

25-28th September 2017



OVERVIEW SCHEDULE

	25th September	26th September	27th September	28th September
08.30 - 09.00 09.00 - 10.00	Workshops on Introduction to Bayesian inference of phylogenies with RevBayes	Three workshops in parallel: Introduction to Bayesian inference of phylogenies with RevBayes; Preparing successful papers in the Biogeographical Sciences; Historical Biogeography	Symposium: Paleoecology, Palaeontology and Paleoclimate of the Indian Plate	Symposium: Building bridges in biogeography - Gondwana to Laurasia
10.00 - 10.30		Coffe	e break	
10.30 - 12.00	Workshops on Introduction to Bayesian inference of phylogenies with RevBayes	Three workshops in parallel: Introduction to Bayesian inference of phylogenies with RevBayes; Preparing successful papers in the Biogeographical Sciences; Historical Biogeography	Contributed session: Defin- ing conservation priorities based on biogeographic value	Contributed session: Speciation and diversification in the Indian Subcontinent
12.00 - 13.00		Lunc	h break	1
13.00 - 14:00		Three workshops in parallel: Introduction to Bayesian	Contributed session:	Contributed session: Hot topics in biogeography
14.00 - 14.30	Workshops on Introduction to Bayesian inference of phylogenies with RevBayes	with RevBayes; Preparing successful papers in the Biogeographical Sciences; Historical Biogeography	Community ecology, phylogeny and biogeography	Mini-Session: Savannah Biogeography
14.30 - 15.30		Registration with Biogeography coffee, soda, ice-cream & snacks	Mini-Session: Biogeography of Rivers	
15.30 - 16.00	Coffee break	Welcome and inaugural session	Biogeography coffee, s	oda, ice-cream & snacks
16.00 - 16.30		Plenary Talk by Ashok Sahni - Paleontology and		
16.30 - 17.00		paleoecology	Poster Session	Poster Session
17.00 - 17.30		Popular Science Talk by Pranay Lal on Indica - The		
17.30 - 18.00	Workshops on Introduction to Bayesian	Deep Natural History of the Indian Subcontinent	_	Plenary Talk by Michael
18.00 -18.30	inference of phylogenies with RevBayes	Biogeography and Society: Talk and Introduction to "Islands in the sky" - A photo-exhibit by Prasen-	Travel to NCBS	biome shifting, and functional traits in a widespread plant clade
18.30 - 19.00		jeet Yadav Discussion on outreach in Biogeography	Plenary: Scott Edwards (at NCBS)	Closing session
19.00 - 19.30				
19.30 - 20.00			Informal discussion on Biogeography and Urban Landscapes led by Harini Nagendra	
20.00 - 22.00			Conference dinner (for registered & invited participants)	

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08.30 - 10.00	3 Workshops in parellel: Introduction to Bayesian inference of phylogenies with RevBayes; Preparing successful papers in the Biogeographical Sciences; Historical Biogeography
10.00 - 10.30	Coffee break
10.30 - 12.00	3 Workshops in parellel: Introduction to Bayesian inference of phylogenies with RevBayes; Preparing successful papers in the Biogeographical Sciences; Historical Biogeography
12.00 - 1.00	Lunch break
01.00 - 02.30	3 Workshops in parellel: Introduction to Bayesian inference of phylogenies with RevBayes; Preparing successful papers in the Biogeographical Sciences; Historical Biogeography
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02.30 - 03.30	Registration with Coffee, soda, ice-cream & shacks
03.30 - 04.00	Welcome and inaugural session
03.30 - 04.00	Plenary Talk by Ashok Sahni on Dynamics and Evolution of South and South East Asian Palaeogene Biota: Science, Speculation and Storytelling!
03.30 - 04.00 04.00 - 05.00 05.00 -05.45	Registration with Coffee, Soda, ice-cream & shacks Welcome and inaugural session Plenary Talk by Ashok Sahni on Dynamics and Evolution of South and South East Asian Palaeogene Biota: Science, Speculation and Storytelling! "Popular Science Talk by Pranay Lal on Hidden landscapes: how geology influences everything, from evolution to climate change
02.30 - 03.30 03.30 - 04.00 04.00 - 05.00 05.00 -05.45 05.45 - 7.00	Registration with Coffee, Soda, ice-cream & shacks Welcome and inaugural session Plenary Talk by Ashok Sahni on Dynamics and Evolution of South and South East Asian Palaeogene Biota: Science, Speculation and Storytelling! "Popular Science Talk by Pranay Lal on Hidden landscapes: how geology influences everything, from evolution to climate change "Biogeography and Society: Talk and Introduction to "Islands in the sky" - A photo-exhibit by Prasenjeet Yadav

27th SEPTEMBER 2017

08.30 - 10.00	Symposium: Paleoecology, Palaeontology and Paleoclimate of the Indian plate	Chair: Vandana Prasad
08.30 - 8.50	Role of Plate Tectonics in the disjunct distribution of plant species	Vandana Prasad
08.50 - 09.10	Palaeobiogeography of Neogene Mammals of India	Rajeev Patnaik
09.10 - 09.30	Late Pleistocene hominin biogeography in the Indian Subcontinent	Parth Chauhan
	Speed-talks	
09.35 - 09.40	Pleistocene land bridges and speciation in Wallacea	Kritika Garg
09.40 - 09.45	Biogeography of seabirds in Bay of Bengal in relation to oceanographic variables	Ravichandra Mondreti
09.45 - 09.50	Faunal Change in the Plio-Pleistocene of the Indian Subcontinent	Advait Jukar
10.00 - 10.30	Coffee break	
10.30 - 12.00	Contributed session: Defining Conservation Priorities Based on Biogeographic Value	Chair: Uma R
10.30 - 10.50	Phylogenomics and conservation	Craig Moritz
10.50 - 11.05	Latitudinal gradients in marine species richness	Chhaya Chaudhary
11.05 - 11.20	Patterns and drivers of endemism in the Western Ghats Escarpment	S P Vijayakumar
11.20 - 11.35	Phylogenetic & evolutionary tools in conservation prioritization- Sri Lanka	Dilini Abeyrama
11.35 - 11.40	Spatio-temporal changes in hornbill distributions in north-east India	Rohit Naniwadekar
11.40 - 11.45	Conservation of endemic leaping frogs -Western Ghats	Nikhil Modak
11.45 - 11.50	Elevational patterns of bird communities in Agasthyamalai Hills, Western Ghats	Madhumita Panigrahi
11.50 - 11.55	Moths of Himalayan Biogeographic Zone	Angshuman Raha
11.55 - 12.00	Anuran distribution pattern along an elevational gradient - E. Himalayas	Jayanta Kumar Roy
12.00 - 1.00	Lunch break	
1.00 - 2.30	Contributed session: Community ecology, Phylogeny and Biogeography	Chair: Jahnavi Joshi
01.00 - 1.15	ТВА	M Dawson
01.15 - 1.30	New biogeographic theory to explain small-island effect and latitudinal gradients	Deepthi Chimalakonda
01.30 - 1.45	Immigration is an important driver of diversity build-up in the Himalayas	Krishnapriya Tamma
01.45 - 2.00	Latitudinal gradients in range size & richness of woody plants - W Ghats	Navendu Page
02.00 - 2.05	Neutral & niche based community assembly of tree species - Sikkim Himalaya	Yangchenla Bhutia
02.05 - 2.10	Evolutionary Assembly of Communities in Butterfly Mimicry Rings	Jahnavi Joshi
02.10 - 2.15	Flowering phenology of Rhododendrons in the high altitude of the Himalaya	Shweta Basnett
02.15 - 2.20	Improving inference from patterns of phylogenetic community structure	Lessard J P
02.20 - 2.25	Lizard community organization in Andaman and Nicobar archipelago	Harikrishnan S
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02.30 - 03.30	Mini-Session: Biogeography of Rivers	Chair: Nachiket Kelkar
02.30 - 02.45	Aquatic Insects of Riverine Ecosystems: Biodiversity and Biogeography	K.A. Subramanian
02.45 - 03.00	ТВА	Jagdish Krishnaswamy
03.00 - 03.05	Fish diversity across river basins in the W. Ghats biodiversity hotspots	Vidyadhar Atkore
03.05 - 03.10	Roles of climate and geography in colonization of India by freshwater snails	Maitreya Sil
03.10 - 03.15	Species richness, elevational gradients in terrestrial & aquatic systems -Himalaya	Kumar Manish
03.15 - 03.30	Discussion on River Interlinking	Led by Nachiket Kelkar
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06.30 - 07.30	Travel to NCBS Plenary 2 : Scott Edwards (NCBS)	
06.30 - 07.30 07.30 - 08.00	Travel to NCBS Plenary 2 : Scott Edwards (NCBS) Informal discussion on Biogeography and Urban Landscapes led by Harini Nagendra	

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08.30 - 10.00	Symposium 1: Building bridges in biogeography - Gondwana to Laurasia	Chair: Praveen Karanth
08.30 - 08.50	Evolutionary history - pan tropical tree family Dipterocarpaceae	Selvadurai Dayanandan
08.50 - 09.10	Phylogenetic studies of some Indian plant taxa	Geeta R
09.10 - 09.40	Molecular phylogeny of Scincines skinks	Aniruddha Datta-Roy
09.40-10.00	Dispersal vs. vicariance: Biotic history of Indian vertebrates	Praveen Karanth
10.00 - 10.30	Coffee break	
10.30 - 12.00	Contributed session: Speciation and Diversification in the Indian Subcontinen	Chair: S. P. Vijaykumar
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10.50-11.05	Diversification in a continental radiation of Hemidactylus geckos	Aparna Lajmi
11.05-11.20	Drivers of diversification of herpetofauna in the Western Ghats Escarpment	Kartik Shanker
11.20-11.35	Speciation in oriental bat radiations in species rich South Asian mountain ranges	Balaji Chattopadhyay
11.35-11.40	Lineage delimitation using an integrative approach in Nyctibatrachus frog	Varun Torsekar
11.40-11.45	Origin and Evolution of the Genus Piper in Peninsular India	Sandeep Sen
11.45-11.50	A phylogeny of open-habitat lizards supports the antiquity of Indian grassy biomes	Ishan Agarwal
11.50-11.55	Non-sister Sri Lankan White-eyes are a result of independent colonizations	Nelum Wickramasinghe
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01.00 - 01.05	Citizen Science as a tool to study urban Biogeography: A case study from Bangalore	Kaberi Kar Gupta
01.05 - 01.10	Homoplasy in egg-eating snake genera in India & Africa - convergence of feeding modes	Avinash Visvanathan
01.10 - 01.15	Mountains, Climate and Biodiversity: A Collaborative Understanding	Carina Hoorn
01.15 - 01.20	Origin and diversification of birds from dry forests in South America	Alexandre Fernandes
01.20 - 01.25	Overview of how Indian birds may have evolved to live amongst humans in cities	Madhusudan Katti
01.25 - 01.30	Competition between birds and ants for nesting cavities in eastern Himalayas	K Supriya
01.30 - 01.35	Convergent evolution of key functional traits confers ecological success of tree species	Shivaprakash Nagaraju
01.35 - 01.40	Elevational and latitudinal diversity patterns of trees along the Himalaya	Suresh K Rana
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Workshops

1. Workshops on Introduction to Bayesian inference of phylogenies with RevBayes

Venue: Lotka - Voltera Lab, Centre for Ecological Sciences, Indian Institute of Science, Bangalore, India

Date: 25-26th September 2017

Instructors: Tracy Heath and Walker Pett

2. Preparing successful papers in the Biogeographical Sciences

Venue: Seminar Hall, Centre for Ecological Sciences, Indian Institute of Science, Bangalore, India

Date: 26th September 2017

Instructors: Peter Linder and Michael Dawson

3. Historical Biogeography

Venue: Reading Room, Centre for Ecological Sciences, Indian Institute of Science, Bangalore, India

Date: 26th September 2017

Instructors: Nicholas Matzke

PLENARY TALKS

Dynamics and Evolution of South and South east Asian Palaeogene Biota: Science, Speculation and Storytelling!

Ashok Sahni

This talk is about the distribution of faunas and floras in S and SE Asia in the context of Plate Dynamics, centres of origin, antiquity of evolutionary lineages and dispersal mechanisms. Based on geophysical studies of the Indian Ocean seafloor, the drift of the Indian Plate as an island subcontinent and its subsequent collision with Asia, is regarded as a major planetary event. Unfortunately, one of the most poorly understood facets of this epic journey is the nature of the biota during its supposed isolation before collision. Equally important are the biotic turnovers that took place after collision and as climate changed with the uplift of the Tibetan Block. Changing climate regimes may have led to biotic dispersals to South East Asia leaving a few relict refugia in South Asia.

The main issues and questions that have now emerged in the drift scenario are discussed below:

• The degree of isolation leading to possible Island endemism, in situ evolution and diversification, and preservation of relict taxa. Current data shows the cosmopolitan character of the biota during its drifting phase which is at odds in an isolated island ecosystem. The reasons for this are not apparent at the moment.

• Analogy to its erstwhile Gondwanan neighbour Australia with its unique fauna.

• The biotic response to the great latitudinal displacement of the landmass passing through a range of climatic conditions ranging from temperate, tropical to equatorial and survival in the midst of one of the greatest volcanic episodes of the Phanerozoic and diversification during PETM.

• A tantalizing absence of faunal data during its drifting phase specially during the Palaeocene while significant data has emerged both from the Cretaceous and the Lower Eocene.

CRETACEOUS

• Cosmopolitan affinities in general with some notable exceptions. Dinosaurs of large size of Gondwanan affinity with the exception of the iconic taxon Troodon a small raptor found in west-central USA and the Cauvery Basin. Mammals with mixed affinity: gondwantheres related to those of South America and Madagascar, while the eutherian Deccanolestes and other forms have affinities to taxa from northern Africa and Europe.

• Oldest global record of grasses and freshwater diatoms. The common presence of the Laurasiatic pollen taxa Aquilapollenites in South Asian late Cretaceous sections.

• Record of the first attempts towards grazing in mammals as evidenced by hypsodonty and enamel structure (gondwanatheres).

• Stable fluvio-lacustrine community (Cretaceous and Lower Eocene) with gar fish (Lepisosteus), osteoglossids, and mesoeucrocodiles. The ostracode assemblage is largely endemic at species level. Molluscan communities dominated by Physa and unionids.

LOWER EOCENE

• Research in the last 15 years in the Lignite Mines of the Lower Eocene of Western India has radically changed our concepts of (a) early mammalian evolution, (b) the spread of the first angiosperm tropical evergreen forests and (c) the centre of origin of social insects.

• The affinities of frogs, lizards, snakes show admixed Gondwanan and Laurasiatic affinity as do the insects preserved in amber nodules.

• "Modernity" of mammalian faunas can be measured by the "APP" quotient, that is the antiquity of artiodactyla, perissodactyla and primates. One of the oldest record of the first two mammalian Orders is found in South Asia during pre-collision. The dichotomy between the Primate groups of the strepsirrhines (lemurs etc.) and haplorhines (tarsiers, apes etc.) is remarkably demonstrated in the Vastan Lignite Mine material by three dimensionally preserved postcranials, a million years after the event was recorded in Eurasia by body fossils. Several reasons are offered.

• The oldest record of whales is from South Asia.

• Adapid primates persist as relicts in the Lower Siwalik of the Himalayan Foreland Basin.

• The finds of diverse mammalian lineages in the Gujarat Lignite Mines including tillodonts, pantodonts, rabbits, bats, rodents, insectivores, artiodactyla, perissodactyla, primates, hyaenodonts (Carnivora) have radically changed established ideas of mammalian evolution, turning the Indian drifting " raft " into a veritable Garden of Eden.

Multilocus phylogeography: from mtDNA to next-gen sequencing on two continents

Scott Edwards

Phylogeography is an essential component of modern biogeography, and yet, as a discipline, phylogeography has evolved constantly since its inception in the late 1970s. As the field first moved from mtDNA into multilocus nuclear genome and more recently into genome-wide analyses, the domain of phylogeography has expanded to include not only biogeographic questions but also the linking of genotype variation to phenotype variation and covariation with the landscape. In this talk, drawing from avian examples in Australia and South America, I will present examples of phylogeographic work from various stages in the evolution of the field from a single locus to a genome-wide discipline. I show that critical concepts, such as gene tree / species tree discordance and the distinction between coalescence time and population divergence time are as critical today as they were in the mitochondrial DNA era. Additional processes that complicate phylogeographic patterns, such as introgression and natural selection, were evident in the mitochondrial DNA era yet are now exquisitely revealed in genome-wide studies. With the new tools of next-gen approaches in hand, the field is poised to produce a global database of phylogeographic breaks and divergence times, a small example of which I will illustrate using the Gulf of Carpentaria in Australia. Genome-wide studies, such as we have recently produced for the blue-faced honeyeater (Entomyzon cyanotis) in Australia, involving analysis of over 6 million SNPs, show that reticulations and natural selection overlay an overall pattern of neutral divergence in isolation across areas of endemism.

Biogeography, biome shifting, and functional traits in a widespread plant clade

Michael Donoghue

In connection with our development of Viburnum (Adoxaceae) as a model lineage for studies of plant evolution and ecology, we have now inferred a comprehensive dated phylogeny based on multiple lines of evidence. Jointly with our phylogenetic inference, we have estimated past geographic movements and shifts between mesic forest biomes. This provides us with reliable estimates for movements within and between continents throughout the Cenozoic, as well as for multiple instances of adaptation to colder climates. Much of the action took place in Asia, with monsoonal broadleaved evergreen (lucidophyllous) forests playing a key role in transitions in both leaf form and phenology. From Asia there were multiple movements both to Europe and to the New World. The radiation of one lineage into montane cloud forests of the neotropics was fueled by replicated ecological speciation that resulted in two distinct leaf types in multiple regions.

08.30 – 10.00 AM Wednesday 27th September 2017

Symposium 1: Paleoecology, Palaeontology and Paleoclimate of the Indian plate

1. Role of Plate Tectonics in the disjunct distribution of plant species: Inferences from Indian plant fossil records

Vandana Prasad

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Genera and species of many tropical plant families show disjunct distribution amongst the Gondwana continent and SE Asian region. Based on the molecular data, the Dipterocarpaceae and Sarcolaenaceae represents core Malvales sister plant families. While Sarcolaenaceae is endemic to Madagascar, Dipterocarpaceae is one of the highly diversified and dominant plant family of SE Asian rain forest and show disjunct distribution in India, Sri Lanka, Africa, South America, Madagascar, Seychelles and SE Asia. Dipterocarpaceae family consists of 15 extant genera distributed in three sub-families Dipterocarpoideae. Pakaraimoideae and Monotoideae. Dipterocarpoideae clade is distributed in India, Sri Lanka, Seychelles and SE Asia, Monotoideae sub family is restricted to Africa and Madagascar and Pakaraimoideae sub family is endemic to South America. Present study provides evidence of fossil pollen of both Sarcolaenaceae and Dipterocarpaceae from late Cretaceous and early Paleogene sedimentary sequences of Indian subcontinent. Based on the phylogenetic analyses of pollen morphological features across the family Dipterocarpaceae, and Sarcolaenaceae 8 fossil genera of family Dipterocarpaceae and 3 genera in the family Sarcolaenaceae were identified. This suggest Gondwanan origin of these plant families. Amongst the identified fossil palynomophs large number of pollen species showing affinity with the extant Monotes genera of subfamily Monotoideae that is restricted to Africa and Madagascar suggesting early divergence of this clade. Profuse occurrence of palynofossils showing affinity with the Vatica, Hopea, Shorea and Dipterocarpus indicate evolution and diversification of Dipterocarpoideae clade during warm and humid climate during Cretaceous on Indian subcontinent. Perhumid climate due to high precipitation and low seasonality must have played its role in the range expression of Diptercarpoideae clade on the Indian subcontinent during early Eocene. In absence of early records of Diptercarpaceae from SE Asia it is interpreted that the Diptercarpoideae clade originated on Indian subcontinent and migrated to excessive wet climatic zones of SE Asia after the India Asia collision. Both Gondwana vicariance and long distance dispersal played their role in the global distribution of Dipterocarpacae. Absence of fossil records of Sarcolaenaceae in Indian subcontinent post Eocene suggests forest fragmentation or changing climatic condition post India Asia collision.

2. Palaeobiogeography of Neogene Mammals of India

Rajeev Patnaik

rajeevpatnaik@gmail.com

The Indian Subcontinent appears like a fortress today, surrounded by the Himalayas in the north, north-west, north-east, the Thar Desert in the west and the Indian Ocean in the south. Today, these barriers confine the biota, particularly terrestrial mammals to this province. However, the Neogene (2.5 to 24 ma) fossil mammalian record tells a different story. The Himalayan foothills preserve an exceptionally continuous record that give us a glimpse of the past biogeography of the Indian mammals. After the India-Asia collision some 50 ma ago, the Laurasiatheres (artiodactyls, perissodactyls, bats, carnivores and pangolins) dominated Eurasian landscape. Afrotheres (proboscideans, hyracoids, embrithopods) on the other hand dominated much of Africa. Around the early Miocene (~23 ma) tectonic movement of the Afro-Arabian plate resulted in a land connection between Afro-Arabia and Eurasia. The proboscideans Prodeinotherium and Gomphotherium were among the first African genera to cross the Afro- Arabia-Eurasia land bridge, followed by Zygolophodon, Choerolophodon, cf. Protoanancus, creodonts (Amphycion and Hyainailouros) and rodents (Kochalia) into the subcontinent. Rhinos, chalicotheres, anthracotheres and suids move in the opposite direction. The cricetid rodents Eumyarion, Spanocricetodon, Democricetodon and Primus followed by chipmunks Tamiops, Orienscuirus and gundi Sayimys disperse into the subcontinent from east (China). A little later, sometime between 17 and 16 Ma, African proboscidean Deinotherium, carnivore Dissopsalis and primate Dionysopithecus and east asian rodents Aliveria, Funambulus, Punjabemys, Mellalomys, Potwarmus and Kanisamys immigrate to the subcontinent. The bovid Eotragus and the suid Listriodon moved from Asia to Africa. During the Middle Miocene exchanges of bovids and rodents within Eurasia are prominent. Late Miocene saw the first appearance of the American horse Hipparion in the Indian subcontinent, whereas the mouse ancestor Progonomys disperses west and northwards from the subcontinent. The Siwalik bovids Kobus porrecticornis and Prostrepsiceros disperse towards Arabia and Africa around this time. The langur Presbytes makes its first appearance in the Siwaliks around 6.3 ma. The first lepoirds appear in the Siwaliks around 7 Ma from America. Hexaprotodon sivalensis and Elephas planifrons were immigrants from Africa to the Siwaliks in the Late Miocene (~6 ma) and Late Pliocene, respectively. The Indian bush rat Golunda appears at several places in Africa in the Pliocene time. Camelus and Equus were prominent American immigrants to the subcontinent followed by the African baboon Theropithecus. The constantly changing tectonic, climatic and vegetation scenarios of the subcontinent were most likely responsible for these immigrations, emigrations, extirpations, and endemic evolution.

3. Theorizing about Late Pleistocene hominin biogeography in the Indian Subcontinent using multidisciplinary datasets

Parth R. Chauhan, Ramandeep Singh, Abhimanyu Bhardwaj, Shashi Mehra parthrc@iisermohali.ac.in

The Indian Subcontinent has a diverse environmental history with a mosaic of ecological and climatic patterns spread across the entire region. Combined with palaeoclimatic fluctuations such as the monsoon regime, faunal, floral and related ecological attributes must have had major implications on early human dispersal and colonization events as well as on subsequent behavioral and technological adaptations. This paper provides a brief update of the South Asian Paleolithic record including recent debates and discoveries, followed by a general review of multidisciplinary studies done in geology, geochronology, geochemistry, palynology, vertebrate paleontology and so forth. An attempt is made to integrate these respective datasets to theoretically understand specific geographic barriers, corridors and related factors of faunal and human movements across time and space during the Late Pleistocene. Additionally, the compilation of the published data reveals the geographically and thematically uneven Quaternary research histories and highlights key gaps that need to be addressed in relation to current human evolutionary studies. One of the most critical issues lies with the lack of multidisciplinary paleoenvironmental reconstructions and associated geochronological applications at well-preserved Paleolithic sites. Other lacunae in our knowledge are related to the marginal presence of Early Pleistocene contexts south of the Siwalik Hills and the lack of absolute ages for specific vertebrate taxa including reliable First and Last Appearance Datums. Finally, human behavioral ecology and related factors are explored to explain the extinction and/or gradual geographic marginalization of select taxa over time, such as the ostrich and hippo.

Speed-talks

4. Biogeography of seabirds in Bay of Bengal in relation to oceanographic variables, Chlorophyll a (CHLa) and Sea Surface Temperature (SST)

Ravichandra Mondreti, Priya Davidar, David Grémillet ravichandra.mondreti@gmail.com

Seabirds only form about 3% of all bird species but their collective biomass far outweighs that of the land birds. It is therefore essential to map and analyze seabird distribution patterns across all oceans, to evaluate their functional relevance within marine food webs. In the Indian Ocean, there is a great scarcity of at sea bird surveys, especially in the Bay of Bengal, except for some stray records. We carried out at-sea surveys to study the seabird distributions in Bay of Bengal Large Marine Ecosystem. We analysed the patterns of seabird distribution in relation to oceanographic parameters, Chlorophyll a (CHLa) and Sea Surface Temperature (SST). Chlorophyll a (CHLa) is considered an important proxy of primary productivity while Sea Surface Temperature (SST) was known to be the main indicator of fronts where the prey aggregate. Sooty Tern and Wedge-Tailed Shearwater accounted for more than 90% of the total sightings, with 2200 and 239 individuals respectively. Mean densities of Sooty Terns was 15.46-57.38 birds km-2 whereas that of Wedge-Tailed Shearwaters varied from 1.89-4.64 birds km-2. Highest densities of Wedge-tailed Shearwaters (4.64 individuals/ km-2) and Sooty Terns (57.38 individuals/ km-2) were recorded in areas of low Chlorophyll concentrations (CHLa), as the CHLa values are uniform throughout the study region. Wedge-tailed Shearwaters were occurring both in the areas of low as well as high SSTs whilst Sooty terns had shown a preference for low SST regions. One of the prime objectives of the study was achieved by making the first attempt to look in to the relationship of seabirds with SST and CHLa, one being physical and the other a biological one. We suggest a better understanding of the seabird community along with the underlying ecological processes in least studied ecosystems like BOBLME is essential to include in marine conservation management planning.

Pleistocene land bridges and speciation in Wallacea Kritika Garg, Balaji Chattopadhyay, Dewi Malia Prawiradilaga, Frank Rheindt dbskg@nus.edu.sg

Cyclical periods of global cooling are important drivers of biotic differentiation on our planet. During periods of global cooling, large parts of the world's seawater are locked up in ice, leading to worldwide drops in sea level and formation of land bridges, allowing for potential gene flow across landmasses. Further, species biology plays an important role in genetic differentiation and speciation. In this study, we compared two insectivorous forest passerine species complexes (golden whistlers and henna-tailed jungle-flycatchers) across two Wallacean islands (Taliabu and Peleng) that have repeatedly been connected through Pleistocene land bridges. Although the two bird complexes are similar in ecological attributes, the forest and edge-inhabiting whistler is comparatively flexible in its diet and niche requirements than the flycatcher, which is largely restricted to the forest interior, suggesting higher levels of differentiation between flycatcher populations compared to the whistler. We used genome-wide SNPs and mitochondrial data to understand population differentiation and divergence across islands. Further, we performed coalescent simulations to estimate levels of gene flow across islands and divergence time. We observed high level of differentiation between the two island populations of the diet specialist henna-tailed jungle-flycatcher compared to the more generalist golden whistler populations. The divergence time between two populations of henna-tailed jungle-flycatcher was earlier than the golden whistler populations. Further, we observed much lower levels of gene flow between henna-tailed jungle-flycatcher compared to golden whistler populations. Our results show that Pleistocene land bridges act as semipermeable agents of gene flow in Wallacea, allowing only certain taxa to connect between islands while others remain isolated. Land bridges during Pleistocene are not equally accessible by all species and depend on species biology, as species with specialised niche are more isolated and differentiated compared to generalist species.

6. Faunal Change In The Plio-Pleistocene Of The Indian Subcontinent

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Advait Jukar

The Plio-Pleistocene mammal faunas of the Indian Subcontinent are best known from the Siwaliks, and can be divided into two faunal zones: Tatrot, which extends up to the Neogene-Quaternary boundary, and Pinjor, which spans most of the Early Pleistocene. While fossils of this age have been collected since the mid 1800s, it is only recently that magnetostratigraphy has allowed us to analyze more detailed patterns of faunal change in this region. Here, I characterize the species-level turnover of artiodactyls, perissodactyls, and proboscideans. Species lists were collected from the published literature from the Indian and Pakistani Siwaliks, and correlated with the paleomagnetic time scale. Taxa were binned into five time periods from 3.6Ma to 0.78Ma. Turnover was calculated using the Sørensen-Dice dissimilarity index, and its compositional difference and nestedness components. Changes in the proportional representation of families and faunal body mass distributions were also assessed. Faunal turnover is seen after 3.1Ma and 2.58Ma, largely driven by changes in species composition. A smaller peak after 1.77Ma is also present, but is likely caused by sampling effects. A gradual decline in suids, and a proportional increase in bovids is seen after 3.1Ma, resulting in an assemblage resembling modern subcontinental faunas. The average and median body mass also increases through time. The turnovers between 3.6Ma and 0.78Ma are characterized by the immigration of large herbivores after 3.1Ma, and the replacement of smaller herbivores by other large taxa after 2.58Ma. These two events coincide with the onset of northern hemisphere glaciations, sea-level change, and global aridification. Further investigations of the functional change of the Siwalik herbivores will help determine whether the patterns of turnover observed are consistent with the expectations of climatically induced habitat change. Due to sampling issues, it is unclear whether more turnovers take place after 2.58Ma.

Posters

7. The Impact Of Mid And End-Permian Mass Extinction Events On Terrestrial Ecosystem Of The Godavari Graben, India.

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The Permian has witnessed two major mass extinction events during the mid and end-Permian. The impact of these global events on the terrestrial ecosystems and biodiversity is diachronous. The Godavari Graben preserves a thick pile of late Permian and early Triassic sediments in the form of Kamthi Formation. Here, a detailed palynological data from different palynologically well-dated mid Permian (Guadalupian) to early Triassic sequences of Godavari Graben is presented to decipher the impact of Permian mass extinction events on terrestrial ecosystem and biodiversity patterns of different plant groups. The palaeovegetational inferences have been made based on pollen affinities and biodiversity changes by accounting the variations in palynofloral composition of different plant groups. The palynological analysis reveals seven floral phases between the late Permian to early Triassic. The five floral phases of late Permian are chiefly dominated by glossopterids while pteridophytes and other gymnosperms like Cordaites, peltasperms, conifers were the subsidiary elements of the palaeovegetation. The glossopterids had their bloom and diversified under the warm and humid environments till the end-Guadalupian mass extinction. Post-Guadalupian, the glossopterids started to decline while other plant groups like, peltasperms and conifers expanded their ecological niches. This replacement of glossopterids by different plant groups due to environmental perturbations (seasonally drier environment) resulted in high biodiversity during latest Permian (Changhsingian). But with the onset of Mesozoic, the floral diversity has considerably declined as many plant groups like, glossopterids, Cordaites witnessed a major set-back due to end Permian mass extinction. This aftermath has reshaped the terrestrial vegetation into stress-tolerant lycopsid dominated palaeoflora. The presence of achritarchs and abnormal pollen grains also infer unfavourable conditions. The study reveals a subsequent increase in the aridity of environment which transformed the closed arborescent glossopterid dominated forest of the late Permian to an open lycopsid forest in the Triassic.

8. Biogeography Of The Tropical Plant Family Ebenaceae: Fossil Evidences From The Indian Subcontinent

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Ebenaceae, a low generic diversity family is widespread in the tropical and subtropical regions of the world having its affinity to the Rainforest, Deciduous and Savanna biomes. In the present study, 10 fossil species of pollen belonging to this family were recovered from the Eocene succession of Vastan Lignite Mine, Gulf of Cambay, India. Phylogenetic and S-Diva analyses were carried out using 62 pollen representatives, extant as well as fossil, by incorporating their morphological and distribution data. The results articulate that five of the ten fossil species share synapomorphic characters with D.crassiflora, D.fischeri, D.macrocalyx, E.tomentosa and D. monbuttensis. The remaining five are plesiomorphic to the taxa of their respective clades. S-Diva resolved the ancestor of the family to be in the region of Africa and India. The presence of utmost extant diversity and maximum endemism in Africa also subsist its origination in Africa during Gondwana period. The family diversified with time following 47 dispersal events (when maximum area was set at 4 in S-Diva) and obtained the present pantropical allocation. The present disjunct distribution can be supported by the India Asia collision, long distance dispersal (LDD) events and the migration of species along the margins of NALB (North Atlantic land Bridges) in the North Atlantic Ocean and the Indomalayan islands in the Indian Ocean.

10.30 – 12.00 PM: Wednesday, 27th September 2017

Contributed Session 1: Defining Conservation Priorities Based on Biogeographic Value

Invited Talk

1. Phylogenomics and conservation

Craig Moritz

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An enduring goal of conservation is to sustain biological diversity in all its forms. This entails protecting both the species and genetic diversity that has arisen through past evolution and the processes that will enable persistence through future environmental change. Tropical biomes present a major challenge in that their high and often unique diversity is often poorly described let alone understood. Our recently acquired ability to obtain and analyse genetic information at genome scale combined with spatial modelling and traditional systematics and field work is transforming our knowledge of such systems identifying vast taxonomically unrecognized diversity and novel hotspots of endemism. Applying phylogenetic (or network?) approaches to these increasingly extensive data enables us to describe diversity and assess conservation value in a way that is robust to changing taxonomy and can be applied to real world problems now. That said the issue of how to translate phylogenomic results to taxonomy $\hat{a} \in$ i.e. genetic species delimitation $\hat{a} \in$ remains a work in progress. These issues will be illustrated using results from recent studies of low dispersal vertebrates across tropical Australia and the Atlantic rainforests of Brazil.

Contributed talks

2. Latitudinal gradients in marine species richness

Chhaya Chaudhary, Hanieh Saeedi, Mark John Costello <u>ccha961@aucklanduni.ac.nz</u>

Latitudinal gradients in species diversity is a well debated topic in the field of biogeography. Bimodal latitudinal gradient is, when species diversity dips at the equator and peaks on either side of it. Bimodality in overall marine species diversity has contradicted the age-old paradiam, that suggested highest biodiversity at the equator. Diversity dip at the equator has widely been attributed to sampling bias in the past literature. We used species distribution data from Ocean Biogeographic Information System (OBIS) to analyse the latitudinal gradients in overall 51,670 species of Animalia. The study shows influence of sampling on bimodality. We used three diversity indices i.e., alpha (average species in latitude-longitude cells in a latitudinal band), gamma (total species in a latitudinal band) and ES50 (Hulbert index) at two spatial scales (i.e., 5° latitudinal band and Hexagon ~ 50,000 sq. km). We found that alpha diversity was highly significantly correlated to the sampling effect as compared to gamma diversity. Furthermore, when the sampling effect was minimised using ES50, the equatorial diversity dip remained consistent. However, the diversity peaks were found symmetrical on either side of the equator, contradictory to the asymmetric gamma diversity peaks. The results suggested that sampling does play an important role in determining the species diversity patterns and needs to be considered. Also, the diversity dip is not an artefact of sampling bias. Our findings support the hypothesis that sea surface temperature at the equator is already too hot for some species and could be one of the main reasons for the equatorial diversity dip.

3. Patterns And Drivers Of Endemism In The Western Ghats Escarpment

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S P Vijayakumar, Vijay Ramesh, Kartik Shanker, Uma Ramakrishnan vijay_rhaco@yahoo.com

Endemism has long been used as a parameter to recognize biogeographic regions globally. Here, we identified areas of paleo- and neo-endemism for bush frogs in the Western Ghats Escarpment and tested whether the areas have served as refugia. Location: Western Ghats, Peninsular India, Oriental Realm. We used distribution models - based on primary field data - to determine the geographical range of bush frog lineages. Endemism was calculated using multiple measures: WE (weighted endemism), CWE (corrected weighted endemism) and PE (phylogenetic endemism). For PE, we used a well-resolved clade of bush frogs. Endemism was calculated at a grid resolution of 0.05 degrees (5*5 km) at multiple spatial scales (0 (5 ' 5 km), 2 (15 ' 15), 4 (25 ' 25), 6 (35 ' 35), 8 (45 ' 45 km) neighbouring cells). Categorical analysis of was used to identify areas of paleo- and neo- endemism. Finally, we used climatic velocity estimates to test whether the endemic areas occur in climatically stable areas. A majority of the bush frogs lineages (>75%) showed narrow geographical ranges (< one degree latitude). Multiple (10) endemic centres were discernible at different spatial scales. These endemic centres showed different characteristics: paleo, neo and mixed. Endemic centres were coincident with major massifs in the southern and central regions of the Escarpment. We suggest a link between paleo- and neo-endemic centres in the massifs and the observed persistence of older lineages and underlying lineage diversification processes (allopatric speciation across massifs and in-situ radiation within massifs) in this clade. These results also provide insights into climatic stability and endemism. The centres of the endemism identified here provide a framework to implement conservation measures aimed at areas with unique evolutionary histories.

4. The use of phylogenetic and evolutionary tools in conservation prioritization for Sri Lanka

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All the components of biodiversity cannot be treated equally due to the limitations of resources available for conservation. Therefore biodiversity should be prioritized in effective conservation and site based conservation is one such model to achieve that. However parameters related to ecology, sociology and economics are primarily used for this prioritization process. Genetic and evolutionary history is broadly ignored. Using Important Bird Areas (IBAs: areas of high avian diversity or density) as a model, here we test the effectiveness of evolutionary tools in biodiversity prioritization for Sri Lanka. A phylogenetic tree for the total species of birds (342) recorded in Sri Lanka's IBAs (71) was generated from DNA sequence archives at www.birdtree.org using bioinformatics tools and higher-order phylogenetic backbone. Using this phylogenetic tree the Phylogenetic Diversity (PD), Evolutionary Distinctiveness (ED) and Evolutionary distinct endangered lineage (EDGE) scores of species and IBAs were ranked. Sri Lanka's premier Dry-zone National Park, Yala is the top ranked IBA in PD, ED and EDGE scores. Except Sinharaja Rainforest, all other Wet-zone IBAs, which are characterized by their high endemicity and biodiversity were not ranked among the top ten IBAs with high PD, ED or EDGE. Batrachostomus moniliger (Ceylon Frogmouth) is the most ED species while Otus thilohoffmanni (Serendib Scopesowl) is the most EDGE species of Sri Lanka. Use of ecological parameters in conservation prioritizing is costly as it requires ground surveying and expert knowledge on identification. Molecular parameters such as EDGE scores which are developed using data available in global databases can be used at relatively low costs to refine the conventional indices used in prioritization. PD, however is not informative in setting conservation priorities for an island like Sri Lanka as there are many endemic species that have diverged recently and do not contribute much to PD.
Speed-talks

5. Change for the worse: Spatio-temporal changes in hornbill distributions in north-east India

Rohit Naniwadekar, Karthik Teegalapalli, Raghunath R, Aparajita Datta rohit@ncf-india.org

Asian hornbills face high extinction risks due to their vulnerability to anthropogenic threats like hunting, logging and forest loss. Hornbills have potentially lost more than 60% of their original habitat. However, reliable information on their extant distribution and extent of distributional change over space and time is still lacking. We carried out a large-scale interview to assess the extant status of hornbills in north-east India and also estimate the changes in habitat-use probability over 20 years across five north-east Indian states spread over an area of 1,49,013 km2. The entire area of five states was gridded into 49 km2 grids which approximated known hornbill home ranges. We used an occupancy-based modeling framework to generate detection histories of five hornbill species found in north-east India at two time points (1993 and 2013). We conducted over 700 interviews across 283 villages between November 2013 and May 2014. Multi-season occupancy models were used to assess changes in habitat-use probability and detection probability. Single-species, multiseason surveys revealed that the habitat-use probability of all the hornbill species across space had decreased and the detection probability of the species which is often strongly associated with the abundance of the species had significantly reduced from 1993 to 2013. Overall habitat-use probability of Great Hornbill and Rufous-necked Hornbill has declined by more than 30%. Both these species had relatively high extinction probability (> 0.3). No hornbill species appears to have colonized unoccupied landscapes of the past. This is the first systematic assessment of hornbill distributions in north-east India. Questionnaire-based, detection/non-detection surveys allowed us to generate baselines for monitoring hornbill distributions in the future which is otherwise difficult to conduct with field-based surveys. The survey enabled identifying important sites for hornbill conservation in the future.

6. Conservation status of endemic leaping frogs (Anura: Ranixilidae) of the northern Western Ghats, India based on SDM and ecological observations

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Leaping frogs are endemic to Western Ghats of Southwestern India. Recent studies have revealed several cryptic species of these frogs, but little information is available on their distribution, ecology and threats affecting their populations and habitat. Such information will be vital for defining their conservation status. In this study, we looked at niche preference of Leaping frogs from Northern Western Ghats (NWG) viz. Indirana leithii and recently described species I. chiravasi and I. salelkari and threats prevalent in their habitats and use this information for their conservation assessment. We used field observations and species distribution modelling (SDM) for assessing ecological and climatic requirements of these species. Raster layers for altitude, bioclimate and soil features were used for SDM. Conservation assessment was done using red list assessment strategy of IUCN.Indirana leithii prefers basaltic cliffs for breeding while other two species mainly breed on lateritic surfaces. SDM also showed that I. leithii and I. chiravasi prefer areas having two different soil types. Indirana leithii prefers soil related to high erosion areas such as basaltic formations and I. chiravasi prefers soil type related to clayey material such as lateritic soils. Predicted area of occurrence for I. leithii with >40% probability of presence was 1603 km2 while, it was 8253 km2 for I. chiravasi. Effect of variables is determined through response curves. Based on this analysis, we define new conservation status of all Indirana species from NWG e.g. vulnerable status of I. leithii has been retained however, it is now based upon area of occupancy (AOO) rather than extent of occurrence. This is first conservation assessment of any species of family Ranixalidae based on field observations and SDM. Results of SDM have been used to determine AOO. The study also highlights the importance of using SDM in conservation assessment.

7. Influence of abiotic and biotic variables on the elevational patterns of bird communities in Agasthyamalai Hills, Western Ghats, Kerala, India.

Madhumita Panigrahi, Jins VJ, Rajah Jayapal <u>madhumita.panigrahi7@gmail.com</u>

Understanding the distribution patterns of biotic communities and the underlying mechanisms have long been a central theme in ecology. One of the most widely tested patterns is the apparent decrease in species richness along latitudinal gradient from the tropics to the poles. Alternately, altitude has been used as a surrogate for latitude and species richness often shows a mid-elevation peak or 'Mid-Domain Effect' (MDE). We examined species distribution patterns of birds along an elevational gradient in Agasthyamalai (50-1860m), southern Western Ghats. Birds were counted using variablewidth circular plots across 18 elevational bands. Quadrat method was used to measure vegetation attributes. ASTER global Digital elevation model was used to find out area availability in each elevation band. Environmental variables like temperature and precipitation data were taken from WORLDCLIM data base. Potential evapotranspiration (PET) and Normalized vegetation Index (NDVI) values were taken from Global Aridity index and Bhuvan database respectively. We found that bird species richness, decreased with altitude and deviated from the expected values as predicted by the MDE models (r = -0.372, p=0.234). On the contrary, endemic bird species richness showed a weak correlation with MDE (r=0.617, p=0.033). Also, bird species richness declined with decreasing area in higher elevations (r=0.808, p=0.001). Results of stepwise multiple linear regressions revealed that temperature (r2= 0.802, p=0.001) was the most influential factor in explaining overall bird species richness. In case of endemics, MDE, Mean litter cover & area together influenced endemic richness pattern (r2= 0.899, p=0.001). We infer that an area-effect perhaps constrains the diversification of taxa, triggered by historical climatic events for overall bird species richness. Our results indicate that both historical and contemporary ecological factors may play significant roles in distribution of endemic taxa in tropical montane ecosystems.

8. Moths Of Himalayan Biogeographic Zone: Data Digging For Climate Change Monitoring

Angshuman Raha, Abesh Kumar Sanyal, Susmita Khan, Kailash Chandra adroitangshuman@gmail.com

Indian Himalayan Region (IHR), due to its sheer latitudinal and altitudinal expanse, harbours diverse biomes and habitats, which are the centre-stage of mixing of different biogeographic faunal elements. In the perspective of global climate change scenario, we aimed to introspect into the known diversity of Himalayan Lepidoptera, particularly moths, which are potential focal group for ecological monitoring due to their huge diversity and functional importance. A database on moths recorded from IHR including state-wise distribution and altitude records was prepared from secondary literature and museum collections. Sampling points were transformed into richness grids which were overlaid on altitude, annual precipitation and vegetation layers separately in DIVA GIS to show moth richness patterns along major environmental gradients. Altogether a total of 7853 entries of moths were encountered, of which 5751 entries with valid GPS coordinates were used for spatial representation. Among six Himalayan states, Sikkim is the epitome of moth diversity, while family Geometridae had highest number of species. While in North-western Himalaya 3000m-3500m altitudinal band was the richness hub, in Arunachal Pradesh highest richness was documented in altitudes above 3500m. In Uttarakhand and Himachal Pradesh, middle elevation zone between 1000m to 1500m encompassed high species richness. In the Trans-Himalayan biogeographic zone of Jammu & Kashmir, areas receiving <500mm annual rainfall representing alpine meadow vegetation had significant species distribution record. In Himachal Pradesh, and almost through the entire stretch of Himalaya, Temperate Conifer Forest vegetation associated with 1500-2000mm rainfall zone was dominant habitat harbouring maximum species richness. The information compiled and analysed in the current study would be a valuable source for comparable studies in future. The dataset will be useful to identify species who are altitudinally restricted and thus more vulnerable to extinction in the face of habitat shrinkage and degradation due to ongoing climate change and anthropogenic disturbances.

Posters

9. A problem on the biogeography of the aquatic beetle genus Peschetius Guignot

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The estimated origin of the insect group Coleoptera (beetles) is 285 MYA and it diversified in four extant suborders that inhabit all continents except Antarctica. Coleoptera have invaded aquatic ecosystems more than 20 times during their evolution. The true water beetle family Dytiscidae is a hyperdiverse taxon in which Hydroporinae is one of the most species rich subfamilies. The hydroporine genus Peschetius is distributed in the Afrotropical, Oriental and Palearctic regions with most of the diversity in the Afrotropics. The information on the morphology and distribution of all Peschetius species is based on our studies and available literature. The distribution maps were prepared in QGIS. Based on the highly diagnostic median lobe of the male genitalia the Oriental and Palearctic species are distinct from Afrotropical species. The apex of median lobe of Afrotropical species is extended except in P. aethiopicus which is restricted to the East Africa. On the contrary, apex is not extended in the Oriental and Palearctic species except P. taprobanicus, which is endemic to Sri Lanka. The similarity of the median lobe of P. aethiopicus to the Oriental and Palearctic species and, P. taprobanicus with the African species is interesting. The distribution of Peschetius species only on the Southern continents could be due continental breakup of ancient Gondwana. Inter-continental dispersal as, single migration event of P. aethiopicus-like ancestor from Africa to India, independent colonisation of P. taprobanicus-like ancestor to Sri Lanka, or dispersal of single common ancestor and independent evolution of Indian species could have led to the current distribution. Additionally, structural changes in the median lobe of male genitalia are significant in reproductive isolation and taxonomy of this group. A detailed study on molecular phylogeny and biogeography of the genus Peschetius is essential to resolve this problem.

10. Avian Biogeography of Northern Province, Sri Lanka – A Landscape Worth Conserving

Saumya Wanniarachchi, Chaminda Wijesundara, Tharangi Hettiarachchi, Packiyanathan Rajkumar, Supun Galappaththi, Asela Weerawardhana <u>csaumyaw@gmail.com</u>

The Northern Province of Sri Lanka, with an area of 8,884 km2, provides an atmosphere suitable for many types of migratory and residential birds due to the presence of wetlands. Present Study aims to estimate the bird diversity and distribution throughout the Northern province focusing on the migratory bird species. The study was carried out from October 2015 to present, with two counting days per month. Point counts were used to asses the diversity and abundance of birds. Each point was separated approximately by 300 m to prevent double counting. Standard birding binoculars (8×40) and spotting scopes (20×50) were used to observe the birds. Peak observation hours were from 0700- 1100h and 1300-1830 h each day. A total of 189 bird species (96 migratory, 92 residential) belonging to (59) families and (18) orders were recorded. Among the migrants vagrant species such as Blacknaped Tern (Sterna sumatrana), Fulvous whistling Duck (Dendrocygna bicolor), Gadwall (Anas strepera) and Great White Pelican (Pelecanus onocrotalus), rare winter migrants such as Bar-tailed Godwit (Limosa lapponica), Malayan Night Heron (Gorsachius melanolophus), Common Ringed Plover (Charadrius hiaticula), Spotted Redshank (Tringa erythropus), uncommon winter migrants such as Greater Flamingo (Phoenicopterus roseus), Common Teal (Anas crecca), and fairly uncommon winter migrants such as Ruff (Philomachus pugnax), Sanderling (Calidris alba) were observed. Among the resident birds rare breeding residents such as Crab plover (Dromas ardeola), Indian courser (Cursorius coromandelicus), Spotted-billed Duck (Anas poecilorhyncha) were observed. Total population counts were well above 1200 for 19 bird species including Greater Flamingo, Eurasian Wigeon (Anas penelope), Brown-headed Gull (Chroicocephalus brunnicephalus) and Spoted-billed Pelican (Pelecanus philippensis). Results indicate the ability of Northern Province to attracts different types of rare migratory and residential birds. Thus, as a fast-developing landscape coexistence of conservation activities and development activities is essential for the survival of rare birds.

11. Delimiting the bioclimatic niche of backswimmers Enithares hungerfordi and Enithares ciliata (Hemiptera: Notonectidae) in the Western Ghats and Southeast Asia

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For the current study, we chose two backswimmer species common to temporary habitats in the Western Ghats (WG): Enithares hungerfordi Brooks, found only in WG and Enithares ciliata (Fabricius), distributed from India to Southeast Asia. After detecting minor morphological differences in males, the localities for *E. ciliata* were divided into two groups: (1) WG and Sri Lanka, (2) Southeast Asia. Discriminant Analysis (DA) was carried out to examine whether the hypothesis of two isolated populations is reflected in their abiotic requirements. Data extracted from selective, non-co-linear GIS layers of bioclimatic variables, altitude and soil characteristics for collection localities of both the species were used for DA. The same layers were used to build Species Distribution Models (SDM) in MaxEnt. All analyses will be repeated after adding more locality data. DA showed distinct clusters for the two E. ciliata populations, while the E. hungerfordi and 'WG + Sri Lanka' E. *ciliata* clusters overlapped due to habitat similarity. SDM for E. hungerfordi showed >50% probability of presence (PP) only in the montane part of WG. The 'WG + Sri Lanka' E. ciliata population showed >50% PP over a wider area (northern and central WG, southeast India and central Sri Lanka) and very low PP (<25%) in Indochina and western Malaysia, while the Southeast Asian E. ciliata population showed >50% PP only below the latitude 11°N (southern WG, central and south-central Sri Lanka and Southeast Asia) and in eastern Vietnam. The near-absence of prediction of *E. ciliata* in Indochina and northern part of Southeast Asia indicates paucity of data, not true absence. Results of SDM support the hypothesis that Indian and Southeast Asian *E. ciliata* populations are morphologically distinct and may represent two species. Because the type locality of *E. ciliata* is dubious, taxonomic conclusions cannot be drawn yet.

12. Distribution of Himalayan pikas and modelling impacts of climatic fluctuations

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The Himalava, and the sub - Himalavan ranges include 25% of the total pika diversity. High species richness in these relatively specialized species provides a unique opportunity to understand evolution in the context of montane habitats. Unfortunately, studies on Himalayan pikas are limited, probably because of rugged terrain, remote and inaccessible region. We explored distribution of pikas along the elevation gradients and patterns of pika species assembly to understand if they exhibit a high niche overlap among congeners. Finally, we compared estimated climatic niche breadth to infer robustness towards climatic variation. Armed with this knowledge, we developed climatic models for four Himalayan pika species using occurrence records. The combination of genetics and field observations were used to generate accurate occurrence records. Niche overlap and breadth were quantified using principle component analysis. Correlative models were developed using maxent which were then projected to past and future climate change scenarios. Comparisons of climatic niche change across pika species inhabiting varied altitudinal ranges were made to infer on the patterns of their range shifts. We captured six pika species from the study area. Four out of six species were unevenly distributed along the elevation gradient. Species belonging to the older sub – genus, Conothoa showed broader niche breadth. Correlation between niche overlap and genetic distance between species pairs suggested phylogenetic niche conservatism (PNC). Climatic niche models contrasting range in past, current and future climates indicated range loss in lower elevation and range gain in the higher elevation region. PNC is known to influence species distribution patterns in many taxa. However, among Himalayan pikas PNC seems to influence distribution of younger species with isolated (allopatric) ranges. No signature of PNC was observed within older species pairs with sympatric distribution range. The climatic models for different species consistently indicated signature of range shift to higher elevation.

13. Genetic variation and geographic isolation in the Indian blackbuck (*Antilope cervicapra*)

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The endemic blackbuck (Antilope cervicapra) has been threatened by habitat destruction for decades. This continued loss of grasslands does not bode well for the species, which has never been found, even as a fossil, outside the sub-continent. Although listed as a Schedule I species under the Wildlife Protection Act, 1972, by the Government of India, limited research has been done on this species, particularly with respect to genetic consequences of population decline and isolation. The fragmentation and isolation is known to cause inbreeding depression due to the accumulating deleterious mutations, threatening their longterm survival. Given this scenario, it becomes important to look at how genetic variation is partitioned within and between populations from different geographic regions. Our study aims to improve the understanding of their underlying genetic diversity and the fitness consequences of isolated populations, which would allow us to chalk out efficient strategies for conservation. We use non-invasive sampling methods for DNA extraction. The extraction is done using both Qiagen kits and the swab method. We PCR-amplified mitochondrial Dloop fragments and microsatellite markers. Genotyping and sequencing was outsourced. We analyse the data using multiple softwares which will help identify self-sustainable populations that exhibit high genetic diversity. Preliminary results show that the different geographic regions seem to have some unique haplotypes. Further work is underway. Addition of more samples and more sequences will give us a better understanding. Though our preliminary data shows some structure, more work is needed for a conclusive inference. This project will identify distinct populations of A. cervicapra, to be treated as Evolutionary Significant Units (ESUs), based on genetic divergence and taxonomic classification. It will provide vital information regarding which populations could be potential sources for restocking. We also expect possible taxonomic revisions based on genetic studies making it imperative prioritize their conservation.

14. Global warming and migration constraints: Predicting distribution of Himalayan amphibians under climate change

Barkha Subba, Sandeep Sen, Michael Nobis barkha.subba@atree.org

Global climate change is a threat to biodiversity across several ecosystems and is one of the major drivers for the sixth mass extinction. The Himalayan mountain chains are one of the largest geomorphological features of the world which supports three major biodiversity hotspots. Temperature in the Himalaya is rising at twice the rate of the northern hemisphere. Despite the existence of large patches of climate refugia, studies have shown that the Himalayan species will not be able to keep pace with and adapt to the changing climate under the present accelerated rate of global warming. Among other taxa, amphibians are particularly vulnerable, since 46% of the described species falls under the threatened category and are rapidly declining worldwide. One of the current approaches in quantifying the future distribution of species under climate change is by using Ecological Niche Models. However, one of the most implausible assumption of ENM is that, the species distribution is in equilibrium with climate, i.e., species will immediately react to the changing climate by shifting, expanding, or contracting their range, but this assumption is highly improbable as it does not consider the species' dispersal inhibition or migration dynamics thus resulting in under or over estimation of the species' abiotic niche. Migrational capacities of species is an important factor for predicting its future distribution. To address the effect of climate change on amphibians in the Himalayas, we developed ENMs for four species of high elevation frogs belonging to genus Scuitger for the current and three future time periods. We simulated three possible migration rates (low, medium, and high) to the projected ENMs to estimate the changes in these three scenarios. The future accessibility maps show a significant deviance from the conventional ENMs. These findings are significant in identifying areas of species distribution in future and can further guide judicious identification of areas for conservation prioritization.

15. Macro-ecological and phylogeographic analyses to understand Passerine species richness gradients in the Himalayas

Bela Arora, Vivek Ramachandran, Uma Ramakrishnan arorabela@gmail.com

The Himalayas are amongst the most species-rich regions of the world with a clear southeast-to-northwest declining trend in avian species-richness. What explains this gradient in bird species richness from south-eastern Himalayas (SEH) to north-western Himalayas (NWH)? The answers might lie in understanding how geographical, environmental and ecological barriers have restricted Himalayan bird distributions (particularly from the warmer and wetter SEH to the colder and drier NWH) and facilitated diversification in the context of species' unique evolutionary histories and their biology. These can include physical barriers such as wide or deep river valleys, environmental constraints such as the cold dry climate of the north-west, and eco-evolutionary barriers related to species' biogeographic origins, phylogeny, morphology, habitat preferences and dispersal abilities. I will examine patterns in spatial turnover of resident Himalayan birds in the context of topography and climate to elucidate putative geo-climatic barriers to dispersal. A conclusive signal of restricted dispersal (and thus gene-flow) across putative barriers (physical, environmental or ecological) may emerge from consistent patterns of repeated genetic differentiation and, in some cases, in-situ allopatric speciation across taxa. To determine the level of genetic differentiation across this gradient, I will quantify genetic distances for four nuclear (myoglobin, gapdh, musk and odc) and three mitochondrial (cytb, nd2, cox1) genes across SEH and NWH populations of 22 Himalayan passerines. I will examine the correlation of dispersal ability (hand-wing index data), number of sub-species and genetic differentiation data for select Himalayan Passerines to test the hypothesis that geographic ranges are limited by dispersal (White 2016). Study species include those with tropical and temperate affinities to allow us to examine the effect of species' evolutionary histories on their current distributions and levels of differentiation. This integrated approach will highlight the role of barriers in influencing distribution of bird species (and their sub-species), link species' ecology and dispersal ability with population differentiation at different spatial scales and, ultimately, enhance our understanding of the mechanisms that have shaped avian diversity gradients across the Himalayas.

16. Phylogenetic endemism in Neotropical snakes

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The Neotropical region is the most diverse area in the World in terms species of snakes. This diversity peaks at forests but is still impressive in the open vegetation biomes. There are many endemic species over islands, especially in the Caribbean region, in different valleys over the Andes or isolated over the table mountains of the Central Brazilian Plateau. Many of these areas are highly endangered by human activity and it is important to know where are the places in which there are more species with restricted distribution and at the same time, the places where a great proportion of the evolutionary history of the region can be preserved. Phylogenetic endemism (PE) is a measure that can help us to find the areas with a great number of evolutionary ancient lineages that have a very restricted geographical distribution. The goal of this work was to find the areas with the higher PE for snakes in the Neotropical region, contrast these values of PE for snakes with values found for other organisms. We found that areas with the highest PE for snakes are concentrated over the narrowest parts of Central America, Caribbean islands and in a very smaller extent, to portions of the Atlantic Forest. This pattern is different from what was found for Mammals and indicates that one group should not be always used as a surrogate for conservation for another one.

17. The Critically Endangered Forest Owlet *Heteroglaux blewitti* is nested within the currently recognized Athene clade: a Century-old debate addressed

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Range restricted species generally have specific niche requirements and may often have unique evolutionary histories. Unfortunately, these are also the species on which basic research is severely lacking, resulting in poor conservation strategies for the species. The phylogeny of the Critically Endangered Forest Owlet Heteroglaux blewitti has been the subject of a century-old debate. The current morphology-based classification groups Indian small-sized owls in three genera, namely, Athene, Glaucidium and Heteroglaux. Based on morphological and anatomical data, H. blewitti has been hypothesized to be either a sister species to Indian Athene brama, congeneric to Athene or Glaucidium, or a monotypic genus Heteroglaux. To test these competing hypotheses and resolve the phylogeny, we collected owl feathers from the field, sequenced six loci, generated ~4300 bp data, and performed standard phylogenetic analysis. Mitochondrial and nuclear trees were not congruent at H. blewitti node. However, both mitochondrial and nuclear datasets showed a strong statistical support with high Maximum Likelihood bootstrap (>/=90) and Bayesian posterior probability values (>/=0.98) for H. blewitti being nested in the currently recognized Athene group, not sister species to Indian A. brama. The broader divergence of H. blewitti from its sister taxa was around 3.6 – 7.1 Ma, in the Pliocene – a period with drastic climatic changes in the Indian subcontinent. With the current phylogeny and molecular dating and the previous hypothesis on the origin of Athene genus we hypothesize an African ancestry for the Indian Athene species. This study provides the first genetic data of H. blewitti addressing the long debate on Athene-Heteroglaux-Glaucidium phylogeny. We recommend further studies with more data and complete taxon sampling to understand biogeography of Indian Athene species.

18. Anuran distribution pattern along an elevational gradient in the Dibang River basin, Eastern Himalayas

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Few studies have explored anuran species distribution pattern along an elevation gradient in the Eastern Himalayas. We conducted extensive amphibian survey from 250 - 3500 m asl during 2014 - 2016 by using visual encounter surveys in the Dibang River basin. We sampled the elevation gradient 100 m intervals and collected data on anuran species encountered, habitat and abiotic variables. We tested Bergmann's rule on two selected species: Amolops marmoratus and A. viridimaculatus, as they occupied large elevation range 297 – 1294 m asl and 679 – 2538 m asl respectively. We analyze Topographic Habitat Characteristics (THC) at a 30 m resolution digital elevation model on anuran species abundance in the Dibang River basin. We encountered 39 anuran species, 72% of them were clearly identified taxonomically to species level and the remaining 28% were not identified. Mid-domain null model did not explain the observed anuran species distribution pattern as there was a monotonic decline in species richness with elevation above 1500 m asl. Species richness increased between 224 – 1500 m asl with no anurans record beyond 3300 m asl, although there is conducive anuran habitat at this elevation. We found Bergmann's rule was not consistent with our observation on body length of two selected species with increase in elevation (Pearson Correlation, r = 0.08 and -0.05, n = 43, 26). From TCH analysis, we found that west-facing mountains have the highest abundance followed by south-facing and southwest-facing slopes. This has influence on each of the anuran species in different months of the year. Therefore, topography characteristics are important determining anuran species distribution followed by elevational factors.

01.00 – 02.30 PM: Wednesday 27th September 2017 Contributed Session 2: Community ecology, phylogeny and biogeography

Invited talk

1. Comparative biogeography

Michael N Dawson and Lauren M. Schiebelhut

The challenge for biogeography, like other observational sciences, is to extract general relationships representing causes and effects from complex natural data. Moreover, approaches must, ultimately, link local scale processes to regional, or even global, scale patterns. This likely requires methods that are robust to integration across diverse places and times. I outline one such approach using synchronously diverging co-distributed species, which has potential to clarify the effects of traits — e.g. fecundity, dispersal syndromes — on population genetic structure and elucidate differences in the balance of processes shaping communities.

Contributed talks

2. A New Biogeographic Theory To Explain Small-Island Effect And Latitudinal Gradients Of Diversity.

Deepthi Chimalakonda, Ryan Chisholm

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We propose a new theory to understand an ecological anomaly called the small-island effect. Small-island effect is a phenomenon where species richness does not vary with area under a certain island size threshold but increases linearly beyond the threshold. By integrating principles of The Equilibrium Theory of Island Biogeography, The Unified Neutral Theory of Biogeography and Niche Theory, we show that this bi-phasic species-area relation is due to a transition from niche-mediated regime on small islands to immigration-dominated regime on large islands. Using data from 205 published studies, we make specific predictions as to when this transitions occurs for different taxa and archipelagos. Using the same data and model, we present a case for why and how latitudinal gradients of biodiversity can be explained through the lens of biogeography and not just by deterministic localised processes as traditionally dealt with. Using a mechanistic mathematical model that incorporates niches and neutral processes, we show that niches do not explain variation in diversity gradients. We present evidence on immigration and meta-community diversity being crucial factors for the global diversity trends, thereby highlighting the role of stochastic biogeographic processes in maintaining biodiversity.

3. Immigration Is An Important Driver Of Diversity Build-Up In The Himalayas

Krishnapriya Tamma, Uma Ramakrishnan priya.tamma@gmail.com

The Himalayas are amongst the most biodiverse regions of the world, and their topographical complexity renders them as an excellent microcosm of the study of biogeography and species community assembly. The Himalayas are dominated by tropical forests at the lower elevations and temperate forests at higher elevations, especially in the eastern Himalayas. The topographical complexity of the Himalayas in conjunction with strong habitat differentiation along elevation could result in isolation leading to in situ speciation. Furthermore, the Himalayas, are adjacent and connected to tropical southeast Asia and the Tibetan plateau; subsequently, immigration from these regions could also contribute to diversity here. In this study, we reconstruct small mammal phylogenies to evaluate the contribution of in situ speciation and immigration in driving diversity build up in the Himalayas. Fieldwork was conducted across 7 sites in the Himalayas, and tissue samples collected from three genera of live-trapped rodents. Phylogenies were reconstructed using one mitochondrial and three nuclear genes, and divergence times were estimated using BEAST. Diversification in these clades events mostly occurred during the Pliocene-Pleistocene. From the dated phylogenies, we find no strong support for in situ speciation being an important mechanism for diversity build-up the Himalayas. Most species in the Himalayas are also distributed in other parts of Southeast Asia and adjoining mountains. Other mechanisms such as allopatric speciation and colonisation from surrounding biogeographic realms could be driving the observed patterns.

4. Latitudinal Gradients In Range Size And Richness Of Woody Plants In The Western Ghats

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Understanding the determinants of range location and size has been the focus of many macroecological studies. However, few studies have simultaneously investigated the role of climatic stability as a determinant of species range, richness and turnover. In this study, we tested the effect of climatic stability on range sizes of tropical woody plants and their combined role in influencing latitudinal patterns in species turnover and richness. We built a biome-wide species database using primary data from 156 (0.06 ha) plots comprising of 20,400 occurrences of 400 species of tropical evergreen woody plants from the Western Ghats to decipher latitudinal patterns in species richness and turnover. We then calculated the range sizes of woody plants to test the predictions of the Rapoport's Rule. Finally, we estimated the climatic tolerance of individual species to temperature and precipitation, and calculated their elevational ranges. We used a null model approach to test the validity of Stevens' climatic stability hypothesis by randomizing species ranges across the latitudinal domain of the Western Ghats and examined the relationship of both range size and range position with climatic tolerance of species. Our results show a strong latitudinal gradient in species richness and turnover where alpha, beta and gamma diversity increase monotonically from higher latitudes to lower latitudes of the Western Ghats. We found that species at higher latitudes exhibited both larger ranges and greater temperature and precipitation tolerance compared to species at lower latitudes. Contrary to earlier work, the findings from this study show that Rapoport's Rule and Stevens' climatic stability hypothesis can operate over regional scales, and even at lower latitudes. Our results suggest that climate driven trends in species ranges can explain latitudinal patterns in beta diversity which in turn can result in latitudinal patterns in species richness.

Speed-talks

5. Disentangling The Relative Roles Of Neutral And Niche Based Process On Community Assembly Of Tree Species Along An Elevational Gradient In Sikkim Himalaya

Yangchenla Bhutia, Gudasalamani Ravikanth, Shivaprakash K. Nagaraju yangchenla.bhutia@atree.org

Understanding of processes shaping evolution and maintenance of biodiversity across environmental gradients has always been a challenging question for ecologist. A small gradient can lead to extensive variation in the biotic and abiotic interactions. However, elevation gradient is of great interest, as it provides a natural setting to investigate the different mechanisms of community assembly with changing environments. In this study, we assess the relative importance of neutral (dispersal limitation) and niche based (habitat filtering and competition) processes on tree community assembly along elevation gradient using community phylogenetic approaches and species pool null models. The community data sampled from different forest types (ranging from warm broad-leaved to coniferous forest) distributed across elevation gradient (900m-3200m amsl) in Sikkim, one of the Eastern Himalayan biodiversity hotspot revealed decreasing trend for both species richness and phylogenetic diversity with elevation. Further, the phylogenetic clustering at higher elevation and overdispersion at lower elevation suggest that habitat filtering and competition as predominant mechanisms structuring community assembly in these elevations. However, the phylogenetic community structure among different forest types did not significantly deviate from regional species pool null model. Whereas, phylogenetic clustering in high elevation mixed coniferous forest was non-random and significant. These results indicate that communities in different forest types have been deterministically assembled from regional species pool. Overall the observed non-random pattern of phylogenetic structure and turnover suggest predominant role of niche based processes in assembly of tree communities along the elevation gradient.

6. Evolutionary Assembly Of Communities In Butterfly Mimicry Rings Jahnavi Joshi, Anupama Prakash, Krushnamegh Kunte jj.jahnavi@gmail.com

Species co-occurrence in ecological communities is thought to be influenced by multiple ecological and evolutionary processes, especially colonization and competition. However, effects of other interspecific interactions and evolutionary relationships are less explored. We examined evolutionary histories of community members and roles of mutualistic and parasitic interactions (Müllerian and Batesian mimicry, respectively) in the assembly of mimetic butterfly communities called mimicry rings in tropical forests of the Western Ghats, India. We found that Müllerian mimics were phylogenetically clustered, sharing aposematic signals due to common ancestry. On the other hand, Batesian mimics joined mimicry rings through convergent evolution and random phylogenetic assembly. Since the Western Ghats are a habitat island, we compared species diversity and composition in its mimicry rings with those of habitat mainland to test effects of biogeographic connectivity. The Western Ghats consisted of fewer mimicry rings and an overall smaller number of aposematic species and mimics compared to habitat mainland. The depauperate mimicry rings in the Western Ghats could have resulted from stochastic processes, reflecting their long temporal and spatial isolation and trickling colonization by the mimetic butterfly communities. These results highlight how evolutionary history, biogeographic isolation, and stochastic colonization influence the evolutionary assembly and diversity of ecological communities.

7. Flowering Phenology Of Rhododendrons In The High Altitude Of The Sikkim Himalaya: Phylogenetic Constraints And The Influence Of Abiotic Factors

Shweta Basnett, Shivaprakash K. Nagaraju, Gudasalamani Ravikanth, Soubadra Devy

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The flowering phenology events are key to the reproductive success and long-term persistence of plants in a given environment. These events are considered to be highly lastic due to their flexible response to environmental cues and have therefore gained importance in the context of climate change. The high altitude temperate and alpine plant communities are of particular interest as they are strongly dependent on climatic variables for their phenological events. These ecosystems are also believed to experience highest warming trend globally. However, the phenological events of plants can also be strongly constrained by their phylogenetic relationship (phylogenetic conservatism). Here we used comparative phylogenetic approaches to evaluate the relative importance of environmental constraints and evolutionary history on flowering phenology of Rhododendron, a phenologically plastic plant clade occupying a wide variety of habitats from the temperate forests to the alpine meadows. Our three-year field study in Kyongnosla Alpine Sanctuary, Sikkim Himalaya covered an elevation gradient between 3400 to 4200 m. Our results showed that flowering phenology events substantially differ among Rhododendron plant communities occurring across the elevation gradient. We found phenological traits such as the opening of bud, peak flowering, fruiting and dehiscence of fruits were phylogenetically conserved for Rhododendron communities found at higher and lower elevation. Phylogenetic generalized least squares analysis results suggest that the influence of climatic variables (temperature and day length) on flowering phenology of Rhododendron across an elevation gradient is constrained by the phylogenetic relationship of species. Our study for the first time strongly links flowering phenology events of high altitude Himalayan plant communities with climatic variables and evolutionary history of species and also provides a better approach to predict the adaptive potential of Himalayan plant communities in response to future climate change.

8. How do communities assemble? Inference from global to local patterns of phylogenetic structure.

Lessard J P

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A persistent challenge in ecology is to tease apart the influence of multiple processes acting simultaneously and interacting in complex ways to shape community structure. We implement a heuristic null model approach that relies on explicitly defining species pools and which permits assessing the relative influence of the main processes thought to shape community structure: environmental filtering, dispersal limitations and biotic interactions. We illustrate our approach using data on the community composition, global distributions, phylogeny and morphological traits of hummingbirds.

9. Lizard Community Organization In Andaman And Nicobar Archipelago Explained By Historical And Stochastic Processes

Harikrishnan S

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Various environmental, geographical, and biological factors including interspecific competition can influence patterns of species co-occurrence, species abundance distributions (SADs), and size distributions of communities. We explored patterns in the assemblage of insectivorous lizards in the Andaman & Nicobar Islands (ANI) at regional and local scales. We collected distribution, abundance, and body mass data for lizards through field surveys and secondary records. We used probabilistic pairwise analyses, using geographical distribution matrices and guild membership matrices to explore co-occurrence patterns and causal factors, across ANI, the Andaman Islands (AND), and the Nicobar Islands (NIC). To explore SADs, we fit fourteen models to the data using a Maximum Likelihood Estimation approach. We used a null model analysis using body mass data, with variance ratio as a metric, to examine whether local communities exhibited a constant size ratio. We found negative co-occurrences among species pairs between the two groups of islands (AND & NIC) separated by the Ten Degree Channel. There were a few negative cooccurrences within NIC, but not within AND. Guild co-occurrence analyses did not indicate any significant interactions between species pairs. Among the several models considered, pareto distribution explained SADs in both metacommunity and local communities. The variance ratios observed in body sizes of co-existing species in all local communities were not different from null expectation. The co-occurrence analyses show that the distribution patterns of lizards are due to historical allopatry maintained by geographic barriers such as deep ocean channels. The failure of most niche and neutral models to explain observed SADs and the absence of consistent size differences among species indicate that competitive niche division may not be a major factor structuring these communities. Therefore, regardless of geographic scale, lizard communities seem to be shaped by historical and stochastic events.

10. Phytogeography Of Western Ghats: A Community Phylogenetic Approach

Divya B, Ramesh B R, Praveen Karanth whyisrumalwaysgone@gmail.com

The Western Ghats is a biodiversity hotspot extending along the west coast of India. It has a high endemism and harbours over 5000 plant species. Whereas, the evergreen forests populating the wet zone on the western slopes have existed since 65 million years ago, the deciduous forests populating the eastern plateau were established during the Miocene aridification about 10 million years ago. Additionally, the wet zone also has a latitudinal gradient in length of dry period that was established after the intensification of the monsoons and thus affects species composition, with the relict evergreen species largely confined to the southern refuge pocket. In this study, we tested the antiquity of the evergreen forests, the southern refuge hypothesis, and the relationship of species across these forest types. We used a community phylogenetic approach and analyzed decoupling between phylogenetic (PD) and taxonomic diversity. We worked on the premise that older forests show high PD whereas recently establishes forests show low PD. Presence data of all woody angiosperms above 10cm diameter from 23 defined forest types was used. We calculated phylogenetic turnover to assess relationship between different forest types. While the deciduous forests all showed negative PD, evergreen forests all showed positive PD. Within the wet zone, a latitudinal decrease in PD was observed with the southern forests exhibiting high PD values. Phylogenetic turnover was highest between two evergreen forests, while that across evergreen-deciduous forests was lower than expected. Evergreen forests indeed show antiquity compared to deciduous forests, and PD patterns corroborates the southern refuge hypothesis. Most interestingly, deciduous species show shared evolutionary histories with evergreen species, suggesting shifts in this trait, whereas evergreen forests show greater disparate histories possibly due to their antiquity and sharper gradients in the wet zone.

Posters

11. Combining range and environment to understand species richness patterns in the Western Ghats, India

Anisha Jayadevan, Kartik Shanker anisha.jayadevan@gmail.com

Macroecological patterns in species richness have been attributed to multiple factors including area, climate, productivity, evolutionary history and more recently, geometric constraints on species range boundaries. The latter, termed the mid-domain effect (MDE), leads to a hump-shaped pattern in species richness. The Western Ghats of India spans a latitudinal range from 8 to 20°N, with all four sides presenting hard or soft boundaries to dispersal. Within this domain, many taxa such as trees and frogs exhibit a monotonic increase in species richness from north to south. In this study, we simulated how range affects (through MDE), and interaction of ranges with temperature within the bounded domain of the Western Ghats, influenced patterns in species richness. Simulations were carried out in NetLogo, an agent-based modeling environment. We examined three environmental scenarios: a) no environmental gradients b) a linear temperature gradient and c) empirical temperature. Ranges were defined as cohesive or scattered, depending on whether they occupied adjacent or disjunct cells and representing different dispersal patterns. When interacting with temperature, cohesive ranges moved towards higher temperature cells, while scattered ranges moved towards random cells. We found that for all scenarios, scattered ranges led to a uniform gradient in species richness. Cohesive ranges produced a hump-shaped curve in richness for no environmental gradients, a curve that resembled empirical species richness for the linear temperature gradient and a multi-modal curve for empirical temperature. Our results corroborate other studies which have found that even in the absence of ecological and evolutionary mechanisms, the predicted species richness pattern is not uniform. The similarity between the curve produced in the second scenario and the empirical species richness curve suggests that interaction of ranges with both suitable environmental factors (here, temperature) in southern Western Ghats and boundary constraints, may likely influence species richness patterns in the Western Ghats.

12. Drivers Of Ant Species Richness Across Elevation Gradients In The Eastern Himalaya (India)

Aniruddha Marathe, Priyadarsanan Dharma Rajan, Jagdish Krishnaswamy, Kartik Shanker aniruddha.pravin.marathe@gmail.com

Search for mechanisms behind gradients in species distribution and diversity has been an important objective of ecology and biogeography. Elevation gradients offer a unique opportunity to test these mechanisms as large variation in climate and habitat occurs across small spatial scale. This facilitates addressing questions about patterns in diversity and distribution of species using primary data. Traditionally, the patterns have been explored in context of a range of environmental variables while effects of geometric constraints were tested more recently. However, most studies especially on invertebrates only test the simplest and most uninformative form of the geometric constraints model. In this study, we use modified forms of the geometric constraints null model to include effects of climate and geography. We study ant species richness on an elevation gradient between 600 – 2400 m in the Eastern Himalaya. We sampled ants in nine elevational zones of 200m with four transects in each zone. We find a linear decrease in species richness with elevation. This pattern is best explained by gradient in temperature and edge effect between plains and the mountain range. We present hypotheses relevant to the Eastern Himalaya to test mechanisms behind this relationship.

02.30-03.30 PM Wednesday 27th September 2017

Mini-Session 1: Biogeography of Rivers

Invited Talks

1. Aquatic Insects of Riverine Ecosystems: Biodiversity and Biogeography

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Aquatic insects are one the dominant and key component of freshwater ecosystems. Nearly ten thousand species of invertebrates and vertebrates are recorded from freshwater ecosystems of India, of which about fifty percent are insects. Aquatic insects of riverine ecosystems are characterized by high diversity and endemism. Most of the species are restricted within a drainage and have specific habitat and microhabitat preference. Several taxa have ancient evolutionary history and are good model system to understand biogeography of freshwater ecosystems. The aquatic insect community of riverine ecosystems of India have Gondwanian relicts, Laurasian spill overs, Palaearctic, Afrotropical and Oriental south east Asian colonisations. Based on studies conducted Ephemeroptera (Mayflies), Odonata (Dragonflies and Damselflies) and aquatic Hemiptera (aquatic bugs) current knowledge on this model system is analysed and shortfalls identified for future biogeographic and conservation research.

Speed-talks

2. Drivers of fish diversity across river basins in the Western Ghats biodiversity hotspots in India.

Vidyadhar Atkore

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Ecologists are interested in understanding fresh-water fish community organisation at multiple spatial scales in river basins. This assumes importance because of increasing hydrologic regulation and abstraction of freshwater. In this study we investigated patterns of fish species diversity in the Western Ghats at multiple spatial scales across four river basins. Using a nested study design, we sampled Bhadra (670.12 km2), Tunga (328.60 km2), Malaprabha (1141.06 km2) and Mhadei (3685.78 km2). A total of 152 stream segments across 32 streams of varying stream orders (1–7) were sampled. We used generalized linear model (GLM) to evaluate the role of stream habitat and water quality variables on fish species richness and fish abundance. We recorded a total of 93 species belonging to nine orders and 18 families with 18,322 individuals. About 98.97% of the diversity was comprised of three orders – Cypriniformes with 49 species (17174 individuals), Siluriformes and Perciformes, each with 13 species (497 and 464 individuals). Malaprabha river basin showed highest species richness (53 species in 11 sites) followed by Mhadei (47 species in 32 sites), Tunga (45 species in 52 sites) and Bhadra (24 Species in 41 sites). Comparison of species accumulation curves suggest that highest spatial turn-over in Malaprabha followed by Mhadei, Tunga and least in Bhadra basin. Generalized linear model (GLM) suggested that species richness and abundance were best predicted by stream habitat characteristics and water quality parameters. Fresh-water fish diversity in the Western Ghats is driven locally by water quality and by stream order at larger scales. About 50 species were Western Ghats endemic. Of which certain endemic genus like Barilius, Barbodes were restricted only to the Bhadra and Tunga river basins while other genus like Sicyopterus and Mugil were confined to the Mhadei river sub-basin alone highlighting the biogeographic differences among the four sub-basins. Monitoring is urgently needed in order to assess the impact of hydrologic regulation and climate change.

3. Tales of salt and drought: roles of climate and geography in governing colonization of India by freshwater snails.

Maitreya Sil, Aravind N.A., Praveen Karanth maitreya.sil@gmail.com

India-Asia collision during early to middle Tertiary unfolded a biotic exchange event that shaped the evolution of floral and faunal communities in both the landmasses. Ever since the first connection was established, the rate of dispersal to and fro the Indian subcontinent has fluctuated over time owing to physiographic and climatic shifts- the slow withdrawal of the Neotethys ocean and the late Miocene aridification to name a few. Freshwater organisms are of particular interest owing to their dispersal limitations and our gap in knowledge. Hence, we wanted to explore the temporal dynamics of the biotic exchange with freshwater gastropod family Viviparidae as a model system, a family which is known to have colonized India from Asia. Genus Bellamya was particularly targeted for the inference of dispersal time, since it is the only Viviparid genus found in the Indian biogeographic subregion.We collected all the described species of Viviparidae from India from multiple locations to capture cryptic diversity. A five gene phylogeny was built from these individuals and Viviparidae sequences from other part of its distribution range. Phylogenetic analysis, molecular dating and ancestral area reconstruction were followed to infer the time of the dispersal event. Preliminary results suggest that two distinct lineages of Viviparid snails have colonized India from Asia independently. Although the Bellamya cf. dissimilis group seems to have colonized India during mid-Miocene, the Bellamya cf. bengalensis lineage may have dispersed much later after aridification has set in. Contrary to our expectation the aridification event did not restrict the spread of Viviparidae snail lineage to India. A detailed discussion on the fine scale niche preference of the lineage concerned will shed light on the apparent oddity of the event.

4. Varying patterns of species richness along elevational gradients in terrestrial and aquatic ecosystems of the Himalaya

Kumar Manish, Jay Bhatt, Maharaj Pandit kumarmanish910@gmail.com

Understanding the patterns of species richness and various factors influencing their distribution is central to ecological biogeography; this knowledge is important for the conservation and management of biological diversity. The success of macroecological studies of elevational diversity lies in unraveling the drivers of the distribution patterns of varied taxonomic groups and ecosystems within a region. Fish and plant (angiosperm) species occurrence data were collated for Sikkim Himalayan region using primary field surveys and secondary data sources. Generalized linear models (GLM) and generalized additive models (GAM) were used to examine spatial patterns of species richness along an elevational gradient from 300 m to 5300 m. GLM was also used to determine the predictive ability of various environmental variables in driving fish and plant species richness patterns; modelling involved stepwise procedure including elimination of collinear variables, best model selection, based on the least Akaike's information criterion (AIC) and the highest percentage of deviance explained (D2). Total and non-endemic fish species richness showed a monotonous decrease with increasing elevation, while endemic fish species richness peaked around 700-1500 m. The richness patterns of non-endemic and endemic plant species showed a non-overlapping and humped pattern: non-endemics peaked at 1100-2500 m while endemics peaked at 3500-4500. Fish species richness patterns supported Rapoport's elevational rule while both fish and plant species richness patterns showed poor fit to Mid-Domain Effect (MDE). Water discharge emerged as the best predictor of fish species richness pattern while ambient energy and water availability were the main drivers of plant species richness patterns. This study points out that species richness patterns and their drivers in aquatic and terrestrial ecosystems within the same region are likely to be different. We highlight the consequences of undermining this important fact while generalizing a common macroecological pattern for a study region.

Posters

5. Acoustic populations in the endangered South Asian river dolphin?

Sunil Kumar, Nachiket Kelkar, Tadamichi Morisaka, Subhasis Dey chaka@bio.mie-u.ac.jp

The South Asian river dolphin Platanista gangetica is a remarkable, 'almost blind', monotypic cetacean endemic to the murky, sediment-laden floodplain rivers of the Indus-Ganga-Brahmaputra basins of South Asia. This dolphin relies almost entirely on echolocation for navigation, foraging, and communication. In this paper we test whether echolocation characteristics of Platanista vary in different river habitats. For this we conducted acoustic studies on Platanista in Bihar, India, and compared their echolocation characteristics with published information from tidal rivers of the Bangladesh Sundarbans. Acoustic studies were conducted in the Ganga River at Bhagalpur and Kahalgaon, Bihar, India. Two A-Tags (MMT Corp., Japan) and a hydrophone were used to measure echolocation click peak frequencies, inter-click intervals, and sound source levels. We compared our results with those reported by Jensen et al. (2013) from the Bangladesh Sundarbans. We found that river dolphins in the Ganga River had significantly higher peak frequencies (74.3 ± SD 8.8 kHz) as compared to those in the Sundarbans (58.8 ± SD 6.8 kHz; z-test, z=8.6, p<0.01). Peak-to-peak soundsource levels (176.5 dB re 1 µPa @ 1m) and inter-click intervals (24.4 ms) were significantly lower for the Ganga river population than for the Sundarbans (z-test, z=-7.0 & -2.9 respectively, both p<0.01). Our preliminary study suggests that habitat differences (tidal influence, salinity, depth, clutter) might influence background noise and detection distances for echolocating dolphins. Environmental factors could thus explain acoustic divergence in the two dolphin populations. In the Sundarbans, Irrawaddy dolphins Orcaella brevirostris cooccur in some areas with Platanista gangetica, and observed differences in the latter's echolocation may also possibly result from competitive interactions. These results offer exciting possibilities for future studies. Comparative acoustic studies could help identify potential barriers to genetic connectivity between river dolphin populations disconnected by large dams and barrages in the Indo-Gangetic plains.

6. Bridging the 'Wallacean shortfall' for subterranean fishes of Kerala, India

Tanvi Vasan, Arjun CP, Rajeev Raghavan, Philips Siby, Liju Thomas, Neelesh Dahanukar, Rajani MB, Binoy VV tanvi165@gmail.com

Subterranean fishes comprise one of the most poorly known components of India's ichthyofauna, with many species assessed as 'Data Deficient' on the IUCN Red List. Of the nine such fish species known from the hypogean habitats, seven, belonging to three genera, Monopterus, Kyptoglanis and Horaglanis occur in dugout wells in the southern Indian state of Kerala. Of these, the synbranchid eel genus, Monopterus is the most frequently observed and widely distributed, compared to the blind catfish genera. Horaglanis and Kryptoglanis. However, opportunistic encounters have rendered their true distribution obscure leading to the 'Wallacean shortfall'. To overcome this, we studied the geographical distribution of members of the three genera and tried to understand their ecological niche by overlaying distribution records on environmental variables including altitude, precipitation, temperature, bioclimate, soil type and soil carbon content. Sites harbouring subterranean fish species were located within an average altitude of 50m ASL, at a distance of 30km from the coastline, and associated with river basins, lateritic surface soils and an aquifer type of 'charnockite, basic gneissic complex, gneiss and laterite'. Subterranean species distribution was also affected by organic carbon, temperature and precipitation. Principle component analysis of the extracted environmental variables suggested that while Monopterus was adapted for a wide range of environmental variables, Horaglanis and Kryptoglanis showed preference for relatively lower altitudes, organic carbon and calcaric regosol and higher values of Eutric fluvisol. A MaxEnt model revealed that Monopterus has the widest predicted range, from 12°N to 9°N, with the highest probability being in locations in and around 12°N, while Horaglanis has a distribution range spread across two disconnected regions, the first between 10.7°N to 10.3°N, and the second between 9.5°N to 9.2°N; with the highest probability in and around 9.5°N. Kryptoglanis has the narrowest predicted distribution range, restricted to regions between 10.4°N and 10.5°N.

7. Comparative Study of Freshwater Fish Communities in two ecoregions of India: West Bengal and Madhya Pradesh.

Rubina Mondal

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Freshwater fish communities are controlled by a host of biotic and abiotic factors. In this study the role of these factors are dissected to examine their influence on structuring these communities. Our study compares communities from two contrasting ecoregions, Madhya Pradesh and West Bengal, and the composition and distribution abundance patterns which may exist despite being in different ecological conditions. Our study aims at answering how environmental factors determine the fish community composition. Are there common factors involved? 10 sites in MP and WB were sampled thrice a year in the seasons of winter, premonsoon/summer and post monsoon for fish abundance and environmental data. This work contains data of 3 winters, and 2 pre-monsoon and 2 post monsoon sampling. Environmental data was used to explain Shannon diversity of the unpooled abundance values using stepwise regression. CCA was plotted using the factors explaining the variation in MLR. Conservation status was assessed for the species found.73 species were observed in MP and 69 species were observed in WB based on species accumulation method by rarefaction.26 percent of species are common to both MP and WB out of the total 100 species found in both regions combined. Stepwise regression yielded pH and temperature as common factors for explaining the diversity in both regions. 9 species in WB and 12 species in MP were found to be under high risk. Presence of common species and common driving factors indicate at underlying patterns of community structure. Anthropogenic activities such as river bed sand mining, cattle and electrofishing and bulk fishing may affect the communities which would drive the species into greater risk. Further analysis of community structure may reveal common patterns in fish communities from these contrasting eco-regions.

8. Differential Turnover Rates And Temporal Beta-Diversity Patterns Of Native And Exotic Species On An Oceanic Archipelago

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A key component of assessing the impact of invasive species in island systems involves the development and testing of biogeographical theories and models relevant to alien species. Burns (2015) recently introduced an extension of the equilibrium theory of island biogeography which he termed a †theory of island biogeography for exotic species' (herein â€~TIBE'). TIBE is a graphical island biogeographic model that makes a variety of different predictions regarding the species richness and turnover of native and exotic species. However, predictions of TIBE have only been tested using a single taxon and study system (Burns 2015) and the generality of its predictions are unknown. In this study we test two of the predictions of TIBE in combination with an examination of temporal beta-diversity patterns using a unique and novel time-series dataset of arthropods sampled in native forest fragments every three months over five years in the Azores. Based on TIBE (Burns 2015) we predict that 1) exotic species will have higher turnover rates than native species; and 2) colonisation rate will be greater than extinction rate for exotic species whilst colonisation rate will be roughly equivalent to extinction rate for native species. Following on from the above two predictions we further predict that 3) temporal beta-diversity will be greater for exotic species than for native species. We use a linear modelling framework to determine whether any environmental factors (e.g. altitude) can explain variation in the number of turnover events between plots and a null model approach to determine whether the turnover of exotic species will be the result of stochastic dynamics. We found that the rate of turnover and the degree of temporal beta diversity was higher for exotic species in accordance with the TIBE. Our null model and linear regression analyses indicated that turnover of exotic species is the result of stochastic processes which has important implications for the management of invasive species

9. Distribution and biogeography of fish fauna in Godavari Estuary, Andhra Pradesh: a preliminary assessment

Paromita Ray, Giridhar Malla, J.A. Johnson, K Sivakumar paromitaray20@gmail.com

Godavari River is India's second longest river and the largest in peninsular India. After traversing a distance of 1465 kms, it empties to sea in form of two major distributaries namely Vasistha and Gouthami. The confluence of Gouthami River with Bay of Bengal in Andhra Pradesh gives rise to an extensive river estuarine ecosystem characterized by one of the largest patches of mangroves in east coast. This estuary was surveyed between December, 2015 and November, 2016 to study the spatio-temporal pattern of fish fauna. Locally-available trammel nets were kept for 1 hour at each sampling site before which environmental parameters such as salinity, depth, water temperature, dissolved oxygen, pH, turbidity and conductivity were recorded. A total of 115 species were recorded during the study out of which Leiognathus equulus, Mystus gulio, Dichotomyctere fluviatilis and Dendrophysa russelii were the most abundant species. Multivariate analyses revealed salinity to be the most important factor responsible for distribution of fishes in the estuary followed by water temperature. Fish assemblage differed across a gradient of salinity which was most pronounced in the summer season. M. gulio mainly preferred the mangrove-lined creeks with lower salinity values while D. russelii preferred the Bay. When compared with other studies, salinity seems to be a strong determinant of estuarine fish composition particularly in estuaries with a strong seasonal influence. It was also found that the fish assemblage of Godavari Estuary is similar to that of other estuaries in eastern coast of India. Majority of the species recorded during this study have an Indo-West Pacific distribution but to assess the biogeographical pattern of estuarine fishes in India more detailed studies are required.

10. Eurasian otter records across India in 2016: unfolding surprises Aditya Joshi, Vivek Tumsare, Milind Pariwakam aditya@wctindia.org.in

Three species of otters, namely, the smooth-coated otter Lutrogale perspicillata, Asian smallclawed otter Aonyx cinereus, and the Eurasian otter Lutra lutra, have been reported to occur in the Indian subcontinent. Smooth-coated otters are found throughout India, and Asian small-clawed otters are known from NE India, the Western Ghats, and Eastern Ghats. However, the regionally most widespread species, the Eurasian Otter, which occurs in Europe, Africa, and Asia, was only known from a skin described by Pocock in 1939. In 2015-16 we documented the first photographic record of the species from the Satpura hill ranges in Madhya Pradesh, central India. Around this time, surprisingly, the species was also confirmed from four other locations in India. Otter footprints and spraints were recorded along rivers/streams in the Satpura hill ranges in December 2015. For confirmation we placed camera traps at 21 sites, near rock boulders with spraints, sandy banks along streams/rivers and slopes near deep pools in flowing streams. The otter species photographed were identified from field guides and consultation with otter biologists. We also reviewed other reported information on confirmed records of Eurasian otters from India. In the Satpura hills, we recorded Eurasian otters in the hill streams (elevation 300-480 m ASL) and smooth-coated otters (550-700 m). Eurasian otters were clearly distinguished from smooth-coated otters based on their nostril and pointed muzzle, bedraggled coat, conical tail, whiskers, and less robust build. In 2016, researchers across India confirmed four records of the species, from low-lying areas around the Kanha Tiger Reserve (central India), tropical forests of the Valparai Plateau (Tamil Nadu), and Nagarahole (Karnataka, from an old record), and the Sikkim Himalaya. The surprising occurrences of Eurasian otters from five distinct geographic settings point to some fascinating guestions. How did such a successful and common species evade detection for this long a time? Previous unsubstantiated reports of the species have been from the Western Ghats and the Himalayas, and hence our record from central India is thus of great significance. Finally, we discuss potential reasons for why this species might have remained undetected across India.
11. Freshwater turtle assemblages in the Indus-Ganga-Brahmaputra basin: effects of floodplain hydrology and life history traits

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The Indus-Ganga-Brahmaputra basin (IGB) is a global hotspot for freshwater turtle diversity. Thirty-one species of turtles are known from this region, of which about 22 depend on river floodplain hydrology for their breeding and survival. So far, studies have mainly focused on taxonomy, distribution, breeding biology, and threats to turtle species, mainly from hunting, in this region. However, there is limited work in the IGB on how life-history traits of turtle species, and hydrological factors maintaining river-floodplain processes on the other, shape turtle assemblages. We reviewed information on the distribution of 22 floodplain-associated turtle species in 17 rivers of the IGB, and compiled a database of turtle traits associated with breeding biology, feeding preferences, basking (thermal) activity, and periods of activity. Further, we compiled data on hydrological characteristics of these rivers, in relation to the contribution of monsoonal precipitation and snowmelt to seasonal discharge and flooding, source type, vegetation controls on river floodplains, and extent of human modification. To understand how turtle traits were filtered by different hydrological factors we used multivariate RLQ and fourth-corner analyses. We found that turtle species traits and assemblage composition were correlated with hydrological factors. Turtle assemblages differed mainly in relation to 1) impact of anthropogenic modification of rivers, 2) rivers originating from hilly regions of peninsular India, and 3) rivers with low human impact, heavy flooding, and receiving two monsoons per year. As expected, turtle assemblages in highly modified rivers were characterized by summer-breeding species preferring lentic, alluvial floodplains. Winter-breeding, herbivorous turtles were mainly associated with flood-prone, near-natural rivers. Monsoon-breeding species and summer-breeding species formed separate clusters, correlated with flooding intensity and degree of anthropogenic modification, respectively. The most significant finding of our study was that human modification of rivers and resulting impacts on flooding extent might have affected freshwater turtle assemblages in the IGB.

12. Zoogeography of some passive dispersers on the Indian subcontinent

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The Indian sub-continent has a unique tectonic history which has influenced its biota. Various hypotheses were proposed describing the distributional patterns observed in different taxa, but these are not universally applicable. There are few studies on biogeography of the Indian sub-continent using freshwater invertebrates. Here we explore the possibility of using some passively dispersing freshwater invertebrates, which lack fossil records, for such studies. Based on available distribution records, the beta-diversity measure (ßsim) was used to generate clusters with Unweighted Pair-Group Method. Significance of distribution was tested using Analysis of Similarity. Geo-informatics tools were used to extract environmental data (19 bioclimatic variables, altitude and terrestrial ecoregion composition) for random and species locality points in the study region (divided into 100X100km2 grids). Principle Component and Canonical Correspondence Analyses were used to determine differences in environmental variables among zones, and their influence on distribution patterns respectively. Our analyses show (a) a distinct northern zone harbouring mostly Palaearctic taxa and (b) peninsular region harbouring diverse endemic faunal assemblages of anostracan branchiopods, Daphnia and diaptomid copepods. These zones differed in climatic as well as terrestrial ecoregion compositions; altitude, latitude and temperature influenced species' distribution. Global distribution data were not available for all groups, however available data show the Indian fauna to be a mixture of Gondwanan. Oriental, Palaearctic and Indian endemic taxa. The biogeography of the Indian plate is discussed referring to specific cases from these groups. Our analyses suggest that (a) passive dispersers exhibit distinct biogeographic patterns - this was initially thought to be a limitation in using these taxa for such studies and (b) these understudied taxa are important candidates for studying biogeography. Detailed investigations with further surveys and integrative taxonomic methods on these animal groups can provide better perspectives regarding the biogeography of the sub-continent.

08.30 - 10.00 AM Thursday 28th September 2017

Symposium 2: Building bridges in biogeography - Gondwana to Laurasia

1. Evolutionary history and diversification of the pan tropical tree family Dipterocarpaceae

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The pan tropical tree family Dipterocarpaceae, which consists over 500 species, shows remarkably high diversity and ecological dominance in the Asian rainforests. Based on the occurrence of high diversity of dipterocarps in southeast Asia, dipterocarps have been considered to have originated in the Laurasian tectonic plate and subsequently dispersed to African and American continents. However, the fossil data and phylogenetic evidence suggests a Gondawanic origin of dipterocarps and subsequent diversification in the Asian forests. To assess these two alternative scenarios and to gain insights into the diversification of the family Dipterocarpaceae, we carried out a biogeographical and phylogenetic analyses of the family Dipterocarpaceae. The dated phylogenetic analyses using fossil data and nucleotide sequences of the chloroplast and nuclear genes of 265 species of Dipterocarps revealed early Cretaceous (122 – 120 Mya) origin of the family in the Gondwana and divergence of the Asian subfamily Dipterocarpoidae from the African subfamily Monotoidae during Cretaceous to early Paleocene (106 to 61 Mya) period. The speciation and extinction rates specific for clades as well as geographical regions have contributed to the overall diversification of the Dipterocarpceae. The high diversification of dipterocarps due to high speciation and low extinction in the early Eocene (45Mya) coincided with the optimal climatic conditions that favored the expansion of tropical wet forests. Furthermore, our results suggest that the limited dispersal and in-situ speciation events promoted the radiation of Dipterocarpaceae in islands such as Sri Lanka. Overall, our findings support the view that ancestral stocks of Dipterocarps dispersed from the African landmass to the Deccan plate and migrated to the Eurasian plate and diversified in Southeast Asia giving rise to the current species richness distribution patterns of dipterocarps in tropical forests.

2. Making, baking and laying bricks to build bridges: Phylogenetic studies of some Indian plant taxa

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Out-of-India movements of taxa are important as bridges between Gondwana (G) and Laurasia (L) in studies of the global distributions of taxa. Regionally, there may be interest the bridge itself—not just as a path—for what it says about the assembly of the flora and fauna of South Asia (SA), a hybrid subcontinent (SAG+SAL). In this context, the Out-of-India hypothesis might be fine-tuned: for instance, a Gondwanan (SAG) taxon may go into Laurasia (through SAL) or vice versa; having entered, it may go "Out" leaving no traces today; it may enter, remain and speciate, then go out; it may do this and, in addition, reenter; it may enter and go nowhere. Before we can evaluate diverse scenarios, the bridges first need to be built-bridges require bricks. Here, we present bricks in the form of phylogenetic and preliminary biogeographic analyses of a few angiosperm taxa. Indian species of the study taxa—Dioscorea, Impatiens, Crotalaria and Rhododendron—were sampled; plastid and/or nuclear regions sequenced; new sequences combined with those from existing global studies; and analysed using maximum likelihood and Bayesian methods to estimate phylogenetic trees, divergence times and ancestral areas and to infer the movements of taxa as they diversified into, within, and out of India. The phylogenetic relationships and broad biogeographic patterns discovered are consistent with previous studies. In India, the different taxa show different patterns and times of diversification, keeping in mind caveats due to the general paucity of fossils for dating. For example, Impatiens shows a pattern of multiple entries, much diversification, and multiple exits (L-SAL-SAG; <15 ma; secondary calibration), while Dioscorea shows multiple entries, minimal diversification and no further movement (L-SAL-SAG; <30 ma; fossil and secondary calibration).

3. Not quite Gondwanan: Molecular phylogeny of Scincines reveal independent evolutionary origins for Indian and Sri Lankan skinks

Aniruddha Datta-Roy, Matthew Brandley, Praveen Karanth datta.roy82@gmail.com

Scincid lizards (Squamata: Scincidae) of the subfamily Scincinae are not as diverse as Lygosominae, contributing only about 19 % of the total skink diversity. Much of the diversity within Scincines are distributed in the Afro-Malagasy region and Arabian peninsula with only a few isolated lineages in Southeast Asia, India and Sri Lanka. We built a molecular phylogeny of Scincines from across its distribution using eight nuclear genes and one mitochondrial gene for an alignment consisting of ~8k base pairs. The results reveal that Scincines are monophyletic and are largely Gondwanan with the exception of a smaller Laurasian clade. The split between these two clades occurred around 90 mya which is much younger than the tectonic split between Gondwanan and Laurasian plate boundaries. Although the Indian and Sri Lankan scincines are nested within the Gondwanan clade they seem to have independent evolutionary origins. The endemic Indian Scincine genera Barkudia and Sepsophis are sister to a clade consisting of the African and the Malagasy Scincines, while the endemic Sri Lankan Scincines are sister to a clade consisting of the Seychelles scincines. The dates for the split between the Indian clade and the Afro-Malagasy clade are younger than the break-up of the Indo-Malagasy tectonic plate boundaries suggesting that the ancestors of the Indian genera may have dispersed onto the Indian plate while it was drifting northwards and was in glancing contact with Africa. The Deccan volcanism in India may have played a major role in extinction of many lineages that India and Sri Lanka may have shared in the past.

4. Dispersal vs. vicariance: Biotic history of Indian vertebrates Praveen Karanth karanth@ces.iisc.ernet.in

The origins of India's unique biota has been ascribed to its extraordinary geological history. particularly the separation of Indian plate from Gondwana in the Cretaceous and subsequent accretion with Eurasia in the Eocene. This provides an interesting setting to study the contributions of vicariance and dispersal, the two competing paradigms in biogeography, in shaping India's biotic assembly. Here I review published molecular phylogenetic and dating analysis of South Asian taxa to address this guestion. A literature review was undertaken to come up with a list of molecular studies on Indian vertebrate groups or studies that included Indian taxa. Taxonomic groups whose root age predated the separation of India-Africa (160-110 million years ago, mya) or India-Madagascar (100-80 mya) were considered as a strong candidate for vicariance. Those that underwent diversification after 80 mya were categorised as intrusive elements that dispersed into India. Furthermore, the topologies of these phylogenies were also considered to distinguish vicariance and dispersal events. Five vertebrate systems-fishes, amphibians, reptiles, mammals and birds- were considered in this study. Among these groups mammals and birds underwent recent post K-T diversification (65 mya) and therefore have dispersed into India. Among amphibians and reptiles most studies suggest recent dispersal into India and in the case of fishes there is data deficiency but the few studies on this group suggest dispersal. The overall pattern for Indian vertebrate biota suggests that dispersal into Indian plate has been the major factor shaping their current assembly in India. A similar exercise needs to be undertaken on other biota particularly plants and invertebrates. This will help us better understand predominant biogeographical process that has contributed to the origin and evolution of Indian biota.

10.30 – 12.00 PM Thursday 28th September 2017

Contributed session 3: Speciation and Diversification in the Indian Subcontinent

Invited talk

1. Origins Of The Western Ghats Endemic Birds

Sushma Reddy, V.V. Robin, C K Vishnudas, Pooja Gupta, Uma Ramakrishnan <u>sreddy6luc@gmail.com</u>

The origins of montane species in the Western Ghats, a biodiversity hotspot in southwestern India, have long been debated. Current taxonomy suggests that most endemic birds are single species of more widespread genera. The prevailing hypothesis for birds is that Himalayan taxa were able disperse to the Western Ghats at a time when peninsular India was covered in moist forest and subsequently these populations were isolated due to progressive aridification of the subcontinent. However some groups show connections to lineages in other surrounding regions. We conducted a comparative biogeographic study to examine the phylogenetic relationships of endemic species and investigate how these lineages colonized India. Our analysis included almost this entire avifaunal community of the Western Ghats, 48 of 66 endemic species or subspecies. Here we show that the Western Ghats species have their closest relatives in all the five possible geographic regions surrounding India and colonized India at various times. We propose that the assemblage of the Western Ghats avifauna is driven as much by island biogeography dynamics as vicariance events.

Contributed talks

2. Lineage And Morphological Diversification In A Continental Radiation Of Hemidactylus Geckos

Aparna Lajmi, Anjilee Verma, Praveen Karanth aparna.lajmi@gmail.com

Adaptive radiations are characterized by diversification of a single ancestor into multiple ecologically diverse species. While these radiations are frequently coupled with an early burst in lineage diversification, corresponding patterns of morphological diversification are rare. However, these generalizations stem from extensive studies in insular systems and very little is known about them at a continental scale. In this study, we investigated an endemic radiation of Indian Hemidactylus geckos through complete taxon sampling to understand the patterns of lineage and morphological diversification. Hemidactylus species are found in a variety of microhabitats - rocky outcrops, open grasslands, tree trunks and human habitation – and the relationship between these habitat specialists and their morphology was assessed. Molecular data was generated for multiple markers and species delimitation methods were utilized to identify putative species. A time-calibrated phylogeny was used for diversification analysis. Phenotypic data for 42 morphometric characters was measured from~225 specimens representing 32 species. We examined models of species and morphological diversification, along with the morphological disparity-through-time. We found significant differences in morphology between terrestrial (open grassland species) and scansorial species (rupicolous, arboreal and human-commensal species). Species diversification followed a density-dependent model, and y statistics also suggested an early burst in lineage diversification. Morphological diversification shows a delayed burst in the evolution of subclade disparity. The Indian Hemidactylus radiation began diversifying 37 MYA, soon after the Indian plate collided with Asia 35 - 55MYA. The mass extinctions due to extensive Deccan volcanism coupled with the rapid drift of the Indian plate across the equator could have served as ecological opportunity and caused an early burst in diversification. However, the accumulation of morphological disparity is concurrent with the evolution of terrestrial lineages, and coincides with aridification in peninsular India.

3. Drivers Of Diversification Of Herpetofauna In The Western Ghats Escarpment

Kartik Shanker, SR Chandramouli, KP Dinesh, Aditi Jayarajan, Ashok Mallik, Saunak Pal, Vijay Ramesh, Priyanka Swami, Varun Torsekar, S P Vijayakumar <u>kshanker@gmail.com</u>

Mountains have been considered as centres of diversity and biodiversity hotspots across the globe. However, the fundamental drivers of diversity, diversification and dispersal remain poorly explored. Location: Western Ghats, Peninsular India, Oriental Realm. We studied diversification in multiple clades of frogs (Hylarana, Indirana, Micrixalus, Nyctibatrachus, Duttaphrynus and Raorchestes), lizards (Calotes) and snakes (Aheatulla, Trimeresurus) using a combination of dated molecular phylogenies, morphological and ecological data and geographical distributions. We used ancestral area reconstruction methods and alternative models of diversification to understand patterns of diversification and dispersal in space and time. The different clades showed broad scale spatial and temporal patterns of congruence and incongruence in the degree of importance of speciation modes. Temporal patterns of lineage diversification varied across the clades and showed signatures of both adaptive and non-adaptive radiations. The Palghat gap was found to be a major biogeographical barrier driving diversification and dispersal at different temporal scales within clades. Across all the clades, many deeply ancient lineages were found to be distributed in the southern Western Ghats. Comparative analysis of diversification across clades with differing biology reveals several underlying evolutionary and biogeographic processes. Both adaptive and nonadaptive radiations contribute to the underlying patterns of lineage diversification. The study highlights Western Ghats as a major centre of lineage and clade diversification. The persistence of several ancient lineages in the southern massifs highlight the significance of this Escarpment as a museum of evolutionary novelties in Peninsular India.

4. Speciation In Oriental Bat Radiations In Species Rich South Asian Mountain Ranges

Balaji Chattopadhyay, Kritika Garg, Sripathi Kandula, Paramanantha Swami Doss D, Uma Ramakrishnan, Frank Rheindt balaji@nus.edu.sg

Diversification of bats in the Indian subcontinent is a poorly studied discipline with reports of great potential of cryptic diversity, specifically within the species rich mountain ranges of Southern and Northeastern India. In the present investigation we collated data obtained from three species complexes (least horseshoe bats, rufous horseshoe bats and Cynopterus fruit bats) of oriental bat radiations to address speciation dynamics and diversification of bats within the subcontinent. We used a suite of morphological, vocalization data and multi-loci DNA sequence data for the insectivorous horseshoe bats. For the Cynopterus fruit bats we used genome-wide data for both contemporary and century old ancient DNA samples. We performed phylogenetic reconstructions, assessed population genetic differentiation and performed coalescent simulations to understand gene flow and isolation among distinct lineages within each species complex. We also performed historical biogeographic reconstructions to assess if the Indian subcontinent acts as source or sink to these bat radiations. Our results reveal the presence of new species level lineages in the Indian subcontinent. The Western Ghats drives divergence and speciation for multiple bat species. We observed deep phylogeographic divide across the Palghat gap within insect bats and discovered a hybrid zone in Northeastern India. Further, observations reveal that Indian continent serves as both source and sink to bat radiations. We obtained evidence from multiple bat taxa revealing that the mountain regions of the Southern India serve as hotspot of speciation in young bat radiations. The Palghat gap impedes gene flow at least in insect bats. Analyses for the fruit bats are ongoing. The Indian subcontinent, specifically the biodiversity hotspots of Western Ghats and Northeastern India harbors great cryptic diversity and serve as engines for speciation and diversification of biotic taxa.

Speed-talks

5. Lineage Delimitation Using An Integrative Approach In Nyctibatrachus, An Ancient And Endemic Frog Genus From The Western Ghats, Peninsular India

Varun Torsekar, Kartik Shanker

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Frogs belonging to the genus Nyctibatrachus are endemic to the drainages of the Western Ghats mountain range, a biodiversity hotspot located in peninsular India. Although several new species of Nyctibatrachus have been described in the last decade, the species diversity in this genus still remains underestimated. In addition to this, there is widespread confusion regarding the systematic status of many species, which have been mainly delimited and described based on morphological criteria. To address both these issues, we carried out lineage delimitation by employing a unique stepwise protocol, along with a systematic spatial sampling strategy. Fieldwork was conducted to ensure the spatial coverage of the topographic and ecological heterogeneity of the Western Ghats. Therefore, first and second order streams belonging to all major drainages distributed across different hill ranges were sampled across the entire elevational gradient of the Ghats. We then used a stepwise integrative approach by incorporating multiple criteria like molecular phylogeny, genetic distance, bPTP (Bayesian Poisson Tree Processes) models, geographic distribution and morphology. Our analyses revealed the existence of number of hitherto unknown lineages with different levels of genetic divergence. We identified 21 new lineages, which is a 60% jump over the currently known species diversity. Out of these, more than half (57%) were shallow divergent lineages. This number is much higher than the number of shallow divergent lineages (38%) among described species. Our results highlight the gaps in historical sampling for genus Nyctibatrachus, and emphasize the significance of adequate taxon sampling for poorly studied tropical herpetofaunal groups. This study also manifests the importance of using biogeographic sampling and a hierarchical framework in uncovering a large number of shallow divergent lineages, which would have remained undiscovered using conventional or ad-hoc methods.

6. Origin And Evolution Of The Genus Piper In Peninsular India Sandeep Sen, Selvadurai Dayanandan, Thomson Davis, Rengaian Ganesan, Jagadish MR, Mathew PJ, Gudasalamani Ravikanth sandeep.sen@atree.org

Piper is one of the highly speciose plant genera (about 2000 species) in the world, consisting of several economically and medicinally important species. In the Indian subcontinent, Piper is naturally distributed in the northeastern Himalayas and in Western and Eastern Ghats of Peninsular India. Despite their high diversity and economic importance, the taxonomic and biogeographic affinities of this group remain poorly understood. Using a dated phylogenetic and biogeographic analyses, we shed light to the understanding of the historical biogeography and diversification of Piper in Peninsular India with respect to other South East Asian and South American elements. The multi-locus phylogeny revealed that the Peninsular Indian Pipers are nested within the South Asian group. Ancestral area reconstructions indicated three independent dispersals into India from South Asia during Oligocene period. This mainly contributes to the extant diversity of Piper in Peninsular India to South Asia during Miocene. Overall, our findings further support the evidence of Eocene-Oligocene biotic exchange between Peninsular India and South Asia. We further discuss taxonomic groupings and potential synapomorphic characters of Piper.

7. A Phylogeny Of Open-Habitat Lizards (Squamata: Lacertidae: Ophisops) Supports The Antiquity Of Indian Grassy Biomes

Ishan Agarwal, Uma Ramakrishnan

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India is dominated by Tropical grassy biomes (TGBs), usually considered seral stages or degraded forest and low diversity relative to the highly restricted, ancestral wet zone. It is unclear if Indian grasslands are anthropogenically derived, or native, old-growth habitats; with no clear timescale of grassland evolution. Studying diversification in taxa that are restricted to open habitats is one way to understand grassland evolution. We use a dated phylogeny of Ophisops to address questions on the origin, diversification and interrelationships of Indian and Saharo-Arabian Ophisops.Location :The Indian subcontinent and the Saharo-Arabian Realm. We generated up to 2736 base pairs of aligned sequence data including one mitochondrial and two nuclear genes for Indian lacertids and reconstructed phylogenetic relationships using maximum likelihood and Bayesian inference. We used a fossil-calibrated timetree, diversification analyses and ancestral area reconstructions to reconstruct the timing and tempo of Ophisops diversification. The monophyly of Ophisops is strongly supported, with a basal split into a large-bodied (LBC) and small-bodied clade (SBC). The Saharo-Arabian species are nested within the Indian species in the LBC. Species diversity in Indian Ophisops is grossly underestimated, with 26-47 candidate species. Ophisops began diversifying in the late Oligocene with significant rate shifts in the late Miocene- Pliocene and Pleistocene within the SBC.Our results are consistent with an ancient origin of grassland taxa and TGBs in India. Ophisops is a dramatic example of overlooked cryptic diversity outside forests, with ~30 species where five were known. Ophisops shows a novel biogeographic pattern, dispersal into-India from the Saharo-Arabian Realm in the Oligocene with a back dispersal in the Middle Miocene. Diversification in the SBC of Ophisops increased about eight-fold during the time of global C4 grassland expansion. Indian TGBs are old-growth ecosystems that need urgent conservation attention.

8. Non-Sister Sri Lankan White-Eyes (Genus Zosterops) Are A Result Of Independent Colonizations

Nelum Wickramasinghe, V.V. Robin, Uma Ramakrishnan, Sushma Reddy, Sampath Seneviratne

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Co-occurrence of closely related taxa on islands could be attributed to sympatric speciation or multiple colonization. Sympatric speciation is considered to be rare in small islands however multiple colonizations could be common in both oceanic and continental islands. Sri Lanka is a continental island in the Indian continental shelf of the Northern Indian Ocean. We carried out phenotypic and phylogenetic analyses to understand the origin and relatedness of Sri Lankan white-eyes (genus Zosterops), that include endemic Z. ceylonensis and its widespread regional congener Z. palpebrosus. Using multivariate morphometrics, we identified two phenotypically distinct clusters corresponding to the two species of white-eyes. Maximum Likelihood and Bayesian analyses with ~2000bp from two mitochondrial (ND2 and ND3) and one nuclear (TGF) gene indicated that the above two clusters are phylogenetically distinct, and not sister to each other. Sri Lankan Z. palpebrosus egregius and Western Ghats (India) Z. palpebrosus nilgiriensis clustered within the Z. palpebrosus clade having a common ancestor. In contrast, the divergence of the endemic Z. ceylonensis appears to be deeper and basal to other Zosterops white-eyes, and the first to originate in Sri Lanka. Despite high endemism, Sri Lankan biodiversity is long considered to be a subset of southern India. This study on a speciose group of songbirds with high dispersal ability, rapid diversification rate, and predominance on islands provide evidence for the contribution of multiple colonizations in shaping Sri Lanka's biodiversity. It also highlights the complex biogeographic patterns of the South Asian region, reflected even in highly vagile groups such as birds.

9. Aridification Driven Diversification And Abiotic Factors Influencing Current Distribution Of Fan-Throated Lizards In The Indian Subcontinent

Deepak Veerappan, Praveen Karanth <u>veerappandeepak@gmail.com</u>

The establishment of monsoon climate and the associated aridification has been one of the most important climate change episodes in the Indian subcontinent. However, little is known about how these events might have shaped the diversification patterns among the widely distributed taxa. To address this issue we studied the fan-throated lizards (Genus: Sitana, Sarada), which are diurnal and restricted to the semi-arid zones of the Indian subcontinent. Furthermore, there is no information on the factors influencing current distribution of these lizards. We sampled fan-throated lizards in 107 localities across its range. We used molecular species delimitation methods to delineate species. Five iguanian fossils were used to calibrate and date the phylogeny. We used bioclimatic layers and google earth to identify potential climatic and topographic barriers respectively. Using species delimitation methods we delineated 15 species in the Sarada & Sitana clade. Lineage diversification of fan-throated lizards began 15 mya onwards which corresponds to the time when monsoon climate was established. This was followed by a period of intensification of monsoon and initiation of aridification which is also when we observe rapid lineage accumulation in these lizards. The current distribution of fan-throated lizards is confined to the dry zones of the Indian subcontinent. On the other hand, the species poor sister lineage Otocryptis (3 species), a much older lineage, probably represents relict lineages now confined to forested areas. Thus, the seasonality led changes in habitat, from forests to open habitats, appear to have driven diversification of fan-throated lizards. River gorges and high mountain ranges are potential barriers for their dispersal.

Posters

10. Did Indian Monsoon Drive Diversification Of Amphibians Of The Western Ghats?

Anwesha Saha, Aparna Lajmi, Praveen Karanth, Aravind N.A. anwesha.saha@atree.org

The Western Ghats, a biodiversity hotspot in India, harbors an extraordinarily high level of taxonomic diversity and endemism which is probably due to various geological and ecological processes influencing the evolutionary patterns. The unique life history strategies of flora and fauna of the Ghats might be expected to be evolved due to the onset of major climatic events. In the present study, we chose amphibians as the model system to address whether the Indian monsoon is driving the diversification in amphibians of the Western Ghats All molecular sequence data and the corresponding secondary time-calibrations were collected from published studies to reconstruct the dated phylogenies for individual Anuran and Gymnophiona families of the Western Ghats. Furthermore, macro-evolutionary analysis was performed to detect the uncertainties in the phylogenies, the diversification rate and its variation with the climatic factor. The initial results show that two families, Rhacophoridae and Micrixalidae diversified around 10-0 Mya, whereas the diversification of the genus Indosylvirana(Ranidae) occurred around 12-3 Mya which corresponds to the establishment of Indian Monsoon. Other families have a peak diversification around ~26-22 Mya and a gradual decline in diversification is observed post mid-Miocene optima (~17-15Mya).Based on this preliminary analysis, it is observed that out of seven anuran families, three have diversified after the strengthening of Indian monsoon between 12 to 7 Mya. This major climatic event also resulted in aridification and high seasonality. Probably due to this, the obligate freshwater breeding species (eg: Nyctibatrachidae) declined after the mid-Miocene optima, and those families or genera which are either post monsoon (Micrixalidae) or terrestrial breeders (Rhacophoridae) showed an increased diversification rate.

11. Multi- Locus Phylogeny Of A Taxonomically Problematic Frog Genus Fejervarya From South Asia Reveals Cryptic Diversity.

Prudhvi Raj

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The genus Fejervarya, also known as Cricket frogs of the family Dicroglossidae are distributed across South and Southeast Asia. However they had been difficult to study since the group is plaqued with taxonomic issues. Lack of distinctive morphological characters has lead to problems in validating the true species diversity of this group. In this study I attempt to resolve taxonomic issues in this group using molecular data. Broad sampling of this genus was undertaken across its range in India. To assess the phylogenetic relationships of this group, we utilized two mitochondrial (12sSr RNA and 16S rRNA) and one nuclear (Rhodopsin) DNA markers. Maximum likelihood and Bayesian approaches were used to build phylogenetic trees. Maximum likelihood and Bayesian analyses resulted in identical and highly supported trees. Phylogenetic analysis retrieved many well supported clades that are not defined by traditional morphological characters. Many of these species can only be distinguished from other congeners using molecular data. On the basis of our phylogenetic analyses, they are seven south Asian clades and three south East Asian clades. These clades represent regional radiations. Both analyses show strong support for the monophyly of the genus Fejervarya with good bootstrap values. The analyses support derived clades in both south and south east asian lineages. From the current study it was considered that Fejervarya crancivora group to be the basal for both the lineages. The current distribution can be explained through dispersal of the group through main land and in some cases by overwater rather than vicariance.

12. Phylogenetic Relationships Among Civets In The Genus Viverra, Including The Malabar Civet (Viverra civettina)

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Current species distribution patterns across Southeast Asia and India have been shaped by complex geological history and repeated climatic fluctuations since the Pleistocene. However, the advent of human activities, especially trade, has altered distributions, especially affecting species of commercial importance. Civets in the subfamily Viverrinae are harvested for their aromatic product (civet), and this practice has been well documented in several species. The Malabar Civet Viverra civettina, one of only two small carnivores in the world listed as Critically Endangered, is endemic to the Western Ghats, India. However, it has never been sighted with certainty in the wild and it's 'known' ecology is based on speculation, not fact. A review of its history of collections and published and unpublished literature on the species led to persistent uncertainties about the species. All known skins have changed hands before reaching their current destinations, and the primary origin of each remains unknown. The Malabar Civet is so close morphologically to the disjunct Largespotted Civet V. megaspila of South-east Asia that the two are often considered conspecific. Discrepancies in the early field descriptions attributed to Malabar Civet suggest that they refer to other, non-congeneric, species (no other Viverra is suspected to occur in southern India), yet most of these descriptions have been repeated verbatim. In this study, we examine the phylogenetic relatedness amongst species of Viverra civets across Asia, as well as test the hypothesis that the Malabar Civet is not a real species. We will present results from Bayesian, maximum likelihood and parsimony analyses with data from 4 genes for over 7 species of civets. Genetic diversity within the geographic lineages and subspecies of the Viverrinae civets will also be calculated, in order to allow for a better understanding of the trade-related movement of species by humans.

13. Phylogeny And Biogeography Of Peninsular Indian Bulbuls Ashish Jha aashishiha@ccmb.res.in

Globally 139 species of bulbuls (Pycnonotidae) are recognized, of which 24 species are found in Indian subcontinent and 8 species are found in Southern India. Previous studies on Bulbul phylogeny suggest two endemic radiations- African and Asian. Peninsular India has 6 endemic bulbuls. We wish to decipher patterns in speciation in peninsular India of extant bulbuls and identify factors that might have influenced the biogeographic patterns. Samples from 11 Bulbul species were collated from various sources and 6 genes (3 mitochondrial and 3 nuclear) were sequenced for this study. Sequences were also obtained from NCBI and the concatenated sequences thus created was subjected to phylogeny tools; RaxML, MrBayes and BEAST. Our phylogenetic tree and ND2 gene tree retrieved topologies that were identical to those obtained previously on bulbuls. Though 6 out of 8 Bulbul species of peninsular India are endemic to the region, they group within different clades. Yellowthroated bulbul is basal to the clade containing Himalayan bulbul, white-eared bulbul, redvented Bulbul and red-whiskered bulbul while yellow-browed bulbul is sister to white-browed bulbul and forms a separate clade with bulbuls belonging to Malay Peninsula. Flamethroated bulbul, as expected appears well nested among congeneric black-capped bulbul and Black-crested Bulbul which were all once a part of Pycnonotus melanicterus species complex. Square-tailed Bulbul is sister to Black Bulbul and forms a clade with Ixos and Hemixos spp. of Himalayas and Indo-Myanmar region. Phylogenetic placement of endemic bulbuls such as yellow-throated bulbul, square-tailed bulbul and yellow-browed bulbul was deciphered. Using newly generated sequences and those from NCBI, a phylogenetic tree for 57 species covering all valid genera in Asia was generated. There is no evidence of in-situ speciation of bulbuls in India. Bulbuls of peninsular India show two groups with distinct biogeographic affinities- (i) Western Ghats and Himalayan bulbuls; (ii) Peninsular Indian and South Asian bulbuls. Indian bulbuls are phylogenetically diverse and we hypothesize that distinct colonization events and allopatry might have occurred due to historical habitat transitions in peninsular India.

14. Through The Eyes Of The Blindsnakes: Understanding The Biogeographic History Of India

Chinta Sidharthan, Akshay Khandekar, Praveen Karanth chinta.sidharthan@gmail.com

The Indian subcontinent's association at different time periods with different landmasses, and the intense climatic changes it has undergone have been evident in the presence of taxa with various biogeographic affiliations on the subcontinent. Due to their fossorial nature, blindsnakes have been a largely unexplored group. They are an excellent system to study to further understand the role of India's geological history in the present faunal distributions, given the evidence that they have various modes of dispersal, including oceanic dispersal (Vidal et al., 2010). This study aims to decipher the various biogeographical affiliations of the four genera of blindsnakes- Indotyphlops, Grypotyphlops, Argyrophis and Gerrhopilus- found in India using an integrative approach. We also attempt to study the actual diversity of this highly understudied group and resolve their taxonomy in the process. Extensive sampling from the described type localities was done in order to have a comprehensive sampling for the four genera of Typhlopoids found in India. A phylogeny was built using 3 nuclear markers generated from the collected individuals and sequences obtained from GenBank for the blindsnakes distributed worldwide. Morphological measurements and scale counting data were also collected to identify species and to study the presence of cryptic diversity in species with very wide distributions. Initial results show that the four genera of blindsnakes found in India have very distinct evolutionary origins and biogeographical affiliations. The results confirm the various biogeographic affiliations for the four Indian blindsnake genera. Molecular dating and ancestral area reconstruction analysis will further help us understand the geological processes that led to the current distribution and diversity of this taxa in India. This is an ongoing project and the results and discussion sections are based on what information we have so far. These sections may be subject to modification.

15. Genetic Drift Among Isolated Populations Of Tree Euphorbias In The Western Ghats

Bruce De Jong, Mihir Sule, V.V. Robin, Nandini Rajamani tbdejong2000@yahoo.com

India is home to 85 recognized species of the genus Euphorbia L, with 15 species of succulent euphorbias (Euphorbia subgenus Euphorbia). The giant genus Euphorbia is one the most numerous groups of plants globally (2050 species), ranging widely in form and ecology. Few succulent euphorbias in India are generalists, with most species being restricted to pockets across the country. Four succulent Euphorbia species are endemic to the Western Ghats of Tamil Nadu and Kerala, and we propose one or two new species and five distinct varieties (possibly species complexes). Numerous isolated valleys and pockets in the southern Western Ghats have provided the ideal conditions to encourage genetic drift among these plant populations. It appears that for geographical and botanical reasons, these mountain euphorbias have been unable to spread from their isolated habitats for a significant period of time. These plants possibly require higher altitudes with cooler temperatures and more water and are therefore restricted to hills, unlike lowland species, which can live and reproduce both in the foothills and on the plains. We use morphological and genetic information to determine the relationships of the south Indian Euphorbia subgenus euphorbia plants with their relatives across India, Asia and Africa. We present Bayesian, maximum likelihood and parsimony analysis of genetic data from 6 markers (>50 samples, ~10 species) in addition to trait reconstruction and evolution. We also take into account collection histories and description records to determine the veracity of species.

16. Comparative Biogeography Of Vine Snakes (*Ahaetulla, Colubridae*) And Asian Pit Vipers (Trimeresurus, Viperidae) In Peninsular India.

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The evolution and biogeography of various taxa in Peninsular India are of particular interest as this region, a Gondwanan fragment, is critical to our understanding of historical biogeography in the Oriental realm. Though most Indian snakes are considered to be Malayan relicts, they remain poorly studied with regard to their biogeographic affinities despite their spectacular diversity. Here, we present patterns of dispersal and diversification within Peninsular India using two distantly related snakes with broad differences in ecology; an arboreal, non-venomous genus, Ahaetulla (vine snakes), belonging to the family Colubridae, and the genus Trimeresurus (pit vipers)a group of terrestrial and arboreal, venomous snakes belonging to the family Viperidae. First, using an extensive taxon sampling of snakes from Peninsular India and adjoining Northeast India, we delimited species using a coalescent method and a multi-criteria approach including genes, geography and morphology. We sequenced five mitochondrial and nuclear genes and constructed dated phylogenetic trees for both genera. We then carried out a comparative biogeography of species across Indian subcontinent with special reference to the Western Ghats. We found a deeply divergent clade in vine snake, which was unrecognized earlier and seven new lineages within Ahaetulla genus. Similarly, we found six new lineages in Trimeresurus. We found that diversification and radiation for both the genera occurred in the Middle Oligocene to Early Miocene.In contrast to earlier hypotheses, Peninsular India emerged as a centre of snake diversification and Western Ghats as a major centre of in-situ radiation for both clades. Patterns of dispersal show signatures of congruence and contrast between the clades, with the Western Ghats acting as a major source for colonisation of ancestral lineages into the arid regions in Peninsular India and adjoining Sri Lanka as well as SE Asian regions.

17. Genomic Diversity And Phylogeography Of Sino-Australasian Lauraceae

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Evolutionary and biogeographical studies of highly speciose tropical tree groups are hampered by extensive geographic ranges, lack of diagnostic morphological characters and limited success of traditional molecular studies due to the use of easy to obtain, but generally low-informative markers. This continues to play a role today and becomes apparent in the fragmented knowledge on the evolutionary history, genetic diversity and ecological functioning of widespread, key plant families of tropical ecosystems. Contrary to traditional molecular studies, advances in genomics and next generation sequencing techniques allow us to open the treasure chest of tropical genomic diversity and investigate plant diversification and evolutionary history on levels that are out of reach using standardised marker approaches. Here we present results of the first large-scale study to investigate the geographic distribution of genomic-level diversity using NGS-techniques in Lauraceae, an ecological and structural key component of (sub-) tropical forests in Asia. Our aim is to clarify the origin, diversification and ecological functioning of regional Lauraceae assemblages, against the backdrop of past palaeogeographic changes and geological events. Results provide essential insights into the geographic distribution of genomic diversity within southern China, and its evolutionary connections to South- and South-East Asia, Malesia and Australasia. Our study is timely in an era where we face a global loss of biodiversity due to unsustainable use of biological resources, climate change and deforestation, as we struggle to understand and define the origins and distribution of diversity in order to ensure its conservation for future generations.

18. Phylogeny And Biogeography Of The Genus Hedychium J. Koenig (Zingiberaceae)

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Hedychium J. Koenig (Zingiberaceae) is represented by c. 80 taxa mainly from Eastern Himalaya, North East India (NE India), South West China (SW China), Indo-China, Thailand and Peninsular Malaysia. Distribution of Hedychium is very disjunct as some taxa are endemic to the Western Ghats (India) and Madagascar. Taxa which are not accepted as true species are considered to be part of a species complex. At least four major species complexes exist among Hedychium in the NE India alone. The members within these complexes show high degrees of overlap in their morphological (especially, floral) characters. The only molecular phylogeny of Hedychium has a very narrow representation of taxa from the Indian subcontinent, leaving the confusions even at the molecular level. For a clear understanding of the genus Hedychium and its interspecific relations we are currently building the Hedychium phylogeny using different nuclear and plastid markers. We will be testing if the homoplasy in the floral characters within Hedychium can be explained by their similar ecological conditions and overlapping distributional ranges. Supporting Wood's phylogeny, our tree topology also supported the monophyly of Hedychium, but challenged many of the established morphological affinities. Four clades were distinguished within Hedychium based on the biogeographic associations. Clade 1 consisted of species from peninsular Malaysia, Clade 2 consisted of Chinese and higher elevation Himalayan species, Clade 3 consisted of Hedychium acuminatum alone and Clade 4 consisted of species from the Indo-Myanmar ecoregion. The phylogeny reconstruction can give better insights into the factors which shaped the current diversity patterns of Hedychium. We will try to validate most of the intermediate clinal forms using our multi-pronged approach of morphometric, ecological and molecular evidences. We are trying to understand the evolutionary switches occurred in floral traits among different Hedychium.

19. Phylogeography Of An Old, Low Vagility And Fragmented Species From The Chilean Hostspot: Genetic Diversity Of The Endemic Wet Meadow Crayfish Parastacus pugnax (Parastacidae)

Pedro Victoriano, Guillermo DÉlía, Carla Muñoz-Mendoza, Karina Vega, Lorena Rivera

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Low connectivity of habitat, low vagility and the age of taxón, are recurrently associated with high levels of inter-population diversification and cryptic diversity. Parastacus pugnax is part of a Gondwanic family, it is an endemic freshwater burrower crayfish in Chile, and with high economic and cultural importance. Although it is a highly exploited resource, its phylogeographic patterns, which could form the basis, both for conservation, and to infer historical processes explaining its evolutionary diversification, are unknown. Considering its association with highly fragmented habitats in Central-Southern Chile (wet meadows), preliminary estimation of age of Parastacus, and its low vagility, we evaluated the hypothesis of the occurrence of high and old inter-population genetic diversity. Methods: Based on a mitochondrial gene (COI), we estimate levels of spatial genetic diversity for populations from all the distributional range of the species. Results: According to summary statistics (Hd, pi, S, D', Fs), and genetic structure, we detected high levels of interpopulation variability and geographical differences in demographic histories which could be associated with the Chilean geography and palaeoclimate. Bayesian estimates suggest high number of intraspecific lineages with restricted distribution. TMRCA for P. pugnax is approximately 38 Ma. Topologies and estimated ages for clades suggest the occurrence of cryptic diversity at species level. The results are discussed in terms of probable historical causes that would account for the recovered pattern, both in the Biogeographical scope, and about delimitation of conservation units (ESUs) for P. pugnax.

20. Diversification of Impatiens in India: From Where and When? Renu Puri, Ramachandran Geeta

Western Ghats and northeastern India are two disjunct hotspots of biodiversity in South Asia. These regions are known to contain disjunctively distributed taxa. Impatiens is one such taxon that, in India, comprises about 200 species mostly distributed disjunctively in Western Ghats and Himalayas. This disjunct pattern raises questions regarding the history of these distributions: What is the shared history of the Impatiens species of these two regions? Do they form a clade? Where did the ancestor come from? When did Impatiens diversify in India? We address these questions by phylogenetic analysis of an expanded set that includes about 55 Indian species, from both regions, to understand the diversification of Impatiens in India. Species of Impatiens were collected from Goa, Bangalore, Kerala, Sikkim and Meghalaya and DNA isolated. We analyzed new sequences of ITS and atpB-rbcL regions combined with existing data. Divergence times were estimated by using Bayesian methods as applied in BEAST ver. 1.75 (Drummond et al., 2012). Ancestral areas were reconstructed using programmes implemented in RASP (Yu et al., 2015). The results suggest that there have been multiple migrations between India and Africa and India and China; these migrations occurred around 10 million years ago. There were not only dispersals from China and SE Asia into India, but also dispersals out of India into Africa and back into China and SE Asia. The northeastern species form a distinct group closely related with some Chinese species. Divergence times suggest that migrations between India and Africa are recent and must have occurred by long distance dispersal either over land or by transoceanic dispersal. Impatiens is supposed to have originated in Southwest China; therefore it is plausible that Impatiens migrated first into India and, from there, to Africa via Southwest Asia.

01.00 – 02.00 PM Thursday 28th September 2017 Contributed Session 4: Hot Topics in Biogeography

1. Citizen Science as a tool to study urban Biogeography: A case study from Bangalore

Kaberi Kar Gupta, Hari Prakash JR, Vidisha Kulkarni,Harshitha C,Soumya Kori,Rajeev Bacchu, Arun PV, Poornima Kannan,Yateesh Kumar lorises@me.com

While a focus on conserving biodiversity in protected landscapes is important, biodiversity outside protected areas is also critical for conservation. A growing number of studies show that urban habitats can be rich in species diversity. Our understanding of urban ecosystems remains lacking even as cities continue to sprawl worldwide. Cities are now recognized as complex dynamic social-ecological systems, studying which requires interdisciplinary collaborative approaches, with quantitative and qualitative data gathered over large spatial and temporal scales. Involving local communities in scientific research helps in not just gathering data but also in conservation policy and action. Engaging the public directly in research through Citizen Science is therefore an important tool for conservation in cities. The Urban Slender Loris Project documents how citizen science can be used to study urban biogeography in Bangalore, India. A collaborative team of citizen volunteers and scientists are mapping spatial and temporal distribution of lorises as well as the extent of forest cover in the city. To estimate loris abundance, volunteers conduct nocturnal censuses using a standardized protocol within a 5kmX5km sampling grid. An online survey of residents helps document local knowledge of loris distributions. Ethnographic interviews of long-term residents help build an oral history archive of nature in the city. The project has engaged over 300 citizens, with 60 formally trained to conduct field surveys. We have confirmed loris presence in forest patches within institutions, parks, and reserve forests. Encounter rate is higher in the institutional campuses than in parks and city forests. Interviews suggest older residents have seen lorises in the past. This project shows interdisciplinary collaborative research initiatives between local communities and scientists are important to understand urban biogeography.

2. Extreme homoplasy in egg-eating snake genera in India and Africa due to convergence of feeding modes.

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The Indian egg-eating snake, Elachistodon westermanni is endemic to Indian sub-continent, and a monotypic species, known from very few specimens. It differs from African egg-eating snakes of the genus Dasypeltis, by absence or reduced number of teeth and presence of modified vertebrae possessing hypapophyses, both specializations for preying on bird eggs. Based on a limited number of specimens, comparison of the two genera must have had a common ancestor that might have been an opisthoglyph or even a proteroglyph, and Dasypeltis had more specialized morphology than Elachistodon. In order to test if the snake genera shared a common ancestry, we employ molecular phylogenetic tools to compare both the genera. We amplified two mitochondrial gene regions: 16S ribosomal RNA and Cytochrome B (Cytochrome B oxidase) and one nuclear gene region C-mos (Serine/ threonine kinase) which has been extensively used in squamate phylogenies. We compared 18 morphological characters between the three genera Boiga, Elachistodon and Dasypeltis. We show that the African egg-eater and Indian egg-eater snakes do not share the most recent common ancestor. Instead, we found that the Indian egg-eater is closely related to a paraphyletic clade of snakes belonging to the genus Boiga. Therefore evolution of similar morphological characters in the African egg-eater snakes and the Indian egg-eater could be a result of convergent evolution driven by diet specialization, independently in two continents - India and Africa. Considering the vast area of their distribution and diversity in colour morphs, we speculate that the Indian egg-eater lineage could be more diverse than represented by a sole representative of the genus.

3. Mountains, Climate and Biodiversity: A Collaborative Understanding.

Alexandre Antonelli, Allison Perrigo, Carina Hoorn <u>M.C.Hoorn@uva.nl</u>

Mountains harbour about one guarter of all terrestrial species in about a tenth of the world's continental surface outside Antarctica. This disproportionate diversity makes mountains a focal point for research on the generation and maintenance of biodiversity. There are complex interactions between plate tectonics and mountain building, climate change and erosion over time scales extending to millions of years. It is now widely accepted that these large-scale processes play a fundamental role in biotic evolution across space and time. Together with ecological interactions among organisms, they form the basis for modern biogeography. But why, when and how the interactions between the geosphere, biosphere and atmosphere resulted in such high biodiversity in mountains is insufficiently understood. We brought together a number of experts to address this shortfall, and as a result produced a reference text that will further promote the study of biogeographic patterns in a greater context. A major collaborative effort was carried out together with international authorities spanning a number of disciplines within biology, geology and climate sciences. We solicited chapters to produce an edited volume that promotes a synthetic view of montane biodiversity in light of geological and climatic processes. This is intended as a crossdisciplinary reference for students and scientists that wish to learn more about these adjacent, yet often overlooked, fields. The result of this effort was the production of a 31chapter edited book, Mountains, Climate and Biodiversity. It brought together a multidisciplinary team of authors to discuss the state of research at the interface between the geo- and biosphere and address major questions, while presenting examples from mountain systems around the world. It provides a three-part presentation of theory, methods and examples that offer readers a useful introduction for assessing montane biodiversity in a broad context.

4. Understanding the origin and diversification of birds from dry forests in South America: the case of the Slaty-Antshrikes, Thamnophilus punctatus species complex (Thamnophilidae).

Alexandre Fernandes, Gustavo Bravo, Andrés Cuervo, Urban Olsson, Helder Araujo, Luís Fabio Silveira, Robb Brumfield, Alexandre Antonelli, Elizabeth Derryberry, Alexandre Aleixo, Graham Derryberry.

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This study aims to infer the biogeographic history of the Slaty-Antshrike species complex (Thamnophilus punctatus), to better understand the origin and formation of open vegetation in South America. Slaty-Antshrikes are an important component of the dry forest avifauna. ND2 gene sequences of 100 individuals were used in a probabilistic dispersal-vicariance likelihood model implemented in the library BioGeoBEARS in R and applying Reconstruct Ancestral State in Phylogenies to estimate event route probabilities (dispersal, vicariance and extinction). We also generated sequence data for 84 exons and 2305 ultraconserved elements (UCEs) for 19 individuals in the Thamnophilus punctatus complex. Concatenated and species-tree analyses are congruent with previous phylogenetic hypotheses based on six mtDNA and nDNA loci. The results indicate that populations in Amazonia are closely related to populations along the foothills of the Andes, whereas populations from the Dry Diagonal are sister to those in the Atlantic Forest. The most likely origin of the Thamnophilus punctatus complex was estimated to the Lower / Middle Pleistocene. Vicariance seems the most important process accounting for diversification in this group, with climatic oscillations probably playing a more decisive role than geomorphological dynamics in South America.

5. Urban biogeography: an overview of how Indian birds may have evolved to live amongst humans in cities

Madhusudan Katti, Christopher Trisos, Vallari Sheel <u>mkatti@ncsu.edu</u>

The Indian subcontinent, starting in the Indus Valley, has been a leading center for urbanization in the world. Historically, the region has also tended to support a higher density of people, living in close proximity to wildlife, than most other parts of the world. This trend has accelerated in recent decades, with some Indian cities becoming exemplars of the biggest, densest megacities in the world, and numerous others poised to join their ranks by 2050. India is now home to 1/6th of Earth's human beings and 1/10th of its bird species. Even as a Cartesian duality separating humans from nature has come to dominate the conservation policy discourse, the reality in India remains one of humans continuing to coexist with a rich diversity of wildlife, even in its largest megacities. We believe this presents an underexploited opportunity to study the evolution of synurbanization, i.e., adaptation of species to urban habitats. Our preliminary analysis of the geographic distribution of avifaunal diversity in urban India suggests: 1) Indian cities harbor rich bird diversity; e.g., a recent global analysis of urban biodiversity (Aronson et al 2014) found Kolkata to be one of the most species rich in a global sample of 54 cities; bird species richness in Indian cities is likely 2x the global median. 2) Unlike in other regions, the Indian avifauna seems robust to invasion by urban exploiter species (like starlings), even as it has exported such birds (like mynas, parakeets) elsewhere. We hypothesize that this reflects a long-term coevolution between birds and anthropogenic landscapes driving greater likelihood of synurbanization. In the context of rapid urbanization threatening wildlife worldwide, we believe that developing an evolutionary understanding of the biogeography of synurbanization is key to biodiversity conservation, and a core research agenda for reconciliation ecology in the Anthropocene.

6. Competition between birds and ants for nesting cavities results in shortage of nesting space at low elevation in eastern Himalayas

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Songbirds show a mid-elevational peak in eastern Himalayas, i.e. species diversity is highest at about 2000m. By contrast, ant abundance declines steeply with elevation such that ants are essentially absent from the mid-elevations. To investigate the potential effect of ants on nesting behavior of birds, we put up 139 nest boxes at low elevation at about 200m in 2015 and 2016. We also put up 30 nest boxes at an elevation of 1200m in 2016. 62 of the nest boxes at the low elevations were occupied by a single bird species, the white-rumped Shama (Copsychus malabaricus) and 19 of these nest boxes were occupied by ant colonies following a nesting attempt by birds. Ants also occupied 6 of the nest boxes unused by birds. Neither birds nor ants used any of of the nest boxes at 1200m. The high rate of occupancy of nest boxes at low elevations coupled with the absence of nest box use at mid-elevations suggests that ants and birds might be competing for nesting cavities at low elevations. Greater availability of nest cavities at mid-elevations may be one of the factors contributing towards the mid-elevational peak of birds in eastern Himalayas.

7. Convergent evolution of key functional traits confers ecological success of tree species in tropical swamp forest communities

Shivaprakash K. Nagaraju, Selvadurai Dayanandan, Jagadish MR, Vasudeva R, Srikanth Gunaga, Uma Shaanker R, Lessard J P. <u>shivaprakash.kn@gmail.com</u>

In tropical forests across the world, communities are comprised of relatively few 'dominant' species and many rare species. However, the processes underpinning such patterns in the structure of tropical tree communities remain widely debated. First, there is disagreement regarding the relative influences of stochastic and deterministic processes, though most would agree that they vary geographically, and that both play a role in determining the relative abundance of species in a community. Second, while we generally think of ecological processes as drivers of species' relative abundances, there may be an important and unexplored role of species evolutionary history. Here, we use data on species' relative abundances, functional traits and phylogenetic relationships within 42 freshwater swamp tree communities distributed over seven degrees of latitude in Western Ghats, India to ask whether the evolution of key ecological traits predicts ecological success. We found that key functional traits, independently of phylogenetic relationships, explain the ecological success of species in these communities. Moreover, we detected a strong signature of habitat filtering, which indicates that species are deterministically filtered from the regional pool into freshwater swamp communities. Finally, we show correlated evolution between key ecological traits that confer flooding tolerance and historical colonization of swampy habitat. In sum, we show that the repeated evolution of key functional traits, together with strong habitat filtering, consistently lead to species ecological success across communities spanning a broad geographical gradient.

8. Elevational and latitudinal diversity patterns of trees along the Himalaya

Suresh K Rana, Gopal S Rawat, Trevor D Price. envsuresh09@gmail.com

To summarise the distribution and richness patterns of Himalayan trees along elevational and latitudinal gradients from east to northwest Himalaya we examined 31 floras on species occurrence and their elevational distributions across six Indian Himalayan states plus Nepal and Bhutan. Further, presence of all species was cross checked in the Indian plains floras and species with underestimated lower ranges in Himalayan floras were updated for their elevational ranges. We conducted field sampling of trees in 50 guadrats of size 0.1ha after every 500m elevation along a single gradient in North Bengal and Sikkim in eastern and Jammu & Kashmir in western Himalaya.1382 species of trees including 1173 natives and 209 aliens have been recorded in the Himalaya. Species richness declines about fivefold from eastern to northwest Himalaya. Along the elevation trees shows a peak between 500m and 1000m in the east and monotonic decline with elevation in northwest in both field sampling and range interpolation methods. Species with tropical affinities shows a lowelevation peak, whereas species with temperate affinities show a mid-elevation peak. Beta diversity along elevation shows maximum turnover of species at 1500-2000m zone indicating a transition zone between tropical and temperate species. Richness is highly correlated with precipitation (R2= 0.77). Average tree densities are higher along elevation in east whereas girth sizes are higher in the northwest. However, tree densities and girth shows no peculiar trend along the elevational gradient. Both field sampling as well as range interpolation method show consistent richness patterns along the elevation, implying that sampling artefacts peculiar to each are not driving the relationship. Bioclimatic variables across Himalaya shows fivefold higher annual precipitation with much lesser temperature seasonality in east than in the northwest Himalaya. The latitudinal and climatic differences may have resulted this gradient with sharp decline in species richness from more tropical east to temperate northwest Himalaya.

9. Hostplant change and paleoclimatic events explain diversification shifts in skipper butterflies (Family: Hesperiidae)

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We explored factors that affected the diversification of skipper butterflies (Family: Hesperiidae) using the most comprehensive time-calibrated phylogeny of this speciose taxon based on a 10-gene dataset. Using estimated times of divergences and ancestral state reconstructions, we show that the early hesperiid lineages utilized dicots as larval hostplants, and the evolution of monocot feeding was a key character innovation that happened once at the K-Pg boundary (ca. 65 million years ago (Mya)), but allowed monocot feeders to diversify much faster on average than dicot feeders. The increased diversification rate of the monocot-feeding clade is specifically attributed to rate shifts in two of its descendant lineages. The first rate shift, a four-fold increase compared to background rates, happened ca. 50 Mya (i.e. 15 million years after the evolution of monocot feeding), soon after the Paleocene-Eocene thermal maximum, in a lineage of the subfamily Hesperiinae that fed on forest monocots. We hypothesize that although monocot feeding was an intrinsic trait that allowed exploration of novel niches, the lack of extensive availability of monocots comprised an extrinsic limitation for niche exploration. The other rate shift happened ca. 40 Mya in a grass-feeding lineage when open-habitat grasslands appeared in the Neotropics owing to gradual cooling of atmospheric temperature. We suggest that the rapid radiation of skipper butterflies on grasses is due to increased opportunity for allopatric speciation rather than the classical insect-hostplant co-evolutionary race.

10. Patterns Of Divergence Revealed Across Biochemical, Morphological, Vocal And Genetic Traits In An Island Endemic: The Flameback Woodpeckers Of Sri Lanka

Saminda Fernando, Rashika Ranasinghe, Sampath Seneviratne <u>saminda@ou.ac.lk</u>

Selection and drift are intense in insular populations, which could lead to rapid divergence and eventual reproductive isolation. Here we studied the patterns of divergence in a group of Dinopium flamebacks in Sri Lanka, a continental island located in the Indian plate, in the light of how barriers to gene flow shape divergence in island populations. Three forms of Dinopium are found in Sri Lanka; endemic red D.psarodes, yellow D.benghalense, and their hybrids comprising of a gradient of orange flamebacks. Using 340 live and 140 museum specimens we examined the variation in morphometrics, plumage, pigment biochemistry, acoustics and genetics of flamebacks across geographic and climatic gradients. Range of techniques such as haplotype mapping, NGS, phylogenetics, TLC, HPLC, and field playback trials. Multivariate analyses backed by cline theory were used for the analysis. Phenotype, genotype and pigment biochemistry showed concordant clinal variation across the hybrid zone, and across geographic and climatic gradient, suggesting a complex trait composition and the role of selection. Mate choice supported the same, psarodes and benchalense are vocally similar compared to other species in Dinopium. Endemic psarodes have a red carotenoid pigment that alters its reflectance spectra – which makes it red in Sri Lanka. There is a significant genetic distance between the two species. The benghalense found in Southern India appears to be sister to the Sri Lankan Dinopium.We found compelling evidence of divergence and local adaptations across multiple trait levels in Dinopium Flamebacks in Sri Lanka. The introgression between mainland congeners and island endemics seems limited, therefore, the distance and climatic barriers might have insulated endemic taxa from introgression. This pattern is reflected in other groups in Sri Lanka as well, where about one third of resident phenotypes are endemic even in a mobile group such as birds.
11. Integrative Taxonomy Of Himalayan Langurs: Molecular, Morphological And Ecological Variations And Its Taxonomic Implications

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Himalayan langur (Semnopithecus spp.) is the northernmost population of Hanuman langur (S. entellus) complex, distributed in the Himalayas from Pakistan to Bhutan and found at an altitude from 700 to 4200 msl (meters above mean sea level). Since the early 20th century, the taxonomy of these langurs has been a topic of debate owing to the presence of multiple classifications; this is because traditional taxonomy is based on morphological characters which are not adequate to differentiate between species and subspecies. Many authors consider Himalayan langurs as a single species with 4 to 7 subspecies whereas some authors have split these species in 2 to 4 species. Here, we will use data from multiple sources viz; morphology, DNA and ecology; to resolve the taxonomy of Himalayan langur. Fecal samples were collected in lysis buffer by using a cotton swab. DNA extraction, PCR amplification and sequencing were done. We amplified one nuclear marker and one mitochondrial marker. DNA sequences were analysed using multiple phylogenetic softwares. Occurrence points were recorded for ecological data analysis. Mitochondrial marker shows that Himalayan langurs are polyphyletic with respect to Hanuman langur. Resolution in the nuclear phylogeny is low, there are no distinct clades. This is an on-going work; addition of more nuclear markers will give robust results. In the mitochondrial phylogeny, Himalayan langur (HyL) populations are not monophyletic. They are polyphyletic with respect to Hanuman langur populations, immediately south of these HyL populations, from the plains. The low resolution in the nuclear phylogeny is because of less information in the single nuclear marker. Addition of more markers might improve the resolution. Our results suggest presence of multiple species of HyL which evolved independently from Hanuman langurs from the plains. Further analysis of morphological and ecological data will give more robust results.

02.00 - 03.30 PM Thursday 28th September 2017

Mini Session 2: Savanna Biogeography

Contributed talks

1. Current issues in savanna ecology

Jacques Gignoux

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Savannas are increasingly acknowledged as important and valuable ecosystems. They occupy ~20 % of global land surfaces, 85 % of the global land area burnt, host an important and spectacular biodiversity, and constitute a significant income for many countries through tourism and ranching. Despite this importance, they are under threat, mainly because of a poor knowledge of their extent and functioning. For long they were considered as degraded forests or croplands – ignoring that most of them are ancient ecosystems that appeared at least 5 million years ago. They are subject to high economic pressure, being easy to tranform either to cropland or to tree plantations, and being found in parts of the world where human population growth is fastest. Savanna science faces the double challenge of the ecological complexity of these systems and of the deep transformations they are currently undergoing. The complexity is due to the many interacting functional groups found in savannas: grasses, trees, grazers, browsers, predators, soil engineers. The balance between these groups is under the control of climate, fire regime and human activities, making the understanding and prediction of changes in ecosystem dynamics very difficult. The transformations currently observed are bush encroachment and/or afforestation, clearing and conversion to cropland, heavy poaching of emblematic species, changes in fire regimes and changes in rainfall regimes. I attempt here to prioritize the hottest issues in savanna ecology with regards to their current global situation. Among the major topics are (1) the socio-ecology of fire, or how governments and societies perceive and decide to manage fire in savannas and how this interacts with their stability ; (2) nutrient dynamics and limitations, in interaction with (3) the effects of CO₂ fertilisation on savannas, including water stress; (4) savanna stability and resilience with regard to their disturbance regimes; (5) the belowground world : when at least 50 % of the biomass is belowground, this has profound effects on the ecosystem functioning. Savannas also pose modelling and questions that have gained interest in the theoretical ecology community.

2. What changed for African trees after the invasion of Eurasian Bovids during the Miocene?

TRISTAN CHARLES-DOMINIQUE, T. Jonathan Davies, Gareth P. Hempson, Bezeng S. Bezeng, Barnabas Daru, Ronny M. Kabongo, Olivier Maurin, A. Muthama Muasya, Michelle van der Bank, William J. Bond

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By the mid-Miocene (16 My), a new land bridge allowed Eurasian bovids and giraffoids to invade the African continent. We investigated the consequences of the arrival of Bovids on the African continent for the evolution of spinescence in trees (1852 species). We revealed which class of mammal browser favours spiny communities of trees and found that trees from unrelated lineages developed spines 55 times subsequently to the formation of the land bridge. The increase in the diversity of spiny plants and bovids are remarkably convergent over the last 16 My. Our findings indicate that herbivore-adapted savannas evolved several million-years before fire-maintained savannas, and are favoured by distinct environmental factors. These findings then question whether spinescence emerged earlier in Asia and how the herbivores present during the early Miocene could have shaped the Asian vegetation.

3. The dynamics of fire and vegetation in northern Australia GARRY COOK, Mick Meyer, Adam Liedloff and Anna Richards garry.cook@csiro.au

Across much of northern Australia's savannas, the frequency of fires is greater than one fire every four years with relatively intense fires late in the dry season dominating many regions. This has arisen from post-colonial depopulation of the landscape and is linked to declines in fauna and some of the less fire tolerant vegetation. Australian tropical savannas are dominated by highly fire tolerant eucalypts and a recent review concluded that water relations rather than fire was the major factor affecting tree stand dynamics in Australian savannas. Here we report data from across the savanna zone and investigate variation in tree stand structure, the factors determining it and what it indicates about vegetation dynamics. We discuss this in the context of drivers of fire behaviour in northern Australia and steps being undertaken to better manage fire to conserve savanna fauna and flora.

4. How do climate change, fire and elevated CO₂ influence the distribution of shrubs in the Tropics?

SIMON SCHEITER, Camille Gaillard, Liam Langan, Mirjam Pfeiffer, Dushyant Kumar, Carola Martens, Steven I. Higgins simon.scheiter@senckenberg.de

Shrubs are a successful growth form in many ecosystems globally. While ecosystems such as the Fynbos in South Africa or Mediterranean shrublands are dominated by a dense cover of shrubs, savannas experience increases in the abundance of shrubs. This 'shrub encroachment' often implies changes in vegetation dynamics and reductions in the provision of important ecosystem services such as livestock production or biodiversity. However, there is no conclusive explanation for shrub encroachment and most explanations include elevated CO₂ and land use, particularly grazing. Despite the importance of shrubs at the global scale, they are often not explicitly simulated in complex dynamic vegetation models. Here, we present a dynamic vegetation model, the aDGVM2, that simulates shrubs as multistemmed woody plants, based on fundamental trade-offs in water availability, resistance to fire and growth rates between trees and shrubs. We show that the trade-offs between shrub and tree strategies considered in the aDGVM2 allow us to simulate the current distribution of shrubs in tropical areas globally, and how the introduction of shrubs influences competitive interactions between grasses and trees. Fire, climate change and elevated CO₂ modify the distribution of grasses, trees and shrubs and these results allow us to identify areas that are susceptible to shrub encroachment. This study provides a novel approach to simulate shrubs in a dynamic vegetation model and it contributes to our understanding of the distribution of shrubs and their potential to invade into grasslands and savannas.

5. Diversity and functions of soil macrofauna in West African savannas: Case study of termites and ants in Côte d'Ivoire and Burkina Faso.

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SOULEYMANE KONATE

African savannas are important and extensive ecosystems of great significance for biodiversity and as a human economic area. Termites and ants represent a very important component of soil biodiversity in West African savannas, delivering essential ecosystem services (by e.g. improving soil water content, soil fertility and carbon sequestration). Our study aims to analyse the diversity and functional roles of these soil organisms along a climatic and anthropogenic gradient in West African savannas, with two case studies in Burkina Faso and Côte d'Ivoire.

Rapid assessment protocol of biodiversity, based on standardized transects, was used to record termite and ant diversities. Termite biogenic structure and soil physio-chemical properties were analysed to access their influence on soil water and nutrient dynamics. Our results showed that termites and ants species richness and functional diversity broadly decrease with the increasing aridity (from moist savannas to dry savannas) and with land-use intensification. The fungus growing termite of the genus *Odontotermes* plays a key role, as ecosystem engineer, in the dry savannas as well as in the moist one; where they impact the vegetation structure and dynamic. This they achieve in first line by modifying soil physio-chemical properties and ants change with the amount of rainfall. These organisms play a key role in soil functioning and perform some essential ecosystems services like soil restoration (in arid savannas) and carbon dynamics (in moist savannas). This is well illustrated in a West African traditional practice, the Zaï system, which can be considered as a true model of ecological engineering for soil restoration based on termite activities.

6. Variation in plant diversity in relation to environmental gradients in a tropical dry forest landscape

Sandeep Pulla, H.S. Dattarajaa, S. Pulla, H.S. Suresha, M.S. Nagarajac, C.A. Srinivasamurthy, and R. Sukumara sandeep@ces.jisc.ernet.in

We examined how environmental factors – primarily precipitation and fire – relate to woodyplant diversity in a seasonally tropical dry forest landscape in Mudumalai, southern India. 19 1-ha permanent vegetation plots were established along a sharp precipitation gradient (about 600-1800 mm mean annual precipitation within a ~45-km distance) that also exhibits considerable variation in long-term fire-burn frequency. Woody-plant diversity exhibited two local maxima separated by a low-diversity central region where fire frequency was highest. This pattern is discussed in the context of annual water balance, fire, productivity, soil nutrient status, and global and regional patterns of plant diversity

Posters

7. How will climate change shift the grassland-savanna-forest biome boundaries in India? A dynamic vegetation modelling approach.

DUSHYANT KUMAR, Liam Langan, Mirjam Pfeiffer, Simon Scheiter <u>dushyant.kumar@senckenberg.de</u>

India is likely to experience drastic climatic changes in the future, but the consequences of such changes on biome distributions are uncertain. Indian vegetation is a complex mixture of forest, savanna and grassland. Many studies have documented that forest has invaded the areas occupied previously by C4 plant communities (savannas and grasslands). Indian savanna systems have often been misinterpreted as degraded dry tropical forest. They are threatened by land-use changes, including conversion to agriculture and government initiatives of tree plantations and hence, their future is influenced by policies promoting afforestation. Therefore, the distribution and diversity of forest-savanna systems under different climate scenarios need to be explored. In this study, we used a trait based dynamic global vegetation model (aDGVM2) to simulate current and future biome distributions in India. We sought to understand how the potential biome distribution and diversity might shift under future climate scenarios (IPCC RCPs) and in response to fire management. Simulated current biome distribution, above ground biomass and tree height agree well with potential natural vegetation and remote sensing products, respectively. Increasing atmospheric CO2 concentrations, rising temperature and changes in precipitation regimes have a substantial impact on the vegetation pattern, mainly by promoting wood dominated biomes. Fire played a significant role in shaping biome distributions as it favors more open savanna type vegetation and reduces forest cover. Our results suggest that large proportions of grasslands and savannas are vulnerable to biome shifts towards more tree dominated biome types. These results have implications for management policy across Indian ecosystems, because they identify how climate change may affect India's unique biodiversity. This knowledge is crucial to maintain important ecosystem services of Indian ecosystems and it can help scientists and decision makers to develop proactive strategies and policies.

8. Nutrient deposition enhances post-fire survival in non-N- fixing tropical savanna and dry forest tree seedlings

Varun Varma and Mahesh Sankaran varunvarma17@gmail.com

Nutrient deposition can modify plant growth rates and potentially alter the susceptibility of plants to disturbance events, while also influencing properties of disturbance regimes. In mixed tree-grass ecosystems, such as savannas and tropical dry forests, tree seedling growth rates strongly influence the ability of seedlings to survive fire, and hence, determine vegetation structure and tree community composition. However, the effects of nutrient deposition, " a major global change driver" on the susceptibility of recruiting trees to fire are poorly quantified. In a field experiment, seedlings of multiple Nfixing and non-N- fixing tropical dry forest tree species commonly found in India were exposed to nitrogen (N) and phosphorus (P) fertilisation, and fire. We quantified nutrient mediated changes in a) mean seedling growth rates, b) growth rates of the fastest growing individuals and c) post-fire seedling survival. N-fixers in general tended to have faster growth rates compared to non-N- fixers. Consequently, N-fixers had substantially higher baseline post-fire seedling survival, which was unaffected by nutrient addition. Fertilisation, especially with N, increased post-fire survival probabilities in non-N- fixers by increasing growth rates of the fastest growing individuals. These results demonstrate how differences in N-fixer and non-N- fixer tree seedling susceptibility to fire can shape tropical savanna and dry forest tree communities. Further, atmospheric nutrient deposition can potentially enhance the relative abundance of non-N- fixers in the resprout community, and thereby, alter adult tree community composition in the long-term.

9. The Savannas of Asia: geographic extent and evidence for an evolutionary history of grazing and fire tolerance

Jayashree Ratnam, Dina Rasquinha, Mahesh Sankaran j.ratnam.bangalore@gmail.com

The savannas of Asia have historically been mis-classifed as degraded forests, and both overlooked and misunderstood by the vegetation scholars of this region. As a consequence of this historical problem, there is no current precise map of the savanna regions of Asia. Here, using a bioclimatic approach to model the savannas of Asia from those of the other continents, we present a first map of the geographic regions where the savannas of Asia potentially exist. We then focus on the areas in the Indian subcontinent in this map, and describe and classify the vegetation types that exist within these regions, highlighting plant characteristics that suggest a long evolutionary history of these ecosystems with herbivory and fire- key drivers of savanna ecosystems globally. Finally, we compare the traits of trees in savannas versus forests in southern India, to show that savanna trees present a suite of traits that are indicative of fire-tolerance.

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