temperature and average precipitation were the main variables explaining species assemblages. Geographic distance explained a high percentage of community variance across the elevation gradient, as documented for other taxa (i.e. vascular plants), suggesting the importance to conserve areas along the altitudinal gradient to effectively protect this diversity.

S4-7

Plant dispersal strategies of mountain top grassland communities across the Tropical Andes

Carolina Tovar, Royal Botanic Gardens, Kew; Inga Melcher, University of Amsterdam; Buntarou Kusumoto, University of the Ryukyus; Antoine Cleef, University of Amsterdam; Francisco Cuesta, Universidad de las Américas

We assess the role of climate and evolutionary history on shaping plant dispersal strategies of alpine grassland communities across the tropical Andes. We combined community, climate, phylogenetic and dispersal trait data for 486 species recorded in 49 mountain summits across the Tropical Andes to analyse: 1) phylogenetic signal of dispersal-related traits, 2) trait/phylogenetic clustering at community level, and 3) association between traits, phylogeny, climate and space using an extended version of the RLQ ordination approach and structural equation modelling. Our results show that the predominant dispersal mode is anemochory (by wind) followed by barochory (by gravity, lack appendages), while herbs are the dominant growth form. While dispersal-related traits are phylogenetically conserved, they are significantly associated with a temperature gradient. Extremely low minimum temperatures occurring at higher latitudes and higher elevations tend to favour barochory and herbs, which are traits common among Caryophyllales, Brassicaceae and Poaceae. Alpine grassland communities located in areas with moderate minimum temperatures (e.g lower elevation/latitudes) tend to have better representation of endozoochorous (dispersed by animal ingestion), shrub/tree species. The dominance of anemochorous species within communities is also indirectly influenced by temperature. Overall, species co-occurring locally tend to be phylogenetically closely related in comparison to the regional pool and phylogenetic relatedness seems to be climatically structured. This study shows that environmental filtering is the major process structuring plant dispersal strategies in mountain summits across the Tropical Andes. Lower minimum temperatures in higher elevation/latitude select less costly dispersal-related traits and certain taxa, leading to functionally converged mountain top communities.

S4-8

Vegetation trends over eleven years on mountain summits in NW Argentina

Julieta Carilla, IER-Universidad Nacional de Tucumán – CONICET; Stephan Halloy, Ministry for Primary Industries, NZ; Soledad Cuello, INBIOFIV – CONICET; Alfredo Grau, IER – Universidad Nacional de Tucuman, Argentina; Augustina Malizia, IER – Universidad Nacional de Tucuman – CONICET; Francisco Cuesta, Universidad de las Américas

Alpine plant communities are expected to move upward following their climatic niche, as climate change leads to warmer and dryer conditions in the central Andes. Species range shifts are predicted to have major impacts on alpine communities by reshuffling species composition and abundances. Using a standardized protocol, we surveyed alpine plant communities in permanent plots on four high Andean summits in NW Argentina, which range from 4040 to 4740 m a.s.l; surveys were done in 2006-2008, in 2012, and in 2017. We found a significant decrease in plant cover, species richness and diversity across the elevation gradient in the three censuses, and a strongly decrease in soil temperature along the elevation gradient. We found a high plant community turnover (37-49%) among censuses, higher in the lowest summit (49%) and on the northern (47%) and western (46%) aspects. Temporal patterns in community changes were represented by increases in plant cover in the highest summit, in species richness in the lower summit, and in diversity (Shannon index) in the four summits, over time. We suggest that the observed trend in plant community dynamics responds to short term temperature and precipitation variability, which is influenced by El Niño Southern oscillation (ENSO), and due to time-lags in plant community response, it may take much longer than one decade for the observed trends to become stables and statistically significant. Our study provides an important foundation for documenting more profound changes in these subtropical alpine plant communities as global climate change continues.

Symposium 5: From the Andes to the Amazon: Zoological elevation patterns from Manu National Park, Peru

Organized by Alessandro Catenazzi & Jill Jankowski

S5-1

Potential indirect impact of climate change on nestling growth for Tropical birds

Karolina Fierro-Calderon, Universidad ICESI; Gustavo Londono, universidad icesi

Changes in temperature and predation risk in montane ecosystems could influence life history traits in ways that are not well understood. Growth rates of offspring exert strong effects on fitness. Temperature and predation risk may influence offspring growth and these factors are likely to change in montane ecosystems due to direct or indirect effects of climate change. Temperatures are increasing and predators may move upwards tracking their thermal tolerances. Yet, to what extent temperature and predation risk currently influence offspring growth in an altitudinal gradient is unknown. We investigated the effect of ambient temperature and nest predation risk on nestling growth of 12 bird species with wide distributions and 20 species of congeners (7 pairs and 2 trios) with narrow distributions in a 2600m altitudinal gradient in Peru. We found that nest predation decreases with elevation. Nest predation had a stronger effect than temperature on nestling growth for all the species. Specifically, growth rates for mass and wings were faster in populations and species under high nest predation risk (low elevation sites). Mass and wing length at which nestlings left their nests were bigger and longer in species under high nest predation risk. Longer wings under high nest predation risk might enhance juvenile survival. Our results highlight the influence that predation risk has on offspring growth, and the potential indirect impact of climate change on Tropical birds′ fitness if nest predators track their thermal niches upslope.

S5-2

Hummingbird Incubation Behavior along a 3000m Tropical Montane Gradient

Gustavo Londono, Universidad ICESI

Incubation behavior varies within and among species. Birds must meet the thermal demands of the developing embryo by transferring constant heat. However, birds have to leave the nest to restore the energy lost during the incubation. These frequent incubation trips can affect the risk of nest predation. Hence, birds encounter a tradeoff between energetic demands and risk of nest predation. These two traits can change at the local, regional or global scale. Tropical mountains offer temperature and predation gradients and thus are well-suited to investigate the relative effect of climate and predation risk on incubation behavior. We aim to disentangle the contributions of external temperature, body mass and incubation behavior, using a novel dataset of tropical hummingbirds from a long-term study from 2007 to 2015 in the Western Andes of Colombia and the Eastern slope of the Peruvian Andes (diurnal temperatures ranged from 26° at 386m a.s.l. to 7° C at 3325m a.s.l.). Using custom novel Bayesian statistical methods (hierarchical multi-species survival models, phylogenetic principal component analysis with hierarchical measurement-errors, and phylogenetic regression with hierarchical measurement-errors), we leverage a data set of 526 days of incubation from 100 nests of 34 species of hummingbirds. Incubation behavior appeared strongly correlated with temperature. Our results illustrate the importance of extreme abiotic conditions in explaining phenotypic diversity.

S5-3

Diversity, distributions and life histories of birds in the Peruvian Andes

Jill Jankowski, University of British Columbia

Tropical mountains have among the most diverse bird communities globally, with communities that change dramatically with elevation and species constrained to narrow zones. Here we highlight findings from ten years of research that describe the elevational ranges, community structure and life-history trait variation displayed by birds across a 3000-m gradient in the Peruvian Andes. We examine patterns in range size, species turnover and phylogenetic community structure with elevation to make inferences on the abiotic and biotic factors that have shaped these communities. We examine variation in two life history traits, basal metabolic rate (BMR) and apparent annual survival, to ask whether these traits show correlated changes with elevation. We found that range sizes are broader at high elevations, where species show overlapping distributions and similar low-elevation limits. Phylogenetic structure, for all family groups, shifts from communities that are overdispersed in the lowlands to clustered in the highlands. We found a negative relationship between basal metabolic rate (BMR) and survival and no indirect effect of elevation on BMR, suggesting that high BMR is associated with low survival, regardless of a species' native altitude. Elevation had significant negative relationship with survival. Thus, high elevation Andean bird communities, largely composed of close relatives with overlapping ranges and coincident range boundaries, may have responded similarly to ecological or evolutionary pressures in the process of colonization and diversification. They are further characterized by a unique suite of traits in their 'pace of life,' in which BMR does not differ from lowland species, but survival does.

S5-4

Phantom of epidemic (recent) past determine the elevational distribution of montane tropical frogs

Alessandro Catenazzi, Florida International University

Humans are disrupting biogeographic patterns globally. The spread of microscopic pathogens increasingly threaten wild plants and animals. Outbreaks of highly virulent diseases can cause the extirpation of populations and species. The fungal disease chytridiomycosis is associated with catastrophic loss of amphibian biodiversity worldwide. I have been surveying anuran communities in the Amazonian Andes near Manu National Park, Peru since 1996. This large national park protects one of the richest amphibian faunas along an elevational gradient from the Amazonian lowlands to the Andean peaks. Epizootics of chytridiomycosis have reached this region around 2002, and were followed by the disappearance of nearly 20 species of frogs, with most vanishing species occurring at middle elevations in the cloud forest where chytrid prevalence is highest. Despite increasing search effort over the past 10 years, most vanishing species continue to be absent from surveys. Whereas species richness of terrestrial-breeding species has decreased little during the epizootic and is now recovering, species accumulation curves for stream-breeding communities have not recovered. These extirpations permanently altered species distribution and community structure of frogs along the elevational gradient of an otherwise well preserved natural area. My findings highlight the catastrophic effect of fungal disease on one of the most diverse anuran faunas, suggest limited population recovery for most species, and show the potential for recently introduced pathogens to disrupt biogeographic patterns. Symposium: From the Andes to the Amazon zoological elevation patterns from Manu National Park.

S5-5
Life history diversification in lowland tropical forests: Why are antbirds successful?
Santiago David, University of British Columbia; Gustavo Londono, universidad icesi; Karolina Fierro-Calderon, Universidad ICESI

Life history strategies vary along a slow-fast continuum, with higher investment in survival over reproduction at one end and the opposite pattern at the other end. Lowland tropical forest birds have long been expected to have a "slower" lifestyle, including higher adult survival, and reduced fecundity and parental care, but variation among coexisting species remains unexplored. This variation could help to explain why some tropical bird families, such as antbirds (Thamnophilidae), attain high species diversity and population densities within Amazonian communities. We compared the life history strategies of Amazonian lowland birds in the Manu National Park, southeastern Peru, to examine how life history traits (e.g. nest attentiveness, clutch size, incubation and nestling periods, nestling growth rate) vary among coexisting species of different bird families, and whether different strategies are characteristic of particular bird clades. We found a continuum of life history strategies larger than previously recognized for tropical birds. A "fast" pace of life characterized by short nestling periods and fast nestling growth rates was common among antbirds, but more generally, species exhibit multiple life history strategies to cope with the high nest predation risk in the region. These results contribute to our understanding of the diversification of avian life histories across elevation in one of the most biodiverse tropical regions in the world.

Symposium 6: Biogeography in the age of genomics: case studies at different spatial and temporal scales

Organized by Patricia Salerno & Monica Páez

S6-1
Revising the role for gene flow in contemporary population ecology, evolution, and conservation
Sarah Fitzpatrick, Kellogg Biological Station; Michigan State University

Understanding the ecological and evolutionary consequences of gene flow among wild populations poses a fascinating puzzle. Gene flow is classically viewed as the 'evolutionary glue' that holds species together over space and time, and should reduce differences among populations, potentially limiting adaptation and population growth. On the other hand, small populations stand to benefit from gene flow through genetic and demographic factors such as heterosis, added genetic variation, and the contribution of immigrants. Understanding the extent to which populations are connected, and the ecological and evolutionary consequences of altering these patterns are crucial challenges for the conservation of biodiversity. Only recently have the molecular tools become feasible and cheap enough to gain this understanding in diverse non-model organisms. I will synthesize what we now know about the consequences of gene flow in contemporary populations and draw attention to outstanding research questions. I will also highlight results from a case study in the Trinidadian guppy system to illustrate our changing view of the role of gene flow in nature.

S6-2

Using genomics to understand local adaptation of a poison frog species along elevational gradients in the Andes

Monica Paez-Vacas, Universidad Tecnologica Indoamerica; Patricia Salerno, Pontificia Universidad Catolica del Ecuador; Brenna Forester, Colorado State University; Christopher Kozakiewicz, University of Tasmania, School of Biological Sciences; Chris Funk, Colorado State University

Population divergence is determined by the interaction between the homogenizing effects of gene flow and differentiation due to genetic drift and adaptive divergence caused by natural selection. To test for selection at the genomic level and the environmental forces driving it, we studied the poison frog, Epipedobates anthonyi, which has a broad elevational range in Ecuador. Populations show phenotypic divergence along replicate elevational gradients in putatively adaptive traits including size, coloration, calls, and thermal tolerance. Interestingly, however, genetic divergence is low at neutral microsatellite loci. Trait divergence can be due to genetically based adaptation and/or plasticity. We used genomic data (ddRAD) to (1) examine genomic signatures of divergent selection using genome scans, and (2) identify the environmental gradients responsible for divergence using genotype-environment associations. Our preliminary analyses show evidence of genetic differentiation between populations from low elevation, while most populations at higher elevations are relatively similar. These overall results contrast with patterns observed with microsatellites that implied gene flow through the lowlands with populations at higher elevations relatively isolated, suggesting that the same loci are involved in adaptation to higher elevations across gradients. By the addition of genomic data, we aim to identify the role of the environmental variation on divergent selection at specific loci associated with phenotypic divergence. This will allow to better understand the mechanisms that generate our exceptional montane biodiversity and its distribution patterns.

S6-3

Diversification in the Neotropics: Insights from phylogenomic patterns, demographic processes and venom variation in lancehead pitviper snakes

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The current diversity and distribution of lineages present in the species-rich Neotropics is in part the result of complex ecological and evolutionary trends determined by environmental variables that have operated at diverse spatial and temporal scales. Recent studies have also demonstrated the importance of demographic processes influencing the structure of present-day phylogeographic patterns. We use pitviper snakes to explore historical diversification patterns in the region by combining genomic, morphological, and venom-protein data to explore diversification patterns and evolutionary mechanisms implicated in the divergence of the Bothrops asper species complex, a medically important group of snakes and a model organism in toxinological research. We identified extensive phylogeographic structure, suggesting the influence of geographic barriers and/or differences in ecological niches in the recent diversification of the group. A deep divergence between a mainly Central and South American clade is evident, but more recently diverged groups in South America show complicated patterns suggestive of recent divergence and/or gene flow among lineages. Next, we used this information to perform model-based analyses to investigate the demographic processes involved in the origin of Andean montane lineages. This approach allowed us to resolve some discrepancies of evolutionary relationships identified with tree-methods, but also to find evidence for the recent isolation of montane lineages in dry inter-Andean valleys. Coupling these results with similar patterns of venom variation highlight the importance of Andean montane habitats as drivers for the diversification of tropical reptiles. NOTE: Presentation invited for the symposium "Biogeography in the age of genomics: case studies at different spatial and temporal scales".

S6-4

Genomics of Lost World frogs reveals complex evolutionary histories of nearby summit endemics

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The Lost World of South America is a treasure-trove of biodiversity, yet little is known about the origins of the enormous endemicity found in this ecosystem. The region is dotted with numerous high-altitude plateaus (2000–3100m) that are currently separated by dramatic geographic, topographic, and ecologic distances; thus, it is no wonder these summits are home to numerous endemics, many of which are isolated to a single summit. Given the discontinuous landscape of this high-altitude ecosystem (Pantepui), teasing apart the effects of landscape, demography, and selection on these summit lineages remains extremely challenging. Here, we focus on the Chimantá massif, a large (~1400km2) fragmented structure that possesses high landscape complexity and unique yet nearby summits where two abundant species of frogs, Stefania and Tepuihyla, co-occur in sympatry. We investigate morphometric, genetic (mtDNA) and genomic (ddRAD nuDNA) patterns of variation and divergence atop three Chimantá summit populations of these two lineages to assess whether these patterns corroborate hypotheses of local adaptation or founder-driven speciation. We find strong support for a highly dynamic summit ecosystem, where even the older summit lineage, Stefania, has likely had recent hybridization and mitochondrial capture events with nearby upland lineages outside the massif. Furthermore, in both lineages we find genomic patterns of local adaptive divergence, suggesting that even within the Chimantá massif, in situ Pantepui speciation is being promoted, contributing to the high level of summit endemicity.

S6-5

No DUH: the Dual-Umbilicus Hypothesis of Philippine Stream Frog Biogeography Reconsidered with More than 10,000 Genomic DNA Sequence Loci.

Rafe Brown, University of Kansas; Chan Kinn Onn, National University of Singapore; Perry Wood, Auburn University; Carl Hutter, University of Kansas

Traditionally viewed as a "fringing" archipelago, the Philippines has served as the geographical setting for the development of biogeographical and evolutionary diversification-via-insular-isolation theory, including one major model of archipelago colonization: a bi-directional invasion pattern, coined the Dual-Umbilicus Hypothesis. Frequently invoked to explain deep, endemic central Philippine phylogenetic divergences and non-monophyly empirically observed in numerous clades of terrestrial vertebrates, the DUH pattern of historical Philippine biogeography has been applied to interpretations of archipelago diversification in freshwater invertebrates, fish, amphibians, reptiles, mammals and birds. Central to this idea is the empirical finding of two or more independent colonization events of the Philippines, derived from island-hopping dispersal to the southern reaches of the archipelago, ultimately from Sundaic sources (Borneo, Sumatra, Peninsular Malaysia)—with two lineages, each situated on the archipelago's western and eastern island arcs, and with each penetrating north only as far as their relative dispersal ability might allow.

Multiple phylogenetic analyses of Philippine amphibians have recovered the DUH pattern, including frogs of the genus Pulchrana, which have been interpreted as dual-umbilicus exemplars in previous analyses of allozyme characters and DNA sequences.

Here we use phylogenomic analyses of data from a novel genomic sequence capture probeset to infer the biogeographical history of Philippine Pulchrana. We harness the power of ≥ 10,000 gene loci to re-evaluate this classic pattern and provide a new temporal framework for diversification in this iconic island archipelago clade. In this presentation, we will showcase new genomic resources for amphibian historical biogeography and re-evaluate the biogeography of an amphibian transgressor of Wallace's Line.

S6-6

On the Evolution of Theraphosidae: Phylogenomics of tarantulas unravels major genetic lineages and suggests a rapid diversification in the Americas

Tim Lüddecke, Fraunhofer Institute for Molecular Biology and Applied Ecology

Theraphosid spiders, commonly referred to as tarantulas, represent some of the largest and most prominent spiders on earth. Given their uniqueness among spiders, it is rather surprising that our understanding of tarantula evolution still remains in its infancy. The analysis of morphological characters for the inference of evolutionary hypotheses still represents the most commonly used practice, although it was recently demonstrated that such approaches in tarantulas are easily biased via morphological homoplasy which consequently led to controversial evolutionary hypotheses in the past. To account for this problem, we inferred a phylogenetic tree for Theraphosidae from transcriptome data, including representatives from most major subfamilies within the family. Our data suggests that some taxonomical placements in Theraphosidae are in urgent need of revision and further shows that subfamilies can often be grouped into distinct biogeographic clades. Interestingly one of these clades, comprising most of the American lineages, accounts for 58% of all species described. Further members of this clade evolved urticating setae as an additional defensive mechanism besides their venom. We therefore conclude that the evolution of such setae in American theraphosids provided the means for the rapid diversification on the species level that we observe today. Finally we discuss priority groups for future studies that need to be included to infer a holistic understanding of theraphosid evolution and biogeography.

Symposium 7: Raices históricas de la biogeografia: de los pueblos andinos, pensadores criollos, Humboldt y los Humboldteanos

Organized by Elisa Sevilla

S7-1

Paradigmas de las verticalidades

Jorge Canizares Esguerra, University of Texas -Austin

A Humboldt se lo asocia con los mapas de biodiversidad de los Andes. Esos mapas fueron posibles gracias en gran parte a concepciones indígenas y criollas sobre las montañas como microcosmos, particularmente sobre los Andes como la localización original del paraíso terrenal (y por tanto microcosmos de la tierra en su conjunto). Este ensayo busca poner a Humboldt en el marco de tradiciones intelectuales andinas e hispanas que el naturalista prusiano encontró en Quito y en Perú. Estas tradiciones por lo general han sido ignoradas por los especialistas y biógrafos de Humboldt, quienes asumen que Humboldt extrajo de la América hispana animales, insectos, plantas, y documentos, y dela América anglosajona ideas. Este ensayo, por lo tanto, disecciona el colonialismo que estructura la mayoría de biografías sobre el naturalista alemán. Humboldt, nos dicen sus biógrafos, rechazó el colonialismo y la esclavitud. Esos mismos biógrafos, al igual que Humboldt, promueven practicas colonialistas que borran legados epistemológicos no europeos.

S7-2

La información histórica para la biogeografía de hoy

Diego Cisneros-Heredia, Universidad San Francisco de Quito USFQ, Colegio de Ciencias Biológicas y Ambientales, Laboratorio de Zoología Terrestre & Museo de Zoología

América fue el escenario de algunas de las más famosas expediciones científicas entre los siglos XVIII y XIX: Misión Geodésica Francesa (1735≈1745), Expedición Malaspina (1789–1794), Humboldt & Bonpland (1799–1804), Lewis & Clark (1804–1806), Expedición científica austríaca al Brasil (1817–1835), Darwin y el viaje del Beagle (1831–1836), Wallace & Bates (1848≈1852). Estas expediciones inspiraron a muchos otros exploradores que viajaron al continente americano y en conjunto generaron una cantidad enorme de descripciones etnográficas, mapas, y colecciones de objetos arqueológicos y naturalistas. Los viajes de todos estos exploradores y los datos que generaron constituyen hoy en día una fuente de información valiosa por su relevancia y aplicación al entendimiento de la biogeografía del continente con la mayor diversidad biológica del planeta. En este marco, analizaré la relevancia de la información generada por algunas expediciones, grandes y pequeñas, que visitaron Ecuador entre los siglos XVIII y XIX: Humboldt y Bonpland, Schmarda, Comisión Científica del Pacífico, discutiendo su impacto sobre el desarrollo y entendimiento de los estudios biogeográficos modernos.

S7-3

Las tecnologías americanas, biodiversidad ecuatorial y la biogeografía de Humboldt

Elisa Sevilla, Universidad San Francisco de Quito

En esta ponencia se discutirá algunas tecnologías amerindias que llamaron la atención a Humboldt en su viaje por la Audiencia de Quito que tienen que ver con el transporte y comercio entre diferentes pisos altitudinales, en particular la balsa de Guayaquil y el puente de maromas de Penipe. Estas tecnologías son reseñadas y dibujadas dentro de su album "Vistas de las cordilleras y monumentos de los pueblos indígenas de América". A partir de estos materiales y el trabajo de Frank Salomon sobre la verticalidad en los pueblos precolombinos y el comercio con los Yumbos durante la Colonia, discutiré el conocimiento indígena y colonial respecto a la geografía de las plantas a partir de una preocupación económica por acceder a productos subtropicales como son la coca, el algodón, (luego, la caña de azúcar), las frutas, tintes y maderas. Además, hablaré sobre Humboldt como viajero y las tecnologías amerindias y coloniales para transitar por la geografía andina tan accidentada a comienzos del siglo XIX.

S7-4

El orientalismo germanista de Humboldt llevado a América. Mesa redonda: Raíces históricas de la biogeografía. De los pueblos andinos, pensadores criollos, Humboldt y los Humboldteanos.

Mark Thurner, School of Advanced Study, University of London

Although it is frequently claimed that Humboldt was influenced by his American voyage, many aspects of his thought are more readily traced not only to German cameralist mining discourse, as several scholars have noted, but also to a neoclassical aesthetic typical of the German Enlightenment. This aesthetic was marked by a notable Hellenophilia and a studied Orientalism. This orientation generally held that the ancient Greeks were the measure of nearly all things, including race, beauty, civilization and intellect; indeed the German Enlightenment tended to trace its origins to this civilization; ancient Oriental civilization was also noteworthy for its great antiquity, and because it was the likely point of origin of the so-called 'indo-european' peoples and languages that later populated the West. For Humboldt, American culture, which was never native, was in most ways ‘Asiatic’ and thus inferior to or behind Western civilization and its more refined, figural aesthetics. Humboldt assumed its ‘semi-civilization’ was probably derived from ancient Oriental civilization via the migrations of Eastern sages to the New World. He thus speculated (and he was not alone in this) that Manco Capac, the first Inca, was likely a wandering Brahmin. Notably, enlightened Peruvian creole intellectuals such as Joe Hipolito Unanue rejected Humboldt's orientalism.

CS1-1

Explosive diversification following continental colonizations by canids

Lucas Porto, UFRGS; Renan Maestri, UFRGS

Colonization of a new environment may trigger an explosive radiation process, defined as an accelerated accumulation of species in a short period of time. Geographic colonization is often linked with key dispersal events. Several groups of mammals have undergone dispersal processes over their evolutionary history, but how often dispersal events precipitate explosive radiations remains to be understood. We studied the worldwide dispersal of Canidae, expecting that the arrival in a new continent was the ecological opportunity for explosive radiation in canids. We estimated ancestral ranges using 56 species of Caninae after comparing multiple models for biogeographical range estimation. Variation in speciation and extinction rates through time and across clades were estimated by comparing birth-death models and also using a data-driven approach. The coupling between ancestral estimation and diversification rates allowed us to associate shifts in diversification with the entrance in new biogeographical areas. We found that the timing of entrance into Eurasia and South America was between 11-10 Ma. Major peaks in speciation and diversification rates were also between 11-10 Ma, suggesting that the two results are related. Our results demonstrated that Caninae lineages presented dynamic rates of speciation over the last 22 Ma. The early-burst patterns of the speciation rates of Caninae lineages are characteristic of explosive radiations. Evidence from paleoenvironmental data suggests an association between peaks in speciation and the climate conditions of the new environments explored, implying that the differences in the ecological settings between continents may be responsible for the disparity among clades′ dynamics.

CS1-2

Environmental change: The extinction of Sparassodonta clade in South America

Kateryn Pino, Universidad de Concepción; Paulo Vallejos-Garrido, Universidad de Concepción; Enrique Rodríguez-Serrano, Universidad de Concepción; Cristian Hernandez, Universidad de Concepcion; Daniele Silvestro, University of Gothenburg; Nicolas Espinoza, Universidad de Concepcion

The mammalian carnivore guild in South America was long dominated by Sparassodonta, a Metatherian monophyletic group, which diversified between the Paleogene to early Pliocene (c. 66–5 Ma). The fossil record documents a general decline of Sparassodonta diversity starting in the late Miocene, which led to their extinction. The demise of this clade has been traditionally linked to two main hypotheses: 1) competitive displacement due to the arrival of placental carnivores (Carnivora order) in the context of the GABI; and 2) the effect of major habitat changes triggered by environmental change (Andean uplift and global cooling after the Middle Miocene). Here, we assess these biogeographic hypotheses using the fossil record and a Bayesian Multivariate Birth-Death (MBD) model to estimate the Sparassodonta extinction rates as a function of multiple time-continuous variables. We analyzed the fossil record of 58 Sparassodonta species and the potential competing groups: 82 Carnivora species and 28 other carnivorous vertebrate species (Sebecidae, Phorusrhacidae, Madtsoiidae), which span from c. 86 Ma to the present. We additionally included in the model two abiotic factors, global temperature, and Andean paleo-elevation, as proxies for environmental changes. We used the MBD model jointly analyze all biotic and abiotic variables and assess which and how many of them best predict changes in speciation and extinction rates in Sparassodonta. Our results show that global temperatures and Andean uplift are the most important predictors for the extinction of this paleo-endemic South-American group, indicating that competition with other carnivores did not play an important role in their demise.

CS1-3

Long distance dispersal or dispersal through land bridges? -- An integrated biogeographic study of Juglandaceae based on molecular and fossil evidence

Qiuyue Zhang, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences; Richard Ree, Field Museum; Yaowu Xing, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences

Despite long-standing interests of the East Asia - North American disjunction, its underlying biogeographic processes remains debate. Most biogeographic analyses based on molecular data of extant taxa have attributed to originate in East Asian then disperse to North America through long distance dispersal. However, this contradicts to the fossil evidence that many fossils occur in North America and high latitudinal region. In this study, we hypothesized that the walnut family, Juglandaceae had a North American origin then dispersed to East Asia via the Bering Land Bridge, and through the North Atlantic Land Bridge to Europe then to East Asia. We assembled over hundred reliable fruit fossils for Juglandaceae. We estimated its divergence time using node dating and Total-Evidence dating under Fossilized Birth Death model in BEAST. Finally, we used DEC model to reconstruct its biogeographic history based on the molecular phylogeny and fossil records. Our results show that the ancestral region of Juglandaceae was in East Asian during the Late Cretaceous then dispersed to North America based on the analysis without fossils, whereas its original region was in North America in the analysis with extant and extinct species, subsequently dispersed to North American Circumboreal Region then expanded to Asian Circumboreal Region and lastly to East Asia. Alternatively, dispersals to North American Circumboreal Region from North America, subsequently expansions to European Circumboreal Region and then dispersals to East Asia were also detected followed by extinction from high latitudinal region. Our study highlighted the importance of integrating fossils into the biogeographic analysis.

Concurrent Session 2: Island Biogeography

CS2-1

Speciation of the genus Urosaurus in the Revillagigedo Archipelago

Juan Gutiérrez, Unidad de Genómica Avanzada Cinvestav-Irapuato; Sean Rovito, Langebio-Cinvestav

The role of demographic history and stochastic events in speciation is still a subject of debate in evolutionary biology. Islands are among the best systems to study the role of geographic isolation and population history in speciation because of the small number of scenarios between which to discriminate. The Revillagigedo Archipelago, known as “Mexico’s Galapagos”, is a group of four volcanic islands 750 km west of Colima, Mexico in the Pacific Ocean. Among the many endemic vertebrates of the archipelago, the two largest islands (Socorro and Clarión) each have an endemic lizard of the genus Urosaurus, and previous studies have shown them to be closely related to the mainland species U. ornatus. These island endemics offer the opportunity to study the role of population bottlenecks in speciation. We generated a SNP dataset using ddRADseq, which we used to infer the demographic history and geographic speciation model for both species. We test alternative hypotheses of demographic histories that differ in assumptions related to migration rates, isolation periods, and population size changes to understand the role of founding bottlenecks in the formation of these endemic species. We also aim to infer the timing and order of colonization events and distinguish between a single colonization from the mainland vs. independent colonization of each island. Our results help us to understand diversity arises in geographically simple systems, shedding light on what may happen in more complex continental landscapes.

CS2-2

Invasion dynamics of a specialist solitary bee and its effect on the pollination system of an endangered island herb

Brittany Harris, Florida International University and International Center for Tropical Botany; Hong Liu, Florida International University and Fairchild Tropical Botanic Garden; Suzanne Koptur, Florida International University and International Center for Tropical Botany

Island ecosystems harbor much of the world's biodiversity but are threatened by their high vulnerability to invasive species. These isolated systems, with their often simplified communities, provide ideal models for studying how invasions influence communities and ecosystems. Shifts in community structure and function are common following invasion, but outcomes are less clear for introduced species that depend on mutualistic interactions. Pollinators are critical for reproduction in most flowering plants, particularly in island communities where mechanisms to avoid self-pollination are diverse. Understanding how introduced pollinators affect the recipient plant-pollinator community is therefore critical for their persistence. Thus far, invasion studies have been limited to social and generalist foraging bees imported for agriculture. Because agricultural bee populations are continuously enhanced by humans, disentangling competitive effects from supplemented populations may be difficult. A recent introduction and expansion of a solitary orchid bee, *Euglossa dilemma* Bembé & Eltz, from the Yucatán Peninsula to the Florida Keys archipelago may provide insight. We assessed invasion dynamics of an introduced pollinator by measuring structural and compositional shifts in the pollinator community and functional shifts in reproduction of an endangered island endemic herb that it frequently forages for pollen. We measured pollinator abundances, richness, and interaction structure via timed flower visitation watches for three years immediately following invasion. We compared these values and fruit-set rates of the endangered herb to the same plant population before the invasion. Fruit set was maintained, but the primary pollinator pre-invasion was nearly completely absent after invasion; this was consistent across all three years. It is likely that high trait overlap led to competitive displacement of the native pollinator. Although the bee is an efficient pollinator of the rare plant, loss of a primary pollinators may have dire implications for conservation, particularly in light of increasing frequency of disturbances in the region.

CS2-3

Extinction-driven changes in island communities: worldwide and in Mauritius and Krakatau

Julia Heinen, Center for Macroecology, Evolution and Climate, Denmark

Global change and human expansion have resulted in many species extinctions worldwide, but the geographic variation and determinants of extinction risk in particular guilds still remain little explored. We quantified insular extinctions of frugivorous vertebrates (birds, mammals and reptiles) across 74 tropical and subtropical oceanic islands within 20 archipelagos worldwide and investigated extinction in relation to island characteristics and species′ functional traits. Out of the 74 islands, 33 islands have records of frugivore extinctions, with one third of the pre-extinction frugivore community being lost. Geographic areas with more than 50% loss of pre-extinction species richness include islands in the Pacific and Indian Ocean. The proportion of species richness lost from original pre-extinction communities is highest on small and isolated islands, increases with island elevation. Large and flightless species had higher extinction probability than small or volant species. Across islands with extinction events, a pronounced downsizing of the frugivore community is observed, with a strong extinction-driven reduction of mean body mass and maximum body mass. The results document a substantial trophic downgrading of frugivore communities on oceanic islands worldwide, with a non-random pattern in relation to geography, island characteristics and species′ functional traits. This implies severe consequences for ecosystem processes that depend on mutualistic plant–animal interactions, including ecosystem dynamics that result from the dispersal of large-seeded plants by large-bodied frugivores. We suggest that targeted conservation and rewilding efforts on islands are needed to halt the defaunation of large and non-volant seed dispersers and to restore frugivore communities and key ecological interactions.

Concurrent Session 3: Biodiversity Patterns & Maintenance

CS3-1

A synthesis of animal-mediated seed dispersal of palms reveals distinct biogeographical differences in species interactions

Gabriel Muñoz, Concordia University; Kristian Trøjelsgaard, Aalborg University; W. Daniel Kissling, University of Amsterdam

We synthesized data on palm–frugivore seed dispersal interactions to reveal emergent broad-scale differences in plant-animal interaction networks between the Neotropics and Afrotropics biogeographical regions. After a comprehensive search in published literature, we recorded a total of 750 unique pairwise interaction records covering 340 frugivores and 126 palms. We aggregated these pairwise observations of palm–frugivore interactions into single meta-networks for each biogeographical region. We then compared their taxonomic composition, network indices and tested whether functional trait matching (i.e., the relationship between palm fruit size and frugivore body size) differs between meta-networks. Moreover, we assessed sampling completeness and estimated knowledge gaps for individual palm species and geographic units within regions. The Neotropics showed a larger interaction diversity and more modular network structure than the Afrotropics. Broad-scale morphological trait matching among plants and frugivores was only observed in the Afrotropics. The lack of a Neotropical trait matching relationship might be driven by the late Quaternary extinctions of mammalian megafauna in this region. Sampling completeness of frugivore interactions within biogeographical regions and for individual palm species was low, geographic coverage limited, and relative knowledge gaps were largest in areas with high palm species richness. Despite increasing the digital availability of palm–frugivore interaction observations, our work shows that massive knowledge gaps of interaction diversity still remain for the tropics, suggesting that deeper insights into the biogeography of species interactions can be gained by extracting ecologically relevant information from increasingly larger volumes of literature.

CS3-2

Plant trait-environment dynamics challenge the Humboldtian view of nature during the Holocene

Pierre Gauzere, Arizona State University; Benjamin Blonder, Arizona State University

The functional composition of plant communities are commonly thought to be determined by climate, in line with the Humboldt's viewpoint of nature. However, plant trait–environment relationships (TERs) are often weak and/or inconsistent. A key hypothesis for these patterns lies with disequilibrium biodiversity responses to past climate change. However, how contemporary distributions of trait values are influenced by past climate is still poorly elucidated, mainly because studies have not been able to investigate the temporal responses of communities during past climate changes.

Here we investigated the long-term functional responses of 426 North American plant communities to temperature changes during the Late Quaternary (21Ka - 0Ka). We assessed evidence for disequilibrium between traits and environment during both periods of warming and periods of stable climate. We then tested two hypotheses for the drivers of disequilibrium: lagged response to climate, or non-climatic drivers (such as human activity).

We found that during warming periods, the functional response of plant communities was consistent with equilibrium climate responses, but the functional composition of communities diverged from equilibrium expectations during periods of stable climate. These results suggest that disequilibrium between functional traits and climate results from the influence of non-climatic drivers, and challenge the common assumption that present-day trait distributions result from lagged biodiversity responses to strong climate change. Non-Humboldtian drivers such as human impact, megafauna, and fire regimes might also have a major influence on the contemporary patterns of functional composition.

CS3-3

Dialects in the high-frequency song of the Ecuadorian Hillstar

Fernanda Duque, Georgia State University; Laura Carruth, Georgia State University; Carlos Rodriguez-Saltos, Emory University; Elisa Bonaccorso, USFQ; Walter Wilczynski, Georgia State University

Differences in vocalization structure across populations of the same species have been described in frogs, birds, whales, dolphins, and humans. These vocal variants, also known as dialects, may have implications for genetic diversification, sexual selection, and vocal learning. The Ecuadorian Hillstar (Oreotrochilus chimborazo) is a hummingbird that produces a complex high-frequency (HF) song (7-16 kHz), composed of introductory motifs with frequency-modulated syllables, followed by trills. We investigated the structure of the HF song among four populations of this species. Recordings were collected along the Ecuadorian Andes, in three locations for the subspecies O. c. jamesonii (Antisanilla, NE; Culebrillas, SE; and Cajas, SW) and one location for the subspecies O. c. chimborazo (Mt. Chimborazo). We found that the song structure described above was maintained across populations in this species. However, important differences were present in the introductory motifs. The two introductory elements in the songs from Antisanilla, Chimborazo, and Culebrillas differed in structure. In addition, the song from Culebrillas had a frequency-modulated element after the beginning of the trill sequence. The song from Cajas included five introductory motifs, making it the longest song across the populations studied. Variability in the HF song of O. chimborazo suggests that these populations are isolated. It also opens the possibility that these dialects may be the result of vocal learning, as hummingbirds are among the few lineages that have evolved this ability.

Concurrent Session 4: Functional Biogeography

CS4-1

The origin and assembly of the alpine biome in the Hengduan mountains

Wen-Na Ding, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences; Richard Ree, Field Museum; Yaowu Xing, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences

Extensive mountain-building during the Cenozoic helped to shape modern terrestrial landscapes and form biodiversity hotspots, including those featuring alpine ecosystems. Yet the biogeographic origins of alpine regions, and the evolutionary histories of the diverse plant species that inhabit them, remains relatively poorly understood. Here we study the alpine biome in the Hengduan mountains (HDM) and adjoining highland ranges (Qinghai-Tibet Plateau and Himalaya), which harbors exceptional alpine plant diversity. We examine the tempo (when, how fast) and mode (through what processes) by which the alpine biome was assembled through time and across regions using the comparative phylogenetic analyses of 3584 species from 18 major clades. We apply a new biogeographic model in which geographic range and biome occupancy jointly evolve with species birth (cladogenesis) and death, and use stochastic character mapping to estimate the dynamics of range and biome shifts and lineage diversification through time. Our preliminary results show that the alpine plants in the HDM are assembled by biome shifts from lower elevations firstly and then followed by in situ diversification. One the other hand, the alpine biome of HDM also serves as mains source of alpine plants for adjoining Himalays and Qinghai-Tibet Plateau though time.

CS4-2

Geographic and environmental determinants of floristic structure in a biodiversity hotspot

Qin Li, The Field Museum of Natural History; Richard Ree, Field Museum

Documenting geographic patterns of species richness and turnover is fundamental to understanding why biodiversity is unevenly distributed on Earth, and for the conservation of biodiversity hotspots. The Hengduan Mountains region in south-central China is a floristic hotspot, but beta diversity within it has not been extensively studied. We compiled a presence/absence dataset of 15,042 species of seed plants across 1,265 sites (county-level 500m-elevational bands), based on a published checklist and database of specimen records across the Hengduan Mountains and adjacent areas of the Qinghai-Tibetan Plateau (QTP) region. We used Grade of Membership (GoM) models, similar to those used to assess population genetic structure, to identify species assemblages (motifs) and explore the relative contributions of spatial, elevational, and environmental gradients to motif boundaries. Motifs fell into two major regions, the QTP and greater Hengduan Mountains, with relatively divergent environmental parameters. In the Hengduan Mountains region, motifs primarily showed spatial and elevational turnover, with relatively little environmental differentiation, except for a distinct motif in the subtropical Gaoligong Mountains. Unexpectedly, in the core Hengduan region we found a clear motif boundary along the Jinsha River, which persisted with increasing values of motif number. This boundary does not correspond to any previously described biogeographical divide, and further studies are needed to determine the precise nature and causes of floristic turnover across this tectonically active zone.

CS4-3

Dacryodes (Burseraceae): un género huérfano en América

Maria Martinez, Universidad del Norte

Estudios recientes en la sistemática de Dacryodes (Burseraceae) revelan la distribución de un alto número de especies en los bosques húmedos del neotrópico, incluso una incursión de este género en elevaciones no esperadas desde Guyana hasta Bolivia. ¿Cómo podemos a través de revisiones de herbario ampliar su distribución, publicar docenas de especies nuevas y saber tan poco de su biología y su historia evolutiva? ¿A qué se debe la relativa "escasez" de material en los herbarios? ¿Es este un fenómeno común o estamos siendo testigos de los últimos ejemplares de este grupo? Pretendo narrar desde el punto de vista de la botánica sistemática a lo que nos enfrentamos cuando el boom de las expediciones sobre la flora se extinguen, cuando la misma legislación (en mi caso, colombiana) desestimula la toma de muestras y el intercambio, cuando los mismos colegas deciden no colectar en campo, y el efecto del posconflicto colombiano en el estudio de la diversidad biológica.

Concurrent Session 5: Island Biogeography

CS5-1
Life-history evolution in contrived communities of invasive livebearing fishes in the Hawaiian Islands

Spencer Ingley, Brigham Young University - Hawaii; Gentrie Maag, Brigham Young University - Hawaii; Ivy Doringuez, Brigham Young University – Hawaii

Of fundamental importance in biogeography are the factors that dictate a species' range, or in other words, its realized niche. A key component of a species' realized niche is the outcome of competitive interactions. Life-history traits can be particularly important when determining the outcomes of competitive interactions, as these traits impact when and how a species reproduces and reflect trade-offs subject to evolution due to competitive interactions. To better understand how life-history traits evolve in response to competition with closely related species, we studied contrived communities of livebearing fishes (Poeciliidae) on Oahu, Hawaii. We focused the Mangrove Molly, Poecilia orri, in locations where it is found either in allopatry or sympatry with respect to other introduced poeciliids. We assessed life-history traits including size at maturity, brood dry mass, reproductive allotment, and fecundity. We found significant variation in life-history traits between populations that occur either in sympatry or allopatry with respect to other poeciliids. In allopatric sites, size at maturity was greater than sympatric counterparts. In sympatry, females allocated more energy to reproduction, and had fewer and smaller offspring than females in allopatry. Overall, our results provide evidence that closely related species can quickly evolve divergent life-history traits in response to competition with closely related species, thus facilitating the occupation of a broader geographical range. These results are particularly important in light of invasion biogeography, in that they highlight the need to consider evolvability of invasive species as a determining factor of their potential range.

CS5-2
Fanged Frogs Reset Expectations of Terrestrial Vertebrate Evolutionary Diversification in an Iconic Island Archipelago

Rafe Brown, University of Kansas; Johana Goyes Vallejos, University of Kansas; Carl Hutter, University of Kansas; Mark Herr, The University of Kansas; Robin Abraham, University of Kansas; Perry Wood, Auburn University

We use a newly-developed suite of phylogenomic resources (the FrogCap sequence capture probeset) to infer biogeographical history, assess the timing of diversification, and evaluate species boundaries in Limnonectes Fanged Frogs, one of the few formally-characterized global examples of amphibian adaptive radiations. We used 100 independently-evolving legacy loci to estimate evolutionary relationships, determine the numbers of invasions of the Philippine archipelago from continental sources, test hypotheses of species boundaries, and estimate the archipelago's timeframe for Fanged Frog diversification.

In this presentation we will summarize a new, comprehensive, archipelago-wide analysis of evolutionary diversification in this amphibian adaptive radiation to evaluate the relationship between the Philippine geographical template and hypothesized drivers of Fanged Frog species diversity: (1) the archipelago's east versus west island arc systems, (2) its well-characterized Pleistocene Aggregate Island Complexes (PAICs), today's (3) modern island landmasses, and (4) environmental gradients of atmospheric variation associated with elevational topography.

Our results resolve questions of species diversity, modes of archipelago colonization, and comparative lineages' timeframes for speciation. Surprisingly fewer species were identified by our analyses of genomic data than expected (or predicted by current taxonomy) and cases of in situ diversification along elevational gradients were substantiated on the larger islands of Luzon and Mindanao.

CS5-3

Narrow-range endemic ground beetles in Ecuadorian páramos: Towards a biogeography of Andean sky islands

Pierre Moret, CNRS; Alvaro Barragán, Pontificia Universidad Católica del Ecuador; Mauro Gobbi, Museo delle Scienze, Trento; Jerome Murienne, Museum national d'Histoire naturelle

The tropical Andean páramo ecosystem emerged after the final uplift of the Cordilleras, leading to the rapid radiation of species-rich clades. It is debated whether these mountain clades mostly originated from local lowland taxa or from cool regions north or south by long range dispersal, and to what extent the fragmentation of isolated high-altitude island-like páramos contributed to the multiplication of narrow-range endemic taxa..

To answer these questions, our project focuses on ground beetles of the family Carabidae. These insects are good markers of endemism areas, due to their low dispersal ability (all the páramo species are wingless), which gives the opportunity of an exceptionally fine-grained analysis of endemism patterns. Two hypotheses are tested: (i) that most of the endemic ground beetles found above 4000 m have evolved by niche shift, from local ancestors in the montane forest, and (ii) that the high level of microendemism observed in several genera is the result of recent speciation events, related both to Pleistocene climate fluctuations and to the volcanic and tectonic history of the Andes.

Carabid beetles were collected above 4000 m on 13 superpáramo "sky islands" in central and northern Ecuador, using standardized sampling methods. COI sequencing was performed to strengthen species delimitations, and mitogenome sequencing of selected species is underway for phylogeographic analyses. The first results of this ongoing project are presented with a highlight on the Llanganatis non-volcanic mountain area, one of the major biodiversity hotspots among Ecuadorian páramos.

CS5-4

Diversification patterns of ground beetles and rove beetles from the highlands of Ecuador

Sofia Muñoz-Tobar, Pontificia Universidad Católica del Ecuador; Michael Caterino, Clemson University

The tropical Andes are considered a biodiversity hotspot for numerous evolutionary lineages. Allopatric speciation and paleoclimatical events appear to be the main drivers for species diversification in the tropics, especially for páramo species which show high diversity and endemicity. The present research aims to elucidate speciation and diversification patterns of widely distributed species of beetles from isolated páramo patches across Ecuador. The study of high elevation faunas can give us an insight into basic evolutionary processes for Andean insect species. Sampling targeted 17 sites in the páramo ecosystem (3500 – 4000 m), through pitfall traps, hand collecting and leaf litter. One nuclear and one mitochondrial marker were used to assess the genetic diversity of four beetle lineages within the ground beetles (Coleoptera, Carabidae) and ant–loving beetles (Coleoptera, Carabidae, Pselaphinae), through a combination of phylogenetic methods, divergence time estimates and population genetics. Results from these analyses reveal there is no general pattern of diversification in beetle lineages from páramo. The effect of mountain isolation varies across lineages, where the distribution of the genetic diversity for each beetle lineage appears to be influenced by several factors such as divergence time, range size, dispersal capability, and geological and paleoclimatical events that occurred in the Miocene–Pleistocene, as recorded for plant lineages from páramo.

CS5-5

Connecting spatial trophic ecology with processes of population differentiation and speciation in Galápagos marine iguanas (Amblyrhynchus cristatus)

Timm Reinhardt, Leipzig University; Juan Guayasamin, Universidad San Francisco de Quito; Sten Anslan, Braunschweig Unviersity; Nicolás Peñafiel, Memorial University of Newfoundland; Sebastian Steinfartz, Leipzig University; Amy McLeod, Leipzig University

Marine iguanas (Amblyrhynchus cristatus) are the only seagoing lizard worldwide. They graze specifically on green and red macro-algae in the tidal zone. San Cristóbal is the easternmost and oldest island of the Galápagos archipelago and is inhabited by two genetically differentiated marine iguana populations that were recently described as distinct subspecies (Amblyrhynchus c. mertensi and A. c. godzilla). Previous investigations have shown that intermixing between the two subspecies is rare; this contrasts with the relatively high frequency of hybridization of these subspecies with individuals from adjacent islands. Here, we provide the first data that shows differences in feeding ecology between the two subspecies. To this end, we analyzed food composition of adult marine iguanas of both subspecies using a DNA-metabarcoding approach, which aimed to identify consumed algal species from feces samples and signatures of stable isotopes in accumulated skin tissue. We find differences in the composition but not in the number of consumed algal species between sites (subspecies). Further, the variability in the trophic niche between iguana populations is low and is predicted by the site specific macro-algal community composition. At the same time, isotopic values of iguana tissue also indicates a very small range of food items throughout the iguana life cycle, and indicate only very restricted spatial expansion. Therefore, we suggest that small home ranges and low mobility might be relevant factors in the separation between the two subspecies on the island scale.

CS5-6

Use of drone and satellite images to map native and invasive vegetation distributions in island systems: The Galapagos example.

Gonzalo Rivas-Torres, Universidad San Francisco de Quito; Lorena Benitez, USFQ; Carlos Mena, USFQ

Here we present the results of a mixed, systematic and low-cost methodology to map native vegetation and the distribution of pervasive invasive plants that generally affect island resident ecosystems. After obtaining preliminary legends defined by experts, i. satellite images were used to perform an object classification analysis; ii. high resolution images obtained by drones were taken for mapping validation; and iii. verification was performed in the field and in workshops to obtain the vegetation map and the distribution of main vegetation occurring in the iconic Galapagos National Park (GNP). This project, (which includes mapping of species using drones), allowed defining that 53.63% of the GNP is covered by nine native ecosystems and ~2.2% of this protected land is canopy dominated by invasive species. The so-called "dry" native ecosystems cover 40.8% of the GNP and only 12.8% of this protected area is covered by "wet" and "transitional" native ecosystems. Among the latter, those distributed in the highlands, covered only 4.8% of the protected area and are very threatened by the invasive species mapped here. In addition, three native ecosystems occurring in the mountaintops of the GNP were spatially described for the first time.

The methodology detailed here proved useful to provide accurate spatially-explicit vegetation data and biogeographical details of main Galapagos vegetation types, but also the potential for replication in time, and is expected to aid suitable management of highly endangered and unique biotas in this and other tropical island biomes.

Concurrent Session 6: Conservation Biogeography

CS6-1

Conservation priorities for Romerolagus diazi based on Species Distribution Models including biotic interactions

Luis José Aguirre López, Universidad Nacional Autónoma de México; Tania Escalante, UNAM; Perla Espiritu, Universidad Nacional Autónoma de México

Volcano rabbit (Romerolagus diazi) is an endemic species with restricted geographical distribution inhabiting the center of Transmexican Volcanic Belt. This rabbit has been cataloged as endangered by Mexican Legislation. A large part of its distribution is within a protected natural area: Iztaccíhuatl-Popocatépetl National Park. Ilegal logging, poaching, agriculture, livestock and private property expansion threaten to modifying, fragmenting or destroying the habitat where volcano rabbit lives. Our aim is provide key considerations for volcano rabbit′s conservation through four main tasks within the Izta-Popo National Park: (1) to develop a catalog of directed or indirected captured mammals to identify species that may have an effect on the volcano rabbit; (2) describing biotic or abiotic factors that may affect the geographical distribution of volcano rabbit; (3) to perform a potential distribution model based on the ecological niche of volcano rabbit; and (4) to prioritize sites for conservation of volcano rabbit. Our methods are divided in two processes: obtaining field data with different techniques and using correlative algorithms focus on propose microscale priority zones. Our main result was a priority area that must be isolared from disturbances, tourism or negative factors if the volcano rabbit population decrease. In this area, the environmental conditions, like the NDVI, topography or biotic interactions, are optimal for the survival of volcano rabbit populations. One of the conclusions is that the protected areas does not guarantee the biodiversity conservation and its ecological networks if management strategies are not applied and updated properly.

CS6-3

Through the extinction filter: historical and contemporary patterns of vulnerability of the most extinction-prone bird family

Lucile Leveque, University of Tasmania; Scott Carver, University of Tasmania; Jessie Buettel, University of Tasmania; Barry Brook, University of Tasmania

Patterns of extinction risk can fluctuate, leading some taxa to be particularly vulnerable to extinction. Rails (Aves: Rallidae) represent one of the most extreme cases of mass extinction within a modern vertebrate group: about 80% of rail species became extinct after human expansion during both the Holocene and the Anthropocene eras. The majority of recent rail extinctions affected island endemic and flightless forms, largely attributed to introduced predators and hunting by people. However, the relative importance of the factors that lead to vulnerability in contemporary rails remains enigmatic. Here we hypothesised that both intrinsic and extrinsic attributes play specific roles in the threatening processes leading to elevated vulnerability in rails. Specifically, we expected that i) island endemic, large-bodied and flightless species would be more threatened and ii) developing or human dense countries will support more threatened species. We used the IUCN Red List status to model contemporary vulnerability, along with life-history traits, geographic context, and socio-economic status of their countries of occurrence. We found that at global scale island endemism was the strongest predictor of current rail vulnerability, but within island endemic species, no threatening processes could be explained. Interestingly, we did not find that body size or being flightless contributed to contemporary vulnerability, indicating the most vulnerable rails with these traits are already extinct. Collectively, this research identifies that islands continue to be a high priority for rail conservation efforts and highlights disparities between historical, contemporary and regional threatening processes.

CS6-4

Bioregionalization approaches for conservation: methods, biases, and their implications for Australian biodiversity

Cristian Montalvo-Mancheno, University of Tasmania; Stefania Ondei, University of Tasmania; Barry Brook, University of Tasmania; Jessie Buettel, University of Tasmania

Biogeographic classification schemes have been developed to prioritize biodiversity conservation efforts at large scales. While these schemes can make conservation more effective, they can only do so if the biogeographic divisions (hereafter referred as bioregions) accurately inform about the biodiversity present in those areas. We hypothesized that there would be marked disparities in our knowledge of biodiversity across bioregions—such as spatial and taxonomic bias in sampling effort—which could weaken the effectiveness of such schemes for conservation planning. We systematically reviewed the literature on Australia's bioregional planning scheme (the Interim Biogeographic Regionalization for Australia; IBRA) to understand how biodiversity research at macroecological scale relates to the biogeographic classifications. We identified 67 relevant studies, finding that the majority investigated biodiversity exclusively within a single bioregion (65.7%). Most studies used inferential techniques (74.6%) or pattern-based measures (68.7%), and few studies (9%) both considered biodiversity across multiple bioregions and compared findings between IBRA bioregions. Species were investigated ten times more frequently than ecosystems' attributes, with mammals and birds monopolizing scientists' attention. These findings show that our knowledge of biodiversity at bioregional scales is patchy, even for well-studied taxa in a developed nation. This knowledge gap limits our understanding of the synthetic relationships between biodiversity and the planning units of bioregionalized conservation schemes (which, like IBRA bioregions, are demarcated according to other biophysical factors). This creates a barrier for systematic conservation planning, which requires unbiased information on the spatial attributes of biodiversity, and therefore this knowledge deficit warrants more attention.

CS6-5

The spatial and temporal dynamics of interspecific associations under global changes

Stanislas Rigal, Université de Montpellier; Vincent Devictor, Institut des Sciences de l'Evolution de Montpellier

The consequences of global changes on biodiversity dynamics are still poorly understood. Traditionally, ecological studies have either focused on how individual species respond to specific pressures or on the spatial distribution of more integrative descriptors such as species richness. But whether and how global changes are shaping the structure and composition of local assemblages in space and time and across large areas remain poorly analysed. We investigate the synergies among several candidate variable of environmental perturbations to understand the magnitude and direction of changes in the "interaction milieu" defined as the specific interrelations among species within communities. We apply a network approach to a large and high resolution dataset in birds collating co-occurrences of more than 100 species for 16 years in 1,977 sites monitored with a standardized protocol across France. We propose new metrics reflecting three aspects of the relationships among species to describe the interaction milieu of bird communities. We then test the relative contribution of random processes versus more deterministic filters to explain the state and fate of bird communities facing climate and anthropogenic stressors. Overall, we found that global changes are most likely responsible for homogenising the diversity of interrelations among species. This study opens new avenues for bridging the gap between network ecology and community ecology under global changes and highlight a neglected issue for conservation science. p { margin-bottom: 0.25cm; direction: ltr; color: rgb(0, 0, 10); line-height: 120%; text-align: left; }p.western { font-family: "Liberation Serif", serif; font-size: 12pt; }p.cjk { font-family: "Noto Sans CJK

CS8-1
Are tropical thermal barriers 'higher' on the way up or down?

Pol Pintanel, Pontificia Universidad Católica del Ecuador; Luis Gutiérrez-Pesquera, Estación Biológica de Doñana; Freddy Almeida-Reinoso, Pontificia Universidad Católica del Ecuador; Gustavo Llorente, Universitat de Barcelona; Andrés Merino-Viteri, Pontificia Universidad Católica del Ecuador; Miguel Tejedo, Estación Biológica de Doñana

Janzen (1967) proposed that tropical species are specialists to thermally stable environments and thus, they would be more limited to dispersing altitudinally (up or down mountain) than temperate species because of evolved physiological barriers. Yet the relative role that physiological barriers, such as thermal tolerance limits, CTmax and CTmin, may play in tropical ectotherm dispersing to either lower o higher elevations is largely untested. Here, we estimated thermal tolerance limits of 75 species of amphibian tadpoles from an aseasonal tropical mountain range of the Ecuadorian Andes, distributed along a 3500 m elevational range, to test whether moving up or down may be more physiologically challenging. Our results by using ancestral reconstruction of evolutionary trajectories, suggest that moving upwards is physiologically more challenging than dispersing downwards; since moving up implied a drastic evolution in cold tolerances. By contrast, higher heat tolerances were not required when species moved downwards. This contrasting evolutionary pattern may result from divergent local habitat selection on both thermal limits to face environmental thermal extremes (tmax and tmin). Specifically, within the same altitudinal window, exposure to extreme maximum temperatures can be avoided through habitat shifts from temporary ponds to permanent ponds or streams, while minimum peak temperatures remained invariable between habitats. Thereby we propose habitat selection as the main driving mechanism in the evolution of CTmax whereas altitude does with cold resistance.

CS8-2
Thermal tolerance across latitudinal and elevational gradients in Neotropical plethodontid salamanders

Sean Rovito, Langebio-Cinvestav; Ana Mayela Ornelas Morin, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional

Among the many hypotheses that attempt to explain high species diversity in the tropics, Dan Janzen's 1967 hypothesis linking annual temperature variation to physiological adaptation and dispersal ability is one of the few that mechanistically links environmental variation with speciation rate. A key prediction of this hypothesis is that physiological tolerances will become more narrow with decreasing latitude, limiting the ability of organisms to cross climatically unsuitable habitat and decreasing gene flow, ultimately resulting in higher rates of allopatric speciation in the tropics. While evidence for this prediction does exist, most studies divide organisms into tropical and temperate groups, while annual temperature variation varies continuously with latitude. To test this prediction while explicitly accounting for latitude, we measured critical thermal minimum and maximum temperatures of Mexican plethodontid salamanders spanning 10 degrees of latitude and 4000m of elevation. We tested the relationship of CTmin, CTmax, and temperature range using both standard and phylogenetic regression methods. In agreement with Janzen's hypothesis, salamander species' temperature range increases with latitude. In contast to more recent predictions, species' temperature range decreased with increasing elevation, largely because of decreased CTmax at high elevation. These results imply that high elevation salamanders at low latitudes, where many endemic species are found, may be the least able to deal with increasing temperatures as a result of global warming because of their narrow thermal ranges.

CS8-3

Functional traits, climate and soil drive niche differences of Damburneya (Lauraceae) sympatric species in a Mexican tropical rain forest

Laura Giraldo-Kalil, Instituto de Ecología, Universidad Nacional Autónoma de México; Juan Núñez-Farfán, Instituto de Ecología, Universidad Nacional Autónoma de México; Julio Campo-Alves, Instituto de Ecología, Universidad Nacional Autónoma de México

Understanding the coexistence of closely related species is challenging, especially in long-lived plants. Niche differentiation promotes species coexistence by reducing interspecific competition and allowing each species to exploit different ranges of resources. Niche differences can be characterized from the abiotic conditions that species tolerate, as well as through the analysis of intraspecific variation of functional traits, directly involved in response capacity of the species to their environment, and their performance within communities.
The Lauraceae family is particularly interesting for the study of coexistence: Although trees of this family have great morphological similarity, ecological differentiation seems to be frequent within the group, mainly promoted by altitude, topography, and soil.

This project aims to assess whether there is niche differentiation among four Damburneya species which have contrasting patterns of latitudinal and altitudinal distribution and occur sympatrically in a Mexican tropical rain forest. If so, we expect to detect it at different scales and dimensions of the niche.

To date, we have performed ecological niche models based on climatic variables. Furthermore, we sampled surficial soil and mature leaves from 184 trees within six 1 ha plots along an altitudinal gradient to measure several functional leaf traits (SLA, LDMC, chlorophyll, N, and P content). Our goal is to determine the extent to which closely related species of Damburneya are functionally distinct at local scale, and how this is associated with their climatic and edaphic tolerances.

CS8-4

Polytolerance to abiotic stress and range filling in European and North American woody species

Giacomo Puglielli, Estonian University of Life Sciences; Lauri Laanisto, Estonian University of Life Scienes

Current plant species distribution patterns are predicted to be strongly determined by species' ability to tolerate multiple abiotic stress factors (polytolerance). Nevertheless, species' polytolerance ability is a complex feature shaped by trade-off rates between abiotic stress factors. Our aim was to explore the relationship between species polytolerance to four major abiotic stress factors (lack of light, drought, waterlogging and low temperatures) and range filling for 331 woody species from Europe and North America. We asked whether lower trade-off rates between stress factors (i.e. polytolerance) are positively related to woody species' ability to fill a greater portion of their potential range.

Our results highlighted a main trade-off axis (Mto) positively related to drought tolerance and negatively to waterlogging and cold tolerance, revealing a polytolerance sub-axis for the last two stress factors. Mto was in turn negatively related to range filling estimates. When accounting for the interaction between shade tolerance and Mto, two major trade-offs could be defined in a bi-dimensional stress tolerance space: 1) the shade-drought (SDto) and 2) the shade-waterlogging/cold (SWCto) trade-offs. SDto was found to limit range filling values while SWCto was not, possibly due to the positive relationship between waterlogging and cold tolerance.

Altogether, our findings demonstrate that trade-off rates between abiotic stress factors are strong determinant of woody species' ability to fill a great portion of their potential range and that polytolerant species tend to display higher values of range filling.

CS8-5

Elevational and microclimatic drivers of thermal tolerance in Andean Pristimantis frogs

Pol Pintanel, Pontificia Universidad Católica del Ecuador; Miguel Tejedo, Estación Biológica de Doñana; Santiago Ron, Museo de Zoología, Pontificia Universidad Católica del Ecuador; Gustavo Llorente, Universitat de Barcelona; Andrés Merino-Viteri, Pontificia Universidad Católica del Ecuador

We analysed elevational and microclimatic drivers of thermal tolerance diversity in a tropical mountain frog clade (4230m elevational gradient) to test three macrophysiological predictions: less spatial variation in upper than lower thermal limits (Bretts′ heat invariant hypothesis); narrower thermal tolerance ranges in habitats with less variation in temperature (Janzen´s climatic variability hypothesis); and higher level of heat impacts at lower elevations. We examined variability in thermal limits (CTmax, and CTmin), and thermal breadth in 21 species of Pristimantis frogs. Additionally, we monitored temperatures at the local-scale (tmax, tmin), and estimated vulnerability to acute thermal stress from heat and cold, by partitioning thermal diversity into elevational and microclimatic variation. Our results were consistent with Brett′s hypothesis: elevation promotes more variation in CTmin and tmin than in CTmax and tmax. Frogs inhabiting thermally variable open habitats have higher CTmax and tmax and greater thermal breadths than species restricted to forest habitats, which show less climatic overlap across the elevational gradient (Janzen´s hypothesis). Vulnerability to heat stress was higher in open than forest habitats and did not vary with elevation. We suggest a mechanistic explanation of thermal tolerance diversity in elevational gradients by including microclimatic thermal variation. We propose that the unfeasibility to buffer minimum temperatures locally may explain the rapid increase in cold tolerance (lower CTmin) with elevation. In contrast, the relative invariability in heat tolerance with elevation may revolve around the organisms′ habitat selection. Secondly, on the basis of microclimatic estimates, lowland and upland species may be equally vulnerable to temperature increase.

Concurrent Session 9: Conservation Biogeography

CS9-1

Evaluation of five taxa as surrogates in the Transmexican Volcanic Belt, Mexico

Tania Escalante, UNAM; Leslie Elguea Manrique, Biogeografía de la Conservación, UNAM; Ana Varela Anaya, Universad Nacional Autonoma de México; Elkin Noguera-Urbano, Instituto Humboldt

Many biotic groups have been proposed as surrogates; however different taxa could provide complementary information for choosing conservation priorities. There are two general ways to evaluate the performance of surrogates: (1) using cross-taxon congruency as a priori test, before the application of some prioritization algorithm to select areas for conservation, and (2) developing a system of priority areas as a posteriori test. We have developed these two tests in order to evaluate five different taxa as surrogates (Amphibia, Aves, Insecta, Mammalia and Magnoliopsida), and groupings of them (Invertebrates, Vertebrates and Plants), in order to compare their performance in a priori and a posteriori tests based on their richness patterns and prioritization areas for conservation within the Transmexican Volcanic Belt. The prioritization was run in Zonation software. We performed two correlation analyses in order to evaluate if the patterns are shared, using Pearson and modified t test (to correct spatial autocorrelation). Although we found some positive correlations between the richness patterns of taxa and groupings, there was not a correlation between the prioritized areas. In general, the best correlations were always for mammals and plants, and the worst for birds and insects. We found that patterns of richness and rarity (obtained through the prioritization) are not shared among groups and groupings. Therefore, if conservation priorities are only based in one group and a single test, the risk of leaving other groups unprotected is high.

CS9-2

New guidelines for ex situ conservation- integrating geography and genetics

Sean Hoban, The Morton Arboretum; Patrick Griffith, Montgomery Botanical Center

It is important to safeguard the genetic diversity of threatened species in ex situ facilities (e.g., in seed banks or botanic gardens). For decades, conservationists have used a simple and useful, but perhaps suboptimal, minimum sampling guideline- sampling from 50 individuals per population. However, this guideline neglects realities of biogeography, population genetics, and practical constraints. Here, I use computer simulations as well as empirical data from 10 species to demonstrate two major areas in which sampling can be improved- by considering population structure (population fragmentation and degrees of migration) and by considering ex situ collections maintenance over time (loss of plants, e.g. via disease). I find that sampling seed from approximately 200 to 300 individuals total across a species' geographic range may be a new useful "rule of thumb" for conserving many plant population systems. However this suggestion assumes that all seed or plants survive in perpetuity. I next show that to compensate for losses over time, sampling should be increased by approximately the expected loss rate. Therefore, sampling from 1000 or more individuals may be needed to ensure a robust minimum collection for ex situ gene conservation. I will also discuss how to sample based on ecological diversity, and future directions to incorporate biogeographic history and distinct evolutionary lineages. I conclude that conservation collections planning must consider the species' biology as well as collection maintenance. These results emphasize a need for thoughtful deliberation by collectors and curators, and renewed discussion of long term gene conservation targets.

CS9-3

Implicaciones biogeográficas espaciales para la evaluación de las categorías de amenaza: El caso de las ranas venenosas en Ecuador.

H. Mauricio Ortega-Andrade, Universidad Regional Amazónica Ikiam; Miguel Gómez, Universidad Regional Amazónica Ikiam

Según la UICN, el 19,14% de los dendrobátidos ecuatorianos están en Peligro Crítico, un 17,02% En Peligro y un 12,77% Vulnerable. Los criterios utilizados por la UICN para evaluar la categoría de riesgo dependen directamente del área estimada y de las diferentes amenazas presentes. La metodología utilizada por la UICN para generar las áreas de distribución potencial de las especies: a) Extensión de Presencia (EOO), y el Área de Ocupación (AOO) utilizan únicamente el número y distribución geográfica de las presencias, generando frecuentemente áreas de distribución sobreestimadas, y/o subestimadas. Por tanto, el incluir datos ecológicos, climáticos y/o biogeográficos, a través de MNE, permite obtener información base, incorporando la historia ecológica y evolutiva de la especie. En este trabajo comparamos la metodología propuestas por la UICN con los MNE para estimar los potenciales sesgos en las áreas usadas para aplicar los criterios de amenaza. El área de distribución propuesta por la UICN mediante EOO de 6 especies (17,14%) con categoría de amenaza y 3 especies (8.6%) sin categoría de amenaza fueron subestimadas y 8 especies (22.85%) sin categoría de amenaza fueron sobreestimadas. El análisis de correlaciones (MNE vs UICN), mostró una mayor correlación lineal positiva en especies amenazadas ($r=0,94$ / $R2 = 0,92$) frente a otras categorías ($r=0,84$ / $R2 = 0,7$) que presentaron cierta dispersión en los datos. Estos resultados evidencian que, según la metodología, es posible otorgar distintas categorías de amenazadas a una misma especie, influyendo directamente en la toma de decisiones para la conservación de las especies y áreas prioritarias de conservación.

CS9-4

Diversificación altitudinal en el Bloque Norte de los Andes vista a través de múltiples taxa

Viviana Ayus, Universidad Industrial de Santander; Daniel Miranda, Universidad Industrial de Santander

La distribución geográfica de los organismos puede influenciar cambios en las tasas de especiación y/o extinción en el tiempo. Dado el amplio rango elevacional del Bloque Norte de los Andes (BNA), cuantificamos el ajuste de diferentes escenarios de diversificación altitudinal durante el Mioceno-Plioceno, variando los valores para especiación y/o extinción._
Para el análisis usamos cinco grupos, cuyas divergencias se encuentran entre 35 y 5 Ma, pertenecientes a tres clases taxonómicas. La distribución altitudinal por grupo se optimizó como variable cuantitativa y categórica tanto para la reconstrucción del rango altitudinal ancestral como para la evaluación de hipótesis, en este último, usando modelos SSE-like.

Nuestros resultados sugieren que bajo los dos esquemas de optimización, el rango de tierras medias corresponde a la altitud ancestral para los cinco grupos de estudio, lo cual coincide con la elevación propuesta en la literatura para algunas de las cordilleras en los respectivos intervalos temporales dentro del BNA. Además, los periodos de máxima diversificación estimados para las filogenias coinciden con eventos geológicos, como el levantamiento acelerado de las cordilleras. Aunque al evaluar el comportamiento de las diferentes tasas de especiación y/o extinción dentro de los escenarios y la distribución altitudinal no se encontró compatibilidad en la influencia de la distribución geográfica sobre los parámetros, para los cinco grupos; en general se observa un patrón similar independiente de la identidad taxonómicas en términos de altitud ancestral reconstruida, tasas de diversificación y escenarios con mayor likelihood.

CS9-5

Patrones de distribución de la diversidad Alfa y Beta de murciélagos en las regiones biogegráficas de Columbia: Base para su conservación

Juranny Astorquiza, Estudiante Universidad de Nariño; Elkin Noguera, Instituto de Investigación de Recursos Biológicos Alexander von Humboldt

Se presentarán los patrones de distribución de la diversidad Alfa y Beta de murciélagos en Colombia. Este análisis está soportado a partir de 370,000 registros publicados y almacenados en base de datos (GBIF, SIB Colombia, PUCE Ecuador, SpecesLink Brasil y publicaciones científicas), que corresponden a 204 especies de murciélagos para Colombia. Luego de la revisión y validación de los datos, se procesarán 220,040 registros que sirven para determinar la distribución potencial de 192 especies de murciélagos, basadas en el modo predictivo de nicho ecológico. Mediante la superposición de192 modelos se puede ver un mapa de la riqueza potencial de murciélagos, evidenciar las zonas de mayor diversidad del país. Con esta información,

Toda la información de la riqueza potencial se superpondrá con el mapa de las áreas protegidas de Colombia (SINAP), para evidenciar el porcentaje del área con el mayor potencial potencial de los quirópteros que se encuentra protegida, con el propósito de hacer un análisis de los vacíos de la información actual, En Colombia, se puede utilizar información importante sobre las áreas prioritarias de investigación y conservación de la vida en Colombia.

Concurrent Session 11: Biodiversity Patterns and Maintenance

CS11-1

Southern Philippine Stream Toad Diversification Resolved with a Novel Genomic Probeset and thousands of Sequence-Capture Loci

Marites Sanguila, Fr. Saturnino Urios University; Chan Kinn Onn, National Museum of Singapore; Perry Wood, Auburn University; Carl Hutter, University of Kansas; *Rafe Brown*, University of Kansas

Traditionally considered a textbook "fringing archipelago," the Philippines has been regarded as a typical "downstream" geographical setting for evolutionary diversification, where colonizing lineages only penetrate as far as their relative powers of dispersal allow. "Upstream diversification," or in situ diversification within the archipelago or its larger landmasses, has rarely been considered in the context of this model.

Here we utilize a new phylogenomic genomic sequence capture probeset to infer biogeographical history of southern Philippine bufonid toads of the genus Ansonia. We utilize thousands of sequence-capture loci to perform SNP-based coalescent analyses of (1) species boundaries, which have remained unresolved following a 2010 phylogeographic analysis of mitochondrial DNA sequence data, to (2) reconstruct the ancestral biogeographic sequences of insular range evolution in these high-gradient stream specialists, and to (3) address primary geographic factors of geographic isolation among populations endemic to Mindanao's montane centers of amphibian diversity.

Philippine Ansonia—the first terrestrial land vertebrate from the Mindanao faunal region ever to be the subject of a phylogeographic analysis—now emerges as a unique study system. The clade does not exemplify the expected, pure, west-to-east pectinate set of relationships, nor a sky-island series of montane endemics, nor a paleo-island radiation of old endemics. Rather, this endemic group represents a novel combination of factors and processes: ideal for testing biogeographical hypotheses of diversification in the model Philippine archipelago.

CS11-2

Assemblage dispersion fields reveal the spatial structure of biotic similarity among South American vertebrate distributions

Michael Borregaard, Center for Macroecology, Evolution and Climate; Carsten Rahbek, CMEC Univ. of Copenhagen; Gary Graves, Smithsonian Institution

The underlying cause of continental patterns of species richness has been one of the central questions in biology since the days of von Humboldt, Wallace and Darwin, and continues to spur heated discussion. Hypotheses based on an effect of ambient energy have traditionally dominated the debate, but have in recent years increasingly been challenged by hypotheses that incorporate niche evolution and range dynamics of individual species. At the heart of this controversy lies the question of whether species richness of individual grid cells is mainly controlled by local factors, or mainly reflects the species composition of regional assemblages generated by the spatial turnover of species' ranges. This question is still unanswered, in spite of a recent focus on patterns of spatial turnover, primarily on the geographical configuration of discrete biogeographic regions. Here, we use a new approach that characterizes the orientation and shape of assemblage dispersion fields as a vector field (ADF), to demonstrate the existence of as yet undocumented macro-structures in the spatial pattern of biotic similarity at a continental scale for all birds (n = 2869), mammals (n = 1146), and amphibians (n = 2265) of South America. These structures are highly congruent among vertebrate classes and reflect spatial factors with consistent effect on species distributions, such as the turnover of vegetation biomes at different scales. These patterns are inconsistent with a hypothesis of simple localized energy-richness dynamics across continental scales, and point to the importance of regional-scale processes that are impossible to capture with local regression analysis.

CS11-3

Dimensions of biodiversity and geodiversity across scales

Phoebe Zarnetske, Michigan State University; Annie Smith, Michigan State University; Quentin Read, National Socio-Environmental Synthesis Center (SESYNC); Sydne Record, Bryn Mawr College; Kyla Dahlin, Michigan State University; Andrew Latimer, University of California at Davis; Jennifer Costanza, North Carolina State University; Stephanie Pau, Florida State University; Keith Gaddis, National Aeronautics and Space Administration (NASA); Martina Hobi, Swiss Federal Research Institute WSL; Adam Wilson, SUNY Buffalo

Climate and land use change are affecting the geographic distributions of species, composition of ecological communities, and patterns of biodiversity. In addition to species' physiological tolerances, biotic interactions, and dispersal, species-environment relationships are central to anticipating the ecological effects of climate change. However, ecological analyses tend to focus on mean environmental conditions in space and time. Geodiversity—variation in Earth's abiotic processes and features —is rarely incorporated explicitly into models predicting species distributions. Conservationists have proposed preserving geodiverse landscapes because variable environments that include distinct landscape features are likely to support more unique biota. Quantifying the influence of geodiversity on biodiversity is necessary to guide appropriate selection of geodiversity variables and scales and to identify potential refugia for populations facing changes in climate and land use. We computed and assessed a range of spatial scale-dependent geodiversity measures across the continental United States from NASA satellite remotely-sensed products. We found that relationships between geodiversity and biodiversity of birds and trees varied by ecoregion, scale, and dimension of biodiversity (taxonomic, functional, and phylogenetic diversity). Models incorporating abiotic spatial heterogeneity in addition to abiotic means explained more variation in biodiversity for both taxonomic groups. We present a framework for incorporating geodiversity into models forecasting the effects of climate and land use change, from individual species to dimensions of biodiversity.

CS11-4

Evolutionary cradles and museums of plant diversity in tropical Africa

Thomas Couvreur, Institut de Recherche pour le Développement; Dagallier Léo-Paul, Institut de Recherche pour le Développent (IRD); Olivier Hardy, Evolutionary Biology and Ecology Unit, Faculté des Sciences, Université Libre de Bruxelles ; Steven Janssens, Meise Botanic Garden; Jan Wieringa, Naturalis Biodiversity Center; Gilles Dauby, Evolutionary Biology and Ecology unit, Université Libre de Bruxelles, Belgium

Alexander van Humboldt was one of the first to recognize that biodiversity is not distributed equally across space. Understanding where species diversify (cradles) and persist (museums) over evolutionary time is fundamental to better describe the distribution of biodiversity and for conservation. Here, we identify for the first time cradles and museums of plant diversity across the entire tropical African flora, one of the most biodiverse and unique places on Earth.

Regions containing significant concentration of young -neo and old -paleo endemic taxa were identified by analyzing the distribution of over 1700 angiosperm genera combined with a time-calibrated phylogenetic tree. We match these regions with the current network of protected areas (PA) of Africa.

Across tropical Africa, phylogenetic diversity and endemism are mainly concentrated in the biogeographically complex region of Eastern Africa. We show that mountainous areas are both centers of neo- and paleo-endemism, simultaneously acting as cradles and museums of plant diversity. In contrast, the lowland rain forest of the Guineo-Congolian region is characterized by widespread and old lineages, implying they mainly act as museums of diversity. Overlap between the identified centers of phylogenetic endemism and PA is high suggesting that regions of diversification and persistence of the tropical African diversity might be properly conserved in the future.

This study underlines once again the vital role played by mountains in generating and maintaining tropical plant biodiversity. Further refining our comprehension of the processes shaping biodiversity, potentially at the species level, will be important to confirm our results.

CS11-5
The macroecology of climate stability and change: a synthesis of mechanisms and patterns
Roland Jansson, Umea University

I present a framework describing the effects of climate change on organisms at population, species and assemblage levels, synthesizing recent advances in e.g. palaeoecology, phylogeography and macroecology. I conclude that temporal stability in species' geographic ranges can explain a range of biogeographic phenomena, such as patterns in organism traits, genetic diversity and divergence among populations, and strength of interspecific interactions. I also discuss the role of climate stability for different speciation modes, species diversification and adaptive radiation. The rate of splitting might be favoured by climate shifts, but the risk that lineages do not persist, or that there is insufficient time with stable conditions to allow speciation to be completed increases with the magnitude or frequency of climate change. While lineages may diversify in response to novel conditions offered by climate change, climate stability allows lineages to diversify and radiate by multiple mechanisms. I present a conceptual model for how climate stability affects species richness, incorporating the effects of time and area since these variables are modulated by climate change. Reviewing the evidence, I find that climate stability is positively associated with numbers of range-restricted species, high endemism and species richness, and high community and phylogenetic beta diversity. Knowledge of how climate change has shaped processes at the levels of population, species and assemblages in the past offers insights on how to deal with human-induced climate change. I discuss which lessons that can be learnt from the past and how the Anthropocene is different from previous climate-shift events.

CS11-6
The global distribution of morphological diversity in insect societies
Jean-Philippe Lessard, Concordia University

Morphological diversity in the worker caste is present in ants, wasps, termites and thrips, but is particularly striking in ants, as they can produce distinct or continuous worker subcastes. This is referred to as worker caste polymorphism, which has enabled efficient division of labour and consequently, ecological dominance. Previous research shows that nutrition and colony demography during larval development are important determinants of worker polymorphism, which in turn can be mediated by the abiotic environment. However, little is known about the influence of environmental gradients on the geographic distribution of worker caste polymorphism. Here, we investigated the influence of geographic variation in temperature and precipitation on the distribution of worker polymorphism worldwide using 680 000 ant occurrences and identifying each occurrence point as polymorphic or not. Previous estimates suggested that 13% of ant species are polymorphic whereas our results suggest that 29% of all ants are polymorphic. Moreover, the occurrence of polymorphism was highest in arid and tropical ecosystems, suggesting that it may be an adaptation to regions with extremely scarce or diverse resources. Our results further indicate that warm climate is a pre-requisite for the evolution of worker caste polymorphism. Taken together, this work sheds light on the factors promoting complex social lifestyle in insects.

CS11-7
Application of the 'Humboldtian' interdisciplinary approach to reconstruct phytogeographic history
Carina Hoorn, University of Amsterdam; Giovanni Bogotá-Angel, IBED, UvA; Universidad Distrital; Christine Bacon, University of Gothenburg; Guillaume Dupont-Nivet, Potsdam University, Department of Earth & Environmental Science ; Hong Xiang Zhang, Chinese Academy of Sciences; Amber Woutersen, University of Amsterdam; Natasha Barbolini, Stockholm University; Delphine Tardif-Becquet, Institut de Physique du Globe de Paris, Equipe Paléomagnétisme 1

Alexander von Humboldt was a great advocate for interdisciplinary research. The 'Humboldtian' approach to conducting science enabled him to identify the intimate relationship between plant geography and climate. This insight diverted from the traditional perception of species as single entities that were disconnected from their surroundings. His conceptual advances culminated during his research in Ecuador where he observed the changes in plant composition along the altitudinal gradient. Although at the time the geological sciences were still developing, his holistic approach is also of great importance in historical biogeography. In this presentation I will highlight the potential of integrating geological and biological datasets when reconstructing plant history, and I will illustrate this point with examples from South America and Asia. The integration of palynological, geological, climatic and molecular data enable us to make more sophisticated reconstructions of plant evolution and the habitats they represent than any of the individual disciplines could do on their own. Taken together, the 'Humboldtian' approach is still highly pertinent to apply in 21stcentury science.

CS11-8

Biogeographical insight into evolution of bird migration

Bela Arora, Centre for Macroecology, Evolution and Climate (Natural History Museum of Denmark); Kasper Thorup, University of Copenhagen

Billions of birds modify their distributions seasonally. How these movements have evolved and what consequences they have on the colonization routes, species distributions and gene flow is poorly understood. Earlier discussions on the evolution of migratory movements mainly dichotomized into 'Northern Home' hypothesis (moving for non-breeding) and 'Southern Home' hypothesis (moving for breeding) (Cox, 1968, 1985). Lack of single conclusion implies peculiar origin of migration within and amongst avian lineages (Zink, 2011). Migration routes likely evolved as gradual changes. We hypothesize that the current migration patterns, at least partially, reflect historical colonisations, with migration resulting from range expansion of either migratory species (dispersal from one or more of the original breeding, stop-over or wintering sites) or sedentary species. Recent tracking technology has made it possible to study detailed spatio-temporal migratory patterns of birds. We use these data from breeding, stop-over and wintering sites of numerous species to investigate their likely biogeographic origin. Origins were inferred from genus phylogenies with main focus on closest relatives to ensure contemporary origin. We demonstrate many cases of origins, likely extending breeding and wintering grounds from mid-point of route, seemingly from shorter-distance migrants in Asia, as well as more commonly inferred patterns of extension from wintering to breeding grounds and vice-versa. We conclude that biogeographic origin likely varies greatly among Afro-Palearctic long-distance migrants, concordant with their inferred colonization routes. The diverse origins point to complex inferences from current distributions and the importance of considering migration in shaping distributions and prioritizing conservation grounds.

Concurrent Session 12: Neotropical Phylogenetics and Phylogeography

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CS12-1

The origin of exceptional diversity in the widely distributed New World songbird, the House Wren (Troglodytes aedon)

Jaime Chaves, Universidad San Francisco de Quito; Patricia Escalante, Instituto de Biología, Universidad Nacional Autónoma de México, México, D.F., México; Garth Spellman, Department of Integrative Biology, Denver Museum of Nature & Science; Brian Smith, American Museum of Natural History; John Klicka, Department of Biology, University of Washington

Macroevolutionary studies often assume currently recognized species are adequate for comparative methods. However, unrecognized biodiversity can affect downstream analyses, such as estimating the mode and tempo of diversification. Here we explored a recent and rapid radiation in the House Wren complex (Troglodytes aedon), a songbird that is widely distributed across North and South America, to test the effect of taxonomic sampling bias on diversification rates and inferences on the evolutionary history for this group. Using a dataset of three mtDNA and eight nuclear loci we recover a clade comprised of 44 independently evolving evolutionary lineages. Of these, 29 were part of a "House Wren complex" that includes the House Wren (T. aedon) and two Mexican island endemics. Using a model-based approach to estimate ancestral ranges we document that in these wrens, a single ecological shift from high to low elevation habitats occurred near the onset of the Pleistocene. This rapid colonization of lowland habitats throughout both North and South America led to a more than doubling of diversification rates at this time leading to an inter-continental radiation. This study suggests that both ecological and evolutionary

explanations must be invoked to account for the number and geographic distributions of lineages currently this group, and highlights the necessity to include all available taxa, being these phylogroups or unrecognized biological species when seeking a complete evolutionary reconstruction of species' diversification.

CS12-2

Species delimitation and evolutionary history of closely related abundant vs. rare rainforest trees (Eschweilera, Parvifolia clade, Lecythidaceae) in French Guiana

Myriam Heuertz, INRA; Quentin Jehanne, INRA; Sylvain Schmitt, UMR BIOGECO - Université de Bordeaux; Stéphanie Mariette, INRA; Henri Caron, INRA; Caroline Scotti-Saintagne, INRA; Pascal Pétronelli, CIRAD; Julien Engel, IRD; Niklas Tysklind, INRA; Jean-François Molino, IRD; Daniel Sabatier, IRD; Katharina Budde, INRA

Amazonia's tree flora displays a strong skew in species abundance. Some clades, such as the Parvifolia clade of the genus Eschweilera (Lecythidaceae), contain hyperabundant tree species, also known as hyperdominants, which co-occur in sympatry with closely related rare tree species in different Amazonian regions. We here examined the evolutionary implications of species commonness versus rarity in the Parvifolia clade in French Guiana, where abundant species such as E. coriacea and E. sagotiana co-occur with rare congeners. We sampled 11 species in nine forest sites and produced microsatellite data and resequencing data of 130 nuclear loci. We used phylogenetic and genetic clustering methods to delimit genetically coherent putative species and compared genetic and morphological species assignments. We examined evolutionary relationships between species and estimated current and historical effective population sizes as indicators of the evolutionary persistence of common vs. rare species. All species were closely related, as suggested by widespread allele sharing and failure of phylogenetic methods to delimit species. Genetic clustering methods succeeded at taxon delimitation, revealing mismatches with morphological determinations. We did not find any conclusive evidence for cryptic species within abundant taxa such as E. coriacea. A positive trend was identified between demographic abundance of species and effective population size, suggesting a trend for higher evolutionary potential in abundant species, except in E. sagotiana. Our study resolves evolutionary relationships in the Parvifolia clade and enhances our understanding of the causes of hyperdominance in Amazonian trees.

CS12-3

Unravelling the evolutionary processes driving the diversification of a conifer clade after its migration into the subtropics

Juan P Jaramillo-Correa, Institute of Ecologia, Universidad Nacional Autónoma de México; Gustavo Giles-Pérez, Institute of Ecology, Universidad Nacional Autónoma de México; Jorge Cruz-Nicolás, Institute of Ecology, Universidad Nacional Autónoma de México; Alicia Mastretta-Yanes, Comisión Nacional para el Conocimiento y Uso de la Biodiversidad; Norberto Martínez-Méndez, Instituto Politécnico Nacional; Érika Aguirre-Planter, Institute of Ecology, Universidad Nacional Autónoma de México; Luis Eguiarte, Institute of Ecology, Universidad Nacional Autónoma de México

Tropical trees embody an evolutionary dichotomy: they are outcrossing long-lived taxa, which favours evolutionary stasis, but have a predominant position in a highly heterogenous ecosystem, which should prompt disruptive selection and species divergence. Such dichotomy is particularly noteworthy in conifers that have migrated south into subtropical latitudes from boreal regions, given that they are among the most slowly evolving tree clades. We studied this evolutionary puzzle using the genus Abies (firs), which expanded into Mexico ~5Ma ago, and then underwent a rapid diversification. According to our phylogenies, firs colonized Mexico in at least two independent waves, which resulted in at least four modern lineages that do not fit a classic bifurcating model; they are better depicted as a reticulated network in which incomplete lineage sorting and introgressive hybridization are commonplace. They have further accumulated relatively low amounts of nucleotide diversity, although the central and southern clades have a higher contribution of non-synonymous mutations, which points to a more relaxed purifying selection as we move south. A more detailed study of the zone of contact of the two main lineages (central Mexico) revealed that this is not only related to population size, but to the relative distance to the optimal ecological conditions that fir populations have had during the last ~20Ka. The existence of a long-lasting continuum process of (mal)adaptation, genetic drift and introgression should be thus considered for managing and protecting this economically important group of trees.

CS12-4

Phylogeography of an Amazonian tree frog reveals high cryptic diversity and provides insights into Neotropical diversification

Diego Ortiz, James Cook University; Antoine Fouquet, Centre National de la Recherche Scientifique, Laboratoire Evolution et Diversité Biologique; Albertina Lima, Instituto Nacional de Pesquisas da Amazônia; Santiago Ron, Museo de Zoología, Pontificia Universidad Católica del Ecuador; Leandro Moraes, Instituto Nacional de Pesquisas da Amazônia; Lynne van Herwerden, James Cook University; Fernanda Werneck, Instituto Nacional de Pesquisas da Amazônia; Conrad Hoskin, James Cook University

An old debate persist today about how the high Neotropical biodiversity is originated and maintained through history. We aimed at exploring mechanisms promoting speciation in this region by targeting a widespread Amazonian tree frog as study model, the Osteocephalus taurinus species group. Based on previous studies, this group is expected to contain a complex array of genetic lineages and cryptic diversity. Using newly generated and online repository mitochondrial data, we gathered 429 sequences for 16S gene (up to 1500 bp) and 244 for ND1 (1400 bp), covering the entire geographic range of the group. We conducted phylogenetic analyses and found 18 well-supported major clades. Currently, there are only two accepted binomials for these clades, O. taurinus and O. oophagus. Therefore, as many as 16 undescribed taxa may exist in this group. The distribution of groups of clades is mainly delimited by the largest rivers (Amazon, Madeira, Negro rivers), suggesting a role of them as barriers to gene flow, at least at their widest courses. The Guiana Shield seems to be the origin centre of the group, presenting an increased diversity (occurrence of 9/18 clades) and early diverging clades. Such result can be explained by the historical persistence of this area within the Amazonian landscape, coupled with its topographical heterogeneity. Ongoing analyses include incorporation of nuclear data (SNPs), species delimitation and reconstruction of biogeographic scenarios for its diversification. Few vertebrate groups have been sampled at such fine scale over entire Amazonia, thus our overall findings would be representative for other Neotropical species complexes.

CS12-5

Mitogenomics Phylogeny and Historical Biogeography of Neotropical Myotis (Chiroptera: Vespertilionidae)

Carlos Carrion, University of New Mexico

Bats of the widely distributed genus Myotis are an excellent model to study one of the primary processes of evolution, diversification. This genus contains ~103 species and has undergone one of the most impressive mammalian radiations worldwide. However, despite recent advances in description of species and phylogenetics of Myotis, our understanding of the systematics and biogeography of this genus in the New World, particularly the Neotropics, is extremely limited. Defining natural groups within this assemblage has been difficult due to high diversity and the extreme morphological conservatism of the genus. Previous studies based on genetic data hypothesized that New World Myotis is monophyletic and includes 2 clades, Nearctic and Neotropical. Another study based on mitochondrial cytochrome b (cytb), however, revealed multiple paraphyletic assemblages within both clades suggesting the need for expanded sampling for phylogenetic analyses. Here ,we conducted a robust phylogenetic analysis of 35 published mitogenomes together with 61 newly generated mitogenomesand suggest that colonization of the New World was initiated during the Miocene (13.5 MYA) with diversification in South America occurring prior to the onset of the Great American Biotic Interchange (GABI) in the Late Miocene (now dated at about 9 MYA). Herein, we shed light on light on evolutionary relationships, historical biogeography and species boundaries of the genus in the Neotropics Realm

CS12-6
Salamanders of the Trans-Mexican Volcanic Belt: the microbiome in a phylogenetic context

Julio García, Cinvestav; Sean Rovito, Langebio-Cinvestav

The study of microbiomes has flourished in recent years, in part due to the wide range of functions that the microbiome performs in host organisms. In amphibians, little is known about the skin microbiome, yet skin bacteria have already been shown to play a role in protection against fungal pathogens. Despite the major technological advances in characterizing microbiomes using amplicon sequencing, it is still not clear which factors determine microbiome species composition and diversity. Microbiome composition may be influenced by development stage, environmental, spatial, and species-specific factors, but the relative roles of each in shaping the microbiome are not well understood. Therefore, we used phylogenetically controlled comparisons of closely related plethodontid species in order to determine the role that phylogenetic history, environment, and geographic space play in shaping the microbiome. We used amplicon sequencing to compare bacterial skin microbiomes of five closely related, microendemic species of Pseudoeurycea in the Trans-Mexican Volcanic Belt and one widespread species of the same genus (P. leprosa) that occurs in sympatry with the microendemic species. By comparing the composition of the microbiome of these species of salamanders in a phylogenetic and spatial context, we can infer which factors have the strongest influence on microbiome composition. We found that phylogenetic relatedness of the host has an effect on the differences in the composition of the microbiome, even after taking into account the geographical distance between the collection sites. These results have important implications for our understanding of interactions between host, microbiome, and environment.

CS12-7
Worldwide expansions and dispersals between tropical and extra-tropical zones underlay the reticulate assemblage of muscid flies in South America

Peter Löwenberg-Neto, UNILA; Claudio Carvalho, UFPR

The fly family Muscidae originated during the Paleocene-Eocene and today has a worldwide distribution. Spatial and phylogenetic patterns supported that the family had a tropical origin followed by climatic adaptations to occupy temperate zone and highlands. In South America, its composition is reticulated, comprised by endemic, disjunct and cosmopolitan genera. Herein we investigated how muscid genera have evolutionarily assembled in the continent. We departed from terrestrial regionalization scheme and we classified regions into extra-tropical (Andean, Nearctic, Palearctic) and tropical (Afrotropical, Australian, Neotropical and Oriental). Phylogenetic and geographic data were fitted to five DEC models based on dispersal constraints: unrestricted routes, trans-climatic routes, cis-climatic routes (non-stratified), trans/cis routes, and cis/trans routes (stratified). Based on the inferences of the best-fit model, we quantified the direction of dispersal events, absolute and relative numbers of dispersals through time.The best-fit model was 'trans-climatic routes', which inferred 175 events of dispersals; about 45% of these events involved expansions between the same climatic zones. Area to area range expansions were strongly asymmetric: Neotropics was the primary source of lineages to all other regions. Dispersal through time plot indicated dispersal events of two ancestors' lineages from Neotropics to all other areas during Eocene (~41Ma). After that, range expansion frequency relatively decreased through time and ceased during Late Miocene (~11Ma). Climate niche conservatism was not supported as an underlying mechanism for the family global pattern. The reticulate assemblage of muscid flies in South America was caused by, at least, three factors: ancestral origin in the Neotropics; range expansions to tropical and regions of same and different climatic zones, and early events of dispersal responsible for expanding deep ancestral lineages worldwide.

CS13-1

El Río Pastaza como barrera biogeográfica para las poblaciones de la lagartija amazónica Potamites strangulatus (Gymnophthalmidae), Ecuador.

Carolina Reyes-Puig, Universidad San Francisco de Quito; Raquel Betancourt , Instituto Nacional de Biodiversidad; Omar Torres-Carvajal, Pontificia Universidad Católica del Ecuador

Las estribaciones andinas y tierras bajas de la Amazonía ecuatoriana son áreas de alta biodiversidad. Las cuencas hidrográficas y cadenas montañosas son barreras biogeográficas que podrían limitar la dispersión de fauna en esta zona. La lagartija Potamites strangulatus se distribuye ampliamente en esta región; sin embargo, existe incertidumbre taxonómica sobre sus poblaciones. En este estudio, hallamos por medio de morfometría geométrica diferencias entre poblaciones del norte y sur. Examinamos 59 especímenes e identificamos 18 puntos homólogos en la superficie dorsal de las escamas de la cabeza. Realizamos un Análisis Procrustes Generalizado y un desplazamiento vectorial. Además, generamos un PCA, un ANOVA y una prueba de distancias pareada para establecer diferencias entre grupos (norte versus sur) y sexos. Ejecutamos un Análisis de Trayectoria para identificar diferencias entre la magnitud y ángulos de los vectores. La mayor parte de la variación en forma se encuentra asociada al área parietal. Los especímenes de la región norte presentan una constricción pronunciada en esta zona, en comparación con los ejemplares del sur. Existen diferencias significativas en forma entre los grupos y entre sexos. El Análisis de Trayectoria muestra que la manifestación del dimorfismo sexual de los dos grupos se expresa de forma inversa. Las diferencias entre las poblaciones de P. strangulatus deben ser analizadas bajo criterios adicionales (e.g. distancias genéticas) para esclarecer su estatus taxonómico. Nuestros resultados indican que las poblaciones hacia el norte del río Pastaza son significativamente diferentes de las del sur, reflejando una posible ruptura en la conectividad de poblaciones.

CS13-2

Uso del Modelamiento de Nichos Ecológicos para informar áreas con potencial diversidad de mamíferos no descritos en el Choco Biogeográfico.

Jhan Carrillo Restrepo, EAFIT University; Jorge Velásquez Tibatá, The Nature Conservancy Colombia; Juan Díaz Nieto, Universidad EAFIT

El Neotrópico, con cerca de 1701 especies de mamíferos (i.e. 30% de las especies del planeta), es catalogado como una de las regiones con mayor biodiversidad. Colombia posee 518 especies de mamiferos, correspondientes al 10% de la diversidad global. A pesar de estos elevados números de riqueza, recientes estudios demostraron que al menos 2000 especies, principalmente distribuidas en la región neotropical, aún esperan por ser descritas. Por lo tanto, cobra valor validar una metodología que optimice el proceso de descubrir y describir dichas especies de manera precisa y eficiente. El modelado de nicho ecológico ha sido propuesto como herramienta para identificar áreas que alberguen potencial diversidad no descrita, no obstante, dichos alcances han sido vagamente expuestos en la teoría y dificilmente han sido probados en campo. El presente proyecto construyo modelos de nichos ecológicos, mediante MaxEnt y ENMeval, de 7 especies de pequeños mamíferos terrestres cisandinos con el fin de proyectarlos en áreas trasandinas del Choco Biogeográfico. Estos modelos identificaron 4 zonas ambientalmente propicias y paralelo a este estudio se realizó trabajo de campo en una de ellas (Anorí, Antioquia), donde tres especímenes de Nyctomys cf. Sumichrasti fueron colectados, lo cual forma parte de una importante extensión del rango de distribución. Además, debido al alto grado de distribución alopátrica de nuestras poblaciones de Nyctomys con respecto a las de América del Norte, se realizaron análisis filogenéticos y de delimitación de especies para evaluar el estado de especie de estas nuevas poblaciones.

CS13-3

Integración de modelos de distribución y abundancia del ocelote (Leopardus pardalis)

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El ocelote (Leopardus pardalis) es una especie que ha sido ampliamente estudiada y cuenta con estimaciones locales sobre su tamaño poblacional mediante la implementación de metodologías que requieren de un elevado esfuerzo de muestreo. El gran esfuerzo necesario para estos trabajos, limita su alcance en términos de la extensión espacial. Por su parte, los modelos de nicho ecológico abordan la totalidad de las áreas de distribución a partir de una aproximación del nicho de las especies, pero tienen limitaciones en su aplicación a resoluciones finas y a las estimaciones de tamaño poblacional. Este proyecto integra registros de presencia del ocelote obtenidos de manera oportunista y bajo un diseño de muestreo sistemático entre 2013 y 2019, para proveer un modelo de distribución con un mejor desempeño respecto a los modelos independientes. El modelo integrado logra vincular información de ausencias a partir del reconocimiento y estimación de la detección imperfecta de los muestreos a escala local, con la amplia cobertura geográfica y ambiental de los datos de solo presencia a escala regional para generar una predicción de la distribución y la densidad de la especie (número de individuos por área). En esta investigación se incluyeron 406 registros de presencia de ocelote obtenidos de GBIF de toda su área de distribución y 329 historias de detección con datos de presencia/ausencia obtenidos a partir de estaciones de muestreo con cámaras trampa ubicadas en Colombia, en las regiones Caribe, Andes, Pacífico y Orinoquía, con historias de detección de hasta 71 días de muestreo.

CS13-4

Filogenia molecular y biogeografía histórica de un linaje incertae sedis: Una nueva especie de Atopophrynus de los Andes norte del Ecuador.

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El género Atopophrynus se considera incertae sedis dentro de Brachycephaloidea, con una sola especie (A. syntomopus) conocida de la Cordillera Central en Colombia. Aquí, describimos una nueva especie del norte de los Andes en Ecuador, basada en evidencias genéticas y morfológicas, y discutimos sobre su biogeografía histórica. Las relaciones filogenéticas y cronogramas se reconstruyeron con ADN mitocondrial (genes 12S y 16S) y nuclear (RAG1), mediante análisis bayesianos y máxima verosimilitud. Los patrones biogeográficos de las nuevas especies y sus parientes se analizaron mediante la construcción de un modelo de dispersión-extinción-cladogénesis (DEC) para la evolución del rango geográfico, mediante el software RASP. Los árboles filogenéticos revelan que Atopophrynus está relacionado con linajes antiguos, con el género Crossodactylus como taxón hermano, apoyando hipótesis previas de Hylodidae como monofilético. La nueva especie tiene una distribución restringida relacionada con el bosque siempreverde montano en las laderas amazónicas de los Andes del norte en Ecuador. Fue recuperado como el linaje hermano de Crossodactylus aeneus + C. caramaschii+ C. werneri + C. schmidti, todos ellos distribuidos a lo largo del bosque Atlántico sudeste en Brasil. De manera interesante, la nueva especie es parte de uno de los clados más antiguos dentro de Anura, con un origen sudamericano de hace 29.89 Ma, y una especiación geográfica por eventos de dispersión (desde el escudo Brasileño hacia los Andes orientales del norte) y vicarianza. Es necesario seguir trabajando para comprender las relaciones filogenéticas y la taxonomía del grupo.

CS13-5

La macroecología argentina: ¿una subdisciplina en vías de desarrollo?

Julieta Filloy, CONICET - Universidad de Buenos Aires; Paula Fergnani, CONICET

Desde la aparición de Areografía y la consolidación de la Macroecología como una subdisciplina dentro de la Ecología en la década del 80, la investigación inspirada en las ideas de von Humboldt y centrada en las leyes generales que gobiernan la distribución de los organismos en el planeta se ha incrementado marcadamente. Eduardo Rapoport ha dejado un legado tanto local (en Argentina) como mundial. Nos preguntamos en qué medida los ecólogos argentinos hemos incorporado el enfoque macroecológico en nuestros programas de investigación, y en qué aspectos nos hemos centrado. Realizamos una búsqueda de artículos en la base de Scopus, conteniendo "macroecology", "areography", "macroecologia" y "areografia" y "argentina" en la filiación. Evaluamos la tendencia en el tiempo de la cantidad de publicaciones y la contribución relativa de los autores involucrados. Encontramos 282 artículos que muestran que, con aproximadamente una década de retraso, el número de publicaciones de macroecología publicadas por autores argentinos a través del tiempo es creciente y con una tendencia similar a la global. Las áreas temáticas son variadas y la mayoría de los autores publicó dos artículos como máximo mientras que la minoría publicó entre 3 y 19. Esto sugiere que Argentina acompañó la tendencia global, en mayor medida por contribuciones eventuales que por programas regulares de investigación en la subdisciplina. La macroecología, si bien en vías de desarrollo, es un área de investigación relativamente vacante en Argentina.

CS13-6

Distribución de las aves en la gradiente altitudinal de la cuence media del Río Marañón

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Los rangos altitudinales, el tipo de vegetación y las barreras geográficas definen la presencia y distribución de las especies; los estudios biogeográficos permiten obtener herramientas para proponer medidas de conservación. El estudio determinó la diversidad de aves y su variación en cuatro estratos diferentes a lo largo de las gradientes altitudinales de la Cuenca media del río Marañón en los distritos de Utco y Balsas en la región Cajamarca y Amazonas en Perú. Se identificaron cuatro estratos en base a características de vegetación y altitud: Jalca (J), Bosque Montano (BM), Bosque Seco Alto (BSA) y Bosque Seco Bajo (BSB) desde los 850 – 3427m en la gradiente Oeste y 845 – 3663m en la gradiente Este. Se estableció 160 puntos de conteo, 20 por estrato, donde se aplicó las técnicas convencionales de monitoreo de aves. Se registraron 161 especies, con las familias representativas: Thraupidae, Tyrannidae y Trochilidae. Los estratos que presentaron mayor riqueza fueron el BSA con 70 especies para Cajamarca y el estrato de BM con 82 especies para Amazonas. En el distrito de Utco se identificaron 3 especies distribuidas en todos los estratos. El coeficiente de Sorensen indicó similitudes para ambas gradientes de BSB (94%), BSA (64%), BM (49%) y J (27%). La gradiente Oeste presenta mayor similitud en los estratos BSB - BSA (60%) y la gradiente Este mayor similitud en BSB – BSA (44%). La similitud entre comunidades se reduce a medida que la distancia entre estratos aumenta, el río Marañón actúa como una barrera geográfica.

CS13-7

Fauna urbana de la región metropolitana de São Paulo, Brasil: Antecedentes de un Proyecto Educacional de Biogeografía del antropoceno

Yuri Rocha, Department of Geography, University of Sao Paulo; Patricia Oliveira , Universidade de São Paulo

La región metropolitana de São Paulo (Estado de São Paulo, Brasil) es una de las mayores regiones metropolitanas del mundo y su crecimiento en el área del Bosque Atlántico cambió su paisaje natural en paisaje cultural. Esta ciudad presenta flora y fauna nativas y especies que fueron introducidas por distintas razones culturales. El primer paso del estudio biogeográfico urbano fue identificar áreas donde se sitúan tanto las plantas como los animales. Desde 2010, se ha desarrollado un proyecto educacional con estudiantes de la disciplina de Biogeografía, carrera de grado en Geografía, del Departamento de Geografía, de la Facultad de Filosofía, Letras y Ciencias Humanas Universidad de São Paulo, para ejercitar la ubicación e identificación de especies encontradas en el vecindario de su casa y en la cartografía de los individuos utilizando el Google Maps. En nueve años, ya fueron identificadas y registradas 113 especies de 61 familias zoológicas de moluscos, crustáceos, quilópodos, arácnidos, insectos, anfibios, reptiles, aves y mamíferos. Del total, el 25% de las especies son exóticas, el 75% son brasileñas. La mayor cantidad de especies pertenece a la clase aves.

CS13-7

Variabilidad genética y estrucura poblacional del sapo endémico de Columbia Osornophryne percrassa ruíz-carranza y hernández-camacho,1976 en risaralda, caldas y Quindío

Manuela Montoya-Marín, UNISARC; Kevin López-Molina, Universidad del Quindío; Juan Guayasamin, Universidad San Francisco de Quito; Ghennie Rodríguez-Rey, Universidad de Caldas

Osornophryne percrassa es un sapo endémico de Colombia catalogado como Vulnerable (IUCN), distribuido en seis departamentos de las Cordilleras Central y Occidental de Colombia entre los 2700-3700 m.s.n.m. Esta especie ha sido estudiada desde diferentes aspectos biológicos, pero aún no hay estudios de su estado genético poblacional. Por esto, nuestro objetivo es evaluar la variabilidad genética y la estructura poblacional de O. percrassa mediante el gen mitocondrial COI en los departamentos de Risaralda, Caldas y Quindío con el fin de gestar estrategias de manejo y conservación con soportes moleculares. La recolección de muestras de ADN provenientes de la falange III del dedo pedial IV se realizó durante seis meses en las localidades de Campoalegre-Risaralda, Salento-Quindío y Villamaría-Caldas. Posteriormente, se hizo extracción de ADN, amplificación del gen COI y secuenciación de los fragmentos de ADN amplificados. Se calculó la variabilidad genética y la estructura poblacional mediante diferentes métodos y adicionalmente, se hizo una red haplotípica. Se espera que la variación genética entre la población de cada departamento es alta, por lo tanto, la estructura poblacional también; también se espera encontrar por lo menos un haplotipo único para cada población evaluada y que la red de haplotipos sugiera que estas secuencias no se comparten entre los individuos de diferentes poblaciones. Lo anterior indicaría que es muy probable que las poblaciones a nivel genético se conserven a través del tiempo. Incluir la genética de la conservación en planes de manejo ayudará a conservar poblaciones de esta especie tan poco conocida con base a evidencia molecular.

Concurrent Session 14: Diversity patterns along gradients

CS14-1

Distribución altitudinal de escarabajos del estiércol (Coleoptera: Scarabaeinae) en paisajes de la Amazonía ecuatoriana.

Jorge Celi, Universidad Regional Amazonica Ikiam; Nereida Guerra, Universidad Regional Amazonica Ikiam; Marina Rodes Blanco, Universidad Regional Amazonica Ikiam; Ximena Herrera, Universidad Regional Amazónica Ikiam; Miguel Gómez, Universidad Regional Amazónica Ikiam; Ernesto Villacrés, Investigador independiente; Leonardo Pereira, Universidad Regional Amazónica Ikiam; Marja De Kraker, Wageningen Research University

Las poblaciones de escarabajos peloteros, subfamilia Scarabaeinae, son indispensables para impulsar diversos procesos ecológicos como la eliminación de estiércol (lo cual beneficia al ciclo de nutrientes), el entierro secundario de las semillas, la aireación del suelo y la supresión de parásitos. Su distribución y selección de hábitat depende de varios factores; la altitud y el tipo de hábitat son considerados los principales. En el presente estudio se han realizado colectas de especímenes de escarabajos peloteros utilizando trampas de caída (pitfall) con dos tipos de cebo (carroña y heces) en diferentes paisajes de las provincias amazónicas, abarcando un rango altitudinal desde los 230msnm hasta los 3450msnm. La finalidad de este estudio es determinar la distribución de estas especies en este rango altitudinal así como la influencia de distintas variables abióticas y geomorfológicas propias de cada lugar en la abundancia, diversidad y riqueza de los escarabajos del estiércol (Coleoptera: Scarabidae). Se encontró que sí existen diferencias entre las especies de escarabajos peloteros en la selección del hábitat con relación a la altitud, siendo mejor adaptadas a altitudes más bajas.

CS14-2
Is fern diversity highest at the equator?

Laura Salazar, Universidad Tecnológica Indoamérica

Among of the best documented richness pattern in ecology are the latitudinal and elevational gradients. However, little is known about the diversity of ferns at regional scales within the tropics. In this study, we established the first suitable fern transects on the equator, Napo on the eastern (Amazonian) slope of the Andes, and Pichincha on the western slope. Fisrt, we evaluated the elevational patterns of ferns species along both elevational gradient and we relate these patterns to climatic variables in order to assess their relative importance in driving fern richness patterns. Secondly, we set our results in context to comparable data from other neotropical elevational gradients in Mexico, Costa Rica, and Bolivia, setting our new transects in a latitudinal context. Along the Napo and Pichincha transects the species richness showed clear hump-shaped patterns with elevation with peaks at about 2000 m. In general, we found a surprising similarity of the richness and taxonomic composition of the seven elevational transects spanning the latitudinal range between 18°N and 18°S. Only the northernmost and southernmost transects, located at or even slightly beyond the transition from tropical to subtropical conditions showed significantly reduced species numbers.

In conclusion, within the tropics, there appears to be no latitudinal diversity gradient of ferns at the local scale. We suggest that, in tropical habitats, species richness of ferns at the local scale is limited by the number of species that can co-occur and that the available niche space is saturated.

CS14-3
The distributions of morphologically specialized hummingbirds coincide with floral trait matching across an Andean elevational gradient

Jesper Sonne, Center for Macroecology, Evolution and Climate

Morphological trait matching between species affects resource partitioning in mutualistic systems. Yet, the determinants of spatial variation in trait matching remain largely unaddressed. Here, we generate a hypothesis that is based on the geographical distributions of species morphologies. To illustrate our hypothesis, as a study system we use hummingbirds in the tropical Andes. Hummingbirds with specialized morphologies (i.e. long or curved bills) may forage on flowers that are inaccessible to hummingbirds with generalized bill morphologies (i.e. small-to-medium-sized bills with no curvature), yet the vast majority of hummingbirds have generalized bill morphologies. Thus, we propose that trait matching across space is determined by the distribution of morphological specialists. In the Andes, we observe the richness of specialized hummingbird morphotypes to peak at high and low elevations. Therefore, we hypothesize that trait matching should be most influential in predicting pairwise interactions at high and low elevations. We illustrate our hypothesis by field observations along an elevational gradient in Podocarpus National Park (Ecuador). Using Bayesian hierarchical modelling of interaction frequencies in combination with network analyses, we found that hummingbirds at high and low elevations contributed to resource partitioning by foraging on morphologically close-matching flowers. Moreover, at high and low elevations, hummingbirds with specialized morphologies showed a stronger tendency to visit close-matching flowers than morphological non-specialists did. In contrast, at mid-elevations, hummingbirds were not attracted to morphologically close-matching flowers. These results suggest that the spatial distribution of specialized morphotypes determines trait matching and the partitioning of interactions within hummingbird-plant communities.

CS14-4

Elevational Range Sizes Increase with Climate Variability in the Tropical Andes

J. Sebastian Tello, Missouri Botanical Garden; Manuel Macia, Universidad Autónoma de Madrid; Gabriel Arellano, Smithsonian Tropical Research Institute; Alfredo Fuentes, Herbario Nacional de Bolivia; Leslie Cayola, Herbario Nacional de Bolivia; Maria Loza, University of Missouri Saint Louis; Selene Baez, Escuela Politécnica Nacional del Ecuador

The degree of temporal variability in environment conditions changes dramatically across the globe, and this can have important implications for the evolution and distribution of species. Climate seasonality, for example, increases with latitude. This causes populations of temperate species to experience a wider range of environmental conditions than their tropical counterparts. The climate variability hypothesis proposes that temporal variation in environmental conditions selects for broader tolerances that result also in wider geographic distributions. Most tests of this hypothesis have focused on latitudinal comparisons of species assemblages. However, in mountainous regions, climatic variation is often much larger at high elevations than in the lowlands. Thus, if temporal variation in climate influences niche breath and species distributions, species near mountaintops should have more extensive distributions than species in the lowlands. In this study, we tested this idea using data from ~1,800 tree species in the tropical Andes of northwestern Bolivia. We related the extent of elevational distributions to multiple predictors that can shape range sizes, including the maximum temporal variability in temperature that each species experiences. We used a null model to control for geometric constraints that limit the elevational distributions of species. Our analyses demonstrate that the extent of species distributions increases with the size of species, their local abundance and the mean temperature they experience. Importantly, elevational distributions also increase with variation in temperature, supporting the climate variability hypothesis. These results have important implications for understanding how large-scale environmental changes might influence the diversity of forest ecosystems across the Andes.

CS14-5

In the footsteps of Humboldt: species richness and phylogenetic structure of vascular plants along a Neotropical elevation gradient

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Alexander von Humboldt was undoubtedly influenced by his exploration of the Neotropical natural wealth. In this exploration, he visited the state of Veracruz, Mexico, where he ascended the summit of Cofre de Perote. This elevational gradient caused a big impression on Humboldt, as evident in his own description: "Nowhere is it better to see the admirable order with which the different associations of vegetables are happening, one above the other, that when one goes up from Veracruz to the plateau of Perote [...] so that in this wonderful country, in the space of a few hours, the man of science travels the full scale of the vegetation" (Humboldt 1804). Here, we follow Humboldt's footsteps and studied the Cofre de Perote gradient, from 30 to 3500m m.a.s.l., to evaluate the environmental determinants of species richness (SR) and phylogenetic structure (PS) of different plant functional groups using structural equation modelling. Temperature was the most important variable explaining total SR, followed by PET. Similar findings hold for epiphytes, herbs and lianas, whereas precipitation and disturbance influenced only trees and epiphytes. Regarding PS, temperature was the only significant variable for total species and for shrubs, epiphytes and herbs. Precipitation and PET influenced trees and epiphytes PS. Humboldt was correct in suggesting that climate is an important driver of species richness elevational gradients, and here we show that it is also for phylogenetic structure, supporting the energy and productivity hypotheses.

CS14-6
Disturbance and the elevation ranges of woody plant species in the mountains of Costa Rica.

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The role of disturbance—here defined as a transient reduction in competition—in shaping plant distributions along elevation gradients remains unclear. Theory suggests that disturbance may increase elevation ranges, especially at the lower range limits, through reduced competitive exclusion. We explored this idea by comparing the elevation range of woody stems with >10 cm dbh ("trees") observed in plots along two transects spanning a range of elevations in secondary and old growth forest (409 and 249 species, respectively) in Costa Rica. We also estimated these elevation ranges using nationwide species occurrence data. In addition, we examined the influence of stem size and by basal area (as a measure of competition) on species elevation range limits in the two gradients. In general, tree species ranges increased with elevation. Species in the secondary forest had broader elevation ranges (100-318 meters broader than species in the old growth forest). Also, in the secondary transect, individuals with greater diameters had broader elevation ranges than those observed as smaller trees (137 meters broader). As we predicted, the lower range limit of species occurred more frequently in plots with lower (versus higher) basal area than expected by chance in both forest types. We also observed higher-elevation upper limits in old growth, but not in secondary forests. Disturbance relaxes the constraints imposed by competition and extends effective elevation ranges of species, particularly those in secondary forest, to warmer and cooler climates. Thus, suitable disturbance may assist species persistence under climate change.

Concurrent Session 15: Biodiversity Patterns and Maintenance

CS15-1
Regional scale determinants of neotropical plant-herbivore communities: the role of plant defenses

María-José Endara, Universidad Tecnológica Indoamèrica; Phyllis Coley, University of Utah; Dale Forrister, University of Utah

We are investigating the patterns of historical assembly of plant and herbivore communities across Central and South-America using the Neotropical genus of trees Inga (Leguminosae) and its associated herbivore insects. Using phylogenetic and defense-trait diversity metrics, our results show that different processes operate for plants and herbivores. For Inga plants, there is a clear lack of phylogenetic structure suggesting that the metacommunity for any regional community in the Amazon is the entire Amazon basin. Local communities are assembled by ecological processes, with the suite of Inga at a given site more over-dispersed with respect to defenses than if they were drawn at random from the Amazonian regional pool. On the contrary, for insect herbivores, our results suggest that there is a strong geographic phylogenetic structure, with herbivore lineages at a given site, and on a given Inga species, more closely related than expected by chance. Furthermore, local herbivore community assembly has involved a balance between two processes that vary among herbivore lineages: host tracking or ecological sorting and regional diversification.

CS15-2

Climate-based hypotheses for geographic variation among endotherms physiology

Francisco Bozinovic, CAPES, Departamento de Ecología, Pontificia Universidad Católica de Chile

I evaluate the extent to which physiological plasticity and tolerances can be considered as factors that impact on the geographic range among endotherms. I pointed out importance of climatic variability and how our understanding of physiology in a large scale context may contribute to our ability to understand (or not) limits of geographical latitudinal and altitudinal distribution. The extent to which there have been advances in explaining geographical range through constructing and testing hypotheses involving physiological traits and the climatic variability hypothesis is evaluated. This hypothesis requires an understanding of the impact of climate, the physiological mechanisms by which species cope to climate, and the character of the differential effects of climate within and between species along latitudinal and altitudinal geographic gradients.

CS15-3

Principal factors controlling biodiversity along an elevation gradient: water, energy and their interaction

Ole Vetaas, UNIVERSITY of BERGEN, Dept. of Geography; Keshav P. Paudel, University of Tromsø- The Arctic University of Norway.; Morten Christensen, Morten Chr. Consult,

Variation in diversity is a well-documented spatial pattern in biogeography, but an overarching climate-based theory of diversity is lacking. We evaluate two models: the more individuals hypothesis (NPP-MiH), and water-energy dynamics (WED). We use taxa from three kingdoms along an extensive elevation-temperature gradient (Central Himalayas). Both WED and NPP-MiH are based on thermal energy, but the question is whether energy operates through regulating production and chemical (potential) energy only (NPP-MiH), or if kinetic energy as regulator of available liquid water is needed (WED).

The biodiversity, i.e. elevational gamma diversity, of twelve taxa containing animals, plants, and fungi was estimated from range data along an central Himalayan elevation gradient. Generalized linear models were fitted to the species richness data, and assessed by the Akaike information criterion (AIC) and deviance explained. Precipitation and length of growing season (LGS) and their interaction were also tested.

The peaks in richness of the taxa are dispersed along the entire Himalayan gradient from the subtropics to the alpine zone. WED performs best for all taxa along the entire gradient. Including LGS in the WED model improves the AIC for 8 of 12 taxa. WED is superior for combined cross-taxon, but WED and NPP-MiH are equally good in the non-tropical zone.

WED is able to predict peaks in species richness under different climate and primary production conditions; hence, WED is better and more general than NPP-MiH. The interaction with precipitation and the length of the growing season, which also reflects primary production, improve the model for several organism groups.

CS15-4
TNC and OTT (Tropic- and Moisture- related) mechanisms alternatively dominate the latitudinal patterns of evergreen broadleaved woody plants in moisture divergent context in China

Zehao Shen, Peking University; Yue Xu, Peking university

The tropical niche conservatism (TNC) and Out of the Tropics (OTT) hypotheses provide competing process-based interpretive frameworks for the latitudinal diversity gradient (LDG), and predict contrasting latitudinal trends in clade ages and phylogenetic relatedness. However, studies usually focus on the dominance of energy gradient while neglects the effect of moisture, and the applicability of the hypotheses in humid versus arid contexts have rarely been examined. This study tests the applicability of the TNC and OTT hypotheses to the evergreen broad-leaved woody plants (EBWPs) in China, and to explore the ecological and evolutionary determinants underlying the biogeographical patterns of EBWPs in the humid monsoon region and arid westerly region. We calculated the species richness (SR), phylogenetic structure (nearest taxon index, NTI), the mean, maximum, minimum and standard deviation of family age (MFA, MAXFA, MINFA and SDFA, respectively) of EBWPs in equal-area grid cells of the whole nation and in two climatic regions. Then we used generalized linear models and hierarchical variance partitioning algorithm to ascertain the relationship between the biogeographical patterns of EBWPs and climatic variables. The biogeogaphical metrics showed contrasting latitudinal patterns between the monsoon region and the westerly region. Moreover, the effect of precipitation on the biogeographical patterns of EBWPs was more prominent even in the humid region. Both the TNC and OTT hypotheses were found to contribute to the current patterns of EBWPs, dominating alternatively over time. The results imply the importance of humid refugia on the conservation of EBWPs (and possibly other assemblages) in arid regions.

CS15-5
"So tight are the bonds among sciences": Humboldt's botanical arithmetic, climate contours, and the geographic distribution of plants

Stephen Jackson, US Geological Survey

Alexander von Humboldt conceived of plant geography as a broad-ranging science, integrating a variety of disciplines well beyond botany. He also viewed plant geography as one of his most important intellectual contributions. Ironically, his writings on the topic are sparse, compared with his treatises on diverse other topics. Most of his 1807 Essay on the Geography of Plants and accompanying Tableau physique are devoted to the ‘general physics of the earth’. Plant geography receives brief mention in Cosmos and Views of Nature, but Humboldt devoted only one thin volume exclusively to the topic: On the geographic distribution of plants (1817). Although that volume includes extensive descriptions of plant distributions, most of the text is devoted to ‘botanical arithmetic’, aimed at identifying general patterns from sparse and incomplete data, and to ‘isotherms’ (climate contours), which Humboldt viewed as a critical first step toward explaining plant distributions. Both botanical arithmetic and quantitative climatology followed a general trend of the time towards formal, numerical expression in scientific study. Botanical arithmetic applied ratios and proportions, as well as crude area corrections, to identify patterns (“laws”) by which plant diversity, taxonomic representation, and functional types varied with latitude and altitude. Exploration of temperature records from across the globe revealed that, although temperature decreases with increasing latitude and altitude, steepness of temperature gradients varies widely across the globe. Furthermore, seasonal temperatures vary widely. Humboldt recognized that understanding annual and seasonal temperature patterns across the globe was essential for explaining plant distributions.

CS15-6

Gene Flow and unexpected ancient Divergences in Western Palearctic Pond Turtles (Emys spp.)

Melita Vamberger, Senckenberg Natural History Collections of Dresden; Heiko Stuckas, Senckenberg Natural History Collections of Dresden; Uwe Fritz, Senckenberg Natural History Collections of Dresden

Using range-wide sampling, we analyse genetic differentiation and gene flow patterns in pond turtles (Emys spp.), with a special focus on secondary contact zones. Based on population genetic analyses of highly polymorphic microsatellite and mitochondrial markers, we show that genetic differentiation matches well with general Western Palearctic distribution patterns and current taxon delimitation. However, individual contact zones and introgression patterns differ across the distribution range, with limited gene flow between some taxa and broad-scale gene flow between others. Although the distribution pattern suggests that the individual mitochondrial lineages dispersed from former glacial refugia, or are still largely confined to their refuges, fossil-calibrated molecular clock calculations reveal Miocene and Pliocene divergence ages. Our long-term investigations in the genetic differentiation of European pond turtles result in an excellent understanding of the biogeography of a wide-ranging animal species distributed across a major part of the Western Palaearctic.

Concurrent Session 16: Biogeography of the Anthropocene

CS16-1

Challenges and opportunities for biogeography - can we still learn from von Humboldt?

Franziska Schrodt, University of Nottingham; Maria Santos, University of Zurich; Joseph Bailey, York St John University; Richard Field, University of Nottingham, UK

Alexander von Humboldt changed the way that large areas of science are done and communicated. Indeed, he has been called the father of a range of fields, including environmental science, earth system science, plant geography, ecology and conservation. His approach was characterized by making connections between non-living and living nature (including humans), based on interdisciplinary thinking and informed by large amounts of data from systematic, accurate measurements in a geographical framework. However, some key aspects of his approach have faded, particularly as science fragmented into specific disciplines and became more reductionist. We argue that asking questions in a more Humboldtian way is important for addressing current global challenges with particular emphasis on the study of biodiversity-geodiversity relationships. Although progress has been made in explicitly linking living and non-living nature using geodiversity, much remains to be done to integrate geodiversity into biogeography, conceptually and empirically – towards more fully realising Humboldt′s vision, using twenty-first century databases, techniques and theories. We will provide an overview of von Humboldt's approach relevant to contemporary issues in biogeography and provide a roadmap to progress.

CS16-2

Hybridization, species invasions, and conservation: genetic admixture in the Anthropocene

Amanda Chunco, Elon University; Julia Needham , NC State; Sarah Dolce, Elon University

Humans are both intentionally and accidentally moving species around the globe at an unprecedented rate. As a consequence of such movement, many closely related species that have historically been isolated are now in secondary contact, and hybridization is increasingly common. The outcomes of hybridization are difficult to predict: it can be a major threat to imperiled species, even resulting in extinction, but it can also rapidly increase standing genetic variation and therefore the potential for adaptation by native populations. This can be a particularly valuable benefit in the context of climate change. To uncover likely outcomes of hybridization under climate change, we combined a systematic literature review and GIS analysis to create a global map of known hybrid zones between native and non-native animal species. We analyzed taxonomic trends and biogeographic patterns in the distribution of the mapped hybrid zones. Over 140 studies on over 60 unique species pairs were identified in the literature.

Mapping each hybrid zone revealed striking patterns of hybridization, including hybridization hot spots in western Europe and western North America. Fish were the most common taxonomic group to be found hybridizing with non-native species, and the majority of hybridizing species pairs across all taxa involved endemic species of conservation concern. As hybridization is both a conservation threat and being explored as an option for genetic rescue, identifying outcomes of these unintentional hybridization experiments between native and non-native species will become increasingly important.

CS16-3

Can plants predict soil, hydrology, and disturbance regimes in the páramos?

Mauricio Diazgranados, Royal Botanic Gardens, Kew; Martin Baruffol, Royal Botanic Gardens, Kew; Ed Rowe, Centre for Ecology & Hydrology, Natural Environment Research Council; Christopher Barry, Centre for Ecology & Hydrology, Natural Environment Research Council; Boris Ochoa-Tocachi, Imperial College London; Wouter Buytaert, Imperial College London; Charles George, Centre for Ecology & Hydrology, Natural Environment Research Council; Jeffrey Prieto, Universidad Pedagógica y Tecnológica de Colombia; France Gerard, Centre for Ecology & Hydrology, Natural Environment Research Council

Páramos are the most biodiverse high-elevation ecosystem and a main source of water for over 50 million people in Northern Andean countries. They are also socio-ecological systems shaped by human interactions, including crop cultivation and grazing. Understanding the relations among plants, soil, water, and people is therefore crucial to inform ecosystem management and conservation strategies. As a first step of the NERC/AHRC project "How do Paramos store Water? The role of plants and people (PARAGUAS)", we explored how plant species and functional-type diversity relate to soil properties, hydrological characteristics, and anthropogenic disturbance. We studied the páramo complex Guantiva-La Rusia (1,190 km2), in the Eastern Cordillera of Colombia, which feature broad ranges of temperature and humidity. We selected 6 pristine/altered pairs of research catchments across the climatic range. In each catchment, we identified main hydrological response classes (HRC), and sampled plants and soils in 145 5m×5m plots (~12/catchment; >3/HRC), measuring species richness, plant functional type abundance, and hydro-physical soil properties (pH, penetration resistance, soil moisture retention). The effects of biomass and necromass on catchment-scale water storage capacity and water release dynamics in both pristine and altered plots, provide insights on the relative importance of plants. Soils of the region are typically highly organic and strongly affected by disturbance. Interestingly, plant species distributions reveal sharp responses to climate, soil, and land management. As hypothesised, plants show identifiable biogeographic patterns that have predictive power and provide important indicators of the páramo hydrological functions.

CS16-4

Non-native freshwater fishes are morphologically different from native species

Guohuan SU, Universite Paul Sabatier; Sebastien Brosse, Université Paul Sabatier; SEBASTIEN VILLEGER, CNRS

Biological invasions have altered patterns of biodiversity from local to continental scales and resulted in marked ecological and economic impacts. Since the invasion trend is still growing throughout the world. It is urgent to determine which characteristics make a species a good candidate for future invasions. Here we use a global database describing 10 morphological traits for more than 9000 freshwater fish species to test if invasive species are a random sample of species from donor assemblages (biogeographic realm fauna). We here distinguished between non-native species that have been introduced only within the donor zone (translocated species) and species introduced in other realms where they were not present as native (exported species). We showed that translocated and exported species differ from the non-introduced species in all realms, and that exported species have more extreme morphological traits than the translocated species in most of the realms. Traits differences between non-introduced and introduced species also varied between realms, indicating different introduced fish functional profiles among realms. We then predicted potential future translocated and exported species using a morphological distance-based approach and showed the Palearctic zone would remain a strong provider of non-native species in the future. More surprisingly, the Afrotropical and Neotropical which up to now provided only a few non-native species, have the potential to become major non-native species providers in the future, which should be considered to anticipate future fish invasions across the world.

CS16-5

Living on the edge – plant species persistence changes on range margins in Northern Europe during the 20th century

Lauri Laanisto, Estonian University of Life Scienes

Species ranges are constantly changing because of natural and anthropogenic factors. These processes are relatively slow and there is a lack of comprehensive and consistent meso-scale data for most organisms and places. Most significant and fundamental changes in species distributions happen on range margins. Populations living on distribution edges are considered to be under higher stress (less optimal conditions) than in range centre, yet changing climates are expected to favour species living in certain parts of their ranges, where conditions are supposed to get better (northern edge of distribution range). How are these expectations balanced – is living on range edge always more stressful than in the centre, or does it depend where the location margin is (northern or southern edge)?

We compared two generations (covering most of the 20th century) of vegetation atlas data from the UK and Estonia, where presence of each species was recorded in hectad grid cells (100 km2). We found significant differences in plant species persistence between range center and range margin species for both the UK and Estonia. While the average persistence of range center species in the UK was 71% and 78% in Estonia, range margin species had on average significantly lower persistence, 57% and 64%, respectively. Thus, the gap of difference between range center and range margin persistence in both countries was similar (14 %). Being on a range margin resulted in lower persistence in comparison with range center species, regardless on whether the species is in northern or southern edge.

CS16-6

Critical biogeography of Andean treelines: A synthetic and geocritical prospective of the Humboldtian paradigm.

Fausto Sarmiento, Neotropical Montology Collaboratory. University of Georgia

The foundational theory of mountain geoecology accepts without question the principles associated with climate envelopes as determinants of ecological assemblages. This informs the Humboldtian paradigm of altitudinal belts for vegetation physiognomy and the Humboldt law for the latitudinal/altitudinal correspondence. However, new insight provided by political ecology and critical biogeography has brought arguments to contest/complement this narrative. Using social science multimethod approach to bring forth a new narrative that highlights the role of people in shaping Andean treelines, geocriticism evidence debunk/deconstruct the paradigm of vegetation belts with a new transdisciplinary trope of highland-lowland interaction. Montology accepts that other climates (religious, political, investment, otherwise cultural) affect the historicity of the slopes notwithstanding the meteorology of mountains. Human impact, particularly in the late Holocene must be incorporated to understand the geospatial functioning of tropandean landscapes. Syncretic mountainscapes have produced what ecologists name altered ecotones, fusion landscapes, manufactured ecosystems, ancient engineered sites or novel ecosystems. The Chimborazo mountainscape that so inspired Humboldt, Bonpland and Montúfar, as it has already been argued for the highland páramos of the northern Andean highlands, was in reality a palimpsest of several stories and social constructions developing biocultural heritage worth studying.

Concurrent Session 17: Neotropical Biogeography

CS17-1

Testing hypothesized spatial legacies of the Great Biotic Interchange on Central American tree floras

Maria Loza, University of Missouri Saint Louis; Ivan Jimenez, Missouri Botanical Garden; Robert Ricklefs, Department of Biology, University of Missouri-St. Louis

The Great American Biotic Interchange (GABI) began after completion of the Isthmus of Panama three million years ago (Ma), ending the isolation of South America. Gentry (1982) hypothesized that the current spatial structure of lowland and montane Central America floras reflects contrasting GABI legacies. On one hand, the South American affinities of contemporary lowland Central American rainforest assemblages decline with distance from the South American source of most Central American immigrant tree species. This spatial pattern is thought to reflect predominantly migration of lineages from South America. On the other hand, Central American montane rainforests have been considered more influenced by migration of lineages with Northern origins. We tested these proposed spatial patterns for Costa Rican lowland and montane rainforests. We used specimen records for 341 and 142 species in 21 and 8 ca. ~0.3-ha plots distributed in lowland and montane rainforest, respectively. We measured species composition similarity between plots and 25×25-km grid-cells (≥ 200 specimen records) covering lowland and montane rainforest across Central America. For lowland rainforest, we determined whether decay in the similarity of species composition was stronger towards North America than towards South America. For montane rainforest, an opposite pattern must be observed. For lowland rainforest, we found that the decay of species composition similarity towards North America did not differ from the corresponding decay towards South America, contrary to expectation. Moreover, and contrary to expectation, montane rainforests are more similar to Central American montane rainforest towards South America than to Central American montane rainforests towards North America.

CS17-2

Why continental Urania's species have a disjunct distribution?

Claudia Nuñez Penichet, University of Kansas; Jorge Soberon, Biodiversity Institute, University of Kansas; Marlon E. Cobos, University of Kansas

The Urania genus of diurnal moths has three species that feed, during their larvae stages, on plants of the genus Omphalea. U. boisduvalii is endemic of the Cuban archipelago, and U. fulgens and U. leilus are present in the continental Neotropics. Although several researchers have described that the distribution of these moths is mostly related to their host plant distribution, a marked differentiation between the distribution of U. fulgens (present from Veracruz, Mexico to Colombia) and U. leilus (present from Colombia to Peru) exists, even though the Omphalea genus is distributed almost homogeneously through the Neotropics. These distributional patterns may derive from differences in the niches of the two moths. To test this idea, we developed ecological niche models of these two Urania species and calculated niche overlap between them. Our results showed that the niches of these Urania species are similar but not identical. For example, U. fulgens have a broad tolerance of precipitation in comparison that U. leilus. Unexpectedly, the presence of the food plant was not a significant predictor for the distributions. Since a competitive interaction between two species has not been reported and having the host plants are present in most of the Neotropics, either geographic barriers or the light differences between their niches could be the best potential explanations for the disjunct distribution of these Urania species.

CS17-3
Phyllostomid bats as a model to test zoogeographic units in Ecuador

Nicte Ordonez-Garza, Universidad San Francisco de Quito; Juan Carrera-E, Escuela Politecnica Nacional del Ecuador; Carleton Phillips, Texas Tech University; Sergio Solari, Universidad de Antioquia; Sergio Balaguera-Reina, Universidad De Ibague; Robert Bradley, Texas Tech University

Nine Zoogeographic Units (ZU) have been hypothesized for Ecuador with seven of these units located within the continental portion of the country. Each ZU was defined by climate, topography, elevation, and vegetation type. In spite of their historical application, the validity of ZUs has not been tested. The goal of the present study was to treat the ZUs as hyptheses and test their validity. For this purpose, species of the bat family Phyllostomidae were used as a model. A total of 13,262 validated bat records, representing 109 species and six feeding guilds (with confirmed taxonomic identification and geographic information) were analyzed using multivariate statistical analyses and geographic modeling. Results obtained from the Multidimensional Scaling Analysis, Detrended Correspondence Analysis, and Pairwise comparisons provided evidence that the ZUs as proposed were valid, based on information from phyllostomid bats, although no species were restricted to the Temperate Forests and High Andes. In addition, geographic models showed that Tropical Eastern Forests and Subtropical Eastern Forests were the most likely areas to be inhabited by phyllostomids. Bat species in the High Flying Frugivore and Insecti-Carnivore trophic guilds displayed a clear spatial pattern highly related to ZU. The findings of this study provide important information regarding the validity of these ZUs for establishing priorities concerning research, conservation, and management in this group of mammals.

CS17-4
One clade, two histories: Phylogenetic niche conservatism and area drive megadiversity patterns of Dipsadidae, the richest Neotropical snake family

Filipe Serrano, Universidade de São Paulo; Cristiano Nogueira, Universidade de São Paulo

To understand global patterns of diversity, we need to understand how large-scale biogeographical patterns are influenced by historical and ecological aspects. Thus it is important to consider differences between intra-clade lineages and how these shape current distribution and diversity. We map and document richness and macrohabitat use in two major lineages of Dipsadidae, the richest Neotropical snake clade, testing the roles of niche conservatism, area and diversification rates. We mapped richness and distribution of species across both subfamilies (Xenodontinae and Dipsadinae), and calculated relative richness (percentage of Dipsadinae in total Dipsadidae richness) and the percentage of cells in forest habitats for each species. That percentage was used to test for phylogenetic niche conservatism. We tested how richness responded to percentage of forest and available area per latitude, and calculated macrohabitat diversification and diversification rates for both subfamilies. Distribution and richness patterns differed between Dipsadinae and Xenodontinae. Both subfamilies attained higher richness in forests, but Dipsadinae was relatively richer in forests than in adjacent open areas. Dipsadinae is historically associated with forest, while Xenodontinae responded strongly to area. Extinction rate has recently increased for Dipsadinae. The asymmetrical richness patterns of Dipsadidae reflect two major biogeographical aspects: the low richness of Xenodontinae in Central America is mainly limited by area-related features; and a strong historical association of Dipsadinae with forest habitat. The attained diversification rates might reflect the forest contraction in recent geoclimatic events. We show that distinct lineages might respond differently to ecological or geometrical constraints, leading to idiosyncratic biogeographical patterns.

CS17-5

The Andean uplift effect on the Sigmodontinae (Rodentia: Cricetidae) evolutionary radiation

Paulo Vallejos-Garrido, Universidad de Concepción; Kateryn Pino, Universidad de Concepción; Boris Castillo, Universidad de Concepción; Macarena Toledo, Universidad de Concepción; Eduardo Palma, Departamento de Ecologia, Universidad Catolica de Chile; Cristian Hernandez, Universidad de Concepcion; Enrique Rodríguez-Serrano, Universidad de Concepción

Sigmodontinae rodents inhabiting the Neotropics (c.a. 400 species) show a contrasting and geographically exclusive species richness patterns among their tribes. Therefore, this group stands as a relevant ground for testing general hypothesis about the Andean orogenesis effects on the diversification of Neotropical biota. We evaluated the overall effect of Andes paleo-altitude on this subfamily's radiation through Environment-dependence diversification models and several aspects of the influence of Andean orogenesis on the biogeographic and diversification patterns of the three most diverse sigmodontine tribes (Oryzomyini, Akodontini, and Phyllotini) using BiogeoBEARS and MuSSE analyses. The integration of Andean geological data into an analysis of evolutionary diversification reveals that speciation rates of Sigmodontinae subfamily is negatively exponentially correlated with the elevation history of the Andes, while extinction rates appear to be unlinked to mountain uplift. Biogeographically, for Akodontini and Phyllotini tribes, dispersal and sympatry were the most frequent events and occur mainly inside the Andean range, meanwhile that for Oryzomyini tribe the main dispersal events occur from cis-Andean range to Andean range. Therefore, our results show that the Andes induces frequent speciation and dispersal events creating new habitats available for sigmodontine rodents inside Andes, and outside due the consequent environmental differentiation during the Plio-Pleistocene transition. Nevertheless, their fast and geographically defined species accumulation were decreased as the mountain range reached new heights.

CS17-6

What the spatiotemporal distribution of Amazonian bamboo cohorts tells about their synchronised semelparity

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In a synchronised semelparous life cycle of plants, reproduction happens only once in a lifetime and simultaneously among a large number of neighboring individuals. The dominant hypothesis explaining the origin of this life strategy is that the mass fruiting at long time intervals satiates seed predators, thus enabling successful reproduction. This predator satiation hypothesis gives the geographical predictions that the average size of the patch of reproduction is big and that within a given patch, there would rarely be asynchronously reproducing individuals. We have tested these predictions.

We used a Landsat TM/ETM+ composite to map the geographical distribution of the world's largest bamboo forest area in southwestern Amazonia at the resolution of 30m x 30m pixels. For every bamboo forest pixel we identified the year of reproduction as a sudden drop in the reflectance value of the Landsat band 5 over a period of 28 years (1987–2014) which covers the full 28-year life cycle of the bamboo. We found that the patches of synchronous reproduction are indeed large, typically over 1000 km2, but the synchrony in reproduction is often not quite accurate as the period of reproduction usually lasts for two to three years. We also field-verified in four separate patches of reproduction that the abundant fruiting extends over a period of minimum two years. The extended period of bamboo reproduction is not compatible with the predator satiation hypothesis and therefore we suggest that the synchronised semelparity originated to create, via adult mortality, suitable open habitats for the bamboo seedlings.

Concurrent Session 18: Conservation Biogeography

CS18-1

Combining future projections of land use scenarios and species distribution models. The case of native tree flora of southern South America

Patricio Pliscoff, Universidad Catolica de Chile; Cesar Benavidez-Silva, Universidad Catolica de Chile

One of the most common knowledge gaps when project range distributions using traditional correlative species distribution models (SDM) under future climate change scenarios is the lack of future projections of land use which can be combined with model's suitability. The joint analysis between future models and land use scenarios allow us to obtain more reliable models which reflect not only environmental change but also the potential anthropogenic effects over the territory. These improvements in future range projections are fundamentals in hotspots of land use and land cover change (LUCC) as Central-South Chile a recognised biodiversity hotspot which a historical process of natural land cover transformation. Most of species distribution modelling future projections don´t take account the spatial restrictions defined by non-natural land covers, the potential climatic suitability projected extrapolate areas which can be corrected adding dispersal and movement restriction defined by projected land uses. We applied ensemble SDM techniques to calculate range dynamics in time for 105 native tree species of southern South America and evaluate the differences between climatic suitability without and corrected by land use. Finally, we focus inside protected areas network to analyse whether the difference between trees ranges dynamics made with traditional projections and those which including land use could yield different results regarding climate change vulnerability and protection representativeness in the study area.

CS18-2

Amphibians: the biogeography and phylogeny of extinction

Juan Guayasamin, Universidad San Francisco de Quito; Carl Hutter, University of Kansas

Amphibians (8010 species) face one of the most devastating and complex conservation scenarios among any organism. Species are endangered by a combination of factors, including habitat destruction and fragmentation, emerging diseases, introduced species, and climate change; as a result, about 50% of all amphibians are endangered. One of the main factors contributing to population declines and extinction is chytridiomycosis, an infectious disease that affects amphibians worldwide, caused by the chytrid fungus Batrachochytrium dendrobatidis (Bd). In this study, we use the unprecedented dataset on amphibian susceptibility to Bd (Scheele et al., 2019) and combine it with biogeographic and phylogenetic information. We next investigate whether the effect of chytridiomycosis on amphibians has both geographic and phylogenetic components. We investigate how biogeography and climatic conditions of different environments are related to species' chytrid susceptibility. In addition, we address whether chytrid effects are clustered phylogenetically or spread out randomly throughout the amphibian tree of life. Thus, these results may provide valuable insights for conservation initiatives (including research), especially in targeting the most vulnerable lineages in the most vulnerable environments.

CS18-3

Fragmentation Effects on Species Richness and Distribution in Lowland Amazonia

Gabriel Moulatlet, IKIAM; Emmanuel Ambriz, Ikiam; Jennifer Guevara, Ikiam; Karima Lopez, Ikiam; Marina Rodes, Ikiam; Nereida Guerra, Universidad Regional Amazonica Ikiam; Salomón Ramirez, Ikiam; Lizbeth Andi, Ikiam; H. Mauricio Ortega-Andrade, Universidad Regional Amazónica Ikiam; Pablo Meneses, Ikiam

Fragmentation is an important anthropogenic driver of changes in species occurrence and diversity. However, the magnitude and direction of its effects remain unclear. Fragmentation can lead to loss of diversity in many taxonomic groups, but paradoxically, it may also benefit others. To address this issue we evaluated the occurrence and diversity of four taxonomic groups −birds, orchid bees, dung beetles and amphibians− along a fragmentation gradient in the buffer area of the Yasuní National Park. As part of the newly implemented Ecuadorian National Biodiversity Program we installed fifteen 250 meters-long tierra-firme plots where we sampled these taxa. We calculated a set of fragmentation metrics and analyzed our data using explanatory and predictive models. On the one hand, our explanatory models showed that each taxonomic group is affected by some fragmentation metrics. Overall, birds and dung beetles responded positively to fragmentation, while bees and amphibian were negatively affected. On the other hand, our predictive models showed that dung beetles had the highest probability to increase in richness near fragmented zones, while amphibian species richness significantly decreased. Both modelling approaches showed great variation in species responses to fragmentation, and we did not find a direct relationship between richness and landscape fragmentation. Predictive models are useful tools for evaluating the magnitude and direction of species responses to landscape modifications. We highlight the importance of single-species models in order to understand the complex effects of landscape fragmentation in current and future species distributions.

CS18-4

Persistence of priority effects and their impact on the spatial structure and soil seedbank of a restored grassland

Kiri Staiger, University of Maryland; Nathan Swenson, University of Maryland; DOUG Gill, University of Maryland (Emeritus)

Priority effects may be an important mechanism structuring plant communities at relatively fine scales, with the random initial arrival of species impacting later community structure and spatial patterning. In tree communities, where long-lived individuals are common, priority effects are likely maintained via niche pre-emption and competitive exclusion of similar species by those already established. In herbaceous communities, where large portions of the aboveground vegetation will die or die back each year, we hypothesize that belowground mechanisms such as accumulation of propagules in the soil seedbank may be important to maintaining species' priority on any patch of landscape. We leverage data from a 20-year grassland restoration project with known initial seed applications, along with soil-seedbank surveys and short-term experimental plots, to examine vegetative and soil-seedbank signals of priority effects in an herbaceous system. Specifically, we ask the following questions: 1) Is there a signal of initial seed mixes—and thereby, priority—in the later composition and spatial structure of grassland plots? 2) Does this signal persist across the 20-year span? And 3) Are signals of priority amplified, diluted, or approximately equivalent in the soil seedbank compared to aboveground vegetation, and can this signal be mediated by removal of aboveground biomass or alteration of the soil-seedbank?

CS18-5

Conservation for a post-normal world

Stephen Jackson, US Geological Survey

Post-normal science applies where fundamental scientific uncertainties are high, and societal consequences are large. Paleoecology and historical biogeography indicate that we live on a dynamic planet characterized by natural change and novelty, and that human ecological impacts across much of the planet are of higher magnitude and greater antiquity than recognized even a decade ago. Continually emergent ecological novelty, driven by climatic change, is now well-documented across the globe for the past 25,000 years. Imminent appearance of climates and communities with no historical analogs, together with multiple future ecological pathways laden with historical contingencies, impose high uncertainties in predicting ecological outcomes. These findings challenge deeply held values and assumptions in the conservation community, which were largely developed under 20th century science. Conservationists can find both solace and opportunity in the knowledge that the natural world we've inherited is rich and functional, despite substantial human imprints and alterations, and despite a long history of natural environmental change and ecological disruption. Conservation is undergoing reinvention to reconcile it with changing scientific understanding as well as evolving societal values. Accelerating and facilitating that reinvention process will provide more robust conservation strategies for a rapidly changing world.

Concurrent Session 19: Biogeography of the Anthropocene

CS19-1

Invasiveness, chimerism and genetic diversity

Rachel Ben-Shlomo, University of Haifa – Oranim

Anthropogenic endeavours in the last millennium have triggered the transfer of numerous species from their natural habitat into new, distant locations, far beyond the boundaries of their geographic ranges. Biological invasions have fundamental impacts on ecosystems; nonetheless, the current knowledge of factors that influence and shape invasiveness are far from fully understood. Adaptation for invasiveness should comprise the capability to exploit and prosper in a wide range of ecological conditions, and is therefore expected to be associated with a certain level of genetic diversity. Paradoxically, however, invasive populations are established by only a few founders, resulting in low genetic diversity. As a conceivable way of attaining high genetic diversity even when a small number of founders is involved in invasiveness, I suggest here chimerism, an intra-organismal genetic heterogeneity, resulting from fusion between different individuals—a common phenomenon found in numerous phyla.

The composite entity offers the chimeric organism genetic flexibility and higher inclusive fitness that depends on the joint genomic fitness of the original partners. The ability to form a chimeric entity is also applied to subsequent generations and, consequently, the level of genetic diversity does not decline over generations of population establishment following invasion.

As an example of the association between chimerism and worldwide invasion, I genetically analysed the colonial ascidian Botryllus schlosseri, a well-documented global invader, originally distributed in the Mediterranean Sea. Chimerism is a general phenomenon in Botryllus and is detected in most tested populations; hence, a considerable level of chimerism is noticed in numerous invading populations.

CS19-2

Strong phylogenetic and spatial patterns found in the distribution of anti-infective activities across the flora of Java

Alexandra Muellner-Riehl, Leipzig University; Laura Holzmeyer, Leipzig University; Anne-Kathrin Hartig, Leibniz Institute of Plant Biochemistry; Katrin Franke, Leibniz Institute of Plant Biochemistry; Wolfgang Brandt, Leibniz Institute of Plant Biochemistry; Ludger Wessjohann, Leibniz Institute of Plant Biochemistry; Jan Schnitzler, Leipzig University

The continued high rates of use of antibiotics in healthcare and agriculture has led to a dramatic increase in antimicrobial resistance, with multidrug-resistant bacteria emerging as a major public health problem worldwide. To help battle the global antimicrobial crisis, we here evaluate the phylogenetic patterns of anti-infective compounds across taxonomic and biogeographic scales in one of the most species-rich regions on Earth (Indonesia) and assess the predictive power of phylogenies to identify clades with naturally occurring substances potentially suitable for the development of new active pharmaceutical compounds. Specifically, we (1) estimate the degree of phylogenetic signal of anti-infective compounds using a genus-level phylogeny of the flora of Java, and (2) identify 'hot nodes' in the phylogeny, indicating overrepresentation of anti-infective compounds in a given clade. Finally, we (3) assess the spatial patterns of plants with anti-infective compounds relative to total plant diversity across the region. We found strong phylogenetic and spatial patterns in the distribution of anti-infective activities across the flora of Java. Areas with the highest number of species were found in mountainous regions across Java. The number of metabolites shows a very similar pattern. Indeed, plant diversity and metabolite diversity appear to be strongly correlated. In summary, our study highlights that the combination of phylogenetic, spatial and phytochemical information is a useful tool to guide the selection of taxa for lead compound discovery.

CS19-3

Models and simulations to understand biological invasions: the case of Duttaphrynus melanostictus invasion in Madagascar

Marlon E. Cobos, University of Kansas; A. Townsend Peterson, University of Kansas; Claudia Nuñez Penichet, University of Kansas; Jorge Soberon, Biodiversity Institute, University of Kansas; Luis Osorio-Olvera, Universidad Nacional Autonoma de Mexico; Steven Goodman, The Field Museum of Natural History; Achille P. Raselimanana, University of Antananarivo

Invasive species represent one of the main threats to biodiversity conservation around the world. These species are known to cause several problems because they destabilize ecosystem dynamics, so understanding invasion processes is crucial in preventing or mitigating negative consequences. We used different modeling and simulation techniques to characterize populational, ecological, and distributional characteristics of the Asian common toad as an invasive species. Our goal was to understand and anticipate the potential dynamics of invasion of this species in Madagascar. Population matrix-based models were used to find potential growth rates for this species at local scales. Ecological niche models were used to find areas of potential distribution of these species in Madagascar. Dispersal simulations were performed to identify potential dynamics of invasion considering existence and non-existence of dispersal barriers. Our results indicated that this toad has the potential to invade a large portion of Madagascar thanks to its high population growth rates, the presence of suitable conditions across swaths of the country, good dispersal abilities, and the presence of factors that may facilitate spread (e.g., rivers). Although in general distinct modeling methods and simulation procedures come to similar conclusions, differences among them help to identify variability in predictions. The importance of using different methods is that they allowed us to understand implications of distinct assumptions when modeling populational and distributional potential, and when simulating the potential for spread by this species. Multiple approaches may be needed to obtain a rigorous characterization of the invasive potential of a species.

CS19-4

La Guayaba en Galápagos: Genética e historia de una especie invasora

Diego Urquía, USFQ; María Torres, USFQ; Bernardo Gutiérrez, Oxford University; Gabriela Pozo, USFQ

La guayaba (Psidium guajava) es una planta invasora muy agresiva en Galápagos, y su estudio genético es importante para su control. Para entender la historia y la genética detrás de esta invasión, analizamos 11 marcadores SSRs de individuos de guayaba provenientes de Galápagos (islas San Cristóbal, Santa Cruz, e Isabela) y del Ecuador continental. Según análisis bayesianos y las distancias genéticas encontradas entre estos individuos, sugerimos que las guayabas de la región Sierra Centro y del Sur del Ecuador continental serían las más vinculadas genéticamente con las de Galápagos. Esto coincide con el hecho de que a las islas llegaron varios colonizadores e inmigrantes provenientes de estas partes del país, notablemente de las provincias de Tungurahua y Loja. Seleccionamos utilizando también análisis bayesianos, el escenario tentativo mejor sustentado del proceso de colonización de la guayaba en Galápagos. Éste describe que la guayaba habría llegado primeramente a San Cristóbal, quizás en la segunda mitad del s.XIX, traída por el colonizador Manuel Cobos y sus trabajadores. Posteriormente, la planta invasora habría pasado hacia Isabela, posiblemente a fines del s.XIX junto con el ganado del colonizador Antonio Gil. Por último, a partir de Isabela y San Cristóbal, la guayaba habría llegado durante la primera mitad del s.XX a Santa Cruz, la última isla en ser habitada. Es interesante cómo la genética de una especie introducida, la guayaba en Galápagos, refleja la historia de la colonización de las islas, a la vez que nos provee de valiosa información para el manejo de esta plaga.

Concurrent Session 20: Neotropical Biogeography

CS20-2

Climatic and dispersal filters drive phylogenetic and taxonomic beta diversity patterns of Amazon tree communities

Juan Guevara, Universidad de las Américas

Understanding the tree species composition and turnover in Amazon forests has fascinated ecologists and evolutionary biologists since the first botanical expeditions from the 19th century. More recently, the advent of community phylogenetics and phylogenetic beta diversity methods has been demonstrated to be powerful tools to investigate the patterns and causes of Amazonian tree species assemblage.

However, the lack of a comprehensive tree species sampling using well standardized taxonomy across gradients of soils, geology and climate has precluded a better understanding of the relative importance of these environmental filters on the patterns of lineage and species turnover. Here we test the relative influence of climate, spatial scales, geomorphology and soils on the patterns of Phylogenetic Beta Diversity (PBD) and Taxonomic Beta Diversity (TBD) in Amazonian tree communities. In order to test the role of these variables we compiled data from 150 floristic inventory plots recently established in the Ecuadorian and Peruvian Amazon. We employed 28 climatic, edaphic and geomorphological variables to perform Generalized Additive Models, variation partitioning via Redundancy Analysis and Multiple Regression on Matrices (MRM) and Structural equation models in order to assess their contribution as predictors of PBD and TBD. Climate was a significantly better predictor of PBD and TBD than geomorphology and soils. The influence of climate was stronger at broader spatial scales (50 km2) whereas geomorphology and soils appear to be better predictors of species turnover at mid (5 km2) and fine spatial scales (0.5 km2) but a weak predictor of lineage turnover at broad spatial scales.

CS20-3

Recent diversification of Cratylia genus in South America: From Atlantic forests to Peruvian Andes

Maria Cristina Lopez Roberts, Universidad Mayor Real y Pontificia de San Francisco Xavier de Chuquisaca, Cassio van den Berg; Luccio Paganucci de Queiroz

Cratylia is a genus of legumes endemic to South America, with species distributed east from the Andes and south from the Amazon River Basin to Paraná River Basin in Brazil. Until the present study, five species were recognized: Cratylia argentea, C. bahiensis, C. hypargyrea, C. intermedia, and C. mollis. Several morphological and phylogenetic studies have shown the close relation between Cratylia and the genera Bionia and Camptosema, although without robust results on the phylogenetic relationships of Cratylia species. Biogeographic hypothesis (Queiroz and Coradín 2006) suggest the origin of Cratylia in Brazilian Cerrado. Phylogenetic approach and molecular dating were applied to test this hypothesis and to understand patterns of diversification of Cratylia species. Phylogenetic analyses were conducted using Maximum Likelihood and Bayesian inference to determinate the relationships within Cratylia and then to estimate the absolute ages for lineage divergence (stem age, crown age). Molecular data supported the morphological identity of nine species within Cratylia, adding to the initial list: C. pauciflora from Bolivian and Peruvian Andes, C isopetala and C. spectabile (to be transferred from Camptosema), and a new species from Bahia state in Brasil. The most recent common ancestor of Cratylia genus was dated in 4.78 Mya with a crown age of 3.08 Mya. Diversification of this group took place recently in the Atlantic Rainforest, Caatinga, Cerrado-Amazonia-Andes, and seasonal forest of Brazil and Argentina (0.74, 0.61, 0.54 and 0.40 Mya, respectively). Our results suggest ecological factors for diversification (e. g. transition between mellitophilous and ornithophilous flowers) in Cratylia.

CS20-4

Speciation of birds from savanna-like vegetation in South America: the case of a pair of nighthawk Nannochordeiles pusillus (Aves: Caprimulgidae) in and out of the Amazon

Alexandre Fernandes, Universidade Federal Rural de Pernambuco, Unidade Acadêmica de Serra Talhada; Alexandre Aleixo, Museu Paraense Emílio Goeldi/Departamento de Zoologia, Belém, Brazil; Mario Cohn-Haft, Instituto Nacional de Pesquisas da Amazônia/Coleções Zoológicas; Luís Fábio Silveira, Museu de Zoologia da Universidade de São Paulo, Brazil; Nathália Nascimento, Universidade Federal Rural de Pernambuco, Unidade Acadêmica de Serra Talhada; Urban Olsson, Department of Biology and Environmental Sciences/University of Gothenburg

Current research continues to identify critical information gaps in attempts to describe the true avifaunal diversity of the Neotropics. The Least Nighthawk (Nannochordeiles pusillus) is an interesting case. This taxon has a wide distribution across open and low-stature vegetation in the South American tropics, including such different biomes as Cerrado, Caatinga, and Amazonia. Currently up to six subspecies are recognized but have not been critically revised. Our dated phylogeny based on mtDNA and nuclear genes, using samples from the entire range, revealed two genetically divergent and monophyletic groups in N. pusillus, which can also be distinguished by morphological and vocal characters currently not recognized in the literature. The separation between these two main lineages is estimated to have occurred about 3.5 mya. One of these clades apparently corresponds to the subspecies esmeraldae, restricted to whitesand “campinas” in Amazonia, and is diagnosable by broad ventral barring through the undertail coverts and a slower, lower-pitched vocalization. The other morphotype is basically circum-Amazonian in distribution, occuring in savanna-like vegetation in regions with lower rainfall; this lineage includes nominate pusillus and has finer ventral barring, unmarked vent, and a faster, higher song. These two phenotypes are found in sympatry at the border of Amazonia, but maintain their habitat distinction and show no signs of intergradation. This suggests that the two are probably best treated as different species, separated by high genetic divergence and distinguishable by song and morphology. Plumage and vocal differences are consistent with Gloger`s Rule and the Acoustic Adaptation Hypothesis, respectively.

CS20-5

Biogeografía histórica y diversificación de tres clados de Pristimantis (Anura, Strabomantidae) en relación con la orogenia andina

María José Navarrete, Pontificia Universidad Católica del Ecuador; Nadia Páez-Rosales, Pontificia Universidad Católica del Ecuador; Mario Yánez-Muñoz, Instituto Nacional de Biodiversidad INABIO; Santiago Ron, Museo de Zoología, Pontificia Universidad Católica del Ecuador

Pristimantis es el género más especioso entre los tetrápodos. Se ha sugerido que su diversidad y procesos de diversificación podrían estar asociados históricamente a la orogénesis andina bajo modelos que asumen un rápido levantamiento de los Andes a partir del Plioceno. Bajo esta hipótesis, aumentos en las tasas de diversificación deberían estar asociadas temporalmente con eventos de levantamiento de la cordillera andina. En el presente estudio inferimos la historia biogeográfica y la dinámica de diversificación de 54 especies pertenecientes a tres clados andinos de Pristimantis: el grupo de especies de P. chloronotus, el subgénero Huicundomantis y el clado conformado por los grupos de especies P. devillei + P. myersi con la finalidad de evaluar sus tasas de especiación y comprender la evolución de su nicho térmico. En base a un cronofilograma densamente muestreado (estrategia “top-down”) utilizando 226 secuencias de ADN (16S, ND1 y RAG) estimamos las tasas de diversificación y exploramos su correlación con modelos de paleoelevación andinos. Adicionalmente, reconstruimos el rango de elevación ancestral de los taxa. Nuestros resultados muestran que la tasa de especiación aumenta con el tiempo, pero no existen picos de diversificación que puedan asociarse a eventos de rápido levantamiento andino. Los tres clados se originaron en el Mioceno (~10–12 Ma) a una temperatura aproximada de ~15ºC y ~2500 m de elevación. La distribución de especies hermanas sugiere especiación vicariante en bosques nublados bajo un nicho térmico conservado. Finalmente, los estimados de colonización de ambientes fríos (i.e. páramo) coinciden con el periodo cuando se originaron.

CS20-6
Biogeographical patterns of dry inter-Andean valleys in Ecuador

Catalina Quintana, PUCE

Dry forests in the American Andes and other mountains have provided excellent agricultural lands since millennia. Besides agriculture, wood extraction and the establishment of urban areas have diminished the native vegetation of these valleys. Consequently the original vegetation is now mostly found on steep slopes and in ravines. These areas of original dry vegetation preserve many wild relatives of cultivated plants on the one hand and old lineages of other wild plant groups. Dry inter-Andean valleys (DIAVs) in Ecuador therefore makeup a biodiversity hot spot for both plants and animals. Our analysis focused on diversity patterns, species migration and conservation showed that the influence of disturbance, water availability and low temperature are important in shaping species composition and occurrence for the vegetation of DIAVs. The majority of the species found in DIAVs (72%) are shared amongst dry forests and neighboring habitats like mountain forests, páramos, Pacific and Amazonian lowlands. The Amotape Huancabamba zone in Ecuador, that represents a barrier for certain taxa, is a bridge for the migration of DIAVs species. No prior study of dry valleys anywhere in the Neotropics has explored how species are shared with other habitats. We reinforce the idea that for preserving the patches of native inter-Andean vegetation friendly practices in agriculture can contribute to biodiversity conservation.

Concurrent Session 21: Climate Change Biogeography

CS21-1
Effects of Climate Change and Deforestation on the Distribution of Dung Beetles (Scarabaeinae) in the Amazon Biome

Jorge Celi, Universidad Regional Amazonica Ikiam; Nereida Guerra, Universidad Regional Amazonica Ikiam; Marina Rodes Blanco, Universidad Regional Amazonica Ikiam; Marja De Kraker, Wageningen Research University; Pim Van Hooft, Wageningen Research University; Miguel Gómez, Universidad Regional Amazónica Ikiam; Pablo Meneses, Ikiam; Jesús Toro, Universidad Regional Amazónica Ikiam

The Amazonian Biome has had a lot to endure during last decades due to climate change (CC), logging, etc. We used a model to determine their effect on the distribution of dung beetle species in the biome. Dung beetle distribution data mostly in Ecuador was obtained from publications, museum collections, and field sampling. Maximum Entropy Modelling (MaxEnt) was used to model the distribution area under four different CC scenarios of six dung beetle species: Canthon aequinoctialis, C. luteicollis, C. fulgidus, Dichotomius podalirius, Eurysternus cayennensis and E. velutinus. In the current situation the six species shared a large predicted overlapped distribution area that shrank considerably in the future. All four scenarios resulted in a smaller distribution area (mean difference -59.4%) for the six species in comparison with the current situation. For all species the predicted distribution area shifted to the west, with major contractions on the eastside. Under the CC scenarios the median elevation range changed upwards for nearly all the species. However, a large part of the predicted distribution area for the six dung beetle species in Ecuador is currently deforested and probably would not be part of their distribution area if deforestation was taken into account. In conclusion, CC is expected to have a negative effect on the distribution of dung beetle species in Amazonia, although it is difficult to determine the impact of deforestation on dung beetle communities. In future studies we need to consider where deforestation occurs to determine whether that limits future distribution of dung beetles.

CS21-2

Unique responses to climate changes in geology-dependent habitats from the Mata Atlântica biodiversity hotspot

Luíz Esser, Federal University of Rio Grande do Sul; João Jarenkow, Federal University of Rio Grande do Sul; Danilo Neves, University of Arizona

The Atlantic Forest Domain (AFD) comprises six vegetation types, where half of them present a geological attribute as the major species filter (azonal habitats), while the other half is mainly sorted by climate (zonal habitats). Nevertheless, ecological studies tend to cluster those habitats in one unique entity despite distinct environmental conditions, which might lead to erroneous interpretations in studies aiming to evaluate the impacts of global change in this biodiversity hotspot. In order to assess the impact of climate change in AFD azonal habitats, we modelled the responses of 150 indicator tree species, using multiple algorithms, distinct scenarios of climate change and multiple general circulation models (146,850 models), restricting models to habitats geological attributes. Potential loss of suitable environment summed 58.6% in riverine forests, and 66% in rock outcrop dwarf-forests, reinforcing the hypothesis that climate filter will shift, restricting its intersection with the geological filter (the main driver of species assembly in these habitats). Predictions for coastal white-sand forests (7.6%) showed that overall loss of suitable environment will be relatively less severe for this habitat, which, although restricted to the coast, is present in a larger latitudinal gradient (ca. 30 degrees). Rock outcrop dwarf-forests and riverine forests are less studied and will likely suffer the greatest loss of biodiversity because their species are more dispersal limited. This reinforces the importance of our approach and urge for conservation strategies that account for habitat heterogeneity in the AFD.

CS21-3

Tree species distribution comparisons across latitudinal gradients on the Pacific coasts of North and South America under climate change

Taryn Fuentes-Castillo, Pontificia Universidad Católica de Chile; Matthew Kling, University of California Berkeley; David Ackerly, University of California - Berkeley; Rosa Scherson, Universidad de Chile; Patricio Pliscoff, Universidad Catolica de Chile

The Pacific coastal regions of North and South America exhibit remarkably similar gradients of climate and vegetation across both a subtropical to boreal latitudinal gradient and a steep coastal to montane elevation gradient, inviting comparisons between the biogeographic patterns that have developed independently on these parallel geophysical stages. A correspondence analysis of climate and species distribution of these Northern Hemisphere (NH) and Southern Hemisphere (SH) counterparts has never been explored simultaneously. Following these similar geographical settings, it could be expected that climate change will produce similar responses in distribution changes in both areas.

We analyzed the projected distribution of native tree species in each of these two Pacific rim vegetation zones. As a first step, we compared spatial climate patterns and evaluated the spatial correspondence between vegetation formations in NH and SH to find the most suitable bioclimatic variables for species distribution modelling in both areas. Finally, we compared current and projected future distributions of native tree species.

Our results showed a similar bioclimatic spatial pattern across the two regions; these findings are reflected into a geographic correspondence of climatic units. We found an upward elevational displacement of tree species in SA but a downwards displacement in NA as the most frequent response. Finally, we identified a displacement of tree distributions from central zones of NA & SA toward poleward latitudes. These results point out important conservation issues, with the highest future tree diversity losses projected within two highly-threatened biodiversity hotspots (California Floristic Province and Chile winter rainfall-Valdivian forests).

CS21-4

Multi-population seedling and soil transplants simulate climate-driven migrations of a common tropical montane cloudforest tree species (Weinmmania bangii)

Richard Tito Leon, University of Miami & Universidad Nacional de San Antônio Abad del Cusco; Heraldo Vasconcelos, Universidade Federal de uberlândia; Kenneth Feeley, University of Miami

In response to climate change, tropical plant species will need to either tolerate warmer temperatures or migrate to higher elevations. Through a set of 3yr field transplant experiments in the Peruvian Andes, we simulated these two possible responses for common tropical montane cloudforest tree species, Weinmmania bangii (Cunoniaceae), to global warming: (1) “upward migration”, in which seedlings were grown at their current elevation/temperature but in soils transplanted from higher elevations; and (2) “no migration”, in which seedlings were transplanted downslope along with their home soils into areas that are 1°C or 2°C warmer. We conducted separate experiments with populations from the upper/leading edge, middle and lower/trailing edges of W. bangii’s range to assess the influence of local adaptation on responses to the changes in temperature or soil. We found that seedling survival and growth were not affected by planting soil, regardless of the origin population. An experimental 1°C warming caused a significant reduction in the survival for seedlings transplanted from the mid-range population, and the 2°C warming caused a severe decrease in the survival of seedlings transplanted from both the mid-range and bottom-edge populations. Our findings reveal that rising temperatures are a serious threat to tropical plants, especially in populations growing in the hotter portion of their species' range. At least in the case of W. bangii, novel soil conditions will not limit the establishment of seedlings at higher elevations and thus decreases in the survivorship at lower elevations may be offset through upward migrations.

CS21-5

Humpback whale winter distribution and core habitats in relation to SST in offshore and coastal areas off the coast of Ecuador

Judith Denkinger, Universidad San Francsico de Quito; Ana Eguiguren, Proyecto CETACEA; Laia Muñoz, Proyecto CETACEA USFQ; Francisco Rubianes, Proyecto CETACEA/ USFQ; Javier Oña, Proyecto CETACEA/ USFQ

Humpback whales migrate along the South American coast from feeding grounds off the Antarctic peninsula and Southern Chile to breeding areas off Peru, Ecuador, Colombia and Panama. In temperate and tropical regions, climate change, may cause shifts in cetacean distribution away from tropical waters towards higher latitudes; however, whether these shifts affect humpback whales in their wintering grounds, is unclear. With visual and acoustic surveys from the South to the North of Ecuador on board a sailboat in 2013 and 2014, we determined core habitat characteristics for humpback whales breeding off the coast of Ecuador in inshore and offshore waters. We analysed changes in distribution patterns in relation to El Niño Southern Oscillation (ENSO) events with Generalized Additive Models (GAMs) for the surveys and with long-term sighting data collected in a subtropical and a tropical breeding ground. Humpback whales were observed both in inshore and deep offshore waters with songs recorded as far as 100 km from the coast in depth of up to 2000m. They preferred shallow continental shelves off the coast with areas of relatively warm surface temperature (24-27oC) and within 10-20km from the coast. Sighting rates during years that had been preceded by ENSO conditions were significantly lower in subtropical breeding grounds than those in cooler years. Our data evidence that humpback whale distribution in their wintering grounds is influenced by local SSTs as well as region-wide phenomena (ENSO), and thus could indicate that in the future their distribution may shift with warming ocean temperatures.

CS21-6

Climate Driven Changes in the Composition of New-World Flora

Kenneth Feeley, University of Miami; Tim Perez, University of Miami; Belen Fadrique, University of Miami; Daniel Zuleta, University of Colombia; Catherine Bravo, Florida International University

Climate change is widely predicted to drive changes in species′ ranges and hence the composition of ecological communities. However, data on the effects of climate change on plant communities in sparse and is typically limited to small-scale, plot-based studies. In this talk, we present a new hemispherical-scale analysis of climate-driven changes in plant communities over the past 40+ years. Specifically, we use a database of >25 million plant observations and ca. 20,000 species to characterize the functional composition and diversity of 191 new-world ecoregions (covering all of North, Central, and South America) at annual time-steps from 1970 to 2011. We show that the majority of ecoregions (65%, P < 0 .0001) have experienced ″thermophilization″ – i.e., directional shifts in their composition to include greater relative abundances of heat-loving plant species over time. Thermophilization rates vary between ecoregions (mean=0.017oC yr-1, 95% CI=0.011-0.023oC yr-1) but are related to concurrent rates of warming (R2 = 0.064, P=0.0004) and are driven primarily by the local extinction of less-thermophilic species. Because of an overall positive correlation between species' thermal and precipitation optima (R=0.55, P < 0 .0001), a byproduct of thermophilization is that most (65%, P < 0 .0001) ecoregion plant communities are also becoming more mesophilic, and thus potentially more drought-sensitive. This is despite the fact that annual rainfall has been decreasing over time in most (61%) ecoregions. These results show that climate change is driving marked changes in the floral composition of ecoregions throughout the new-world, and that these changing may be increasing their vulnerability to species loss due to future droughts.

CS21-7

Mountain species lag behind current warming: What does it take to reach equilibrium?

John-Arvid Grytnes, University of Bergen

Species are responding to the current warming by shifting their ranges polewards along latitudinal gradients or upwards along elevational gradients, and this make the species currently living in the coldest area susceptible to extinction. However, so far, there exists little evidence of species extinctions and several studies have shown that species are not fully catching up with the climate warming resulting in a lag of colonization and extinction. Here we use a dataset of repeated plant surveys from 302 mountain summits across Europe, spanning 145 years of observation, to quantify the overall lag in species response to climate warming and assess the different effect of colonization and extinction lags. The summer temperature has overall warmed by 1.5K since 1980 and the plants have only caught up with 0.3K, indicating a considerable lag in species responses. The species colonizing the summits are also lagging behind the observed temperature changes, but not as much as the overall species assemblages. Randomizations suggest that a considerable proportion of the species currently on the summits has to go locally extinct from the summit vegetation; 30-75% depending on the amount of new species colonizing from below. Despite the large fraction of large extinctions expected modelling indicates that around 2-5% of the alpine species will totally disappear from all summits investigated in this study.

CS22-1
The Hidden eruptions: revisiting paleoecological evidence in the search for past volcanic activity in the northern Andes

Catalina Gonzalez Arango, Universidad de los Andes; Natalia Pardo, Universidad de los Andes; Nathalie Martínez, Universidad de los Andes

The northern Andes of South America is a highly complex region in terms of its geology, biodiversity, climate and cultural history. A vast collection of palynological records in the area has provided a comprehensive understanding of the response of vegetation to climate variability at different time-scales. However, despite the area comprises more than 20 active volcanoes that have modified landscapes for millennia, the impacts of volcanism on terrestrial ecosystems have been rarely addressed by paleoecologist in the region. Here, we provide information on early successional pathways developing on volcanic substrates in the tropical Andes of SW Colombia based on local knowledge, observational descriptions, and vegetation plots that might be used to interpret palynological records in similar volcanic settings. Furthermore, we synthesize all the available C14 dates derived from volcano-borne charcoal and paleosoils buried under tephra all over the region for the Holocene and compare them to existing, well-dated, palynological records. We found that many sites might actually contain "hidden" information on the response of vegetation to volcanism and could potentially inform on the timing and intensity of past eruptions. Volcanism should be then considered as one of the primary factors promoting temporal and spatial environmental heterogeneity in the area with important implications for the maintenance of tropical biodiversity.

CS22-2
Quaternary Biogeography of Creosote Bush (Larrea tridentata) in the North American Deserts

Camille Holmgren, Buffalo State College; Kimberly Hunter, Salisbury University; Julio Betancourt, U.S. Geological Survey

Creosote bush exhibits a disjunct distribution with four species in South America and one in North America. It is the most abundant and wide-ranging shrub in the warm deserts of North America and is also a classic example of an autopolyploid complex. Since its arrival in North America, creosote (here represented by Larrea tridentata) evolved into diploids, tetraploids, and hexaploids. These ploidy races exhibit an allopatric distribution with diploids primarily found in the Chihuahuan Desert, tetraploids in the Sonoran Desert, and hexaploids in the Mojave and western Sonoran Deserts, a pattern hypothesized to reflect a SE-NW gradient of increasing summer aridity. Determination of ploidy races from fossil creosote leaves shows these distributions have shifted through time. Much remains unknown, however, about the history of the diploid-tetraploid boundary in southeastern Arizona and southwestern New Mexico, USA. To better understand this history, we determined ploidy levels for modern plants and ancient creosote leaves preserved in fossil packrat middens (3170-145 cal yr BP) from SE Arizona. Ancient creosote was all diploid, suggesting co-occurrence of ploidy races along this boundary is quite recent. This area is a contact zone hot spot for birds, mammals, and phylogeographic breaks, which has been surmised to reflect post-glacial expansion out of refugia. As climatic barriers were eliminated, diploids appeared first around 3170 cal yr BP with more recent arrival of tetraploids. The late appearance of tetraploids mirrors the recent arrivals of other Sonoran Desert plants at its eastern margin and suggests ongoing expansion into the area.

CS22-3

Integrating fossil, environmental, and genetic data in historical biogeographic inference

Allan Strand, College of Charleston/Biology/Grice Marine Lab; Andria Dawson, Mount Royal University; Sean Hoban, The Morton Arboretum; John Robinson, Michigan State University; Adam Smith, Missouri Botanical Garden

A major goal of ecology and evolutionary biology is to document and understand biogeographic history: where species existed, when, with what abundance, and why. Towards this goal, different scientific communities have used disparate approaches based on different data types (e.g., DNA data, contemporary specimen records, fossil remnants, etc.). Each data type reflects different historical processes, has different limitations, and varies in resolution--none alone captures the entire biogeographic history. As a consequence, despite continued improvements in data quality and quantity, questions about species past range shifts remain hotly debated. There is community consensus on a need to quantitatively integrate information from disparate data and models. In this talk we will present an ongoing effort to develop novel, comprehensive, statistically robust informatic methods to estimate species genetic, demographic, and biogeographic history. The specific objective is to leverage information from multiple sources spanning space and time to estimate: (a) key demographic and genetic parameters, (b) post-glaciation (Holocene) species distributions, and (c) observation and process uncertainty. A modified Approximate Bayesian Computation (ABC) approach, developed in R, will link and expand the state-of-the-art in spatially explicit demographic inference. Here we demonstrate the use of this approach to provide new estimates of Holocene range expansion in green ash based upon rangewide SNP and microsatellite data, a rich dataset of fossil pollen, and a large database of contemporary occurrence points. We infer the speed of migration as well as the number of refugia. This work represents a new integrative direction for historical biogeography.

CS22-4

Influence of the Quaternary on the vegetation dynamics of western Ecuador

Sebastián Escobar, Aarhus University; Thomas Couvreur, Institut de Recherche pour le Développement; Rommel Montúfar, Pontificia Universidad Católica del Ecuador; Henrik Balslev, Aarhus University; Andrew Helmstetter, Institut de recherche pour le développement (IRD); Scott Jarvie, Aarhus University

The role of the Quaternary climatic fluctuations on plant species distributions is unknown in many regions. Within the Neotropics, past vegetation shifts in the Amazonia have been studied under different approaches; however, almost null attention has been given to the forests at the other side of the Andes. In particular, the coastal region in western Ecuador may suffered the change of tropical rain and dry forests for desert during the Last Glacial Maximum (LGM; 25 k – 15 k years ago) due to a reduction in precipitation. Therefore, forests with current distribution in this region may developed recently after the LGM. We aim to understand the influence of the Quaternary on the vegetation dynamics of western Ecuador using the evolutionary history of the palm Phytelephas aequatorialis inferred through both phylogeographic and paleodistribution modeling approaches. Tagua, as it is commonly known, is endemic to this region, growing from sea level up to 1500 m asl. For this study we ask: 1) were the distribution of tagua restricted to the western Andean foothills during the LGM?; 2) do areas of historical climatic stability harbor higher genetic diversity than areas where climate fluctuated during the LGM?; 3) does the evolutionary history of tagua reflect a major vegetation shift scenario caused by the LGM? This study looks to fill a knowledge gap about the influence of the Quaternary in the Neotropical region, and to generate valuable information that contributes to the conservation and management of the tagua palm.

CS22-5

Tempo of postglacial recolonization of the Laurentian Great Lakes by ciscoes (Actinopterygii, Coregoninae): a new phylogeographic hypothesis

Julie Turgeon, Université Laval; Gabriel Piette-Lauzière, Université Laval; Mark Ridgway, Trent University & Ontario Ministry of Natural Resources

Ciscoes (Coregonus spp.) comprises – or alas, comprised - the most diverse freshwater fish fauna of coldwater lakes in North America. It is now widely accepted that multiple forms evolved repeatedly in several lakes following postglacial recolonization by two refugial lineages. We recently showed that the blackfin form (aka C. nigripinnis) discovered in an outlet of proglacial Lake Algonquin was not genetically related to the admixed lineage currently present in the Laurentian Great Lakes. The occurrence of the sole Atlantic lineage in this critical connecting landscape suggested that the western lineage, presumed of Mississippian origin, arrived later in the Laurentian Great Lakes. We compiled published and new genetic information (mtDNA, microsatellites, SNP) for ca. 1000 fish from 60 sites throughout the range of ciscoes, including key locations in proglacial lakes and temporary outlets near the Laurentian Great Lakes. Results confirmed the existence of two glacial lineages with distinct distributions and restricted areas of admixture. The Atlantic lineage is the only lineage in all but the latest outlet of Lake Algonquin. It indicates an early dispersal into the area, with plenty of time to invade Lake Barlow-Ojibway. The absence of the western lineage indicates a much later arrival in the area, and suggests dispersal from an unsuspected Missourian refuge via Lake Agassiz, with late connection to L. Barlow-Ojibway. Our phylogeographic approach provides a more detailed view and a new hypothesis on the recolonization of the Laurentian Great Lakes by one of its major fish fauna component.

CS22-6

Persistent Quaternary climate refugia are merely hospices for biodiversity in the Anthropocene

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Climate stability leads to high levels of speciation and reduced extinction rates, shaping species richness patterns. Hotspots of species diversity often overlap with regions that experienced stable temperatures and, perhaps, variable rates of precipitation during the late Quaternary. These hotspots potentially harbour many species with low vagility and small geographical ranges, making them more vulnerable to future ecoclimatic change. By comparing global and regional patterns of climate stability during short periods of unusually large and widespread climate changes since the Last Glacial Maximum with 21st century patterns, we show that (i) human-driven climate change will disproportionally affect biodiversity in late Quaternary climate refugia, ultimately affecting the species, communities, and ecosystems that are most vulnerable to climate change; and (ii) changes in absolute temperature will likely erode the mechanisms theorised to sustain biodiversity hotspots across time. These impending shifts, from stable to unstable temperatures, projected for the majority of the world's biodiversity regions, threaten to reduce the size and extent of important climatic safe havens for diversity. Where climate refugia are forecast to persist until the end of this century, temperatures in these refuges will likely exceed the acclimatisation capacity of many species, making them at best short-term hospices for biodiversity.

CS22-7

Global-scale patterns of plant diversity in relation to mountain geodiversity and past climate change: the “mountain-geobiodiversity hypothesis” put at test

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The objective of our study was to analyse global-scale patterns of mountain biodiversity (vascular plants) and the driving forces leading to the observed patterns. More specifically, we tested the “mountain geobiodiversity hypothesis” (MGH) which is based on the assumption that it is not mountain-uplift alone which drives the evolution of mountain biodiversity, but rather the combination of geodiversity evolution and Neogene and Pleistocene climate changes. We addressed the following questions: 1) Do areas of high geodiversity and high biodiversity in mountains overlap, i.e., can mountain geodiversity predict mountain biodiversity? 2) What is the role of Pleistocene climate change in shaping mountain biodiversity? 3) Did diversification rate shifts of mountain plants occur predominantly with the onset of more pronounced climate fluctuations in the late Neogene and Pleistocene fostering a “species pump” effect, as predicted by the MGH? We used generalized linear models to test to what extent vascular plant species diversity in mountains can be explained by net primary productivity, geodiversity and Pleistocene climate fluctuations. In addition, we compiled dates of diversification rate shifts from mountain systems and investigated whether these shifts occurred predominantly before or after the global major climatic fluctuations of the Late Neogene and Pleistocene. We found that both net primary productivity and elevation range show a positive relationship, whereas Pleistocene climatic fluctuations show a negative impact on plant species diversity. Shifts to higher diversification rates or starts of radiations showed the highest concentration from the late Miocene towards the Pleistocene. Our findings thus support the MGH.

Concurrent Session 23: Biodiversity Patterns and Maintenance

CS23-1

Biogeographical patterns in American Asclepiadoideae (Apocynaceae)

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Asclepiadoideae are represented in the Americas by four lineages. One of these lineages is mega-diverse with more than 1,000 species in 70 genera. While most of the larger genera have their center of diversity in South America with few, species extending into Central America, Metastelma is most diverse in Central America. Metastelma is characterized by a simple five-partite staminal corona and barbate corolla lobes. Analyses of cpDNA using maximum parsimony, maximum likelihood and Bayesian inference reveal that the closest relatives of Metastelma s.str. are South American, but only two small clades are still extant there. In the Caribbean, three Metastelma clades are found. The Caribbean M. anegadense-M. lineare clade is sister to a strongly monophyletic clade comprising all Central American mainland species. The latter clade shows a clear geographical structure with a center of diversity in central Mexico and two radiations along the Sierra Madre Occidental and one radiation along the Sierra Madre Oriental. Morphologically highly similar entities are retrieved in different clades. Biogeographic analysis using RASP suggests that South America was the source for multiple invasions to the Caribbean. The genus possibly reached Central America via the Caribbean and the Yucatán peninsula, rather than the Panamanian landbridge, a pathway not yet known from other Angiosperm genera.

CS23-2

New insights on the role of the Ecuadorian Andes in generating evolutionary diversification

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Andres Cuervo, Tulane University; Catalina Campuzano, Universidad San Francisco de Quito; David Prieto-Torres, Universidad Nacional Autónoma de México; Laura Rosado , Universidad Central del Ecuador; Juan Freile, Comite Ecuatoriano de Registros Ornitológicos

The Andes are the most important biogeographic barrier in the Neotropics. With their impressive topography, they separate foothill and lowland ecosystems of the Amazon from those on the South American Pacific coast. To date, there is extensive information about broad-scale differentiation at both sides of this barrier. However, it is possible that for a number of species, more detailed analyses may reveal some degree of gene flow among populations Amazonian and Pacific populations. This is particularly interesting in Ecuador, where the Andes reach relatively low elevations allowing a higher degree of connection between populations. We analyze genetic differentiation in a group of birds, in order to explore potential connections between east and west, as well as how the roughness of the Andes in the southern part of the country may act as a species pump. Our preliminary results show a complex scenario, where different species seem to show diverse idiosyncratic responses generated by isolation, gene flow, and even secondary contact and introgression.

CS23-3

Divergent melanism strategies in Andean butterfly communities structure diversity patterns and climate responses

Pablo Padron, Universidad del Azuay; Pauline Dufour, School of Biological Sciences, The University of Hong Kong, Hong Kong SAR, China

Geographic distributions are driven by a combination of species sensitivity and exposure to climate. We quantified colour lightness, a trait that mediates the interaction between sensitivity and exposure, of diverse butterfly communities to test whether colour lightness is associated with community assembly across climate-elevation gradients. We used a long-term dataset of museum specimens for two of the most speciesrich genera of Pieridae butterflies in Ecuador, Catasticta and Leptophobia.Within a phylogenetic framework, we examined how communities assemble based on four traits across elevation: colour lightness, species-specific heating rate, maximum temperature (under experimental solar exposure), and elevation breadth. We found that colour lightness in both genera was related to elevation, but the two genera exhibited opposite patterns; Catasticta are darker and Leptophobia are lighter with increasing elevation. The two genera have opposite configurations of body and body + wings colour lightness but achieve comparable thermoregulation, assessed via their rates of heating under experimental solar exposure. The two genera exhibit divergent relationships between eleva- tional and colour lightness patterns, with evidence that these relationships evolved multiple times in Catasticta. Communities from these two genera have likely been shaped by selection on different traits, with Catasticta colour lightness more responsive to temperature than Leptophobia. The observed geographic patterns of colour lightness in both body + wings (Catasticta) and body (Leptophobia) correspond strikingly with the distribution of montane cloud forests. Habitat fragmentation and cloud lifting from climate change documented across the Andes may therefore significantly impact communities through increased exposure to solar radiation, highlighting the complexity of conserving these diverse montane communities.

CS23-4

Biome Phylogenetic Conservatism: How birds colonize new environments? ... an approach for Galliformes

Jonathan Pelegrin, Universidad Santiago de Cali; Juan Cantalapiedra, Universidad de Alcalá; Manuel Hernández Fernández, Universidad Complutense de Madrid

The relationship between past climatic events and evolutionary processes at a broad-scale has an outstanding significance to understand current diversity. Similarly, processes related to the retention of ancestral ecological traits (Phylogenetic Niche Conservatism) aim to explain many geographical distribution patterns in relatively recent times. However, the integration of diverse evolutionary hypotheses related to the ecological specialization can lead to consolidate a complex explicatory frame. In this sense, the biome becomes a key macroecological level that integrates climatic variables, a particular age, and geologic processes. These features can arrange them like "evolutionary arenas" with their own dynamics of extinction and speciation. Therefore, what factors would have been decisive in the processes of colonization of the different biomes by species during their diversification along time? Also, can we evaluate the level of Phylogenetic Biome Conservatism (PBC) and evolution of climatic niche spectrum? Our work evaluates the biome colonization in different species of Galliformes, one of the most ancient bird group (since Upper Cretaceous), It is present in all environments and it has a variety of ecological traits. It can also allow us assess the effect of biome shifts in the evolution of climate niche and the differences of PBC between them to understand their biogeographical patterns under a historical perspective. Overall, our findings suggest a tendency towards the phylogenetic biome conservancy and the importance of global climate changes during the Miocene in the adaptation and evolution of climate niche for families. Finally, the historical dynamics of dry and seasonally biomes seem to be key processes that promote fowl´s diversification.

CS23-5

Spatial patterns of biodiversity and biogeographic regionalisation of north-western South America

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North-western South America is celebrated for its megadiverse flora and fauna. Synergic interactions between geologic, geographic and ecologic factors in the region are some of the factors producing complex spatial patterns. Over the course of a complex 200-year history, scholars have proposed a multitude of frameworks delineating local, national and international biogeographic regions. Plants, birds and mammals have historically been the main biogeographic model groups in NWSA, driving most biogeographic and conservation proposals. However, the study of the spatial biodiversity patterns and biogeographic regionalisation of several vertebrate and invertebrate groups in NWSA remains incomplete. In the absence of quality data, global and regional biogeographic regionalisation proposals based on more exhaustively studied animals have frequently been applied without necessary further validation. The aim of this study is to provide a set of multi-taxonomic analyses to reveal region-wide patterns of the biodiversity composition of amphibians, reptiles and birds of NWSA in order to describe and compare their spatial patterns. These data are based on a database that combines a comprehensive, manually compiled distribution dataset that allows an integrated and updated assessment of the species richness and distribution patterns of more than 3000 species of anuran amphibians, squamate reptiles and birds; generating calculations and comparisons of species richness and endemism patterns for the most relevant supra-generic clades and allowing evaluations of the biogeographic regionalisation of NWSA based on cladistics methods.

CS23-6

Patterns of beta diversity of Neotropical salamanders

Zeltzin Rodríguez Ortíz, Unidad de Genómica Avanzada. Cinvestav-Irapuato; Sean Rovito, Langebio-Cinvestav

The interaction of environmental, evolutionary and ecological factors influences patterns of species diversity across landscapes. Examining beta diversity (species turnover between sites) allows inferences about the role of environmental conditions, biotic interactions and geographic barriers in shaping diversity patterns. We examined different aspects of beta diversity in the geographically complex region of Mesoamerica and northern South America to infer the main modes of geographic speciation that produced the high species diversity of the region. We used the Neotropical salamanders (tribe Bolitoglossini) as a study system because of their high taxonomic diversity (over 300 species) and great variation in morphology and habitat use. Salamanders have very specific environmental requirements and their low dispersal ability means that geographic signatures of speciation are retained over long periods of time. We measured phylogenetic, taxonomic and functional beta diversity between assemblages of salamanders and compared the observed beta values with null distributions from process-based null models to determine which pairs of sites differ significantly in their beta diversity. In general, the three components of beta diversity show great turnover between sites, reflecting the high degree of endemism in this group. The results of this study help us to understand how speciation is related with environmental gradients and geographic barriers, and how environment and geography interact to produce patterns of biodiversity.

CS23-7

The role of behaviour in community assembly: Social spiders as a case study

Leticia Aviles, Dept. of Zoology and Biodiversity Research Centre, University of British Columbia; Jennifer Guevara, Ikiam; Jessica Purcell, University of California Riverside; Philippe Fernandez-Fournier, Simon Fraser University

Among the factors that may lead to differences in resource use among closely related species, body size and morphology have been traditionally considered to play a role in community assembly. Here we show that for animals that live and forage in groups, level of sociality, reflecting differences in group size and cooperative tendencies, can be an additional and powerful dimension separating species in niche space. We first show that in 50+ communities of the social spider genus Anelosimus across the Americas co-occurring species differ in body size or level of sociality more than expected by chance and that differences in level of sociality yield greater differentiation in the size of the prey captured than body size. We then focus on specific communities to demonstrate how co-occurring species differ in their use of space, time, and dietary resources, consistent with known mechanisms of species coexistence. We further show that differences in individual behaviours, such as cooperative tendencies, reaction times, etc., act above and beyond differences in body or colony size to lead to resource use differentiation among co-occuring species. We conclude by considering the role that species sorting, character displacement, and sympatric speciation may have played in determining the species composition of these communities and argue that behavioural traits, including level of sociality, may be a fast and efficient way to separate the niche spaces of closely related species.

CS24-1

Comparative phylogeography and adaptive genomics in the Atlantic Forest of Brazil, using genome-wide SNPs and spatially explicit climatic data

Laura Bertola, City University of New York; Mariana Vasconcellos, City University of New York, New York Botanical Garden; Roberta Damasceno, Universidade de São Paulo; Ivan Prates, Smithsonian National Museum of Natural History; Marcelo Reginato, University of Campinas; Andressa Nuss, Universidade de São Paulo; Nick Steiner, City University of New York; Ashfaq Khan, City University of New York; Natalia Quinteros, City University of New York, New York Botanical Garden; Cristina Miyaki, Universidade de São Paulo; Fabio Raposo do Amaral, Universidade Federal de São Paulo; Karina Brandão, Universidade de São Paulo; Luiza Magaldi, University of Campinas; Andre Freitas, University of Campinas; Miguel Trefaut Rodrigues, Universidade de São Paulo; Fabian Michelangeli, New York Botanical Garden; Kyle McDonald, City University of New York; Ana Carnaval, City University of New York; Mike Hickerson, City University of New York, City College

The South American Atlantic Forest domain is a biodiversity hotspot characterized by steep climatic gradients and high environmental heterogeneity. Here, we use genome-wide RADseq data collected from 20 taxa distributed throughout the domain, inlcuding plants, amphibians, lizards, birds and butterflies, to investigate if and how shared climatic gradients correlate with genomic adaptation in the individual taxa.

To quantify the climatic features corresponding to the landscape, we extracted highly resolved spatial information about seasonal temperature and precipitation gradients from multiple remote sensing data sources, including MODIS, AMSR-E and CHIRPS. We also included bioclimatic variables, both derived from remote sensing data and from weather stations, as well as projections of historical climate.

We used the LEA pipeline and the approach using latent factor mixed models (LFMM) to detect signatures of selection driven by the climatic gradients across the 20 taxa, while accounting for taxon-specific population structure. Depending on the taxon and its distribution, our approach flagged 1-15% of the sampled SNPs as potentially under selection.

We explored spatial patterns of these flagged SNPs across the taxa, to gain insight into concordance and discordance between the included taxa. Data collected in this study 1) give us insight into community-level responses to shared environmental gradients and shifts; 2) provide new views on the evolutionary history of the species in the Atlantic Forest; and 3) give us guidelines on how to preserve regional biodiversity.

CS24-2

Unveiling the biogeographic history of Ecpleopodini tribe (Squamata: Gymnophthalmidae) through genomic data

Sergio Marques de Souza, Universidade de São Paulo, Zoology Department, Herpetology Lab; Roberta Damasceno, University of California, Berkeley; Miguel Trefaut Rodrigues, Universidade de São Paulo; Tuliana Brunes, Universidade de São Paulo, Instituto de Biociências, Zoology Department

The Ecpleopodini lizard tribe (Squamata: Gymnophthalmidae) shows an interesting and enigmatic distribution pattern on South America. Most species inhabit the leaf litter of Neotropical Forests, and are distributed on Atlantic Rainforest (Ecpleopus, Dryadosaura, Leposoma) or in the Amazon (Arthrosaura, Amapasaurus, Loxopholis, Marinussaurus). However, some genera are able to occurr in open habitats, as Colobosauroides and Anotosaura, both endemic of Brazilian Caatinga, or occupy the Gran Sabana and the summit of Venezuelan Tepuis, as Pantepuisaurus, Kaieteurosaurus and some species of Arthrosaura and Yanomamia. To elucidate how this intriguing biogeographical pattern was stablished, we need a robust phylognetic hypothesis for the tribe. However, the few Ecpleopodini phylogenies available are based on few loci and have several poorly-supported clades, being the relationships among genera, therefore, highly uncertain. In this study we present a Ecpleopodini phylogeny based on reduced-representation genome data (RADseq), besides a reconstruction of the biogeographic history of the group using BioGeoBears. We expect this approach to provide clues about the expansion, contraction, fusing and isolation dynamics of South American biomes, in particular the ombrophilous forests, and to clarify which evolutionary process acted on the adaptation of a strictly forest group to be able to occupy open and dry environments, as the Brazilian Caatinga.

CS24-3

Genetic structure of an ancient tropical tree species at multiple geographical scales: divergence across continents, regional gene pools and within-populations

Santiago Gonzalez-Martinez, INRA; Myriam Heuertz, INRA; Paloma Torroba-Balmori, INIA; Katharina Budde, INRA; Thomas Parchman, University of Nevada, Reno; Sanna Olsson, INIA; Caroline Scotti-Saintagne, INRA

Symphonia globulifera L.f. (Clusiaceae) is a widespread tropical tree species. Considered a living fossil, the species colonized the Americas from Africa ca. 18-15 Ma ago. Previous work based on microsatellites (nuSSRs) has shown African populations to display stronger fine-scale genetic structure (FSGS) than Neotropical populations, which may reflect less efficient seed dispersal, and a clear altitudinal stratification of genetic diversity in this range. In this study, based on 4,921 SNPs genotyped in 367 individuals (including two differentiated ecotypes) from nine populations, three from the Neotropics and six from Africa, we inferred population splits and mixtures and discovered more ancient divergence events in Africa than in the Neotropics in a full coalescent analysis, which also allowed us to date the time of population split across continents. In addition, the French Guiana terra firme ecotype was inferred to have a Neotropical origin and we also found São Tomé island population was closer to Neotropical populations than those from continental Africa (Cameroon, Benin and Gabon). At the regional scale, several differentiation outlier loci associated to climate and soil were identified in the African range, which points to locally adapted gene pools. Finally, adaptation at the within-population scale resulting in FSGS associated with altitude was investigated, to confirm previous results using nuSSRs. Overall, we show that standing genetic variation in ancient and widespread tree species, such as S. globulifera, may reflect multiple overlaying levels of population structure in response to environmental drivers acting at different spatial scales.

CS24-4

Comparative geogenomics of three mountain species of Geonoma Wild. (Arecaceae) in the Cordilleras of Colombia

María Sanín, Universidad CES; Margot Paris, Université de Lausanne; Michael Kessler, University of Zurich; Fabian Mejía, Universidad CES; Juan Jaramillo, Universidad Nacional de Colombia; Agustín Cardona, Universidad Nacional de Colombia; Nicolas Salamin, University of Lausanne

The Northern Andes are one of the most biodiverse regions in the Neotropics, exhibiting high levels of species richness and endemism but lacking much knowledge about the temporality of the origins and evolution of its plant life. In this work, we aimed to use genomics to explore the evolutionary patterns that may have determined the distribution of genetic variation among the northernmost mountains of the Andes. We sampled 111 individuals of two highland and one lowland species of one the most diverse and representative palm genus in montane biomes, GeonomaWild., from populations along the geologically least known ranges of Colombia (the Western and Central Cordilleras). DNA sequences were captured and filtered for a total of 12.750 SNPs that were used to test the species delimitation for sympatric species and track populational genetic boundaries from multivariate analyses and genetic structuring. We used the recovered spatial structure, and dated phylogenies to validate contrasting scenarios of mountain formation in the region. Particularly, if elevation was achieved continuously and synchrounously throughout the ranges, and when. We found overall consistent well-structured groups showing strong spatial structure not correlated to geographical nor ecological distances. We also found this structuring is of Pliocene to Pleistocene origin, suggesting that the phylogeographical breaks found in the three species are the result of irregular and asynchronous pre-Pleistocene distribution of topography in the Western and Central Cordilleras.

CS24-5

Using RADseq to understand the circum-Antarctic distribution of the lichenized fungus Pseudocyphellaria glabra (Ascomycota, Peltigeraceae)

Todd Widhelm, Field Museum; Felix Grewe, Field Museum; Jen-Pan Huang, Biodiversity Research Center, Academia Sinica; Karolis Ramanauskas, University of Illinois at Chicago; Roberta Mason-Gamer, University of Illinois at Chicago; H. Lumbsch, Field Museum

The lichenized fungus Pseudocyphellaria glabra has a disjunct distribution that is separated by the Tasman Sea and the Pacific Ocean. We collected samples from across its disjunct range to test whether major physical barriers resulted in genetic differentiation among populations. We tested two hypotheses (1) if large bodies of water isolate populations of P. glabra, then these populations will be genetically distinct, and (2) given the strong wind patterns in southern hemisphere, P. glabra populations on different landmasses will be connected by frequent and ongoing long-distance dispersal (i.e. gene-flow). We predicted the that the large distances between populations would generate genetically distinct clusters, but given the strong and sustained wind patterns present in the Southern Hemisphere and the microscopic size of P. glabra spores that migration is frequent enough to prevent speciation. We used genomic data from 273 samples using restriction site-associated DNA sequencing to conduct phylogenomic and population genomic analyses. Maximum likelihood analysis recovers P. glabra two distinct lineages that contain individuals from all landmasses. Population genomic analyses found genetic clusters can occur in populations that are isolated by large bodies of water. Coancestry estimation analyses suggest that populations from New Zealand and Chile have higher levels of coancestry than both do with Australian populations. Populations from Australia, Chile, and New Zealand are genetically distinct, but frequent long-distance dispersal may sufficiently prevent speciation.

Concurrent Session 25: Climate Change Biogeography

CS25-1

Geographical history of stoneflies (Insecta: Plecoptera): review and extremes of adaptations in environmentally sensitive species.

Charles Riley Nelson, Brigham Young University; Paul Frandsen, Brigham Young University

Plecoptera are aquatic insects that live in clean, well-oxygenated fresh water as immatures. They are generally more prevalent in temperate streams and lakes than in tropical ones. But numerous exceptions and radiations exist. They have a clear fossil history that extends to the Permian. They are used as bioindicators of desirable water quality by managers and ecologists around the world. The phylogeny of the group is largely stable, with notable exceptions. In this talk I will summarize the rather odd distributional history of the order and highlight research into their use of extreme habitats of glaciers, oligotrophic lakes, hyporheic zones, and life history adjustments to alpine and arctic regions. I will also address some current conservation and extinction issues with respect to local and global change.

CS25-2

Applying fuzzy logic to assess the biogeographical risk of dengue in South America

Raimundo Real, University of Malaga; David Romero Pacheco, Universidad de la República-Facultad de Ciencias-Uruguay; Jesús Olivero, Universidad de Málaga; José Guerrero, Instituto de Ecologia y Ciencias Ambientales, Facultad de Ciencias, Universidad de la Republica

Over the last decade, reports about dengue cases have increase worldwide, which is particularly worrisome in South America due to the historic record of dengue outbreaks from the seventeenth century until the first half of the twentieth century. Dengue is a viral disease that involves insect vectors, namely Aedes aegypti and Ae. albopictus, which implies that, to prevent and combat outbreaks, it is necessary to understand the set of ecological and biogeographical factors affecting both the vector species and the virus. We here contribute with a methodology based on fuzzy logic that is helpful to disentangle the main factors that determine favorable environmental conditions for vectors and diseases. Using favorability functions as fuzzy logic modelling technique and the fuzzy intersection, union and inclusion as fuzzy operators, we were able to specify the territories at biogeographical risk of dengue outbreaks in South America. Our results indicate that the distribution of Ae. aegypti mostly encompasses the biogeographic framework of dengue in South America, which suggests that this species is the principal vector responsible for the geographic extent of dengue cases in the continent. Nevertheless, the intersection between the favorability for dengue cases and the union of the favorability for any of the vector species provided a comprehensive map of the biogeographical risk for dengue. In the current South America epidemiological framework, understanding the vector-illness biogeographic interaction may be useful in decision-making by the public health authorities to prevent, control and mitigate such diseases.

CS25-3

A model for plant growth and application to understand the impact of regional scale warming on the distribution of biomass in Ecuador (BIOc Model)

Paulina Rosero, FLACSO

The accounting of biomass has become relevant as the report of carbon emissions by deforestation and forest degradation (EDD) are important indicators for climate change mitigation. The purpose of the BIOc model is the quantification of biomass in a national-scale basis, considering the diversity of bioclimates in Andean regions such as Ecuador, thus the variation in the altitudinal distribution of biomass. BIOc is structured in three sub-models, the first which estimates biomass as a function of climate; the second which estimates the change in maximum productivity of biomass as a function of changes in temperature and CO2 concentration and the third which estimates the carbon emissions by deforestation.

Ecuadorian Ecosystems produce from 187 to 2969 g DM m^{-2} yr^{-1}. The Evergreen forest of the Amazon and the northern coast are the most productive, followed by the western and oriental slopes of the Andes. The Deciduous

forests and the Paramo are the less productive, the former being limited by low precipitation and the latter by low temperature. The most productive ecosystems are the most deforested, accounting for 33% of deforestation emissions. By 2050, ecosystems could be more productive, where lowlands will evidence a higher increase in productivity than highlands. While the increase in CO2 availability will be positive for biomass production, shifts in the altitudinal distribution of temperature will affect biogeography. As a result, mountainous ecosystems will be isolated to higher altitudes or disappear. To conclude, the BIOc outputs can be useful for conservation purposes and the implementation of REDD initiatives.

CS25-4

Directional Changes in an Amazonian forest

Renato Valencia, Pontificia Universidad Católica del Ecuador; Simon Queenborough, Yale University; Consuelo Hernández, Pontificia Universidad Católica del Ecuador

We study population and functional changes in a large forest plot (25-ha) located in eastern Ecuador. Previous studies suggest that climate change affect species in different ways. For instance, secondary species may become more important in Amazonian forests. And the forest itself is supposed to experience frequent and intense droughts. If these is true, species less tolerant to drought are expected to become more common in more humid habitats, such as the humid valleys and will become less common in less humid areas, such as the hill tops and slopes. In this study we test these predictions. The plot was stablished in 1995. Since then, four censuses has been made. We present results of 12 years (divided in two intervals). We use functional traits such us maximum size, wood density, seed mass and specific leaf area to address these questions. We found that the forest is decreasing in wood density, maximum size and specific leaf area in the second time interval. In the two time intervals, the population of 5 and 6% of the species increased or decreased significantly (>6 times of the original population). Contrary to the expectations, species increased tenfold in (dry) ridges than in (wet) valleys by the second interval. Only two species, one in ridge and another in valley, increased systematically in both time intervals and no species decreased in both censuses. Our results suggest that the secondary species are becoming more important, but not that species are increasing in population in the humid valleys.

CS25-5

Amphibian diversity under climate change and the efficiency of protected areas in the High Paraguay Basin

Matheus Neves, Universidade Federal de Mato Grosso do Sul; Olivier Broennimann, University of Lausanne; Heidi Mod, University of Lausanne; Mario Moura, Yale University - EEB; Diego Santana, Universidade Federal de Mato Grosso do Sul; Antoine Guisan, University of Lausanne

Protected Areas (PAs) are an important tool for biodiversity conservation. However, their capability to protect species may be reduced by climate change. High Paraguay Basin (HPB) covers the world's largest tropical wetland area, Pantanal, and its surrounding plateaus, yet the effectiveness of its PAs have not been properly assessed. We investigate the drivers underlying the amphibian diversity in HPB and assess the conservation status of amphibians within the existing PA-network. We built habitat suitability models for 74 species by combining occurrences covering South-America and information on climate, land-use and topography. We then compared the predicted distribution, richness and turnover of species between current environmental conditions and future scenarios. The efficiency of PAs (5.84% of HPB area) was evaluated by comparison to areas which maintained size and shape of PAs while randomizing the geographic position. Based on the preliminary results, amphibian richness is predicted to decrease by the end of the century, especially in Pantanal. HPB is expected to lose suitable conditions for approximately half of the 74 amphibian species, including four endemic species which may become extinct in the future. Areas predicted to gain species were restricted to the surrounding plateaus. The predicted turnover was high (up to 100%), implying biodiversity changes not only in species richness but also in composition. Currently, only 6.8% of PAs have higher richness than randomly placed areas but, in the future, this percentage will increase. Our findings highlight the need to apply systematic conservation planning to guide the location of PAs in HPB.

Concurrent Session 26: Marine Biogeography

CS26-1

Introgressive hybridisation between two widespread sharks in the east Pacific Region

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With just a handful of documented cases of hybridisation in cartilaginous fishes, shark hybridisation remains poorly investigated. Small amounts of admixture have been detected between Galapagos (Carcharhinus galapagensis) and dusky (Carcharhinus obscurus) sharks previously, generating a hypothesis of ongoing hybridisation. We sampled a large number of individuals from areas where the species co-occur (contact zones) across the Pacific Ocean and used both mitochondrial and nuclear-encoded SNPs to examine genetic admixture and introgression between the two species. Using empirical analytical approaches and simulations, we first developed a set of 1,873 highly informative SNPs for these two species to evaluate the degree of admixture between them. Overall, results indicate a high discriminatory power of nuclear SNPs (FST = 0.47, p 0.05), which failed to differentiate these species. We identified four hybrid individuals (~1%) and detected bi-directional introgression between C. galapagensis and C. obscurus in the Gulf of California along the east Pacific coast of the Americas. We emphasize the importance of including a combination of mtDNA and diagnostic nuclear markers to properly assess species identification, detect patterns of hybridisation, and better inform management and conservation of these sharks, especially given the morphological similarities within the genus Carcharhinus.

CS26-2

Evolutionary history of the Scleractinian corals distribution

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Processes driving biodiversity patterns along the bathymetric gradient are not well known at the global scale. Scleractinian corals are a current conservation focus owing to their ecological importance and susceptibility to extinction from environmental change. These species have a wide biogeographic distribution, with two main functional groups: zooxanthellate, which distribution is restricted to the photic zone, and azooxanthellate, widely distributed in the water column. Understanding the evolutionary interaction between these groups from their origin in the Paleozoic to their current distributions is critical to predict the groups destiny in the future. In the present work, we used a new generated phylogenetic tree and known species distribution in a 3D space to test hypotheses about the Scleractinia origin, the origin of zooxanthellaes and the evolution of the distributional ranges in the horizontal space together with the bathymetric gradient. Ancestral state inference analyses indicated that the ancestor of the group was azooxanthellate, with a three times higher transition rate from az-species to z-species. The depth showed a high phylogenetic signal ($\lambda>0.9$) compared to the latitudinal (λmean = 0.72, λmin = 0.86, λmax = 0.39) and longitudinal distribution (λmean = 0.34, λmin = 0.57, λmax = 0.71). The origin of the group was obtained with a phylogenetic geographical model that accounts for varying speeds of movement and it was placed at 500 m depth (min 31, max 900 m), -5.61 latitudinal degrees (min -44.87, max 27.63) and -54 longitudinal degrees (min -162, max 113). Evolutionary patterns show resilience of the deep species distribution with multiple colonisations of the shallow environment and zooxanthellae gain.

CS26-3

A remotely sensed high resolution map of the giant kelp forest ecosystem in the world ocean

Alejandra Mora-Soto, University of Oxford

Giant kelp (Macrocystis pyrifera) is widely distributed in many temperate coastlines of the world ocean. Despite being a keystone marine species, there is insufficient high-resolution data on its distribution and abundance globally. Here we present the first global map of the distribution of the giant kelp forests of M. pyrifera made employing Sentinel-2 (ESA) imagery, the application programming interface of Google Earth Engine, and a formula and algorithm designed to automatically detect this ecosystem from space or airborne sensors (Mora-Soto et al., in preparation). The result updates previous global estimates and shows the extension of kelp forest patches bigger than one hectare. Their averaged extension is summarized by marine realms, provinces and ecoregions. This biogeographic map is a first step towards a worldwide meta-analysis of kelp forests and their overall status and trends.

CS26-4

Fiddler crabs distribution in Ecuador: using biodiversity as an indicator of ecosystem health

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In 1975, Jocelyn Crane pioneered fiddler crab studies in Ecuador, reporting the occurrence of 14 species from just two coastal locations. Since then, although the Ecuadorean coast has been recognized as one of the planet's biodiversity hotspots, it has lost 20-30% of its natural ecosystems and suffers from extensive pollution. Fiddler crabs occupy riverine and littoral habitats, and are bio-indicators of ecosystem health. Their current status in Ecuador is unknown. Recently, we have documented fiddler crab diversity and distribution along the coast of Ecuador and encountered 28 species at 25 locations between San Lorenzo, Esmeraldas and Puerto Bolivar, El Oro. Nineteen species were collected to the north, and 14 species collected to the south of the Equator. Four were from the Uca genus, 11 from the Leptuca genus, seven from the Minuca genus, and one from the Petruca genus. The ranges of 8 species were extended from Central America and northern Colombia into Ecuador. Although known from Colombia and Peru, we recorded one species for the first time in Ecuador. To put in perspective the all Atlantic coast has 10 species. From our survey, we are filling biogeographical information for this group, in specific for Ecuador. We have elaborated a complete inventory of species diversity, relative abundance and also updated the phylogeny of pacific fiddler crabs. Building upon Crane's legacy, we can now evaluate accurately the conservation status of these Gelasiminae and use them to assess the integrity and health of coastal ecosystems in Ecuador.

CS26-5
Distribución biogeográfica de octocorales de los géneros Muricea y Leptogorgia en el frente ecuatorial del Pacífico Tropical Oriental

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Las poblaciones de corales han sufrido severas reducciones a nivel mundial y los arrecifes de la región del Pacífico Tropical Oriental (TEP en inglés) no han sido una excepción. El grupo de octocorales (Alcyonaceae), siendo el más diverso en ambientes marinos, su distribución va desde aguas intermareales hasta aguas abisales a lo largo de la zona costera del Ecuador. El Frente Ecuatorial, que se caracteriza por encontrarse bajo la influencia de zonas de convergencia de la corriente fría de Humboldt y la cálida de Panamá, produce un marcado gradiente termohalino, además de la influencia de los fenómenos relacionados a los eventos del Niño (ENSO). Estas condiciones oceanográficas modifican las condiciones de la termoclina, imponiendo a los organismos condiciones ambientales extremas. En estudios previos en las Galápagos, se ha demostrado que los octocorales presentan una mayor resiliencia a temperaturas extremas que los corales pétreos. En este sentido, en este estudio se reporta la distribución biogeográfica de octocorales de los 2 géneros más conspicuos para Ecuador que son Muricea y Leptogorgia, basado en registros de especímenes del museo Q-CAZ y del repositorio del CENAIM, estableciendo regiones biogeográficas del frente ecuatorial determinado por sus condiciones ambientales y oceanográficas (temperatura, batimetría, clorofila, corrientes) que influyen directamente en la distribución de especies. Además, se reportó una nueva especie para Ecuador y nuevos registros de distribución de especies, que ayudó a establecer zonas de alto interés por su diversidad y abundancia de octocorales, siendo un estudio base para poder ser replicado en otros grupos de corales.

CS26-6
Diversidad y distribución biogeográfica de ascidias en Ecuador

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El Pacifico Oriental Tropical (TEP en inglés) y su biodiversidad continúan siendo desconocidos. En este estudio se describe la diversidad y distribución de ascidias en la costa ecuatoriana, al extremo sur del TEP, que está influenciada por la convergencia de la corriente fría de Humboldt con las aguas cálidas de Panamá. Estas condiciones oceanográficas crean un gradiente termohalino llamado el Frente Ecuatorial, el cual se subdivide en cinco macrozonas, en sentido norte-sur (Valle y Fuentes 2014). Se conoce que el Frente Ecuatorial posee una gran riqueza de invertebrados sésiles, y que las macrozonas 4 y 5 (Cabo San Lorenzo-Tumbes) serían las más productivas debido a la influencia de la corriente de Humboldt y a las descargas del Río Guayas. Así, en este estudio se reporta la diversidad y distribución de ascidias en las macrozonas 3, 4 y 5 (desde Bahía de Caráquez hasta la Isla Santa Clara). De las 28 especies identificadas, 10 son nuevas especies, y 6 constituyen registros nuevos para el Océano Pacífico. Se registraron 4 especies de manera exclusiva en la macrozona 3, 11 especies en la macrozona 4 (la de mayor mezcla de aguas), y 7 especies en la macrozona 5. La macrozona 4 compartió 4 registros con las macrozonas 3 y 5. Estas observaciones indican que las condiciones oceanográficas influyen sobre el patrón de distribución de ascidias y que las macrozonas de la costa ecuatoriana establecidas por Valle y Fuentes (2014) pueden servir como base para estudios futuros de distribución de otros invertebrados marinos sésiles.

CS27-1

Biogeografía estacional: implicaciones de la variación climática anual en las estrategias ecológicas de actividad y distribución de las especies

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Desde los inicios de la biogeografía, se comenzaron a buscar e identificar los patrones generales de distribución de las especies, resaltando tanto los factores históricos relacionados con la movilidad de la tierra y con la existencia de barreras; así como con factores ecológicos asociados al clima. Para muchos grupos, la dispersión hacia altitudes o latitudes templadas, está limitada por sus estrechas tolerancias fisiológicas a la temperatura; cuya variación anual en regiones tropicales es relativamente baja. La evolución de estrategias conductuales en diversas especies ante las variaciones climáticas estacionales, particularmente en las regiones templadas, donde son mucho más marcadas, es un aspecto que está aún poco estudiado, a pesar de lo relevante considerando las implicaciones biogeográficas y evolutivas. Fenómenos como la migración, la hibernación, así como especializaciones fosoriales, son ejemplos de cambios conductuales y fisiológicos en muchos grupos, para mantener sus nichos ecológicos y sus áreas de distribución. En este trabajo se presentan los resultados de algunos estudios con especies de vertebrados, en donde se analiza la relación de la variación climática estacional y su efecto en los patrones geográficos-temporales de distribución. Se sugiere la hipótesis sobre el origen de diversas estrategias conductuales, en términos del cambio o mantenimiento de sus nichos ecológicos, promovidos por la estacionalidad climática.

CS27-2

Current environmental variables explain the species richness pattern of reef-fishes from the families Chaenopsidae and Labrisomidae in the Atlantic West and Eastern Pacific oceans.

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Several hypotheses have been generated to explain spatial biodiversity patterns at the macroecological scale. The Species-Energy hypothesis states that the latitudinal biodiversity gradient would be generated and maintained as a direct consequence of a large amount of energy available on tropical areas, expecting a positive relationship between species richness and energy availability. To assess this hypothesis, we selected two big biogeographical areas (Tropical West Atlantic - TWA and Tropical East Pacific - TEP) using has study model two wide distributed reef-fishes Families (Chaenopsidae and Labrisomidae) that shows high number of endemic species not shared between these areas. Nine environmental variables were used as proxies of productivity to assess its relationship with species richness (S) based on principal components, OLS and SAR analyses. The results show different variables explaining the richness patterns in both areas; At TWA, 90% of the increase in species richness was explained by temperature and pH; and at TEP, just 24% of species richness variance was explained by temperature, but primary productivity (pp) and pH explained together 94% of increase of S. These results raised the importance of the main proxies of ocean productivity (i.e. temperature and pp) to explain the S, supporting the species-energy hypothesis in both areas. These results indicate that highest biodiversity of reef-fish species is distributed in energetically optimal areas in both biogeographical areas, operating as environmental constrains for the species distribution.

CS27-3

Drivers of acoustic variation at multiple evolutionary scales in glassfrogs

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Here we use multiple phylogenetic comparative approaches to test the impact of acoustic adaptation hypothesis (AAH, regarding vegetation and temperature) and the acoustic character displacement in the divergence of advertisement calls among 97 glassfrog species and 17 recently divergent lineages of one monophyletic widespread clade (Hyalinobatrachium fleischmanni sensu lato). We found that spectral parameters of the call do not behave like expected under traditional AAH regards vegetation density, but temporal parameters (Number of notes and Pulse Rate) do follow the AAH as expected. Regarding temperature, only recently divergent lineages living in warmer localities display shorter calls; hence, metabolic rates and air temperature drives advertisement calls only at small evolutionary scales, but it is not a significant driver of call evolution at macroevolutionary scales. Finally, call convergence among sympatric species and recently divergent lineages was detected, while reproductive character displacement occurs in a handful of cases and it is only detected when the species in sympatry are close related, suggesting that species in communities/assemblages trend to have the same call parameters by the pressure of same environmental drivers and likely the species use alternative strategies (ecological, spatial or temporal) to avoid heterospecific matings.

CS27-4

Using gradient metrics to determine landscape traits that enhance biodiversity

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Geodiversity – variation in Earth's abiotic processes and features – is one of the primary determinants of biodiversity patterns. However, there are many metrics for geodiversity, each representing different facets of landscape heterogeneity. Gradient surface metrics are increasingly being used to quantify landscape diversity, but require proprietary software for their calculation. We introduce a new R package, geodiv, for calculating gradient metrics, relate these metrics to more familiar ways of characterizing landscape heterogeneity, and examine a case study for how these metrics may be used to understand tree biodiversity patterns. For two regions in Oregon, USA and Ecuador, we ask, (1) which metrics are most relevant for predicting biodiversity? and, (2) how does the grain size used in metric calculations alter geodiversity patterns, and biodiversity predictions?

We calculate geodiversity using satellite products representing topography, climate, and geology. For each product, we calculate geodiversity around forest inventory plots in Oregon (82 plots) and Ecuador (28 plots) at two grain sizes using gradient surface metrics, and other metrics such as standard deviation and topographic roughness index. We compare how the metrics represent each region, and discuss the potential for each metric to distinguish ecologically unique areas from the standpoint of biodiversity conservation. Using these metrics, we then model tree species richness in each region with generalized linear models. We find that while the metrics do not explain variation in biodiversity at larger scales and grain sizes, they are useful at smaller scales and grain sizes and in models with additional predictor variables.

CS27-5

Geography and drivers of genetic diversity in terrestrial mammals

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Genetic diversity represents the biosphere's fundamental 'information bank', defining its capacity to persist and evolve under global environmental change. Since genetic diversity is a basic component of biodiversity, knowledge on its interactions with other biodiversity dimensions and its main drivers is vital in preserving life's integrity. Here we assemble a dataset of georeferenced mitochondrial sequences (n = 54,786) representing over 1000 species of terrestrial mammals to test for the role of evolutionary rates (evolutionary speed hypothesis), Late Quaternary climate stability and human footprint in explaining the global genetic geography of terrestrial mammals. We show that deep time evolutionary dynamics, as shown by variation in the accumulation of phylogenetic clades across the planet, largely explain the global geography of genetic diversity, in accordance with the evolutionary speed hypothesis. Additionally, and consistent with theoretical expectations, regions which experienced temperature stability and precipitation variability harbor today higher genetic diversity. Finally, we identify a significant co-occurrence between intraspecific variation and both historical and recent human footprint, indicative of the ever-increasing human activities in biodiversity rich regions of the globe. In summary, we reveal that deep-time evolution molds the global geographical template for genetic diversity, a latitudinal gradient, with both climate change and anthropogenic impacts leaving footprints at regional scales. These findings provide insights on the mechanisms that generate and maintain earth's biodiversity, and further emphasize the role of evolutionary perspectives in nature conservation.

CS27-6

Ecological specialization and Macroevolutionary patterns and process: First analitical approach of resource-use hypothesis in american amphibians.

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The resource-use hypothesis proposed by E. Vrba (1992) predicts that specialist species have higher speciation and extinction rates than generalist. Due to their high susceptinility to resource restrictions, make them more vulnerable to enviromental changes, vicariance and directional selection evolutionary process. We test subsidiary predictions of this hypothesis using the biomic specialization index (BSI) for american amphibian species (6394), which is based on biogeographical range within different climate zones. Our results are consistent with the assumptions of the hypothesis, which predicts: 1. A high frequency of stenobiomic species, 2. A relationship between dietary spectrum and biome specialization, 3. Extreme climatic zones will presented higher incidence of biomic specialists. We found that the tropical rain forest are a important sources of species in several groups, which is due to the large size of these biomes, the high incidence of climatic cycles on them, and the physiological restrictions to wet enviroments, which makes these ecosystems keys to understand the amphibian evolution and promote conservation strategies. Other derivations from predictions of the hypothesis tested here like the outstanding presence in temperate evergreen forest are probably due to the incidence of andes orogeny process in South American and the influence of the Great American Biotic Interchange. The hypothesis and related habitat-theory suggest that a key to present-day macroecological patterns is found in the past: in the history of turnover (speciation, extinction) of clades, tools that can help us in future perspectives to protect habitats and ecosystems for conservate species during current climatic change.

CS28-1

Stream capture and vicariance events in the Northern Andes explains the genetic discontinuity of Hoplias malabaricus (Bloch, 1794) (Teleostei: Erythrinidae) in the Magdalena River

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Hoplias malabaricus is a species complex with a wide distribution at the Neotropical region, from Panama to Argentina. Cytogenetic and molecular allowed accessing the diversity within H. malabaricus in the cis-Andean region, but the trans-Andean region remains unknown. The Magdalena River is the largest trans-Andean basin, separated from the Amazon-Orinoco drainages at the final uplift pulse of the Eastern Cordillera, during the middle Miocene. We aimed to trace the influence of the Northern Andes uplift in the diversification of H. malabaricus. Using mitochondrial and nuclear markers, we inferred phylogenetic relationships and estimated divergence times among H. malabaricus lineages in Northern South America and Central America, with an emphasis on the Magdalena River Basin. We compared three alternative biogeographical scenarios using an Approximate Bayesian Computation framework (ABC) to test for vicariance (paleogeographic hypothesis) and colonization events (hydrogeological hypothesis or stream capture). H. malabaricus samples from Magdalena River do not form a monophyletic clade. Upper and Middle Magdalena individuals cluster with Colombian Pacific and Central America samples, while Lower Magdalena samples group with other Caribbean, Trinidad-Tobago, Guianas, Orinoco and Amazon basins. The ABC analysis indicated that the diversification of H. malabaricus in the Northern Andes involved initial colonization by a stream capture from cis-Andean + Caribbean+Lower Magdalena to trans-Andean basins (Upper and Middle Magdalena), followed by population expansion of the trans-Andean group. The current diversity of H. malabaricus in the Magdalena River exhibits a sharp discontinuity resulting from a stream capture (followed by regional vicariance events) associated with the Northern Andes uplift.

CS28-2

Biogeographical legacies constrain invertebrate and diatom metacommunity structure within a heterogeneous basin

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The relevance of biogeographic and evolutionary processes on community- and metacommunity- dynamics has been long debated; particularly when the study systems are stream networks. The greater connectedness among network tributaries has led to postulate present-day dispersal and environmental conditions as the major drivers of species diversity and distribution. Here, by systematically sampling diatoms and invertebrates in near-pristine streams from the Orinoco basin, we provide evidence on how biogeographical contingencies are shaping the structure and dynamics of stream metacommunities. Our overall results show that historical events (e.g. Andean uplifts and the expansions and retreats of glaciers) have shaped distinct regional pools whose distribution resembles the ecoregionally-patched distributions described by Von Humboldt or Van der Hammen. The statistical models elaborated on these communities suggest that the occurrence of distinct regional pools can override the possible effects of the contemporary spatial structure and environmental heterogeneity within the basin. Collectively, our results indicate that species biogeography is crucial to understand biodiversity patterns at local and regional scales; and therefore, metacommunity structure and dynamics. These results have important implications, as they suggest that the basin scale may not be the most appropriate for biodiversity conservation and stream management.

CS28-3

Pleistocene river systems and frogs: understanding evolutionary history of the Sumatran ranids with gastromyzophorous tadpoles

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The influence of river systems on the distribution and genetic structure of species has been investigated in various taxa and regions. In most cases, the influence of river systems on genetic diversity depends on taxa specific life history traits as well as other geographic factors. Here, we assess the role of the Pleistocene river systems of the Sunda region (with a focus on the island of Sumatra) in shaping the evolutionary history frogs′ genera (Huia and Sumaterana) that are highly dependent on cascading stream habitats during their larval_x000D_
stage. Our phylogenetic analyses demonstrated that Pleistocene river systems had no congruency with the current distribution patterns of Huia and Sumaterana. Our time divergence analyses estimated these frogs to have colonized Sumatra much earlier than the occurrence of the known drainage systems in the Pleistocene. Interestingly, both genera are genetically structured into northern and southern lineages on the island of Sumatra, which may suggest that the genetic segregation observed today dates back to now connected_x000D_
Sumatran precursor volcanic islands. Our data further corroborate the current underestimation of biodiversity on Sumatra and show that frogs of the genus Huia in Sumatra and Java are more diverse than currently known.

CS28-4

Global patterns of coupled genetic diversity and structure across freshwater insect species

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Comparative phylogeography is a fundamental field for understanding the factors driving intra-specific evolution, yet research has remained mostly regional using few co-occurring taxa. Here, we implement a macrophylogeographic approach assessing 33 species belonging to Coleoptera and Ephemeroptera freshwater macroinvertebrate lineages across Neotropical Panamanian regions and Mediterranean, Atlantic, Continental, Alpine and Boreal European regions in order to test the role of biogeography and dispersion in shaping global patterns of genetic variability. At the global scale, a positive relationship between genetic diversity and structure is found, with tropical species showing higher values than their temperate counterparts, likely due to long-term environmental stability. Within Europe, the low genetic diversity found is independent of latitude and the varying genetic structure across species suggests persistent demographic fluctuations most likely due to long-term and present-day habitat instability. Beyond the clear deterministic patterns in the Neotropics, temperate regions revealed a local scale inter-species idiosyncrasy and rejected the non-neutrality of mtDNA for explaining the global pattern of genetic diversity.

CS28-5

Landscape Controls on River Networks and Biodiversity

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The evolutionary diversification of continental species is constrained by landscape structures that change over a wide range of spatial and temporal scales. River capture is a landscape evolution process with powerful capacity to affect diversification in obligate aquatic taxa. By altering connections among portions of fluvial networks, river capture changes the areal extent and degree of isolation of watershed catchments, with direct influences on the macroevolution processes of geographic range evolution (dispersal), lineage splitting (speciation), and linage termination (extinction). We investigated the landscape conditions that lead to river network reorganization and continental aquatic biodiversity using a new modeling tool, SpeciesEvolver, that exists to explore questions of landscape-life coevolution. This tool is included in Landlab, a toolkit for researchers to build models of Earth surface processes. In this study, we simulated landscape evolution under perturbations characteristic of natural climatic (base level fall) and tectonic (rock block-faulting) forcings. Large-scale river network reorganization events occurred within a limited combination of landscape conditions. Speciation increased with the landscape conditions that led to large-scale drainage reorganization, and the widely reported power law relationship observed in natural systems between the number of species and the area that these species occupy emerged during model runs. Our results illustrate the important role that river network dynamics have on the evolutionary origins and ecological maintenance of high diversity of continental aquatic ecosystems. We present an approach for future studies using SpeciesEvolver to model geographic landscape heterogeneities and ecophysiological (functional) differences among taxa.

CS28-6

Efectos ecológicos y biogeográficos en la diversidad de anfípodos en ríos andinos del Ecuador.

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Los anfípodos del género Hyalella (Amphipoda: Hyalelidae) han sido reportado en distintas zonas biogeográficas, principalmente en la región andina; sin embargo, su diversidad es poco conocida. Este estudio pretende determinar el origen de la diversidad de Hyalella en diferentes zonas biogeográficas del Ecuador, en una marco filogénetico, y con un amplio muestreo local y regional. Encontramos que las especies de Hyalella de los ríos andinos tiene diversos orígenes geográficos; también determinamos que, en la cuenca del río Cachiyacu, los ríos de origen termal presentas especies que no están cercanamente relacionadas a los ríos no termales aledaños. A diferencia de las Hyalella de Ecuador continental, el grupo de Galápagos es monofilético y con distancias genéticas considerables a las especies examinadas del continente. Estos resultados nos permiten tener una primera aproximación a la complejidad de la composición de comunidades de Hyalella en América del Sur, con interesantes interacciones geográficas, de colonización y adaptación.

CS28-7

Distribución espacial y relaciones interespecíficas de la macrófita acuática Ranunculus limoselloides con otras plantas en un gradiente de elevación en páramos venezolanos

Milena Cardenas, Universidad Pedagógica y Tecnológica de Colombia; Luis Llambí, ICAE-Universidad de los Andes; Fermin Rada, Universidad de los Andes Venezuela; Carmen Azocar, Universidad de los Andes Venezuela

Estudios de interacciones planta-planta en alta montaña tropical se centran en especies terrestres, siendo así en especies acuáticas. Ranunculus limoselloides es una hierba acuática andino-tropical. Plantear evaluar si existen diferencias en las relaciones espaciales interespecíficas de R. limoselloides con otras macrófitas en un gradiente de elevación y entre épocas climáticas? Si la facilitación entre plantas está asociada con el aumento de condiciones extremas, las hojas flotantes R. limoselloides deben beneficiarse de las plantas sumergidas, disminuir la radiación y aumentar la oxigenación de sedimentos mediante la raíz. Se evaluaron las relaciones específicas de R. limoselloidescon otras macrófitas a 3550m, 3900m y 4200m en páramos venezolanos, en dos épocas climáticas. Se comparó la cobertura y la diversidad de especies con los números efectivos de la diversidad entre parcelas bajo y fuera de la macrófita. Se estimó el tipo de interacción con el índice de interacción (RII). Para establecer si existen diferencias significativas entre situaciones, se hace un análisis de varianza por permutaciones. Se registraron 17 especies de macrófitas, las más comunes fueron Crassula venezuelensis , Isolepis inundata e Isoetes andina ; La riqueza y la diversidad de macrófitas disminuyó con la elevación. Según el IIR en la época seca en Mucubají (3550m), se produjo una interacción positiva positiva entre R. limoselloidesy la riqueza y la época en la época húmeda. En Los Guaches (3950m) se presento Una interaction negativa Significativa al Igual Que en Piedras Blancas (4250m), ESTO indicaría Que un alcalde Elevación La Cobertura de R. limoselloides Tiene Un efecto negativo

Concurrent Session 29: Methods in Biogeography

CS29-1

New satellite observations for developing cloud climatologies at both high spatial and high temporal resolution for biogeographical applications

Michael Douglas, Retired from NOAA Research

Recent publications (Wilson and Jetz, 2016, Douglas et al. 2016) have discussed the potential biogeographical value of MODIS-based cloud climatologies generated from twice-daily imagery with relatively high spatial resolution (250m – 1km). Although these climatologies have global coverage, their utility depends on the assumption that the twice-daily MODIS observations represent a true climatology of cloudiness over all daylight hours. As most tropical coastlines and mountainous areas show a strong diurnal cycle of cloudiness, mid-day satellite cloudiness estimates may not accurately reflect nighttime and early morning cloudiness that can be strong contributors to fog drip. Regions where fog drip may be critical range from tropical cloud forests to slopes along hyper-arid coastlines of tropical and subtropical deserts.
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Developing cloud climatologies over the entire daytime diurnal cycle has become more accurate with the recent launching of improved geostationary satellites that have both higher (500m) spatial and temporal (10-15 min) resolution than previous satellites. Three such satellites are now over the Equator at 140˚E, 75˚W and 137˚W.

In celebration of Alexander von Humboldt's exploration of the tropical Americas and his interest in making climatological measurements, my presentation will focus on cloud climatologies generated for select Neotropical areas (e.g. the Venezuelan tepuis, the eastern slopes of the Andes, and the coastal lomas from Ecuador to Chile) using imagery from the new GOES-16 satellite. The results will be compared with Worldclim products and existing MODIS-cloud climatologies. Finally, I discuss how these products can be improved for applications to biogeography through in-situ calibration efforts.

CS29-2

Delineating parapatric ranges using species distribution models and support vector machines: an example with three-toed sloths

Cecina Babich Morrow, American Museum of Natural History; Peter Galante, American Museum of Natural History; Jamie Kass, City University of New York; Robert Anderson, City College of CUNY; Mary Blair, Center for Biodiversity and Conservation, American Museum of Natural History

Despite growing understanding that biotic interactions may impose important constraints on distributional limits, species distribution modeling (SDM) applications typically focus on abiotic variables without explicitly accounting for biotic interactions. One example of biotic influences on geographic ranges is the common phenomenon of closely related parapatric species replacing each other across geography. We sought to address whether incorporating biotic information via post-processing SDM outputs would improve distributional estimates for three sloth species in the genus Bradypus with parapatric ranges. In a novel approach, we used support vector machines (SVMs) to spatially classify map cells, indicating which of the species is most likely to be present. We then use the SVM output to mask the SDM suitability predictions by removing pixels that the SVM indicated as part of the range of a different species. We implemented two different types of SVMs: 1) purely spatial SVMs, using only occurrence data, and 2) spatial + environmental SVMs, using occurrence data in conjunction with SDM-predicted suitability values. After using the SVM outputs as masks, we found that both SVM implementations were less likely to include occurrence points of congeners in species' predicted distributions than the unmodified SDM predictions. Further, we found that the spatial + environmental SVM resulted in distributional delimitations for contact zones that best matched our ecological expectations for these species. This approach could be widely applied both to pure macroecological studies as well as conservation and management, including IUCN Red Listing.

CS29-3

Expanding Wallace species distribution modeling software to support national biodiversity change indicator calculations

Peter Galante, American Museum of Natural History; Jamie Kass, City University of New York; Beth Gerstner, Michigan State University; Gonzalo Pinilla Buitrago, City College of New York; Matthew Aiello-Lammens, Pace University; Ned Horning, American Museum of Natural History; Peter Ersts, American Museum of Natural History; Robert Anderson, City College of CUNY; Mary Blair, Center for Biodiversity and Conservation, American Museum of Natural History; Cory Merow, Yale University; Jorge Velásquez-Tibatá, Instituto Humboldt

Challenges for conservation are often mitigated through policy changes at various levels. Effective policy responses to changes in biodiversity are facilitated with analytic tools that leverage biodiversity observations. Often, researchers and practitioners rely on graphical user interfaces that lack flexibility and/or transparency, or on command-line interfaces that require knowledge of a programming language. Wallace is a new modular, R-based, open-source software that implements species distribution modeling (SDM) and lowers these entry barriers. We are currently developing R packages that serve as tools for biodiversity conservation and will be integrated as modules in Wallace′s workflow. These tools will allow users to estimate species′ current ranges by processing SDM output using in situ observations of species′ occurrence and ex situ remotely sensed data. From those estimates, users will then be able to calculate biodiversity change indicators such as range size, the upper bound of area of occupancy, percent suitable land cover, or ongoing and even projected trends under future scenarios. Development of these tools will also directly enhance and leverage the Colombia Biodiversity Observation Network by integrating Wallace with BioModelos, an existing tool in Colombia that enables expert validation of species range estimates. We expect this expansion of Wallace will lessen current challenges for linking the application of SDM best practices to biodiversity conservation decision-making, as well as facilitate responsible reporting on biodiversity, leading to effective policy changes.

CS29-4

A biogeographic event model under a dynamic geography

J. Salvador Arias, Unidad Ejecutora Lillo (CONICET); Facultad de Ciencias Naturales (Universidad Nacional de Tucumán)

Although plate tectonics is an important cornerstone in modern phylogenetic biogeography, it is currently used either as subjective dispersal parameter between poorly predefined areas, or as a post-hoc inference after the analysis. Here, a new phylogenetic biogeography method is presented. The method is (1) based on cladogenetic (vicariance, full copy sympatry, point sympatry, and jump dispersal), and anagenetic events (dispersal, extinction); (2) it is explicitly geographic, using a geographic data model (a raster) and ranges of any size in both terminals and internal nodes, instead of predefined areas; (3) the geography is dynamic, so the position of each pixel is estimated using an explicit tectonic model, which might include paleogeographic data (emerged land, epicontinental seas, glacial ice sheets). Implementation details, an empirical example, and potential expansions are also discussed.

CS29-5

Mining literature to unlock primary biodiversity data: Biodiversity Observations Miner v.1.1.

Gabriel Muñoz, Concordia University; W. Daniel Kissling, University of Amsterdam; E. Emiel van Loon, University of Amsterdam

Research in Ecology and Biodiversity science is increasingly demanding for larger amounts of standardized biodiversity data on species (e.g. biotic interactions, functional and/or behavioral traits). However, a considerable portion of such primary biodiversity data still remains digitally stored and often locked inside pdf files on the internet. The mobilisation and interoperability of these data will contribute towards open digital access to global biodiversity knowledge as well as benefiting synthetic, large-scale approaches on biodiversity research. Nevertheless, the amount and diversity of digitally published literature pose many challenges for knowledge discovery and retrieval. Text mining has been extensively used for data discovery tasks in large quantities of documents, but their use has been rather limited in Ecology compared with other sciences. As such, text mining workflows are a promising alternative to retrieve primary biodiversity data from literature and make it available, digitally accessible and machine-readable. Here, we present an updated version of a novel, open source text mining tool, the Biodiversity Observations Miner (BOM). This web application, written in R, allows the semi-automated discovery of punctual biodiversity observations associated with the scientific names present inside a corpus of scientific literature. This tool aims to increase the digital mobilisation of primary biodiversity data and is freely accessible via GitHub.

CS29-6

Testing GDMs as a tool to find new species: a case study with eBird data in Colombia

Jorge Velásquez Tibatá, The Nature Conservancy Colombia

GDMs (generalized dissimilarity models) are a powerful modeling tool to predict the expected compositional turnover among site pairs based on their differences in environmental conditions. This tool has been used in a variety of applications, such as the identification of drivers of beta diversity, the delineation of biogeographic regions and the identification of gaps in protected area networks. Due to its ability to identify areas that are highly dissimilar to already sampled sites, it's been also used to suggest sites that are most likely to harbor new species, either to an area of interest or even to science. However, actual tests of this hypothesis are lacking in the literature. I used data from eBird from years 2015 to 2018, to develop yearly GDMs that were used to estimate the expected compositional dissimilarity between sampled and unsampled areas across Colombia. I demonstrate that unsampled sites with predicted high dissimilarities in years 2015-2017 had three times more probability of harboring previously unrecorded species in the following year than sites with low dissimilarities. I also demonstrate that sampling sites in a way that maximizes dissimilarities at each step reaches the yearly species richness asymptotic value much faster that sampling sites at random. This research, and its accompanying R package, may aid in planning future expeditions aiming to complete gaps in taxonomical and distributional knowledge.

CS29-7

Biogeography of Atacama: from the naturalists' views to modern pattern analysis

Andres Moreira-Munoz, Instituto de Geografia, Pontificia Universidad Catolica de Valparaiso; Vanezza Morales, Instituto de Geografia, Pontificia Universidad Catolica de Valparaiso; Melica Munoz-Schick, Museo Nacional de Historia Natural; Rodrigo Villaseñor, Universidad de Playa Ancha

The Atacama Desert is considered one of the planet's most arid desert, however, it has long attracted botanists and naturalists looking for botanical/biological treasures. Some of the naturalists following Humboldt steps C. Darwin, E. Poeppig, Werdermann, Philippi (father and son), I.M. Johnston, among others. They could report a biota of enormous evolutionary interest due to the remarkable adaptations to aridity, encompassing high levels of endemism at different taxonomic scales. Around 23ºS there is a boundary between two biodiversity hotspots: the Tropical Andes and Mediterranean Chile: it is interesting to evaluate the cohesion of both biotas, their levels of endemism and replacement; and the presence of microhotspots. This in the framework of the study of systematization of a "Rand Biota" of Atacama. We selected disjunct desert plant groups for the pattern analysis, at the base of two scales: continental scale (antitropical disjunction, encompassing genera such diverse like Hoffmannseggia, Larrea, Glandularia, Cistanthe, Cryptantha), and the intracontinental scale for which the most diverse family is the Asteraceae. The database comprises 5,016 georeferenced records, which correspond to unique locations per taxon (at a specific or infraspecific level). The geographical distribution of the collections allows the identification of two distinctive floristic centers of richness and endemism; one at 24-25 ° lat. S, for the altiplano; the second one from 24-32 ° lat. S. The area shows a degree of superposition with the boundary between two biodiversity hotspots. Other biotic groups such as pollinators are being analyzed for informing conservation actions. Fondecyt 1180211.

POSTER SESSION

Biodiversity Patterns and Maintenance

01-BPM

Determinants of distribution of a montane grassland endemic bird

Abhimanyu Lele, University of Chicago; V.V. Robin, Indian Institute of Science Education and Research (IISER) Tirupati; M Arasumani, Indian Institute of Science Education and Research (IISER) Tirupati; CK Vishnudas, Indian Institute of Science Education and Research (IISER) Tirupati; Devcharan Jathanna, Wildlife Conservation Society

Tropical montane habitats support high biodiversity, and are hotspots of endemism. Grassland habitat is an integral component of many such landscapes. The factors determining persistence of specialist species in montane grasslands experiencing loss and fragmentation are poorly known. The montane grasslands of the Shola Sky Islands in the Western Ghats have seen extensive land-use change over anthropogenic timescales, including losses to woody invasives. We studied the relationship between the Nilgiri pipit Anthus nilghiriensis, a threatened endemic bird of these montane grasslands, and its habitat across most of its global distribution. We conducted 663 surveys in 170 sites and used both single-season occupancy modelling and N-mixture modelling to account for processes influencing detection, presence, and abundance. We found elevation to have a strong positive influence on species presence and abundance, making it vulnerable to climate change. We also detected effects of patch size and isolation, as well as of characteristics related to microhabitat structure, including a negative influence of invasive woody species on Nilgiri pipit abundance. The species was absent in grassland remnants created by century-old land-use change, while it persisted in low-density populations in remnants of recent fragmentation, suggesting an extinction debt. Our findings indicate a species distribution shaped broadly by bioclimatic factors and geography, and underscore a need to conserve habitat structure within montane grasslands, as well as to control and reverse the spread of exotic woody invasives to preserve the grasslands themselves and the specialist species dependent upon them.

02-BPM

Dinámica de los nichos climáticos en las ranas del género Pristimantis (Anura: Craugastoridae) de la Cordillera Oriental de Colombia

Aldemar Acevedo, Departamento de Ecología, Pontificia Universidad Católica de Chile; Eduardo Palma, Departamento de Ecologia, Universidad Catolica de Chile; Andrew Crawford, Universidad de los Andes; Angie Tovar, Universidad de Los Andes

El Neotrópico y en especial los Andes tropicales representan una de las zonas geográficas más interesantes en términos de evolución biológica. No obstante, para regiones como la Cordillera Oriental de Colombia los procesos evolutivos y ecológicos correspondientes a la ocupación de diferentes nichos climáticos aún no son claros. Esto último se evidencia para las ranas del género Pristimantis, las cuales son las más diversas del Neotrópico. En este sentido, evaluamos la dinámica evolutiva del nicho climático para 65 especies de Pristimantis de las aproximadamente 100 que se distribuyen en la Cordillera Oriental. Se realizó una reconstrucción filogenética mediante máxima verosimilitud usando cuatro genes mitocondriales y dos nucleares. Se obtuvieron los registros geográficos de todas las especies y se solaparon sobre capas climáticas para extraer los valores ambientales. Para evaluar la dinámica de los nichos se realizaron métodos filogenéticos comparativos, y se estimó un modelo evolutivo que se ajustara mejor a los nichos climáticos de las especies a lo largo de la filogenia. Nuestros resultados sugieran que la evolución del nicho climático en general sigue un modelo de Ornstein–Uhlenbeck, por lo cual, se sustenta un patrón de conservadurismo filogenético de los nichos a lo largo de múltiples ejes ambientales sobre todo de las especies alto andinas. No obstante, se evidencian solapamientos parciales de los nichos climáticos para las especies distribuidasentre las zonas bajas y medias. Por lo tanto, se refuerza la importancia de los nichos climáticos y su evolución en la diversificación de las especies de Pristimantis y posibles alteraciones en su distribución por efectos del cambio climático.

03-BPM

Patrones de distribución del hongo patógeno Batrachochitriun dendrobatidis en diferentes biomas del nororiente de los Andes de Colombia

Aldemar Acevedo, Departamento de Ecología, Pontificia Universidad Católica de Chile; Diego Lizcano, The Nature Conservancy

Las evidencias de la disminución global de anfibios se han presentado desde hace más de dos décadas, y múltiples factores se han sugerido como las principales causas de dicha disminución. No obstante, el descubrimiento del hongo patógeno Batrachochytrium dendrobatidis (Bd) dio luces sobre una problemática en términos de conservación que se ha estado expandiendo a nivel global. Para Sur América, se ha propuesto que Bd presentó múltiples periodos de introducción probablemente entre la década del 70 y 80s con una posterior diseminación a lo largo de la cordillera de los Andes. En este trabajo se evaluaron los patrones de distribución de Bden una la región Andina Nororiental de Colombia dónde se han reportado más casos de infecciones por chitridio. Se realizaron modelos lineales generalizados mezclados (GLMM) a partir de 150 muestras diagnosticados para Bd, los modelos fueron construidos a partir de 88 datos positivos (presencias) y 62 datos negativos (ausencias), obtenidos a partir del diagnostico de 40 especies de anfibios distribuidas entre los 100 y 3700 m.sn.m. Se evaluaron 22 predictores ambientales de los cuales se usaron 16 predictores no correlacionados. Se aplicó un procedimiento de regresión a pasos para seleccionar variables en los modelos usando el Criterio de información de Akaike (AIC). El modelo final predijo geográficamente la infección del hongo como una relación entre la precipitación media anual y la temperatura, con un comportamiento particular para cada género de anfibio evaluado.

04-BPM
Endemics dominate Indo-Pacific bird communities

Andrew Reeve, Natural History Museum of Denmark

The positive relationship between range and abundance is a widely accepted macroecological pattern, which has been reported across a wide variety of spatial scales and organism groups. However, recent studies from isolated tropical regions have reported negative or neutral relationships. Potentially, the geographic isolation and environmental stability of such areas promotes narrow specialization in species, breaking the typical positive relationship. To test this, we surveyed 11 bird communities in mature and degraded forest across four islands in eastern Indonesia and New Caledonia, amounting to over 10,000 individual bird identifications. Linear mixed effect models were employed to measure the relationship between local abundance and global range size. The range size-abundance relationship was negative across all combined mature and degraded forest communities. Negative relationships were found in all individual degraded forest plots, with small-ranged species dominating communities. This indicates that environmental stability and narrow specialization do not cause the observed negative relationships. Instead, we found that common endemic and near-endemic species with broad habitat tolerances drive these patterns. A separate analysis of another group's large New Caledonia bird point-count dataset revealed similar results: community dominance across a spectrum of forested habitats by locally widespread endemic species with broad habitat niches. We suspect that water barriers inhibit dispersal and range expansions by these locally dominant endemic birds, highlighting the potential for geographic isolation to break the positive relationship between local range size and global abundance.

05-BPM
Latitudinal Phylogenetic Diversity gradient of the woody plants associated to the Neotropical Seasonally Dry Forests

Axel Arango, Instituto de Ecologia A.C.; Fabricio Villalobos, Instituto de Ecologia, A.C. (INECOL); Roger Guevara, Instituto de Ecologia, A.C. (INECOL); Andres Lira-Noriega, Kansas University; David Prieto-Torres, Universidad Nacional Autónoma de México

Several studies have suggested that, contrary to most other biomes on Earth, the Neotropical Seasonally Dry Forest (NSDF) presents an inverse latitudinal diversity pattern. Here, we used the most recent species-level megaphylogeny of seed plants and the DRYFLOR dataset to evaluate such inverse gradient on the woody plants of the NSDF considering phylogenetic diversity (PD). Also, we tested the Pleistocene climatic refugia hypothesis as an explanation for the current geographic diversity pattern of the NSDF. To do so, we considered the climatic instability since the Last Glacial Maximum (LGM) and the residual PD (rPD), which controls for the effect of species richness on PD. We found that PD of the NSDF woody plants increases away from the equator and that climatic instability fails to explain this pattern. Instead, current and past precipitation regimes were positively related to the rPD pattern suggesting that environmental filtering could be driving the NSDF geographic diversity patterns.

06-BPM
Comparative phylogeography of two lizard species with disjunctive and overlapped distributions in the Amazon basin

Carolina Farhat, University of Sao Paulo; Sergio Marques de Souza, Universidade de São Paulo, Zoology Department, Herpetology Lab

Present biogeographic patterns can potentially track millions of years of space modifications that ultimately resulted in the species diversity as we know today. Therefore, species with disjunctive distribution patterns can be an evidence of mainly two possible past scenarios: (1) an ancestral population with extensive and continuous range area that was posteriorly separated by a natural barrier; (2) an ancestral population with a more restricted range area followed by a dispersion of a group of individuals to a new area. In both scenarios the consequences in long-term are distinct molecular signals on those separated populations that can differ according to the biogeographic scenario. In this work we intend to analyze molecular signals of two lizard species from the Amazon basin, both with similar disjunctive east-west patterns: Potamites ecpleopus and Anolis trachyderma. Our aim is to test two possible biogeographic events – Pleistocene refuge (i.e. vicariant scenario) and the lake Pebas complex (dispersal scenario) –

that could have led to the observed distributions patterns. We set up a data set composed of 42 samples of P. ecpleopus and 55 of A. trachyderma used for basic statistics, phylogenetics reconstructions and molecular dating to test for possible time congruence between both species. All molecular analyzes and phylogenetic reconstructions are based on the sequencing of 12S mtDNA loci, but for more substantial results we will make a next gene sequencing (NGS) and use the method of Approximate Bayesian Computation (ABC) to test different scenarios for both species diversification.

07-BPM

Análisis de la influencia de las barreras geográficas en la subespeciación de Saltator striatipectus

Catalina Campuzano, Universidad San Francisco de Quito; Jaime Chaves, Universidad San Francisco de Quito; Elisa Bonaccorso, USFQ; Juan Freile, Comite Ecuatoriano de Registros Ornitológicos

El Saltador Rayado, Saltator striatipectus, es una especie de ave neotropical ampliamente distribuida desde Costa Rica hasta Perú, que presenta gran diferenciación geográfica en plumaje. Actualmente, se encuentran descritas 10 subespecies. En la zona en la que habita esta ave existen importantes barreras geográficas, tales como la cordillera de los Andes o el istmo de Panamá, los cuales ejercen un fuerte efecto en la tasa de especiación dentro de la región. Nuestro trabajo se centra en conocer las diferencias genéticas que existen entre subespecies y analizar cómo las barreras geográficas facilitaron diferenciación de las distintas poblaciones. Para esto se realizó una construcción filogeográfica con muestras tomadas en diferentes regiones que abarcan Costa Rica, Panamá, Venezuela, Colombia, Perú y Ecuador, analizando los genes mitocondriales ND2 y citocromo b. Análisis preliminares muestran que las subespecies coinciden con grupos genéticamente bien estructurados y definidos en las diferentes regiones que abarca el rango de la especie.

08-BPM

The “Crayfish Kingdoms” of Western Andes: High genomic structure and lineage diversity in Parastacus Pugnax (Poeppg 1835)

Christian Muñoz-Escobar, Departamento de Zoología. Facultad de Cs. Naturales y Oceanográficas. Universidad de Concepción; Carlos Muñoz-Ramírez, CIBAS. Facultad de Ciencias. Universidad Católica de la Santísima Concepción; Lorena Rivera, Depto. Zoología. Fac. Cs. Naturales y Oceanográficas. Universidad de Concepción; Melissa Pincheira-Solís, Depto. Zoología. Fac. Cs. Naturales y Oceanográficas. Universidad de Concepción. Chile; Karina Vega-Drake, Depto. Zoología. Fac. Cs. Naturales y Oceanográficas. Universidad de Concepción; Guillermo D'Elía, Universidad Austral de Chile; Pedro Victoriano, Depto. Zoología. Fac. Cs. Naturales y Oceanográficas. Universidad de Concepción. Chile

Parastacus pugnax is an endemic crayfish species from central Chile with a fragmented distribution between 32°S and 38°S. One of its main traits is its ancient evolutionary origin, whose populations had been exposed to a number of ecological and historical factors. Preliminary genetic studies have shown high levels of genetic divergence among populations, suggesting the probable presence of cryptic species within the pugnax-lineage. With recent advances of sequencing methods (e.g. NGS) it is possible to have a large genomic coverage to answer such issues. Given the habitat requirements of the species and the landscape discontinuity, we expect limited connections in terms of gene flow, and therefore, highly structured populations at the scale of basins. We obtained genomic information from 95 individuals and 42 localities across the distributional range. Morphological variation for main clades was analyzed too. Our results suggest the existence of at least 4 deeply diverged and allopatrically distributed lineages. The structure analysis did not detect any sign of admixture throughout the distribution range, showing a strong geographic structuring of genetic variation. Our morphological data suggest evidence of differentiation between the clades, which seem to indicate that the shape of chelipeds could be informative for differentiation. These results suggest the occurrence of cryptic species beyond the previous hypothesized taxonomic units for Parastacus and highlight the complexity of its evolutionary history. Fondecyt 1161650

09-BPM

Biogeography of southern Ecuador from a herpetological perspective

Diego Cisneros-Heredia, Universidad San Francisco de Quito USFQ, Colegio de Ciencias Biológicas y Ambientales, Laboratorio de Zoología Terrestre & Museo de Zoología; Mario Yánez-Muñoz, Instituto Nacional de Biodiversidad INABIO

Southern Ecuador includes a mixture of Andean highlands and lowland landscapes, with a unique and rich flora and fauna, with all major biomes occurring—from tropical forests to paramo grasslands. Biodiversity of southern Ecuador has been shaped by major geological events, including uplift of the Andes and geological marine transgressions. Geologic and physiographic events have acted synergistically across the region, promoting interacting longitudinal exchanges in biodiversity across highlands and lowlands, and causing vicariance and dispersion events across the Andes from the Pacific and the Amazonian lowlands. Despite extensive knowledge on the herpetofauna of Ecuador, different sources have referred to the biogeography of southern Ecuador indistinctly and without a proper definition. The objective of this study is to analyse the biogeography of southern Ecuador based on extensive phylogenetic and biogeographic data from amphibians and reptiles, especially members of the families Craugastoridae, Centrolenidae and Dipsadidae.

10-BPM

Plant-hummingbird interactions along gradients of elevation and deforestation in the tropical Andes of Ecuador

Esteban Guevara, Swiss Federal Research Institute WSL; Catherine Graham, Swiss Federal Research Institute WSL; Tatiana Santander, Aves y Conservación / BirdLife in Ecuador; Cristian Poveda, Aves y Conservación / BirdLife in Ecuador; Bryan Rojas, Aves y Conservación / BirdLife in Ecuador; Nicole Büttner, Un Poco del Chocó Nature Reserve and Biological Station; Francisco Tobar, Aves y Conservación / BirdLife in Ecuador; Holger Beck, Santa Lucía Eco Lodge; Andrea Nieto, Aves y Conservación / BirdLife in Ecuador; Friederike Richter, Aves y Conservación / BirdLife in Ecuador; Andrés Marcayata, Aves y Conservación / BirdLife in Ecuador; Ben Weinstein, Stony Brook University; María José Gavilánez, Aves y Conservación / BirdLife in Ecuador

Drivers of global change, such as climate and land-use changes, influence the abundance and distribution of organisms, which, in turn, can modify species interactions. Ecological interactions among plants and animals allow for the maintenance of biodiversity and sustain important ecosystem services, like pollination, yet we lack of a deep understanding of how plant-animal interactions will respond to drivers of global change. In this project, we investigate how interactions between hummingbirds and their food plants change across gradients of elevation and land-use. We perform observations with time-lapse cameras and census of floral resources at 14 sites with two levels of land-use, forest (7) and pasturelands with remnant vegetation (7). Preliminary data - consisting of 15,000 interactions - indicate that networks are more nested at forest in comparison with deforested areas (weighted NODF index 30.4 ± 6.3 SD vs 11.3 ± 3.6 SD) and also more specialized (H2 index 0.3 ± 0.1 vs 0.2 ± 0.03) which might suggest that networks in deforested sites are less resilient to potential extinctions. Additionally, our results indicate that phenology patterns of flower abundance are highly influenced by deforestation and elevation. Further steps of this research will address the influence of flower morphology on hummingbird specialization.

11-BPM

Fog and drizzle contribution in the Andean Páramo

Gina Berrones, Universidad de Cuenca; Patricio Crespo , Universidad de Cuenca ; Rolando Célleri, Universidad de Cuenca

Tropical mountain ecosystems such as the páramos of the northern Andes are among the least studied ecosystems of the world. Low-intensity rainfall is common, mainly as fog and drizzle; however, it is challenging to segregate among different light rain events due to the lack of high resolution monitoring. It is primarily important to obtain a well-rounded characterization of precipitation; further research is still needed regarding the importance of these low-intensity events as a water input to the hydrological system. This study was carried out at the Zhurucay Ecohydrological Observatory (3800 m a.s.l.), in southern Ecuador. Precipitation was measured with a high-resolution laser disdrometer and with three different monitoring techniques for fog quantification; thus it was possible to isolate fog from rainfall. Disdrometer data was available from 2012 and fog data since 2017. We defined different types of events: "fog", "fog +drizzle", "fog +light rain", "drizzle", "light rain" and "rain". Results show presence of fog and drizzle almost on a daily basis, and in more than 80% of the time precipitation occurs. The predominant occurrence of fog was at early morning and at night. During the driest months, fog was more frequent and had an important contribution to total precipitation. Moreover, fog and drizzle were an important input of water to avoid dry spells for certain months. Annual precipitation can be up to 20% more when fog and drizzle are measured. These findings demonstrate that their contribution is very important for hydrological and ecological processes at the páramo.

12-BPM

Primera exploración biogeográfica de hongos microscópicos y bacterias en un gradiente altitudinal de la Reserva Biológica Colonso Chalupas, Napo-Ecuador

Kassandra Bazantes, Universidad Regional Amazònica Ikiam

Los microorganismos son fundamentales en el reciclaje de nutrientes del suelo. Sin embargo, poco se conoce de su diversidad y distribución espacial en zonas tropicales. A pesar de sus características fisiológicas, estudios afirman que las comunidades microbianas se ven influenciadas por barreras ambientales y geográficas. El presente trabajo tiene como objetivo analizar en tres secciones del gradiente altitudinal de la Reserva Biológica Colonso Chalupas: a) si la cantidad, diversidad y velocidad de crecimiento de hongos y bacterias son influenciadas por el gradiente altitudinal, y b) si la disponibilidad de nutrientes en el suelo está relacionada con la cantidad de unidades formadoras de colonias (UFC). Para esto, se aisló, contó, e identificó (secuenciación) hongos y bacterias del suelo, y se analizó variables químicas del mismo. Los resultados no muestran diferencia significativa (ANOVA P = 0.6) en la cantidad de UFC. La diversidad (Índice de Diversidad de Shannon) de hongos disminuyó al aumentar el nivel altitudinal, y en las bacterias se observó el patrón contrario. La velocidad de crecimiento para ambos microorganismos fue menor en el nivel altitudinal más alto. Por otra parte, la cantidad de nitrógeno y potasio no determinó la cantidad de UFC de hongos debido a que presentan correlaciones distintas en los diferente niveles altitudinales. Además, el pH en el nivel más alto es determinante para el desarrollo de bacterias ($r2 = 0.7$). Así, esta investigación demuestra la preferencia de algunas especies de hongos y bacterias por ciertas condiciones ambientales, que en términos ecológicos, fomenta la conservación a nivel de paisaje.

13-BPM

Estructura y diversidad genético poblacional del fitipatógeno Austropuccinia psidii

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Austropuccinia psidii es un hongo patógeno de ciclo de vida incompleto con aeciosporas originario de Brasil causante de la roya en varias familias de angiospermas. La problemática de esta especie consta en que ha sido introducido a varios países de América, Oceanía y Asia afectando en gran medida a cultivos de importancia económica. Esto implica que los estudios en genética de poblaciones son relevantes ya que aportan al conocimiento de su composición genética, los patrones de diversidad genética y las posibles rutas de invasión con el fin de conocer su dinámica epidemiológica. Por ende, el objetivo de este trabajo fue evaluar la diversidad y estructura poblacional actual de A. psidii con sus respectivas implicaciones en la dinámica espacio-temporal de este fitopatógeno. Para esto, se generó un set de datos de individuos reportados en Australia, Brasil, Estados Unidos e Indonesia con 18 microsatélites (genotipos); se analizó la estructura poblacional por medio de un DAPC, se evaluó la curva de acumulación de genotipos, diversidad genotípica y un STRUCTURE. Se obtuvo la diferenciación de las poblaciones de Brasil, EEUU, Australia e Indonesia, pero estas dos últimas entre sí, no presentan diferencias lo que indica que comparten genotipos. También, se corroboró que en el origen de este fitopatógeno hubo mayor diversidad genotípica. En la red mínima de coberturas, Australia obtuvo la mayor riqueza de MLG's. Nuestros resultados indican que su migración pudo haberse dado a causa de las rutas comerciales que poseen los países evaluados

14-BPM

Filogeografía del colibrí pico de hoz Eutoxeres aquila (Bourcier, 1847)

Laura Rosado, Universidad Central del Ecuador; Elisa Bonaccorso, USFQ

El colibrí pico de hoz, Eutoxeres aquila, se distribuye en los bosques húmedos desde Costa Rica hasta el Chocó Ecuatoriano y el valle del Cauca, hasta la vertiente amazónica de los Andes, desde Colombia hasta el norte de Perú. En Ecuador, muchas de sus localidades de presencia se encuentran dentro de áreas protegidas. Sin embargo, también existen poblaciones en zonas amenazadas por actividades humanas, como es el caso del Chocó ecuatoriano (a excepción de la Reserva Ecológica Mache Chindul), y en zonas no estudiadas como el sur del país, donde podría darse una confluencia entre las poblaciones del oriente y el occidente. Este estudio pretende comprender la relación existente entre las diferentes poblaciones de la especie, así como evaluar el estatus taxonómico de sus subespecies mediante un enfoque integrativo, con la aplicación de filogenética molecular, morfología estándar y morfometría geométrica. Resultados filogenéticos preliminares muestran diferenciación genética entre individuos de diferentes poblaciones chocoanas y amazónicas, sugiriendo que existe una separación entre ambas, al menos a nivel de Ecuador.

15-BPM

Patterns of planktonic foraminifera diversity in the southeast Pacific (between 22 ° S and 44 ° S)

Laura Tavera Martínez, Universidad de Concepción; Margarita Marchant, Universidad de Concepción

Phylum Foraminifera is part of the group of heterotrophic protists and is a relevant component of marine plankton. These associations are important because of their use as proxies for paleoceanographic and paleoproductive reconstructions. So the variations in abundance and composition reflect ocean fertilization patterns and biogeographic provinces in planktonic communities. Therefore we hypothesize that there is a pattern of diversity in the planktonic foraminifera, among the biogeographical provinces of the Southeast Pacific, reflecting a greater richness and abundance of species in the Peruvian Province besides being related to primary productivity. The objectives of this study are identify the presence of a pattern of planktonic foraminifera diversity among the biogeographic provinces of the Chilean coast, evaluating the community parameters of richness and abundance. Besides knowing which are the oceanographic variables that would explain the structuring of the community and analyze the latitudinal zonation of species, which contribute to the formation of this pattern. Results indicated that there is a pattern of diversity among the biogeographic provinces. Species richness structuring is given by productivity, chlorophyll and dissolved oxygen. Also the currents that influence the composition of species. Pattern recorded in abundance also depends on productivity, dissolved oxygen and phosphate concentration. The Peruvian Province contains a greater diversity and richness of species, caused by the upwelling and the influence of subtropical currents. While the Magellanic Province contains a higher abundance of foraminifera, due to the strong dominance of species of subantarctic and polar waters, coming from the Humboldt current.

16-BPM

Modelling habitat-land cover associations for mapping species distributions

Maria Lumbierres, Sapienza Universita di Roma; Carlo Rondinini, Sapienza Università di Roma; Paul Donald, BirdLife International

Area of Habitat, the area inside the mapped distribution of a species that is ecologically suitable (also referred to as extent of suitable habitat, or ESH), provides detailed large-scale information on species distribution. Suitable conditions can be inferred from the Habitats Classification Scheme of the IUCN Red List (IUCN habitats). However, the IUCN habitats are not based on a remote sensing product, and therefore they are impossible to map. We established a standard methodology to crosswalk IUCN habitats to the ESA-CCI land cover map. This crosswalk maps each IUCN habitat class to one or more ESA-CCI land cover classes, using species occurrences for mammals and birds from GBIF and eBird. The methodology consisted of three steps: 1) cleaning the data 2) extracting land cover and habitat information for each occurrence, and 3) researching and testing different modelling approaches. A generalized linear model with a logit link function, modelling each land cover type individually as a function of different habitat types, was the best model to represent the data. We calculated the log-odds ratios of coefficients of the logistic regression models, and we transformed them into probabilities that each IUCN habitat is associated with a particular ESA-CCI land cover. The probabilities represent the uncertainty of association of each IUCN habitat class with ESA-CCI land cover classes. The crosswalk will be used to calculate Area of Habitat maps for all terrestrial vertebrate species. These models are useful to guide conservation strategies and to study poorly known areas.

17-BPM

Patrones de biodiversidad a macro y microescala en una turbera altoandina del Ecuador

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Los humedales de alta montaña normalmente contienen especies vegetales con una distribución y funcionamiento similar, por lo que tradicionalmente se les ha agrupado dentro de unidades discretas definidas por la presencia o ausencia de una o varias especies de plantas. Por lo general, en estos estudios no se consideran variaciones topográficas del terreno y nivel del agua a una escala de microhábitat. El objetivo de este estudio fue determinar si los patrones de composición vegetal en un humedal de alta montaña están relacionados con factores físicos y nivel de agua a escala de humedal (macroescala) y de sitio (microescala). El estudio se llevó a cabo en la turbera de alta montaña "Tola Alta", a 3700 m s.n.m, en la zona de amortiguamiento de la Reserva Ecológica "El Ángel". Se describió florística y físicamente a cada zona de vegetación de la turbera. Se establecieron cuadrantes de 3×3 m para registrar la presencia y abundancia de especies vegetales, y transectos de 0.1×5 m donde se registró en subcuadrantes de 10×10 cm la presencia de especies vegetales y la variación topográfica del terreno y el nivel de agua. En este estudio se encontró que existe heterogeneidad entre las distintas zonas de vegetación de la turbera, pero también dentro de cada zona. Las zonas con menor diversidad son las de mayor variación microtopográfica y de nivel de agua, mientras que las zonas de vegetación que se encuentran a mayor altura dentro de la turbera fueron las más diversas.

18-BPM

Avian Biogeography of the Chota Valley, Ecuador

Markus Tellkamp, Universidad Yachay Tech; Nicole Alfaro, Universidad Internacional del Ecuador

The inter-Andean region of the Ecuadorian Andes, is characterized by the presence of dry valleys surrounded by humid ecosystems. Perhaps because of the lack of natural habitats in these valleys today, these dry valleys have been largely ignored by biologists. Closer inspection of the avifauna in these areas, however, is starting to reveal interesting patterns. Observations of birds in the Chota Valley (henceforth simply Chota) over the last four years by the authors, complemented by entries from eBird, show that 26% of the 96 species found here are resident of other inter-Andean valleys as well and 26% are migratory or widespread birds. However, the remaining 48% of species come from adjacent ecosystems: 15% spill over from nearby humid montane forests, 5% commonly occur in the highlands above 3000 meters, and 28% are mostly found in the lowlands. Of the latter group, 48% are trans-Andean in Ecuador, 15% occur 800-1300 meters higher in the Chota than in their remaining range, and 44% have a disjunct population in the Chota, being removed by at least 50 kilometers from the closest range limit. Most disjunct populations may be relictual in nature as their presence in the Chota unlikely results from the release of captive individuals. We propose that during the glacial periods of the Pleistocene a dry forest corridor must have connected inter-Andean valleys to other dry ecosystems. The Chota is also receiving new species through recent range expansions, likely linked to a combination of deforestation of humid forests and global climate change.

19-BPM

Biogeography of the genus Oligoryzomys Bangs, 1900: On the fastest and most expansive Pleistocenic radiation of Neotropical rodents

Natali Hurtado, Centro de Investigación Biodiversidad Sostenible

The genus Oligoryzomys of Neotropical rodents is one of the most diverse and the most wide distributed of the subfamily Sigmodontinae. Nonetheless, some aspects about its systematics have been partially explored based on multiloci approaches. Whereas, the historical biogeography of Oligoryzomys has been depicted from topology of phylogenetic relationships of a half of the currently known species without timing of the divergences. We estimated the species tree of the genus by sampling five genes (one mitochondrial and four nuclear) in 30 species and estimated time divergences. Also, we estimated the most common ancestor distribution, setting the current distribution of the species on a matrix among 13 ecorregions and fitting six biogeographical models; and simulated the dispersal events under the selected model. The species tree revealed hard polytomies, whereas the time divergences took place within the Pleistocene. The most common ancestor of Oligoryzomys was distributed within large area that encompasses Boreal and Southern Amazonia, Cerrado, Atlantic Forest, Pampa, Chaco and Andean Mountains, and raised the actual geographical distribution of species by initial events of vicariance, followed by events of dispersion within a large areas or within a single area, and founder events; against former hypothesis of an ancestor originated and restricted to the Amazonia with posterior colonizations. The hard polytomies, short period of time for the accumulation of 30 species and the large extension of the genus is almost all ecorregions of South and Central America, suggest a fast adaptive radiation, which was achieved by multiple and simultaneous dispersal events.

20-BPM

Phylogeography of the Andean genus Parajubaea in Bolivia

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The Tropical Andes of South America are home to an astounding number of plant species. Among them, several palm lineages have found in this hotspot opportunities for dispersal and/or speciation. Palms of the genus Parajubaea, however, represent a special Andean case of low diversification with only three species recognized despite the genus' origin 22 million years ago. Two of them, P. torallyi and P. sunkha, are endemic to Bolivia and are listed as endangered by the IUCN since they show restricted ranges, where they face rapid habitat degradation and limited regeneration. Contrastingly to several other Neotropical palm genera, research on many aspects of the biology of Parajubaea is still scant, including its genetics. The goal of the study is to infer the historical demography of Parajubaea in Bolivia. We predict that long regeneration time and short-range seed dispersal have led to more isolated populations to be genetically more distinct. A total of 168 individuals from three populations of P. sunkha and four populations of P. torallyi were genotyped using Genotyping by Sequencing for a total set of 1432 SNP markers. Preliminary analyses suggest that individuals belong to seven genetic clusters that correspond to the sampled populations. P. sunkha shows higher genetic diversity than P. torallyi. Genetic structure and diversity suggest that geographically distant populations within each species are genetically more differentiated.

21-BPM

Phylogeography of an endemic crayfish from the western slope of the Austral Andes: a history of geography, past climate changes and cryptic diversity.

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Old species with low vagility, adapted to habitats with low connectivity and distributed in scenarios with a dynamic paleoclimatic history, are candidates to show high levels of intraspecific beta diversity.This seems to be the case of Parastacus pugnax, a burrowing crayfish endemic to western austral Andes, part of the Gondwanan family Parastacidae. In spite of the evolutionary and biogeographical singularity of this species, its phylogeographic patterns and the history that has shaped its intraspecific diversity are unknown. We estimate patterns of genetic diversity (mtCOI) in populations of the entire distributional range of the species, infer their demographic history (BSP, equilibrium-expansion) and contrast with their historical habitat (ENM). Morphological variation (geometric morphometrics) for main clades was estimated too. We detected a high number of ancient lineages and where three main clades are consistent with morphological variation. TMRCA for P. pugnax was estimated at 38 Ma, and the diversification of P. pugnax would have obeyed to orogenetic and paleoclimatic processes that occurred from the middle Eocene in austral Andes. Funds FONDECYT-1161650.

22-BPM

Biases and prospects in the distribution of Brazilian anurans

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Mapping species distributions is essential for ecology and biogeography studies, but to do it is first necessary to gather high-quality biodiversity data. Much of currently available biodiversity knowledge is accessible through emergent open-access databases, although these data hold many information gaps. We gathered a comprehensive database on the distribution of Brazilian anurans using publicly available data from databases and biological collections. We compiled a database of species occurrences from GBIF, SpeciesLink, ICMBio "Portal da biodiversidade" (Brazilian Ministry of the Environment), and herpetological museums and collections. All these data were verified by taxonomy specialists. Currently, our dataset integrates c. 217,000 occurrence records of appx. 950 species belonging to 21 families and 114 genera, including 56,900 records unavailable on open-access databases. Approximately 105,000 of these records provide primary data on taxa, year and location (incl. precise georeference and altitude). Data shows a clear bias towards Brazilian hotspots in the Atlantic Forest (56,37%) and Cerrado (20,3%), although many records were recorded for other biomes. Our dataset represents a major effort to compile occurrence records for the entire country, filling in a large gap in primary data on anuran diversity. The detailed information on species distributions provided by our database is of great relevance to inform conservation prioritization at the scales required to understand global changes and land management scenarios.

23-BPM

Fungal diversity associated with roots in three species of the genus Matisia Bonpl. that show different aggregation patterns in Yasuni National Park

Ricardo Zambrano-Cevallos, PUCE

Tropical rain rainforests presents the largest number of biodiversity in the world. In these forests plant organisms can show patterns of distribution explained by abiotic and biotic factors such as climate, soil properties, pathogenicity or herbivory. However, the exploration of associations between trees and fungi has been suggested as one of the mechanisms that allows trees to present spatial patterns such as aggregation.In this study we determined if tree distribution patterns are related to the presence of certain fungal species associated with roots of Matisia cordata, M. malacocalyx and M. oblongifolia, which show low, intermediate and high aggregation patterns, respectively.The tree species were located in the 50-hectare plot of the Yasuní National Park. Macroscopic and microscopic observations of the roots were made to verify the presence of mycelium. Pure cultures of fungi were obtained, and the species were identified by morphology and the sequence of the ITS region of the ribosomal DNA.Sixteen species of fungi were found in association with the roots. The greatest differentiation of fungi was found in M. oblongifolia, whose level of aggregation was the highest and had species of specialized fungi that might help mitigate the density-dependent negative effects. In contrast, M. malacocalyx presented a set of generalist fungi shared with M. cordata, which could possibly explain its level of intermediate aggregation. It is also proposed that M. cordata might depend on other factors such as the availability of light, and not the fungal species to explain its low level of spatial aggregation.

24-BPM
Cradles of diversity: unlikely relics of regional climate stability

Stuart Brown, University of Adelaide; Damien Fordham, University of Adelaide; Carsten Rahbek, CMEC Univ. of Copenhagen

The stability of regional climates on millennial timescales is theorised to be a primary determinant of nearby diversification. Using simulated patterns of past temperature change at monthly timescales, we show that the locations of climatically stable regions are likely to have varied considerably across and within millennia during glacial–interglacial cycles of the Late Quaternary. This result has important implications for the role of regional climate stability in theories of speciation, because long-term climate refugia are typically presumed to be 'cradles' of diversity (areas of high speciation) only if they remain stable across Milankovitch climate oscillations, which operate on multi-millennial time scales.

25-BPM
Biovolume from Andean communities along an elevational gradient

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We assess the relationship between abundance and frequency of taxa versus the contribution of biovolume at plot and landscape scales. We assess the plot biovolume (PB) from 446 0.1 ha plots (260 to 4350 m a.s.l.) established at Madidi National Park. To assess abundance, we calculated the Simpson Evenness index (E D). For frequency, we calculated the number of plots in which each species was found over the total number of plots, and then we calculated the mean of frequencies of all species present in each plot (plot species frequency = PSF). We used a linear model to assess the following relationships: 1. PB vs. elevation; and 2. PB vs. E D and vs. PSF, and their respective interactions (response variable = PB; predictor variables = elevation, E D and PSF). Mainly, our results show that there was a negative linear relationship between PB and elevation, and a positive linear correlation between PB and PSF overall in lowlands. PB was not significantly explained by E D . Regarding statistical interactions, there was a negative interaction between E D with elevation, a marginal significant negative interaction between PSF and elevation, and a positive effect of E D on PB at lower elevations. Our study shows that the biovolume of aboveground vegetation in the Madidi was concentrated in a few species across of its landscape (the most frequent ones), and that this effect was higher at low elevations. Species that contributed with most plot biovolume did not necessarily had greater abundances, but they had functional conditions that allow them contribute with greater biomass, such as tree size.

26-BPM
Biogeography of plant pH across northern China

Wenxuan Han, China Agricultural University

Plant pH, an emerging plant functional trait, plays important roles in nutrient cycling and physiological processes. How plant pH varies at large scales is unclear yet. Here we showed the biogeography of foliar pH and investigated its potential drivers. We analysed foliar pH of plants from 21 sites across northern China, along an east-west transect of northern China with increasing aridity westwards, and explored its spatial pattern and relations with climate, soil and plant functional type. The results showed that the foliage was generally acidic (5.33±0.04), but was higher in arid northwestern relative to humid northeastern China. Foliar pH value decreased significantly westwards at an average rate of 0.24 units per 10° longitude. Climate, soil and plant type explained 11%, 17% and 59% of the variance in foliar pH, respectively. Foliar pH decreased with mean annual precipitation, soil stress coefficient and aridity index, but increased with mean annual temperature. Foliar pH seemed to be higher in later- than earlier-evolved plants, with herbaceous plants higher than woody plants (6.0 vs 4.9), angiosperms higher relative to gymnosperms (5.6 vs 3.7), and monocotyledons higher compared with dicotyledons (6.0 vs 5.5). Among all the factors, plant affiliation and moisture were most influential on the biogeographic pattern of foliar pH. This study documented the first analysis of the spatial pattern of foliar pH over large scale. Our findings provide a new impetus for understanding functional biogeography, and lay the groundwork for research on the linkage of foliar pH to ecological functions and macro-evolutionary implications.

27-BPM
Latitudinal pattern of herbivory in Oak forests: Ant trophic diversity matters

Yuxin Zhang, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences; Shuang Zhang, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences; Keming Ma, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences

Knowing how biodiversity relates to ecosystem process is important for understanding the maintenance of diversity. Herbivory is a main pathway for energy flow in ecosystem. Ant is an important indirect defender against herbivore in many ecosystems. While research often focuses on how variation in ant abundance influences herbivory, assessing ant species in a food web context, i.e. trophic diversity, can provide further insight into the relationship between diversity and ecosystem process and shed new light on the mechanisms underpinning ant-herbivory relationship. Here, we assessed how ant abundance and trophic diversity affects leaf loss rate of Oak forests along latitudinal gradients (Quercus wutaishansea Mary, range: 34.23 N to 42.91 N and Quercus mongolica Fisch. ex Ledeb, range: 44.23 N to 52.03 N) of China. Our results showed that both Oak species have decreased trend of leaf loss along latitudinal gradient. Ant abundance do not show significant relationship with herbivory, but ant trophic diversity have significant effects on herbivory. Our work shows that ant trophic diversity rather than ant abundance influence ecosystem process. The importance of trophic diversity in determining how biodiversity relates to ecosystem process suggests that simply focusing on species abundance does not give a full understanding of how ecosystems may change with the loss or gain of species.

Biogeography of the Anthropocene

30-BA
Biodiversity impacts of non-native lodgepole pine invasions across trophic levels.

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Human-mediated plant invasions are increasingly becoming a worldwide phenomenon. Among this plant invaders, the lodgepole pine (Pinus contorta) is one of the most invasive species. Pine invasions drastically alter the abiotic environment by changing factors such as light, temperature, and soil nutrient availability. Furthermore, because of mutualistic associations between pine and fungi, Pinus contorta invasions often also implies biotic alterations. Most likely when located outside of the pine native geographical range, pine invasions often involves co-invasions of mycorrhizal fungi. Pinus contorta was deliberately introduced to Patagonia in the '70s and rapidly invaded natural areas outside of the original plantations. We studied a 20 years pine invasion at a non-forested, high altitude, the alpine plateau above the timberline in northern Patagonia, Argentina. We sampled plant, mutualistic fungi, and arthropods species along a temporal axis of pine invasion. We measured changes in plant functional diversity, using leaf traits as a proxy for species responses to the presence of pines. Furthermore, we collected pairwise plant-plant, plant-fungi and pine-fungi interactions. We will aim towards quantifying the total interaction network across multiple trophic levels. Later, we potentially asses the effect of the pine on modifying/reorganizing local interactions, how this translated to observable patterns of species/interactions persistence across trophic levels and their representation in network structure. Results of this study will offer mechanistic insights leading to functional changes and reorganization of communities in the presence of pine invaders. Furthermore, we hope to obtain key insights on how whole communities respond to moving environments (e.g. advancing treelines).

35-CB

Evaluación de la vulnerabilidad potencial de los ecosistemas nativos de Ecuador continental a invasión de seis especies de plantas exóticas

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Predecir la distribución geográfica de las especies mediante el modelado del nicho ecológico representa una línea de investigación en expansión, la cual se sigue aplicando en múltiples áreas de conocimiento. Esta investigación evaluó los niveles de superposición geográfica entre las zonas de distribución potencial de invasión de las especies exóticas invasoras (EEI) con los ecosistemas nativos en Ecuador continental a través del modelado de Nicho Ecológico. Se empleó el algoritmo de máxima entropía (MaxEnt) para el modelo del nicho ecológico de 6 especies de flora para predecir sus distribuciones geográficas en su área nativa y de invasión en Ecuador continental, para el modelado se emplearon registros de presencia de las especies invasoras en su área nativa y de invasión obtenidos de las plataformas de GBIF y TROPICOS, variables climáticas de WorldClim 2.0 y vegetación de Copernicus. La contribución y permutación de las variables de los modelos fue calculada mediante el estadístico Jackknife, no se utilizaron variables con coeficiente de correlación mayor a 0.70, el umbral utilizado fue 10 Percentil y el rendimiento de los modelos fue calculado mediante el área bajo la curva AUC y la prueba ROC Parcial. La Zona Interandina presentó la mayor aptitud ambiental para las seis EEI, seguida de pequeños fragmentos en la amazonia y una leve extensión en el litoral.

36-CB

Cambios en la distribución espacial de la cobertura vegetal en la ciudad de la investigación de la Universidad de Costa Rica, 2012- 2019

Helber Guillén, Universidad de Costa Rica

La Ciudad de la Investigación de la Universidad de Costa Rica (UCR), ha presentado un constante proceso de desarrollo de infraestructura, dichas edificaciones han tomado el lugar de amplias zonas boscosas que se localizaban en el Campus, por lo cual en este escrito se expone la pérdida de cobertura vegetal ocasionada por este proceso. Se plantean las siguientes tres preguntas de investigación, para analizar la presente problemática: ¿Cómo ha cambiado la distribución de la cobertura vegetal en la Ciudad de la Investigación de la UCR, 2012- 2019? ¿Cuáles consecuencias conllevan actualmente los cambios de distribución de cobertura vegetal en la conectividad entre poblaciones? ¿Cómo se presenta la variabilidad espacial de temperatura ambiental con respecto a la actual distribución de cobertura vegetal? En respuesta a las anteriores preguntas de investigación se presentan las siguientes hipótesis: La cobertura vegetal ha disminuido considerablemente producto de la construcción de los nuevas edificaciones, tomando en cuenta que no se ha recuperado las zonas con cobertura perdida. Este cambio en la distribución de cobertura vegetal ha ocasionado una fragmentación del espacio verde, al mismo tiempo que se pueden presentar altas temperaturas a nivel ambiental en las zonas con poca cobertura vegetal en comparación los espacios con mayor cobertura vegetal. Resultados preliminares y conclusiones Se puede observar un alto grado de disminución de la cobertura vegetal en el área analizada, especialmente entre los años 2017 y 2019.

37-CB

Inselbergs as natural refugia for the conservation of Brazilian Atlantic Forest

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The Brazilian Atlantic Forest is a global biodiversity hotspot, with a rich and unique flora (rate of endemism 49.5%), remaining in just 11.7% of its original covering. In southeastern (SE) Brazil, the Atlantic Forest domain harbours a huge concentration of monolithic inselbergs - old landscape elements consisting of granitic and/or gneissic rocks. These are colonized by rupicolous plants, but occasionally forests can be found on the summit and at the base of inselbergs. Due to steep slopes and difficulties of access, those rock-related forests are relatively well conserved in comparison to the surroundings. In order to test if the floristic composition of these forests resembles those of the former (and now disappeared) Atlantic Forest, we studied an isolated summital forest on an inselberg in SE Brazil. The isolated forest (situated c. 900m asl) contained typical elements of the Atlantic Forest and in addition species considered endemic to other biomes. The dominance of ornithochoric species could indicate long distance dispersal and emphasizes the potential of inselbergs as stepping stones. So far we georeferenced c. 1.000 inselbergs in SE Brazil and currently we are quantifying the area of rock-related forests. With this study we aim to show the contribution of the topographic barriers of inselbergs for the conservation of forest remnants, and to raise awareness of their biological importance in a scenario of fast deforestation. Since less than 10% of the Atlantic Forest remnants are in Conservation Units, inselbergs play a significant role as natural refugia and hope spots.

38-CB

Modelos de aptitud para ubicar áreas de conservación para plantas suculentas en la Reserva de la Biosfera Sierra Gorda Guanajuato, México

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En México, las Reservas de la Biosfera poseen la máxima categoría de protección para la biodiversidad, éstas poseen sub-polígonos que excluyen prácticas antrópicas (e.g. ganadería). Sin embargo, las poblaciones humanas modifican constantemente el ambiente, ejerciendo una presión sobre la biodiversidad y generando áreas de riesgo para ciertas especies. Dentro de la RBSGG, habitan varias cactáceas y crasuláceas bajo alguna categoría de riesgo (ECOL-NOM-059), por lo que se seleccionaron para generar modelos de aptitud mediante un análisis multicriterio, que permitan ubicar a escala local áreas prioritarias para su conservación y áreas que representan algún riesgo para su permanencia. Para la construcción de los mapas de aptitud (para 19 especies) se emplearon diversas variables (Uso de Suelo y Vegetación, Pendiente, Distribución de Especies, Cercanía a Caminos y Carreteras, Áreas de Minería). En términos generales se encontró que las poblaciones de algunas especies están dentro de áreas de riesgo (Turbinicarpus alonsoi, Strombocactus disciformis, Echeveria xichuensis); por otro lado, se evidenciaron los sitios en los que su conservación podría ser más probable. Finalmente, se generó un mapa consenso con los mapas de aptitud para ubicar a una mayor escala las áreas prioritarias para la conservación de estas especies. Cabe destacar que las áreas prioritarias para la conservación no coinciden con el área núcleo oficial de la Reserva. Los modelos de aptitud pueden ser empleados como un método rápido, que contribuya a la toma de decisión para la designación de las áreas prioritarias para la conservación, dentro de áreas naturales bajo alguna categoría de protección.

39-CB

Propuesta de áreas prioritarias para la conservación de la Guacamaya Verde (Ara militaris) en dos Reservas de la Biosfera en el centro de México.

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La Guacamaya Verde es una especie en peligro de extinción en la Norma Oficial Mexicana y vulnerable en la IUCN. La disminución de sus poblaciones se debe principalmente a la pérdida de hábitat y su captura como ave de ornato. Por ello, es importante generar información que permita generar propuestas integrales para su conservación. Debido a que usa una amplia variedad de hábitats, aquí se presenta una estrategia para predecir su presencia en base al modelaje de sus fuentes de alimento. De los 422 registros de ocurrencia (áreas de percheo, alimentación y anidamiento), 259 fueron para alimentación, las plantas más visitadas fueron Melia azedarach, Juglans mollis, Pinus cembroides y Carya illinoinensis (con 48, 28, 14 y 7 registros respectivamente). En base a estos resultados se modeló su nicho potencial en las reservas, para posteriormente construir el mapa de aptitud para la guacamaya (escala 1 a 5). Las zonas con valores de aptitud 4 y 5 se consideraron como zonas prioritarias para la conservación de A. militaris, rodeada por un área de amortiguamiento (valores de aptitud 3). Cabe destacar que en la propuesta confluyen sus principales recursos alimenticios y sus zonas de anidación; y que las aves se alimentan y anidan en zonas con alto grado de degradación. Los mapas generados ofrecen un primer análisis para definir las áreas prioritarias para la conservación de A. militaris en tres reservas naturales; y constituyen una base de conocimiento para proponer un corredor ecológico que considere como especie bandera a la guacamaya verde.

40-CB

The vulnerability of endemic frog species in a rapidly changing world

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Global changes are expected to escalate throughout the remaining 21st century, as a result of climate change and land-use transformations, making humans largely responsible for biodiversity loss, population decline and extirpation worldwide. Understanding the synergistic effects and how these threats might affect species distribution is crucial for improvimg conservation policies and strategies. Using a range of ecological niche models (ENMs) in an ensemble forecasting-framework, we evaluated the vulnerability and exposure of anurans to the changing climate in the Brazilian Atlantic Forest for the period of the 21st century. To achieve a more ecologically relevant vulnerability assessment for anurans, we included a high-resolution map of the vegetation remnants in ENMs and considered different scenarios of dispersal and distinct anuran reproductive modes under climate velocity trajectories. We showed that most endemic anuran species should undergo a shift in their suitable habitats, but mainly the water-breeding frog species will be forced to move uphill. Forest stream-dependent species are expected to persist at their same elevational range. By understanding the relative contribution of species' life history, climate change, and land-cover conversion (deforestation), we improved our predictions with respect to the vulnerability assessment of endemic species in this rapidly changing world.

41-CB

The role of a Critically Endangered Black-breasted Puffleg in plant-hummingbird networks in the Andes of Ecuador

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Interactions among animals and plants are the backbone of ecological processes such as herbivory, seed dispersal and pollination. Ecological network approach allow us to determine the relative importance of a species, or group of species, in the maintenance of these processes. This understanding is relevant for conservation, especially in systems where highly threatened species are involved. In this study, we explore the role that the Black-breasted Puffleg Eriocnemis nigrivestis, an endemic and Critically Endangerd hummingbird, has on the stability of plant-hummingbird networks. To this end we described plant-hummingbird networks during two years of field observations using time-lapse cameras, at three sites where the species have been recorded previously. We quantified species-level metrics such as closeness (i.e. high niche overlap with other hummingbird species), betweeness (to what extent the species connect guilds within network) and specialization d′ (deviation of interaction frequencies in relation to the availability of interaction partners in the network). Our preliminary results indicate that the species had intermediate values of betweeness (0.03 vs mean 0.09 ± 0.01 SD), closeness (0.1 vs mean 0.09 ± 0.2 SD) and specialization (0.2 vs mean 0.31 ± 0.2 SD). These results might suggest that despite the species is not the most connected species in the network, it holds a relatively large proportion of links in relation to other species in the community. Further steps in this study will be to appraise the role of the species in other known and isolated subpopulations in the Andes.

42-CB

Efecto de borde en fragmentos forestales y su relación con la dinámica del paisaje (1995-2012) en el norte del Estado de Paraná, Brasil

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El efecto de borde consiste en una de las consecuencias de la fragmentación forestal. Esas consecuencias deben ser comprendidas a largo plazo y su relación con las características del paisaje. En ese trabajo la dinámica de la vegetación arbórea (tasas de mortalidad y reclutamiento de especies) fue analizada en ocho transectos perpendiculares a los bordes de seis remanentes forestales entre 1996 y 2012. Los paisajes del entorno fueron caracterizados a partir de imágenes orbitales de 1995 y 2011. Los resultados indicaron que la proporción de individuos de los grupos de especies tardías / clímax y zoocóricas aumentó, en detrimento de las especies pioneras / iniciales y anemocóricas. La comunidad arbórea presentó menor similitud en su composición a lo largo del tiempo a menores distancias del borde. La distancia media del borde de las especies: pioneros / iniciales, anemocóricos y de pabellón aumentó a lo largo del tiempo. Los parámetros físicos y estructurales de los paisajes presentaron poca variación entre 1995 y 2011. Las tasas de reclutamiento de las especies pioneras / iniciales y las tasas de mortalidad de una especie adaptada a la sombra fueron fuertemente influenciadas por el número de fragmentos forestales en el paisaje. Los modelos sugieren que cuanto más intenso sea el proceso de fragmentación forestal en un paisaje, mayor será el reclutamiento de especies pioneras / iniciales y la mortandad de especies adaptadas a la sombra, en el borde de los remanentes forestales.

43-CB

La conservación de la naturaleza en propiedades privadas en Cataluña (España)

Yuri Rocha, Department of Geography, University of Sao Paulo; Gustavo Schacht, Universidade Federal do Recôncavo da Bahia

La delimitación de áreas protegidas es el principal mecanismo de conservación de la naturaleza in situ. Esa investigación fue desarrollada en Cataluña, que hasta 2017 reconoció 765 acuerdos de custodia del territorio para conservación privada, en cerca de 40 mil hectáreas; tenía como objetivo presentar las características de esa conservación en Cataluña, visitando 9 propiedades/fincas catalanas. Se aplicó un cuestionario de 53 preguntas, que al final indicó el perfil de los propietarios que crearan un área protegida privada. Para archivar los datos se utilizó el software Le Sphinx Plus. Las fincas visitadas tienen en general acuerdos sin registro ante notario porque no es una obligación. Son fincas que pertenecen a familia de sus propietarios hace muchas décadas y en cuatro casos el acuerdo de custodia se presenta en 100% de la finca, normalmente son casos de custodia forestal y agraria. Se puede verificar que 77,8% de las fincas están inseridas o tiene sus límites con otras áreas protegidas; solamente una es aislada en la finca, no teniendo contacto con otros áreas protegidas. Cinco de las fincas tienen uso público: recreación, turismo o visita de público. A respecto de la utilización del bosque, se cita como principal uso el senderismo, seguido por contemplación de la naturaleza; también son citadas actividades como observación de aves, piquinique, paseos de bicicleta, entre otras. La Rede de Entidades de Custodia del Territorio de Cataluña busca el reconocimiento de la conservación privada por el gobierno por medio de una ley específica.

44-CB

Conservation of remaining forest fragments of São Paulo City, Brazil

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The Atlantic Rainforest occupied the part of the Brazilian territory that today concentrates much of the urban population and was reduced to fragments. This study discussed how the structure of the landscape from the theoretical assumptions of Landscape Ecology can influence the conservation of forest remnants protected by Parks that are in isolation in urbanization and the prospects of maintaining these environments in the long term. The hydrographic basin of the Ipiranga stream, one of the tributaries of the Tamanduateí river, is in a consolidated urbanization area and was selected for its presence in the perimeter of the Parque Estadual Fontes do Ipiranga (PEFI).The hydrographic basin of the Aricanduva river, one of the tributaries of the Tietê river, counts on the presence of the Parque Natural Municipal Fazenda do Carmo (PNMFC) and other still unprotected forest fragments. Use maps and soil cover were produced from old aerial photographs for 1962 and 1994 and a supervised classification of a RapidEye 2014 image object that allowed the reconstitution of the past landscape. Land use and land cover maps were produced from 1962 and 1994 and 2014 from which landscape metrics were generated for remaining vegetation cover in the watersheds in the software Fragstats 4.2 that allowed the comparative analysis in a historical series of data on spatial diversity, fragmentation, isolation, connectivity and shape of the fragments. The results obtained evidenced the importance of the establishment of Conservation Units in the preservation of these remaining fragments in the urban landscape.

45-CB

Effects of the land use change in the areographical structure of the endemic species of the Transmexican Volcanic Belt

Tania Escalante, UNAM; Karla Aguilar, UNAM

The Transmexican Volcanic Belt (TVB) is a biogeographical province with high number of endemic species, being an important area for biodiversity conservation; however, it presents high rates of deforestation. The aim of this study was to analyze the effect of current land use change in the geographic distribution areas (GDA) of endemic species of the TVB, on the basis that the anthropogenic land-use change (agriculture, human settlements, cultivated and induced vegetation) will be a negative impact for the species. The land-use change was quantified based on the map of the Serie VI of INEGI, which represents the natural and modified vegetation for 2014. We analyzed the GDA of 167 endemic species belonging to five taxonomic groups (Amphibia, Aves, Insects, Mammalia and Plants), which were overlapped to the Serie VI. The most species analyzed (85.2%) showed changes in the GDA, 10% of them with total loss, while 4.8% did not show any change. Regarding the all GDA with changes, 67% of the species had a loss 50% of their area. The most species had a latitudinal displacement to the South (49%), and longitudinally to the West (45%). The altitudinal ranges with more percent of conserved surface (80%) were < 3 500 masl. Although probably the land-use change does not follow a specific pattern, it was possible to observe trends in the displacements of species, forcing them to inhabit in suboptimal conditions, and trigger their possible extinction.

46-CB

Species distribution model for a micro-endemic hummingbird with vegetation indices as a predictor of habitat structure

Edwin Zarate, Universidad del Azuay - Philipps-Universität Marburg

Species Distribution Models (SDMs) are very important tools to predict geographic distribution of biodiversity via ecological niche modelling mainly using climatic information. The most used information is data from the WorldClim Global Climate database. However, in areas such as Ecuador, bisected by the Andes mountain range, the climatic variations are notable over short distances and ecosystems and landscapes also change abruptly. To improve these predictions, it would be appropriate to work with finer scale. For this reason, we opted to model finer scale variation incorporating Landsat remote sensing images as a proxy for habitat variation. We used texture analysis of NDVI and NDWI indices as a proxy for habitat structure. We focused on southern Ecuador across the known distribution area of a micro-endemic hummingbird (Metallura baroni) found in páramo and shrub in high areas of the Andes, and developed an SDM using MAXENT software. The results were promising and can be mapped to 1:50K, providing a cartographic tool for better planning and direct conservation decisions at a local scale.

47-CB

Una evaluación del estado y futuro de la biodiversidad en las áreas ganaderas de Colombia bajo escenarios de conservación

Jorge Velásquez Tibatá, The Nature Conservancy Colombia; Diego Lizcano, The Nature Conservancy; Andrés Zuluaga, The Nature Conservancy

La ganadería es el uso de la tierra geográfica e históricamente más extendido en Colombia. Por esta razón es considerado como uno de los principales motores de degradación y pérdida de la biodiversidad en el país en sus distintos niveles de organización. No obstante el grado de transformación de las áreas ganaderas en el país, en estas subsisten aun elementos importantes de la biodiversidad al nivel de especies y ecosistemas, muchos de ellos altamente amenazados. Adicionalmente, el sector ganadero se encuentra altamente comprometido en liderar una transición hacia una ganadería sostenible y frenar la deforestación, lo cual presenta una oportunidad para la identificación de acciones para conservar y restaurar elementos claves de la biodiversidad afectados por esta actividad. El presente estudio evalúa primero el estado de la biodiversidad en los paisajes ganaderos con el fin de identificar especies, ecosistemas y áreas que dependan de las acciones de conservación que se realicen en paisajes ganaderos. Luego se evalúa el efecto que tendrían las propuestas de sostenibilidad contempladas en el marco de ganadería colombiana sostenible, las cuales van desde la implementación de prácticas que reducen la presión sobre ecosistemas naturales tales como los arreglos silvopastoriles o agroforestales hasta la exclusión de ciertas áreas de las prácticas ganaderas. Los resultados de esta investigación se convierten en una hoja de ruta para la priorización de acciones de conservación en los paisajes ganaderos de Colombia.

47b-CB

Fragile Biodiversity in The Galapagos Islands

Byron Delgado Maldonado, Charles Darwin Foundation; Nicolas Moity, Charles Darwin Foundation

Ecuador, and especially the Galapagos Archipelago, most accomplish some national and international species conservation management conventions and treaties. Thus, certain species that occur in the Galapagos Marine Reserve (GMR) and the Galapagos National Park (GNP) are ascribed to agreements such as: IUCN, International Union for Conservation of Nature, red list of threatened species (IUCN, 2015). CITES, The Convention on International Trade in Endangered Species of Wild Fauna and Flora. CMS, Convention on the Conservation of Migratory Species of Wild Animals. ACAP, The Agreement on the Conservation of Albatrosses and Petrels. IAC, the Inter-American Convention for the Protection and Conservation of Sea Turtles. CONVEMAR, Sea Rights United Nations Convention. TULAS, Unified Text of Secondary Environmental Legislation (Ecuador). To spatially represent the most important biodiversity according to the criteria of belonging and classification to the agreements and treaties previously exposed and thus be able to obtain a prioritization of the areas to be conserved, an analysis of biodiversity data was carried out from the following sources: (1) Datazone, Natural History Collections database of the Charles Darwin Foundation (CDF) (Bungartz et al., 2009); (2) GBIF, Global Biodiversity Information Facility. (GBIF, 2016); (3) BDMEM, the database of Subtidal Marine Ecological Monitoring of the Galapagos of the CDF (Banks et al., 2014); (4) Movebank, the global database of animal tracking data (Movebank, 2015); (5) Several databases of certain CDF projects (ecological data, fishery data, others). This study integrates the conservation assessment criteria for each species to which the protected areas of Galapagos are assigned and thus spatially identifies the most important areas for conservation. This value of conservation is obtained by assigning a numeric value to the categories that each agreement has according to the degree of threat. To represent more comprehensively (presentation, scalability, and perspective) the value of biodiversity obtained in this analysis, it is decided to use a cartographic generalization technique. In the Geographic Information System (GIS) these data were associated with a 5km grid. The 5km grid is a set of cells that exactly coincide in length and width at 5km, around the entire length of the GMR and the GNP. In this way, all the values of the occurrences of the species valued according to the conservation criteria are added, and consequently, high biodiversity zones are generalized for better management of the protected areas. This combination of meta-analysis and spatial analysis exercise had quantified the flora and fauna species in the Galapagos Islands and had remarked the sites where prior biodiversity exists to protect in the protected areas of the archipelago. The study is an active and iterative process in which new biological databases have to be integrated as they are obtained from current projects, but in this case the results and conclusions are presented based on the data analyzed until December 2015.

48-FWB

Nuevo registro de distribución para Andeancistrus eschwartzae, un pez de agua dulce endémico, y ampliación de su rango de distribución altitudinal.

Fidel Rodríguez , Universidad Central del Ecuador ; Juan Reyes, Fundación Oscar Efren Reyes

Presentamos un nuevo registro de distribución para Andeancistrus eschwartzae, este registro fue encontrado a una altitud de 1210 m.s.n.m en las vertientes sur orientales de los Andes de Ecuador, que drenan hacia el Amazonas, en la provincia de Tungurahua. Nuestros resultados ubican al nuevo registro en las aguas del río Tigre, en las coordenadas (17M 1320413.7, UTM 536541) tributario del rio Pastaza, en su cuenca alta dentro del Biocorredor de los Parque Nacionales Llanganates – Sangay, siendo un nuevo registro altitudinal y latitudinal, que constituye el registro más septentrional y de mayor altitud para la especie aproximadamente (Rodríguez et al., 2017). Andeancistrus eschwartzae reciénteme descrita por Lujan et al., 2015, es una especie endémica del este de los Andes Ecuatoriales, perteneciente a la familia Loricariidae, la localidad tipo para la especie se la registro en la provincia de Morona Santiago, cantón Palora, sector Sangay, localidad rio Amundalo, el cual desemboca en la cuenca media del rio Pastaza en las coordenadas (17M 82888, UTM 9806469) a una altitud de 953 m.s.n.m (Lujan et al., 2015).

Este nuevo registro es da gran valor ecológico ya que las condiciones geo climáticas únicas y la poca información sobre la biogeografía de los peces de agua dulce que habitan esta región nos hace plantearnos la hipótesis de que Andeancistrus eschwartzae, podría distribuirse a lo largo de la cuenca hidrográfica del río Pastaza en ambas vertientes.

49-FWB

Revealing fish endemism patterns in the Andean Orinoco region in Colombia

Guido Herrera, Florida International University; Javier Maldonado Ocampo, Pontificia Universidad Javeriana

The Andean Orinoco has been historically considered as an area of high interest in terms of endemic species in freshwater fish species by experts. In this study, we used Species Distribution Models (SDMs) and Parsimony Analysis of Endemism (PAE) to infer patterns of endemism of freshwater fishes in the Andean region of the Orinoco basin in Colombia. The main purpose was to contrast previous conservation priorities considered for this region using the most updated information about species taxonomy and distribution. The PAE generated 12 equally parsimonious cladograms of areas that were summarized in a strict consensus diagram, which identified three areas of endemism in a nested pattern. The SDMs showed a similar pattern at a lower spatial scale, identifying some areas of a high degree of endemism in the piedmonts where multiple endemic species co-occur. Both approaches, highlighted the uniqueness of the Southern Andean Orinoco with a well-differentiated area adjacent to the Amazon basin, validating the traditional expert opinion. However, the analyses also suggest a higher degree of endemism in Northern sub-basins than expected and that has been underestimated in past conservation assessments. Biogeographical approaches implemented here provide useful baseline data to orientate and delineate future conservation assessments.

50-FWB

Macrófitas como estrategia de conservación en ecosistemas acuáticos de alta montaña de la cordillera Oriental Colombiana

Milena Cardenas, Universidad Pedagógica y Tecnológica de Colombia; Carolina Ramos, Universidad Pedagógica y Tecnológica de Colombia

Los sistemas acuáticos de alta montaña tropical brindan gran número de servicios ecosistémicos siendo el principal la regulación hídrica, lo que los resultados en los principales reservorios de agua de las comunidades locales. Dentro de los productores primarios en estos sistemas de sistemas de almacenamiento de agua, de actividades, de actividades, de actividades, de también, un, la heterogeneidad, de, el, hábitats, acuáticos, para, otros, grupos, biológicos. El sistema montañoso de los Andes presenta la mayor riqueza de macrófitas. Por lo tanto, ¿es necesario determinar cuáles son las características de las especies con capacidad bioindicadora y cuáles son las principales amenazas que enfrentan las macrófitas nativas? Dada la importancia ecológica de la vegetación acuática y su potencial biondicador, Se busca implementar estrategias de conservación para mantener la integridad ecológica de los sistemas acuáticos altoandinos. Se realizó una caracterización de la vegetación en 11 humedales de la Cordillera Oriental colombiana, los cuales se ubican por encima de los 3000 msnm, se detectaron especies con potencial biondicador como algunas macroalgas del géneroNitella y especies del género Isoetes. Se evalúan variables físicas y químicas del agua (temperatura, pH, conductividad eléctrica y oxígeno disuelto). Finalmente, por medio del software Miradi y la metodología Estándares Abiertos para la práctica de la Conservación determinantes que las principales relaciones sobre las macrófitas nativas son: el crecimiento de las exóticas, el desarrollo de las actividades agropecuarias y la sedimentación, la retroalimentación y la retroalimentación. Escenarios de cambio climático.

Functional Biogeography

51-FB

A trait database of birds and mammals exhibiting frugivory in Central and South America.

Beth Gerstner, Michigan State University; Phoebe Zarnetske, Michigan State University

Biodiversity conservation has traditionally focused on areas with high taxonomic diversity; however, conserving areas with high functional diversity can help maintain ecosystem functioning. Spatial patterns of functional diversity can be investigated by combining assessments of community composition, species' geographic distributions, and species functional traits. However, functional trait information is often lacking or exists across disparate data sources. To facilitate analyses involving traits, we compiled a trait database containing life-history and morphological traits for birds (n = 1206; 13 traits) and mammals (n = 494; 28 traits) exhibiting frugivory in lowland and highland montane regions of Central and South America, regions with extremely high biodiversity. We focus on frugivores because they provide essential ecosystem services such as seed dispersal and aid in habitat restoration. The database standardizes taxonomic classifications and aggregates dietary and life history information from EltonTraits and PanTHERIA, the International Union for the Conservation of Nature (IUCN), reference books, and primary literature. We incorporated IUCN statuses, new traits such as endemicity and degree of habitat specialization, and added new species not currently included in existing electronic databases. Along with the trait database, we include code to merge occurrence records for each species from GBIF. By streamlining and collating trait information from disparate sources, this open-access database will allow more comprehensive trait-based studies of frugivorous species in this region.

52-FB

Plant functional diversity across two elevational gradients in serpentine and volcanic soils of Puerto Rico

Claudia Garnica Diaz, University of Puerto Rico - Mayag; Catherine Hulshof, Virginia Commonwealth University

Mountains are hotspots of biodiversity that have been studied to understand the mechanisms that shape biodiversity and the functioning of entire ecosystems. Many studies along mountain gradients, however, use elevation as a proxy of abiotic factors that may have complex relationships with elevation. Further, many studies solely assess taxonomic diversity which cannot explain patterns of community assembly across elevation. Thus, a trait-based approach may provide a more complete understanding of the mechanisms that shape biodiversity patterns across elevation. We investigate trait and assembly patterns across two elevational gradients in serpentine and volcanic soils using four functional traits: Specific Leaf Area (SLA), Leaf Dry Matter Content (LDMC), Leaf Thickness (Lt), and Basic Wood Density (Bwd), and relate trait changes to climate (mean annual temperature and precipitation). This ongoing study suggests that species across serpentine soils have a greater competitive strategy with increases in elevation because soil characteristics are more homogeneous, while in the volcanic gradient community assembly depends more on abiotic conditions which vary more dramatically. In both gradients, areas with stressful conditions present a higher Bwd and Lt, compared to areas with more favorable conditions which had greater SLA. Similar results on both soil types suggest that warm, wet tropical climate may reduce productivity differences between soil types and elevation should not be used as a proxy for complex abiotic factors.

53-FB

Macroecological patterns of marsupials brain size

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The brain is a metabolically expensive organ, consuming a disproportionately large amount of energy. Actually, the large amount of energy necessary for the development of big brains-assigned indirectly cost (Expensive-Tissue Hypothesis) or by increasing energy intake directly (Expensive Brain Hypothesis) is also accompanied by higher parental investment for their development (Developmental Cost Hypothesis). These phenomena, result in significant costs for large-brained species, suggesting a differential cost-benefit effect of brain sizes that could determine their current geographical distributions. Consequently, environmental productivity will be the main driver of the current brain size distribution. To evaluate this hypothesis, we used the geographic distributions of marsupials and their brain sizes to implement spatial regression approaches (i.e. GAM + RAC) and AICc procedure and compare five environmental models that differentially measure the effect of energy over encephalization index (EQ). The full model (energy+temperature+precipitation+topography+spatial autocorrelation) was selected, explaining 60% of the EQ variability. This model shows that the positive effects of spatial autocorrelation, follow by seasonal radiation, are the most important factors to explain the EQ distribution. Consequently, bigger EQ values tend to be spatially near in highly temporal variable energetics environments, and little EQ values tend to be overdispersed in the space, inhabiting wide environmental conditions. These results, together with the fact that bigger EQ inhabiting low species richness areas suggest that brainy species tend to avoid interactions with less brainy species, through inhabiting temporal variable energetics environments, where only brainy species can obtain the necessary energy to survive.

55-HB

Spatiotemporal patterns of the historical connections between Amazonia and Atlantic Forest mastofauna

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Despite the apparent disjunct distribution between the Amazonia and Atlantic Forest, three historical connections were hypothesized: by the forests of the Caatinga, Cerrado and Chaco/Pantanal; in a Northeastern – Southwestern time gradient. We applied a biogeographic approach evaluating the spatiotemporal patterns for these connections using neotropical mastofauna as model. Phylogenetic and geographic data were combined. Minimum time of divergence between species from Amazon and Atlantic Forest within taxonomic families were extracted from dated phylogenies and projected into the geographic space using species' distribution range. The relation between the Northeastern – Southwestern distance gradient for the connection routes and the divergence time between Amazonian and Atlantic Forest species was tested using linear regression models. We corroborate the three connection routes and found oldest divergence times for Amazonia than Atlantic Forest, evidencing the Amazon role as center of origin for Neotropical mastofauna. The previously suggested spatiotemporal pattern was not corroborated considering all species, but rather for some families when considered separately although only for Amazonia. We find an inverted pattern for Atlantic Forest, with most recent divergence times for the Southwestern, revealing connections between this region and Andean Amazon that indicate the importance of the Atlantic Forest role as a source of dispersion. Still, we did not find spatiotemporal patterns as expected for most families. Due to the biogeographic history of each group in Neotropics, they show different connections in different times. Therefore, the connections between Amazonia and Atlantic Forest cannot be explained by a single spatiotemporal pattern.

56-HB

Pollen as a proxy for elevational ecoclimatic gradients – integrating climate, biodiversity, and time dimensions of biogeography

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During his explorations in temperate and tropical mountains, Humboldt made crucial observations about the importance of elevational climate gradients as drivers for biodiversity. We show here that pollen deposition may be a suitable, and statistically robust proxy for climate-driven elevational eco-gradients, thus assisting in the interpretation of modern ecosystem dynamics as well as in past climate reconstructions from fossil records.

Our specific challenges are: (1) to derive consistent pollen-climate relationships in complex mountain regions bearing differences in local climates and intensity of human impact; (2) to find potential indicator taxa useful for paleoclimate reconstructions; (3) to estimate the effect of local parameters on the relationships linking pollen percentages variations, elevation and climate and put forward new hints for calibration of fossil sites; (4) to obtain quantitative climate reconstructions and compare the results with instrumental modelled data and finally (5) to integrate the newly-obtained pollen spectra into larger modern pollen samples datasets.

We analyzed pollen deposition in the European Alps and the Canaries, captured by surface samples (subsampling mosses, forest litter, surface soil in open ground land) and artificial traps both at the ground level and over it. To examine the variance explained by climate parameters, elevational training sets were equipped with site-specific climatologies, together with an array of environmental variables (i.e. proxies for fire, nutrients, pastoralism, terrain parameters, plant cover). The potential for a quantitative reconstruction of sensible climate parameters was tested by canonical correspondence analysis (CCA), enhanced hierarchical logistic regression (extended eHOF models), and weighted averaging (WA).

57-HB

Paleoendemismo y Neoendemismo en la familia Cactaceae del Valle de Tehuacán-Cuicatlán, México

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El endemismo es una cualidad espacio-temporal de grupos biológicos en un área restringida. Se pueden definir tipos de endemismo en relación al tiempo de origen de los taxones: el neoendemismo se refiere a especies de origen reciente que no se han dispersado fuera de su área ancestral, mientras que las especies paleoendémicas son taxones antiguos que permanecen restringidos en un área y que probablemente tuvieron una distribución geográfica más amplia en el pasado. El Valle de Tehuacán–Cuicatlán (VTC) es una zona árida con un alto porcentaje de endemismo en México, dada su alta estabilidad climática probablemente ha fungido como refugio durante los cambios climáticos ocurridos en el Pleistoceno, permitiendo la supervivencia de especies paleoendémicas, y/o promoviendo la especiación, dando lugar a neoendémicas. En este trabajo se llevó a cabo una actualización de la flora endémica del VTC y se estimaron los tiempos de divergencia para las especies de Cactaceae, la familia mejor representada en esta región. Los tiempos de divergencia se estimaron a partir de una filogenia datada usando secuencias moleculares de las regiones de cloroplasto trnK-matK y rpl16; y el criterio para la clasificación en paleoendémicas y neoendémicas fue la transición entre el Plioceno y Pleistoceno (2.58 MA). Los resultados muestran que el origen de la mayoría de las especies de cactáceas endémicas al VTC tuvo lugar durante el Pleistoceno, lo que sugiere que las condiciones climáticas y físicas de esta región fungieron principalmente como "cuna de especies" para especies endémicas de la familia Cactaceae.

58-HB

The Quaternary of the Northern Andes; our legacy of 2 million years evolution of flora, vegetation and climate; in time; in space

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This poster shows temporal and spatial dynamics of the páramo biome in the high Northern Andes (currently ca. 3200-4500 m asl) during the last 2.25 Myr. We present environmental change in a >6000 sample record. We show immigration events of trees, Pleistocene ice-age cycles, suites of changes in (non-analogue) vegetation associations, millennial-scale climate change (mostly 2-3°C), rapid climate change events (up to 10°C), changing lake-levels and sedimentary regimes. We used records Funza09 (2550 m, 2250-128 ka; 1200-yr resolution), Fúquene-9C (2540 m, 280-14 ka, 60-yr resolution), and La Cocha (2780 m, last 14 ka, 30-yr resolution) to develop this unprecedented composite record.

We show quantitatively for the last 1 Myr how elevational shifts of the upper forest line (UFL) in the temporal domain have changed patterns of páramo distribution in the spatial domain. For this aim we introduced new concepts in historical biogeography: the mountain fingerprint (mountain-specific elevational profile) and the flickering connectivity system(changing patterns in isolation and connectivity of páramo areas), driving gene flow, hybridization, isolation and allopatric speciation. This all is in support of molecular phylogenetic studies showing stunning high rates of Pleistocene speciation, and high diversity of the current páramo flora. Presence of mild interstadials and cool stadials are the Pleistocene norm; cold glacials and (current) warm interglacial conditions the exception. Páramo connectivity histories appear to differ much between mountains. In much contrast, montane forest shows high and continuous connectivity during the last 1 Myr in support of a remarkable stable Pleistocene forest composition.

59-HB

Climatic instability and historical refugium during the Quaternary explain genetic diversity of a savanna tree species

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Species distribution and population genetic diversity is often driven by geographical distance or environmental conditions, especially under climate change scenarios such as Quaternary glaciations. Here, we used a multi-model inference approach based on ecological niche modelling (ENM) and statistical phylogeography to unravel the patterns of genetic diversity in the widely distributed Neotropical savanna tree, Hymenaea stigonocarpa (Fabaceae). A total of 494 individuals were sampled from 30 populations and analyzed by sequencing three regions of the chloroplast DNA. Bayesian clustering showed six distinct genetic groups (K = 6) and showed congruence with population geographical distribution. ENM results indicate that the distribution of H. stignocarpa was fragmented in cool periods and broader and more connected during warm periods. Our predictions show a historical refugium occurs in a wide region across the central-western and northeastern Brazil, where higher levels of climatic suitability were maintained most populations throughout the last glacial cycle. However, populations from southeast are located outside of the historical refugium, in region with less climatic stability through time. Moreover, genetic diversity decreased with the distance from the centroid of the historical refugium and the lowest values were found in southeast's populations. The results suggest that populations in the central-western and northeastern regions of the range are marked by historical demographic stability, whereas population in the southeastern region probably experienced population growth. The lower genetic diversity in populations in the southeastern region is probably due to local climatic instability during the Quaternary.

60-HB

Sea currents, retreating glaciers and seabirds in a high-Arctic fjord at a time of climate change

Lech Stempniewicz, University of Gdansk

Long-term trends in environmental conditions observed in the warming and deglaciating Arctic are generally identified, however their ecological consequences are poorly recognised. Here, we present relationships between the variable oceanographic conditions and community structure of seabirds foraging in a high-Arctic fjord. The Hornsund ecosystem depends largely on the advections of oceanic water into the fjord: the predominance of Arctic or Atlantic water masses on the SW Spitsbergen Shelf governs the hydrographic conditions in the fjord. Carrying different zooplankton and small fish communities, these two water masses affect the foraging conditions for seabirds, and consequently, their numbers and community structure. The coincidence of a propitious hydrological configuration in the fjord, stormy weather on the open sea and increased glacial activity is manifested by a spectacular boost in seabird numbers, thus reflecting interannual variability in the fjord ecosystem structure and functioning. Abundance of seabirds fluctuated markedly year-on-year, mainly because of the huge differences in numbers of species which forage alternately in the open sea and in the fjord, as the conditions permit. The coastal seabird community in Hornsund is dominated by kittiwakes preferring glacier bays with intensive subglacial discharges. These, however, are highly variable and depend on the stage of glaciers retreating.

61-HB

Spatial coincidence among climate change, tectonic activity and allopatric phylogenetic events in the Northern Andes of South America

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The tropical Andes of northern South America can be divided into 15 biogeographical regions where events of isolation and diversification played a key role in driving current diversity patterns (Hazzi et al. 2018). The Táchira Depression (Mérida Andes) and Las Cruces pass (Eastern Cordillera of Colombia) are two important geographic barriers that shaped biogeographic regions and were formed by mountain uplift and/or climate change. Phylogenetic studies of plants and mammals echo the presence of these barriers by parallel but independent evolutionary diversification. In this work we focus on these barriers and regions, and study the correlations between biodiversity and dispersal events, on the one side, and tectonic and climatic processes on the other. To evaluate different mountain building events by estimating long-term erosion rates, we use an updated thermochronological ages database in conjunction with seismicity data, faults distributions and short-term erosion rates. Recent studies have criticized thermochronology data to have insufficient resolution to assess whether late-Cenozoic climate change affected erosion rates (Schildgen et al. 2018), and especially the Mérida Andes has been problematic. With our new dataset and previous work (Mora et al., 2008; Bermúdez et al., 2013) we present the latest estimates that provide new insights into the geological and climatic history of Eastern Cordillera of Venezuela and Mérida Andes. Contrasting exhumation rates and tectonic quiescence are a key parameter that could explain the presence of allopatric phylogenetic events in the region. Elsewhere, large landslides caused by faults, torrential avalanches and easily eroded lithology coincide with phylogenetically poor areas.

62-HB

Ancestral origin, dispersal routes and evolutionary history of Ulmaceae: a phylogenomic approach

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Ulmaceae is an important woody family in the northern temperate forests. However, its phylogenetic relationships and biogeographic history remain poorly resolved. In this study, we reconstruct its phylogeny, diversification and biogeographic histories based on complete chloroplast genome and nuclear sequences. Our results show that Ulmaceae s.s. includes seven genera which can be divided into two main clades, i.e. the temperate and the tropical clade. The temperate clade includes four genera and their phylogenetic relationships are ((Ulmus+Zelkova)+Hemiptelea) with Planera having an uncertain phylogenetic position. The tropical clade includes three genera and their phylogenetic relationships are ((Ampelocera+Phyllostylon)+Holoptelea). The conflict phylogenetic position of Planera suggests that it is most likely an ancient hybridization and introgression of the subg. Oreoptelea species of Ulmus (like U. serotina and U. alata) and Zelkova. Divergence time estimates show that the origin of Ulamceae may date back to the Early Cretaceous at ca. 118.3 Ma with most of lineages accumulated from the late Cretaceous to the early Eocene (ca. 50-85 Ma), subsequently slowed down during the middle to late Paleogene (ca. 45-23 Ma) and followed by a rapid diversification in the Neogene duo to the global cooling and expansion of the temperate zone. The ARR analysis reveals that the ancestral region for the crown of Ulmaceae was East Asia and Neotropics and Indochina during the Late Cretaceous. The BLB and NALB could be important corridors for Ulmaceae migrations.

63-HB

Using Online Web-Mapping Tools to Create Accessible Quaternary Ecology Visualizations

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Animated maps of taxa distributions since the last deglaciation offer immediately accessible visualizations of species range shifts in response to past environmental change. These visualizations are useful to experts for understanding past patterns and processes and to educators and science communicators. In addition, they can be developed and shared on a variety of platforms. Here, we are developing new workflows for online animated visualizations of taxon range shifts since the last glacial maximum, using data from the Neotoma Paleoecology Database and Carto VL, a Javascript library that interacts with Carto APIs to build maps and animations. Using the Neotoma Paleoecology Database's R package, we downloaded, cleaned, and temporally interpolated pollen, vertebrate, and diatom records from 21,000 years ago to present. Then, we used Carto VL's formatting tools to define the parameters of the animation and styling. All workflows will be made publicly available on GitHub so that other interested users can extend this approach to other regions, times, and taxa. The completed visualizations are interactive and clearly illustrate major shifts in taxa distribution over the last 21,000 years. The next stage will be to update and improve Ice Age Mapper, a web application initially built by Scott Farley using Open Web technology stack of open-source tools including the Mapbox-GL, D3, and Crossfilter libraries.

64-HB

Chemocoding as an identification tool where morphological- and DNA-based taxonomic methods fall short: Inga as a case study

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Cataloging the world's plant diversity has been an ongoing challenge for centuries, and because of accelerated anthropogenic extinctions, the rapid documentation of biodiversity is more critical than ever. Just over a decade ago, DNA barcodes were proposed as an alternative to morphological approaches for species identification. Although DNA barcodes have proved to be successful for most organisms, these have failed to discriminate within many species-rich genera of plants. Here, we examine how chemical fingerprinting, or chemocoding, may be particularly helpful in distinguishing confusing or closely related species in the species-rich and recently radiated Neotropical genus of trees Inga Mill. (Leguminosae, Mimosoideae). Using untargeted metabolomics in combination with multivariate analysis to characterize small defense-related chemical markers, we constructed phytochemical, species-level fingerprints, which we define as chemocoding. Specifically, we compared the effectiveness of conventional DNA barcoding, next generation sequencing, and chemocoding to discriminate among closely related species of Inga within a single site and between sites. Our results show that chemocoding is faster and more efficient and effective than DNA-based species discrimination methods.

Given that the species is the fundamental unit of analysis for conservation, biodiversity assessment, and for understanding ecological and evolutionary processes, the development of accurate identification methods is essential. Moreover, even after species have been designated, distinct species may not differ morphologically such that correct identification in the field may require a cheap, fast method that will permit confirmation for every plant. We suggest that chemocoding is a valuable tool for distinguishing confusing species, particularly in the diverse tropics where many species-rich genera do not resolve with DNA barcoding.

65-HB

Likelihood approach to the biogeography of Atlantic Rainforest frog family Cycloramphidae

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The neotropical anuran family Cycloramphidae, with 36 valid species in the genus Thoropa, Cycloramphus and Zachaenus, occurs over the Atlantic Forest. Most of the species have restricted distributions, bonded by mountains. Despite that making sense for stream-dwelling species, there is a litter-dwelling clade that could have larger distributions. Also, there are species with disjunct distributions, suggesting that there were widespread ancestors. This brings to debate the historical questions behind the distributional patterns currently observed. Herein, we analysed this historical role in a previous phylogeny of 20 Cycloramphidae species based on 91 morphological characters from the group. We implemented six Maximum Likelihood models in the R package BioGeoBEARS to estimate the ancestor's distributional patterns and the biogeographic processes involved. We defined seven areas for the regionalisation of the Atlantic Forest according with the Biotic Elements from a previous study for anurans of this domain. The best fitted model (BAYAREALIKE+j) suggests that the region between the southern Serra da Mantiqueira and Serra dos Órgãos was the Cycloramphidae ancestors' range of distribution, as for the most part of the internal nodes. It also seems to be the region with the higher diversification on the family, especially between 30—20 mya. The most common biogeographic processes along the phylogeny were founder-event and dispersal. Our results are still preliminary, but this model is a good fit to explain the disjunct distribution in some species, and the inclusion of more Thoropa species could clarify this effect.

66-HB

SSDM: An R package to predict distribution of species richness and composition based on stacked species distribution models

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There is growing interest among conservationists in biodiversity mapping based on stacked species distribution models (SSDMs), a method that combines multiple individual species distribution models to produce a community-level model. However, no user-friendly interface specifically designed to provide the basic tools needed to fit such models was available until now. The "ssdm" package is a computer platform implemented in r providing a range of methodological approaches and parameterisation at each step in building the SSDM: e.g. pseudo-absence selection, variable contribution and model accuracy assessment, inter-model consensus forecasting, species assembly design, and calculation of weighted endemism. The object-oriented design of the package is such that: users can modify existing methods, extend the framework by implementing new methods, and share them to be reproduced by others. The package includes a graphical user interface to extend the use of SSDMs to a wide range of conservation scientists and practitioners.

70-NB

Contribution and impact of the Humboldt's ideas on the study of the complexity of the Mexican Biota during the 19th century

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For more than two hundred years, several naturalists had already recognized the Mexican flora as a complex group of components difficult to be described and studied. Humboldt´s ideas contributed to elucidate the geographical patterns of this flora. In this study, we analyse how Humboldt and contemporarys explained the geographical distribution of the Mexican flora, trying to match adapt it to his classification of botanical regions.

For Humboldt and Bonpland, the complexity of the Mexican flora could be explained as product of convergence between two different floras, the northern and southern ones. Augustin de Candolle (1820) highlighted the 'Mexique' botanical region based on its typical and characteristic plant families. In turn, Alphonse de Candolle (1855) found a high biotic replacement in Mexico due to the convergence of three botanical regions: (1) Pacific south of Mexico to Guayaquil, (2) Gulf of Mexico and Guatemala at Caribe slope, and (3) mountain ranges surrounding the Central Mexican Plateau. Finally, Wallace (1876) considered a Mexican sub-region, belonging to the Neotropical region, as an extensive transition zone.

Naturalists like Alfonso L. Herrera (1891), Grisebach (1878), Sumichrast (1875) and Martens and Galeotti (1887), adapted the Humboldt's system of botanical regions to the Mexican flora. However, all of them found inconsistencies in his system. This was explained because of high amount of endemic species (particularly in all mountain ranges, dry tropical forests, and arid lands) as because of the apparently chaotic overlapping of ranging species which spread toward other northern and southern regions.

71-NB

Diversification in a biodiversity Hotspot: Species discovery and historical biogeography of a burrowing crayfish of southern Chile

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The Chilean freshwater crayfishes of Parastacidae have been little studied at the population genetic level, different hypotheses have been proposed to understand the current distribution of this group in South America (disjunct, with species in Chile, Brazil, Uruguay and Argentina). Parastacus nicoleti is an endemic species of burrowing crayfish from southern Chile, and here we perform a mitochondrial DNA analysis to characterize its genetic diversity, hypothesis of primary species and ancestral areas reconstruction. A total of 170 individuals from 30 populations were analyzed using the mitochondrial gene COI (total 650 base pairs) plus 15 indivudals from South American Parastacidae species. We found profound genetic differences and low gene flow between populations. Our results with mitochondrial DNA show three major clades (north, center and south) and nine groups structured geographically. Single locus species delimitation recover between five and eight putative species. This result can be attributed to the great geographical roughness of the study area, that isolates P. nicoleti populations from each other, this in addition to the lack of dispersion of these organisms plus the presence of geographical barriers, mainly by the Cordillera de la Costa. We suggest that P. nicoleti is a complex of several species. The origin of South American parastacids was in the center-south of Chile. Biogeographical events such as the early marine transgressions that shaped the hydrography of southern America can better explain the historical biogeographic process, rather than later events such as the uplift of the Andes. This work is a novelty in the study of the genetic diversity of P. nicoleti.

72-NB

Biogeography and conservation of Atlantic Forest anurans

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The global biota is distributed non-randomly forming geographic distribution patterns. One of the processes explaining these distributions is vicariance, in which a geographic barrier is responsible for fragmenting the geographical distribution of a population. Species that coexist in a certain area form biogeographic units. Examples of widely distributed biogeographic units are the morpho-climatic domains, such as the Atlantic Forest. The highest diversity of anuran amphibians around the world is found in the Atlantic Forest. However, this domain is highly explored since the beginning of the South America colonization, contributing to the population decline of amphibians. The aim of this study was to analyse the current scenario of anuran amphibians in the Atlantic Forest, identifying biogeographic units, to test the vicariance model predictions and to evaluate if diversity patterns and processes have been conserved. We used the revised polygons of the International Union for Conservation of Nature (IUCN) as a database, and Biotic Element (BE) analysis to identify biogeographic units. The conservation analyses were based on the protected areas (PAs) made available by IUCN and the land use map made available by ESA Climate Change Initiative. We recovered 21 biotic elements, and the predictions of the vicariance model were valid, with sister species present in different BEs. On average, BEs had 33% of forest remnants, and only 12% of its total area was protected by PAs, which means that patterns and processes have not been conserved.

73-NB

Space-time trajectory inferred by a geographically explicit event model: the case of Callicebinae (Pitheciidae) in the Neotropics

Peter Löwenberg-Neto, UNILA; Stephanie Winkelmann, Unila

The Callicebinae subfamily is a diverse group and is widespread across the neotropical region, embracing an extensive range of distribution along South America. There is a small amount of information about the past of these species, the fossil record is low and therefore, this group needs more research. We reconstruct the historical steps the Callicebinae made using a geographically explicit event model, implemented in a computer program called EVS, that does not require predefined areas, which is the differential and one of the main reasons as to why this method was chosen. It gives us a possible idea of what were the biogeographical events that occurred connected with cladogenesis in each different node, and also, infers the internal ranges based on the terminal ranges. We used 18 species from three different genera: Callicebus, Cheracebus and Plecturocebus, based on Byrne et al. (2018) and Carneiro et al. (2018). As a result, two equally best reconstructions showed up, with only one different event. Most of the biogeographical events were sympatries, followed by founder events, vicariances and point sympatry. Much of the data is discussed in comparison to Byrne et al. (2018), showing the historical narrative of the Callicebinae throughout South America and how they became such a diverse group. This reconstruction can help provide information not only for the Callicebinae group diversification but also, it can help show more of the biogeographical history of the Neotropics and explain important biotic connections.

74-NB

Time and direction of dispersal events of the New World monkeys

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The ancestor of Platyrrhini (Primates) arrived in the Amazon region during Oligocene and, since then, the lineage diverged into 5 families, 21 genera and 171 species. Today, species are distributed in the Amazon, Atlantic forests and areas of Caatinga, Cerrado and Chaco. Herein we spatially and temporally quantified the dispersal events during the diversification of the Platyrrhini clade. We adopted the regionalization scheme based on interfluvial zones. Geographic and phylogenetic data of 65 species were fitted to a dispersal-extinction-cladogenesis model. Based on the inferences of the model, we quantified the direction of dispersal events, absolute and relative numbers of dispersals through time. DEC model inferred 87 events of dispersals, 70% of the events occurred among areas within the Amazon. Amazon was the primary source of lineages, while Central Grasslands and South Atlantic Forest were sinks only. Interbiome dispersals occurred more frequently between Central Amazon, Cerrado/Caatinga and North Atlantic Forest. Dispersal through time plot indicated a peak of events during Oligocene-Miocene (~24 Ma), and then a decreasing tendency towards the present. Dispersals from Amazon to Atlantic forests started during Miocene (15 Ma) until Pleistocene and was timely congruent with mammal interchanges by the SE-NW route. Platyrrhini historical narrative is marked by high frequency of events of dispersals within the Amazon region during Oligocene-Miocene when several geological events took place, and by decreasing frequency of events since Miocene until present.

75-NB

Paleomodelaje de las áreas potenciales de distribución de las especies del género Polietina (Diptera: Muscidae) en la región Neotropical

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El calentamiento global que viene ocurriendo desde el Último Máximo Glacial provoca variaciones en los patrones climáticos globales, lo cual afecta la distribución de las especies mediante cambios en su forma, tamaño y/o posición. Las especies del género Polietina son sensibles a los cambios de temperatura y humedad, y se espera que sus áreas de distribución se hayan modificado a consecuencia del cambio climático. El presente trabajo buscó describir y comparar la variación ocurrida entre las áreas de distribución de las especies de Polietina entre el Último Máximo Glacial y el presente, y evaluar la existencia de una estructuración filogenética en dicha variación. Se llevó a cabo el modelaje de las áreas de distribución, para la posterior estimación y comparación de distintos parámetros relacionados a su tamaño y posición, y finalmente se calculó el índice de correlación entre los cambios en el tamaño del área de distribución de cada especie. Los resultados demuestran que las distribuciones espaciales de las especies estudiadas cambiaron a partir del Último Máximo Glacial, ocurriendo la expansión o contracción de las mismas, y no se observa un patrón en su magnitud, reflejando los parámetros específicos del nicho fundamental existente de cada una. Se observó además, en todos los casos, un dislocamiento de las distribuciones hacia el Noroeste del continente Sudamericano. Finalmente, se determinó que la proximidad filogenética no influye en las variaciones encontradas.

76-NB
¿El tamaño del área de distribución de las especies de platirrinos presenta estructuración espacial?

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Los platirrinos comprehenden monos endémicos de la región Neotropical que ocupan una variedad de hábitats en zonas tropicales y subtropicales. La comprensión del patrón de tamaño del área de distribución y sus variables correlacionadas es uno de los principales temas en Aerografía y Macroecología. En el presente trabajo nosotros investigamos si hay variables que presentan correlación con el tamaño de las áreas de distribución de las especies de Platyrrhini. Los polígonos de distribución de las especies (n = 123) fueron obtenidos en el sitio electrónico de IUCN. El tamaño del área de cada especie fue computado y descrita la frecuencia del tamaño de las áreas. Análisis de correlación de Pearson fueran ejecutadas entre el tamaño del área y las siguientes variables: latitud, longitud, altitud y masa corporal. Además, el tamaño medio de las áreas fue mapeado en cuadriculas de 2,5 arco-minuto, los datos de masa corporal fueran obtenidos de los sitios especializados y descriptos en envolturas de restricción triangular. El histograma de la frecuencia de tamaño de áreas en escala aritmética presentó distribución unimodal y derecho sesgado, muestreando que hay gran cuantidad especies con áreas de tamaño pequeño. Ninguna variable analizada presentó correlación significativa con el tamaño de área de distribución de los monos y, por lo tanto, el efecto Rapoport no fue observado en los datos. El tamaño de las áreas de distribución de Platyrrhini no se encuentran estructuradas según las variables testadas y solamente la frecuencia de los tamaños de áreas presento un padrón aerográfico esperado.

77-NB
The biogeography of the birds in the lowest mountain pass of the Tropical Andes: a climatic approach

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The current knowledge of bird diversity patterns on Tropical Andes is related small number of studies from cloud forest of east Andes in Peru and Bolivia. In contrast, dries inter-Andean slopes remain understudied. The lowest mountain pass of the Andes, named Abra Porculla at 2145 m, is allocated in the middle of Huancabamba depression that divides the northern and central Andean chains, hindering the distribution of bird diversity and increasing the endemism levels between them. In order to recognize the distribution of the birds in Abra Porculla – northwest Peru, we surveyed 40 localities between 1000 to 2200 m in both slopes of Andes using the line-transect method. Additionally, to understand the variables that drives such distribution, we performed a Principal Component Analysis using 19 bioclimatic variables dividing the study area in both elevational units and western and eastern slopes. We recorded 169 bird taxa, 138 to western and 122 to eastern slopes of Abra Porculla, three new trans-Andean records from western to eastern slopes: Amazilia amazilia leucophoea, Basileuterus trifasciatus trifasciatus and Euphonia saturata, as well as three remarkable records of range-restricted bird species: Thamnophilus shumbae, Patagioenas oenops and Incaspiza ortizi. Our results reveal that the Abra Porculla allows the dispersion of birds through abnormal climatic events that change the environmental conditions on both slopes. We interpret that drier and colder winters can help birds to go higher, while less hot and humid summers, to cross from one side of Andes to the other.

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