



PROGRAM GUIDE & ABSTRACTS

**GEKKOTA MUNDI II
INTERNATIONAL CONFERENCE
TEL AVIV, ISRAEL
MAY 26-28, 2019**

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SCHEDULE OVERVIEW

Bold: Plenary talks

26.5.2019	27.5.2019	28.5.2019
9:00–9:30 Coffee & Registration	9:00–9:30 Coffee	Field Trip: Negev, Arava & Eilat
9:30–9:45 Opening words: Tamar Dayan	9:30–10:00 Karin Tamar	
9:45–10:15 Aaron Bauer	10:00–10:15 Peter Uetz	
10:15–10:30 Rachel Schwarz	10:15–10:30 Lelani Del Pinto	
10:30–10:50 Aparna Lajmi	10:30–10:45 Gavin Stark	
10:50–11:15 Coffee	10:50–11:15 Coffee	
11:15–11:30 Jendrian Riedel	11:15–11:30 Lukáš Pola	
11:30–11:45 Amanda Kaatz	11:30–12:00 Paul Doughty	
11:45–12:00 Mateusz Hermyt		
12:00–13:30 Lunch		
13:30–14:00 Lee Grismer (1)		
14:00–14:15 Hamutal Friedman		
14:15–14:30 Rocio Aguilar		
14:30–15:00 Coffee		14:30–15:00 Shai Meiri
15:00–15:15 Guy Sion		15:00–15:15 Rikki Gumbs
15:15–15:45 Marco Antonio Ribeiro Junior	Field Trip: Negev, Arava & Eilat	15:15–15:30 Lee Grismer (2)
15:45–16:00 Hinrich Kaiser		15:30–16:00 Coffee
16:00–16:15 Thomas Fieldsend		16:00–16:15 Amos Bouskila
		16:15–16:30 Claudia Corti
		16:30–17:00 Rafe Brown
		17:00–17:15 Concluding remarks
16:15–18:30 Tour, Steinhardt Museum		17:30–18:15 Tour, Zoological Garden
		Pizza & Beer

TABLE OF CONTENTS

AGUILAR, R.	Tracking traces of morphological evolution in Australian geckos: CT Scans wanted	7
BAUER, A.M.	Systematics of the <i>Hemidactylus</i> of West and Central Africa: Cutting the Gordian Knot	8
BOUSKILA, A.	Hiding the entrance of burrows in three species of sand-dwelling ground geckos	9
BROWN, R.M.	Parachute geckos free fall into synonymy: Gekko phylogeny, and a new subgeneric classification, inferred from thousands of UCE-baited loci	10
CORTI, C.	The importance of small islands in maintaining Mediterranean biodiversity: Telling about the leaf-toed gecko, <i>Euleptes europaea</i>	11
DEL PINTO, L.	Geographically structured genetic variation in <i>Gekko smithii</i> Gray, 1942 (Squamata Gekkonidae) from Sundaland	12
DOUGHTY, P.	Zig-zag Geckos (<i>Amalosia</i>) of the Australian Monsoonal Tropics: a jagged path towards systematic resolution of the complex	13
FIELDSEND, T.	First genetic analysis of Florida's invasive Madagascar giant day gecko (<i>Phelsuma grandis</i>) population	14
FRIEDMAN, H.	Testing the niche expansion hypothesis in insular geckos	15
GRISMER, L.L.	Evolution of habitat preference in <i>Cyrtodactylus</i> Gray, 1827	16
GRISMER, L.L.	Phylogeographic structure of the Parachute Gecko <i>Ptychozoon lionotum</i> Annandale, 1905 across Indochina and Sundaland with descriptions of three new species	17
GUMBS, R.	Combining human impact, endemism and phylogenetic diversity to identify conservation priorities for the world's geckos	19
HERMYT, M.	Comparatives studies of egg teeth development in two gekkotan species	20
KAATZ, A.A.	The independent evolution of ecomorphology and habitat preference in a Southeast Asian clade of <i>Cyrtodactylus</i> Gray, 1827	21

KAISER, H.	Use with due care: stories of nomenclature and its insidious impact on gecko research	22
LAJMI, A.	Historical biogeography and diversification of <i>Hemidactylus</i> geckos in South Asia	23
MEIRI, S.	What geckos are – and the lizards geckos are not: an ecological-biogeographic perspective	24
POLA, L.	Phylogeography of the <i>Bunopus</i> geckos (Squamata, Gekkonidae) in the Arabian Peninsula	25
RIBEIRO-JUNIOR, M.A.	Taxonomic revision of the dwarf-lizard genus <i>Tropicolotes</i> (Squamata: Gekkonidae): uncovering cryptic diversity	26
RIEDEL, J.	Parallel evolution of enlarged, adhesive toe-pads in two lineages of rock-dwelling lizards (Gekkonidae; <i>Heteronotia</i>)	27
SCHWARZ, R.	Adaptation vs. plasticity in gecko habitat choice, and the influence of predators	28
SION, G.	Can a Lizard Bite Induce Changes in Steroid Levels? The gecko <i>Ptyodactylus guttatus</i> as a model	29
STARK, G.	Does nocturnal activity prolong longevity for gekkotan species, compared to other lizard groups?	30
TAMAR, K.	Biogeography of Arabian Geckos	31
UETZ, P.	Geckos of the world in the Reptile Database	32

Tracking traces of morphological evolution in Australian geckos: CT Scans wanted

Aguilar, R.^{1,2}, J. Melville², C. Hipsley^{2,3}, J. Sumner², K. Date², A. Evans¹, M. Hutchinson⁴, J. Mueller⁵, S. Meiri⁶, D.G. Chapple¹

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Australia, the land of lizards, is the world's most diverse country for this taxon. Geckos in particular are represented by 4 families with more than 230 species. As many of the other lizards, geckos have evolved some morphological adaptations to colonize and succeed in different habitats. Limb reductions, digit modifications and tail shape variations are typical amongst species of this group. Our recently-funded ARC Linkage project aims to track these adaptations in modern geckos to investigate the association between phenotypic traits and species diversification. We do this using non-invasive X-ray computed tomography, or CT scanning, to generate high resolution 3D models of museum specimens. However, obtaining high quality CT images can be an expensive process. It involves the use of sophisticated X-ray technology, specialised software, and hours of data post-processing. In order to minimize these costs, especially as we want to compare geckos to other Australian lizards, CT scans are wanted. We are currently creating a directory of scans collected by colleagues across the world which we will link to details on species life-history, ecological and morphological traits, and locality and distribution data. This directory will be open-access with contact details of the scan providers, thus ensuring proper acknowledgement and providing new opportunities for scientific collaborations. It will also help to avoid multiple CT scans of the same specimens, allowing us to instead focus on other target species that might not have been sampled yet.

Systematics of the *Hemidactylus* of West and Central Africa: Cutting the Gordian Knot

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African *Hemidactylus* have long proven to be a difficult group to resolve, with many available names, but limited data with which to sort them out. We used a multilocus molecular phylogenetic approach to identify genetic diversity and delimit species boundaries within the *Hemidactylus* of West and Central Africa. Three main lineages are represented in the region, 1) the *H. fasciatus* group centered around Equatorial Africa, 2) the *H. angulatus* group, a group with its chief diversity in East Africa, but represented by several endemics in West Africa, and 3) the Afro-Atlantic clade, including the *H. echinus* group and the *H. mabouia* complex, as well as a diverse group of previously poorly-sampled species ranging from Liberia to Angola. Both *H. mabouia* and *H. angulatus* comprise a large number of geographically circumscribed species that share a similar morphology. In both cases diversity is lower in West and Central Africa than in other areas of the respective ranges of these complexes. *Hemidactylus mabouia* sensu lato includes one supertramp species that occupies the New World as well as Equatorial Africa from coast to coast. However, related forms, nearly all undescribed, have a center of diversity in southeast Africa. The greatest genetic diversity in *H. mabouia* proper is in Uganda, with little variation and no substructure across the remainder of the range. It is likely that human activity, including the slave trade, has shaped the modern distribution of this invasive species. Diversity in Angola has been underestimated due to under-sampling and unwarranted synonymization.

Hiding the entrance of burrows in three species of sand-dwelling ground geckos

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Sand-dwelling geckos often find shelter in burrows that they excavate. We discovered and documented an interesting behavior, which we interpret as hiding the entrance of burrows in sand. This behavior involves blocking the burrow after entering it by pushing sand with the hind feet, leaving the distal part of the tail outside the burrow. After the burrow has been blocked, the distal part of the tail wiggles, smoothing the sand around the entrance, and is then pulled inside, leaving no trace of the burrow entrance. We found this behavior in three Gekkonid species with typical tails whose distal end resembles a thin filament: *Stendocatylys doriae*, *S. petrii* (both observed in the Negev desert) and *Crossobamon eversmanni* (observed in the Karakum desert). The filamentous tail is necessary for the execution of this behavior. Due to the phylogenetic relationships of these species, it seems that this behavior evolved at least on three separate occasions. Burrow temporal usage and burrowing behavior of *S. doriae* was studied in greater details. *S. doriae* approach an existing open burrow in a circular path and burrows were occasionally rejected. To test the hypothesis that predator odors could cause burrow rejection, we experimentally applied scent from snakes to entrances of 42 burrows and the burrow temporal usage was compared to the usage of 42 control burrows. Our hypothesis that *S. doriae* whose burrow was visited by a snake will abandon the burrow was confirmed. The geckos may abandon the burrow because its position is no longer hidden.

Parachute geckos free fall into synonymy: Gekko phylogeny, and a new subgeneric classification, inferred from thousands of UCE-baited loci.

Perry L. Wood, Jr., Xianguang Guo, Scott L. Travers, Yong-Chao Su, Karen V. Olson, Aaron M. Bauer, L. Lee Grismer, Cameron D. Siler, Robert G. Moyle, Michael J. Andersen, Rafe M. Brown

Recent phylogenetic studies of gekkonid lizards have revealed unexpected, widespread paraphyly and polyphyly among major named genera, unclear generic boundaries, and a tendency towards the nesting of taxa exhibiting specialized, apomorphic morphologies within geographically widespread “generalist” clades. This is especially true in the Australasian Archipelago, where the monophyly of *Gekko* proper has been questioned with respect to phenotypically ornate flap-legged geckos of the genus *Luperosaurus*, the rare slender Philippine false geckos, genus *Pseudogekko*, and even the elaborately “derived” parachute geckos of the genus *Ptychozoon*. Here we employ an initial sequence capture targeting 5060 Ultra-conserved element-probed loci (UCEs) to infer phylogenomic relationships among representative gekkonine lizard taxa, selected to definitively address four persistent systematic questions: (1) are *Luperosaurus* and *Ptychozoon* monophyletic and, are any of these named species truly nested within *Gekko*? (2) Does the surprising finding regarding Sulawesi’s *L. iskandari* (sister to Melanesian *G. vittatus*), hold up under phylogenomic inference? (3) Is the high elevation Palawan Island species *L. gulat* (represented by a single specimen and degraded accompanying DNA sample) correctly placed in *Gekko*? (4) And, finally, where do the enigmatic taxa *P. rhacophorus* and *L. browni* fall in higher-level gekkonid phylogeny? We resolve these issues, resolve the systematic position of unplaced taxa, and transfer several *Luperosaurus* all members of the genus *Ptychozoon* to the genus *Gekko*. With our final well-supported topologies, derived from phylogenomic analysis of multiple datasets of varying degrees of completeness we recognize seven newly defined subgenera to accommodate ~60 species within the Australasian genus *Gekko*.

The importance of small islands in maintaining Mediterranean biodiversity: Telling about the leaf-toed gecko, *Euleptes europaea*

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The Mediterranean is an important biodiversity hotspot made of thousands of islands. Numerous are islets and rocks of few square meters, characterized by limited resources. Despite their area, they can host reptile populations, often composed of few individuals. The few species able to live on such small islands (e.g., the Corsican and Sardinian land-bridge islets), where no other non-avian terrestrial vertebrates could survive, are small lizards. One of these is the western Mediterranean endemic Leaf-toad gecko, *Euleptes europaea*. This tiny nocturnal gecko, found up to an elevation of 1500 m, is distributed in France in Provence and Corsica, in Italy in Liguria, Tuscany (Tuscan Archipelago included), Sardinia and, in Tunisia on the Galite Islands where currently the species persists only on three islets while on two others it has become extinct since the XIX Century. The prolonged effect of humans on the Mediterranean ecosystems seems to be responsible for the disappearance of some continental populations. Nevertheless, the supposed extinction of mainland populations could also have a pathogenic origin. In France, in the Marseilles region, where the gecko has never been found on the mainland, *Euleptes* inhabits also small islets few meters far from the continental coast at a depth of even 1 meter. Stable populations survive in some areas of Corsica and Sardinia as well as their satellite, sometimes inaccessible, islets and rocks where this gecko is the only representative of vertebrates. *Euleptes europaea* is able to cope with the presence of diurnal wall lizards as well rats sharing the limited resources. Small islands and rocks can be therefore considered of key importance for the conservation of this species.

Geographically structured genetic variation in *Gekko smithii* Gray, 1942 (Squamata Gekkonidae) from Sundaland

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Gekko smithii is large, commonly encountered habitat generalists that ranges from Myanmar to Sulawesi. Despite it being somewhat of a human commensal, it manifests a moderate degree of geographic variation—most notably in Peninsular Malaysia. Given that it had not been collected from the type locality of Penang Island off the west coast of central Peninsular Malaysia since its description by Gray in 1842, we endeavored to re-discover this population and in so doing, collected six additional specimens. These, and 62 other specimens from throughout Peninsular Malaysia, Borneo, and Sumatra were used to examine the Sundaic phylogeographic structure of *G. smithii* within the context of an integrative taxonomic framework using the mitochondrial gene ND2 and its tRNA flanking regions. Notable genetic substructuring in Peninsular Malaysia was compared with its morphology using both multivariate (PCA) and univariate (ANOVA) analyses.

Zig-zag Geckos (*Amalosia*) of the Australian Monsoonal Tropics: a jagged path towards systematic resolution of the complex

Paul Doughty, Ryan J. Ellis, Conrad Hoskin

The small-bodied geckos of the genus *Amalosia* occurring across northern Australia are known for their elongate body shape and arboreal or saxicoline habits. We carried out a widespread genetic screen using the mtDNA *ND4* gene to assess genetic variation within the group, accompanied by a morphological appraisal, across the distribution of the genus. For the genetic results, we found extreme complexity within the genus, with especially high lineage diversity in Queensland and also the Northern Territory. Morphologically, although there were occasionally characters to diagnose some lineages, in many cases there was wide variation as well as apparent convergence in dorsal patterns across putative groups. Lineages were usually morphologically cryptic, with few useful differences in scalation among groups, although some lineages possessed unique diagnostic characters. One further problem was that many genetically distinct lineages were based on single or very few specimens that were morphologically similar to other groups. Nevertheless, progress on the group will be possible through a “divide and conquer” strategy, with major lineages within regions redescribed or described as new taxa and exceptional lineages flagged for further work.

First genetic analysis of Florida's invasive Madagascar giant day gecko (*Phelsuma grandis*) population

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The Madagascar giant day gecko *Phelsuma grandis* Gray 1870 (Sauria: Gekkonidae) was introduced to Florida, USA in the 1990s and is currently expanding its range within the state. Until recently, breeding populations of *P. grandis* in Florida were known only from the Florida Keys, an island chain lying to the extreme south of the state; however, in 2017 a reproducing colony of *P. grandis* was reported in Miami, FL, suggesting that the species may now be in the process of colonising mainland Florida. To determine the provenance of Florida's *P. grandis* populations, we sequenced the mitochondrial Cytochrome b (715 bp) and 16S (536 bp) genes of Florida-caught *P. grandis*, before comparing them with georeferenced native-range sequences from GenBank. All Florida specimens sequenced thus far cluster with *P. grandis* from the extreme north of the species' native range, but our analyses have also uncovered phylogeographic discontinuities strongly suggestive of both multiple introductions and multiple founder populations. Our findings are discussed in the context of spatially structured intraspecific variation in bioclimatic tolerances, as source population provenance is likely to be a strong determinant of invasion success in this system. Our phylogeographic insights will be used to build and refine Species Distribution Models that forecast the species' spread through Florida, under both current and predicted-future bioclimatic conditions. Our research will inform management of *P. grandis* in this part of its non-native range, as populations with a high probability of invasive success will be identified and prioritized for eradication.

Testing the niche expansion hypothesis in insular geckos

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The Niche Expansion Hypothesis (NEH) suggests that dietary niche-breadth increases as interspecific competition weakens, and thus intraspecific competition is stronger, and prey availability is greater. This can occur via increasing differences between individuals and/or by expanding individual niches. We examined how dietary niche-breadths in island populations of *Mediodactylus kotschy* are affected by inter and intraspecific competition, and prey availability. We collected feces of 222 *M. kotschy* from 17 islands in the Aegean Sea and two sites in the southern Peloponnese. On each, we estimated population density of *M. kotschy*, counted their competitor species, and placed 21 pitfall traps to estimate prey (arthropod) diversity and abundance. We identified the remains taxonomically and counted prey items of each gecko. We quantified the number of prey categories, Shannon–Wiener diversity, and evenness (assessing how evenly prey items distribute among prey categories). We similarly processed and assessed the diversity of arthropods from pitfalls and assessed these indices for males and females separately for 9 islands. *Mediodactylus kotschy* base their spring diet mainly on beetles, cicadas and ants. Mainland geckos have wider dietary niches than insular ones. Prey category numbers per-population negatively correlated with competitor richness. Prey availability and population density were unrelated to niche-breadth at both the individual and population levels. Evenness was similar at individual and population level. We did not find sexual dimorphism in diet. Although competitor richness constrains niche-breadth, as predicted, most of our results contradict the predictions of the NEH. This suggests a reconsideration of this theory is warranted.

Evolution of habitat preference in *Cyrtodactylus* Gray, 1827

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Stochastic character and marginal reconstruction character mapping were used to infer the evolution of eight different habitat preferences across a BEAST phylogeny composed of 239 species of *Cyrtodactylus*. The analysis recovered a general habitat preference as the widespread ancestral condition throughout the tree and that this preference initially gave rise to all other habitat preferences: terrestrial (three times), cave (four times), karst forest (15 times), swamp forest (two times), granite forest (nine times), trunk (four times), and arboreal (three times). Major radiations of karst forest species dominate Myanmar and Indochina with lesser radiations in Vietnam and Malaysia. Two radiations of species with a terrestrial habitat preference occur in southern India and the Ayeyarwady Basin of Myanmar. A number of Wallacean species specialize in inhabiting the trunks of large trees. The remaining habitat preferences arise independently in single species or small clades throughout the tree.

Phylogeographic structure of the Parachute Gecko *Ptychozoon lionotum* Annandale, 1905 across Indochina and Sundaland with descriptions of three new species

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An integrative taxonomic analysis of the *Ptychozoon lionotum* group across its range in Indochina and Sundaland recovers *P. lionotum sensu lato* as paraphyletic with respect to *P. popaense* and composed of four allopatric, genetically divergent, ND2 mitochondrial lineages. Multivariate and univariate analyses of continuous and discrete morphological and color pattern characters statistically and discretely diagnose each lineage from one another and together, with maximum likelihood and Bayesian inference analyses, provide the foundation for the recognition of each lineage as a new species—hypotheses corroborated with a Generalized Mixed Yule Coalescent species delimitation analysis. *Ptychozoon* sp. nov. 1 ranges throughout Peninsular Malaysia to Pulau Natuna Besar, Indonesia; *Ptychozoon* sp. nov.2 is endemic to northern and central Laos; and *Ptychozoon* sp. nov. 3 ranges from southern Thailand south of the Isthmus of Kra northward to Chiang Mai, fringing the Chao Phraya Basin and ranging southward through Cambodia to southern Vietnam. *Ptychozoon lionotum sensu stricto* ranges from northwestern

Laos through southern Myanmar to eastern India. The phylogeographic structure within each species varies considerably with *P. lionotum* s.s. showing no genetic divergence across its 1,100 km range compared to *Ptychozoon* sp. nov. 1 showing upwards of 8.2% sequence divergence between syntopic individuals. Significant phylogeographic structure exists within *Ptychozoon* sp. nov. 3 and increased sampling throughout Thailand may require additional taxonomic changes within this species.

Combining human impact, endemism and phylogenetic diversity to identify conservation priorities for the world's geckos

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Incorporating phylogenetic diversity (PD) in conservation planning is increasingly recognised as an important tool for conserving biodiversity. Thanks to recent advances, it is now possible to conduct spatial prioritisations for reptile groups at a global scale. Here we show that, when mapped at a global scale, significantly more priority grid cells for imperilled gecko PD occur in regions of high human impact than expected if human impacts were randomly distributed. Consequently, we applied two novel metrics—one prioritising regions and the other species—which incorporate human impact, range size and PD to species and regions of conservation importance. Geckos provide the greatest contributions of any clade to global patterns of human-impacted reptilian PD, and our species-level prioritisation indicates that large accumulations of gecko PD are restricted to small ranges under high human impact. Worryingly, Data Deficient species tend to harbour levels of imperilled PD comparable to those which are threatened with extinction.

Comparatives studies of egg teeth development in two gekkotan species

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The egg tooth is a transient structure present in embryos of most oviparous species of snakes and lizards. Embryos use it during hatching to set themselves free from egg membranes. Until now the development of the egg tooth was studied in a small number of closely related species. It is known that geckos along with dibamids possess double egg-teeth in contrast to all other squamates which have only one. However it is not taken into consideration that not all eggshells of geckos are the same. Majority of geckos lay rigid-shelled eggs while the eggs of others are parchment-shelled. This study involves a detailed comparison of morphogenetic processes and morphology of the egg tooth in embryos of two geckos' representatives: leopard gecko *Eublepharis macularius* with leathery eggshell and mourning gecko *Lepidodactylus lugubris* with rigid eggshell. General structure of the egg teeth in both species is similar to structure of typical tooth characteristic for all vertebrates. However, we discovered that spatial orientation of egg teeth in investigated species differ from each other. Egg teeth of leopard gecko are facing outward while egg teeth of mourning gecko are facing inward. Our findings might be useful in future analyses concerning Squamata phylogenesis.

The independent evolution of ecomorphology and habitat preference in a Southeast Asian clade of *Cyrtodactylus* Gray, 1827

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Given that the genus *Cyrtodactylus* is the most diverse gekkotan lineage with over 270 nominal species that range from South Asia to the South Pacific, it is not surprising that this group contains many adaptive types from a broad range of habitats. Nonetheless, the evolution of habitat preferences across even a small clade of species has never been statistically examined. We used a stochastic character mapping analysis to map five different habitat preferences across a monophyletic lineage of 30 species ranging from Peninsular Malaysia to Papua New Guinea. Our analysis indicates that the ancestral condition of this clade is that of a habitat generalist (i.e. occurring in all microhabitats) and that from this, swamp forest, granite forest, karst forest, and arboreal habitat preferences have evolved. In Peninsular Malaysia, karst habitat preference has evolved at least three times independently and swamp habitat preference has evolved at least twice. Whereas arboreal and granite forest habitat preference evolved once. Principle component analyses on two subclades from Peninsular Malaysia indicate that not all karst-dwelling species bear a karst-dwelling species morphology. We suggest that both character state mapping and ecomorphological analyses should be considered simultaneously before labeling any species a distinct ecomorph.

Use with due care: stories of nomenclature and its insidious impact on gecko research

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The origins of the accounting system known as zoological nomenclature lay with the occurrences of duplicate naming by usually well-meaning authors, who were simply disconnected in space, time, or language. This required the establishment of specific criteria and best practices, and the *International Code of Zoological Nomenclature*, as imperfect as it may be, has been very useful in disentangling problems in diverse taxonomic groups. It remains of critical relevance today: taxonomic decisions can be published quickly and sometimes with questionable or no peer review, and it is unsurprising that errors in the formation or presentation of taxon names occur – to err is human. Therefore, the point of this talk cannot be to decry flawed practices or to place blame, it is to point out some of the resulting problems and how to tackle them. We use several gecko stories to illustrate the issues. *Hemidactylus brookii* was considered one of the most widespread gecko species, yet its type locality in Borneo is questionable and molecular studies included not samples of *H. brookii* but of *H. tenkatei*. *Cnemaspis timoriensis* is actually a member of *Gonatodes humeralis*, a younger species name, and this destabilizes a well-established group. Molecular phylogenies that include *Hemiphyllodactylus typus* or *Hemidactylus garnotii* do not include tissue samples from the type localities. As a consequence, only patience and care in dealing with type specimens and type localities, sometimes with a healthy dose of sleuthing through the multilingual old literature thrown in, are often needed to produce stable, verifiable taxonomic outcomes.

Historical biogeography and diversification of *Hemidactylus* geckos in South Asia

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The complex paleoclimate of Peninsular India (PI) and Sri Lanka (SL) have profoundly influenced diversification of biota. Furthermore, this region provides an interesting setting to study biotic exchange between island and mainland. Here, I present work carried out on the *Hemidactylus* radiation endemic to PI and SL addressing faunal exchange between PI and SL, lineage and morphological diversification in this radiation, and the role of past climate in shaping these patterns. Results show that *Hemidactylus* have assembled in SL as a result of seven independent dispersals from PI. While two dispersal events occurred in the Early to Middle Miocene leading to two endemic SL species, other five dispersal events led to range expansion in species largely restricted to open semi-arid habitats and are likely to be more recent. The Indian radiation of *Hemidactylus* geckos show evidence of an early-burst in lineage diversification which began ~36Mya. Subsequent ancestral state reconstruction of wet and dry habitat states revealed the dry-habitat state to be ancestral, suggesting prevalence of arid ecosystems in this region during this period. *Hemidactylus* are found in various microhabitats and the relationship between habitat specialization and morphology was examined. We found significant differences in morphology between terrestrial and scansorial species. Unlike lineage diversification, morphological diversification showed a delayed increase in disparity, which coincides with the evolution of terrestrial lineages that have evolved at least five times independently. The shift from scansorial to terrestrial state began ~15Mya, concurrent with aridification in PI that led to the establishment of open habitats.

What geckos are – and the lizards geckos are not: an ecological-biogeographic perspective

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Geckos ‘sit’ on the first branch to diverge from the rest in the squamate tree of life (no one ever thinks of dibamids right?). They are a remarkably successful group with a near cosmopolitan distribution. Using global datasets of lizard geographic ranges, ecology, and life history, I aimed at identifying what traits, if any, set geckos apart from their non-gecko kin. I use a large lizard-wide trait dataset I accumulated over the last 14 years, combined with a global reptile species map dataset compiled by the GARD working group, to describe the diversity of geckos *per se*, and in relation to lesser lizards.

There are many geckos, some 28% (1875 species) of lizard diversity. These figures are rapidly increasing (38% of described species this decade). Geckos form 28-46% of lizard species Old World realms, but just 13 and 4% of the saurian fauna of the Neotropics and Nearctic, respectively. They generally occur in lowlands (avg. max elevation 870m vs. 1480 in other lizards), and are especially prevalent on islands. Geckos are small animals, on average a third of the mass of other lizards. They lay relatively frequent, but very small, clutches. Despite their small size, however, they reach sexual maturity, and die, at similar ages to other lizards. Over their lifetime, under some horrendous assumptions, they thus lay 2/3 the number of eggs laid by non-geckos. While most geckos are nocturnal, 26% of species are diurnal or cathemeral. Body temperatures of geckos are also 2.5-3 degrees lower than the saurian norms, *after* controlling for activity times. The percentage of geckos taking substantial proportion of plant-based matter in their diet (15.5%) is not much lower than in other lizards (21.2%), but 61% of the geckos scored are sit and wait foragers, vs. 39% in other taxa.

Geckos thus defy simple descriptions – they form a large, extremely diverse clade than by itself encompass much of the ecological, morphological and life history diversity present in lizards as a whole – and they also have some unique tricks up their lamellae.

Phylogeography of the *Bunopus* geckos (Squamata, Gekkonidae) in the Arabian Peninsula

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The geckos of the genus *Bunopus* Blanford, 1874 belong to the group of the Palearctic naked-toed geckos. Members of this genus are widely distributed across arid areas of the Arabian Peninsula, Mesopotamia, and Iranian plateau eastwards to Pakistan and Afghanistan. Currently, this genus contains three recognized species: *Bunopus tuberculatus*, *B. blanfordii*, and *B. crassicauda*. Recent findings indicate the presence of several cryptic species on the Iranian plateau and possible paraphyly of *B. tuberculatus* with respect to *B. crassicauda*. However, a vast part of the genus range – the entire Arabian Peninsula – has not been studied yet. We assembled a dataset of tissue samples and voucher specimens from across the Arabia Peninsula with the aim to reconstruct the phylogenetic relationships of *Bunopus* and understand its phylogeographic history in Arabia. We used a multilocus dataset of two mitochondrial (12S rRNA, COI) and two nuclear markers (c-mos, rag2). Our preliminary results confirm the paraphyly of *B. tuberculatus*. The genus is formed by six distinct clades. In contrast to the pronounced genetic variation found on the Iranian plateau where five of the six clades are present, the entire Arabian Peninsula is inhabited by one monophyletic lineage. This Arabian clade has close relationships to two Iranian clades, one of *B. tuberculatus* sensu stricto and the other of a clade from the western Zagros foothills. Interestingly, this latter clade stretches westward to Jordan where it occurs together with the Arabian clade. More detailed delimitation of the contact zone of the two clades in Jordan pends further investigation.

Taxonomic revision of the dwarf-lizard genus *Tropicolotes* (Squamata: Gekkonidae): uncovering cryptic diversity

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The dwarf-lizard genus *Tropicolotes* comprises 12 species distributed along the Saharo-Arabian region, from western Africa to Asia. Despite some recent taxonomic research, deep and historical nomenclatural problems still persist in the genus. Names and identifications of at least half of the *Tropicolotes* species are controversial, especially because: 1) the absence of diagnostic characters to distinguish some of them; 2) for three species the holotypes are considered lost; 3) some subspecies are sometimes considered valid, sometimes not; and 4) the genus is distributed along an area of historical major politic-religious conflicts, and most of the occurrence area is inaccessible to field expeditions. These issues combined or in separate have led to a series of misidentification of specimens in collections and in the literature. Aiming to solve most of these problems, I am conducting a taxonomic revision of the genus. Based on a comprehensive morphological study of it (osteology and external morphology), I am updating species diversity and distribution patterns. Preliminary results based on specimens housed in museums of the USA and Israel showed that at least two recognized species (*T. nattereri* and *T. steudneri*) are in fact complexes of cryptic species containing undescribed taxa. To the present day and among the specimens previous identified as *T. nattereri* and *T. steudneri* I already recognized six putative new species. The study is in progress, so the next step is to examine specimens housed in the major European collections (including type series). After that I will be able to describe neotypes considered lost, redescribe the valid species, describe new species, produce an updated distribution map for each species, and present a detailed revision of the diagnostic characters of the genus.

Parallel evolution of enlarged, adhesive toe-pads in two lineages of rock-dwelling lizards (Gekkonidae; *Heteronotia*)

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The evolution of morphology is one of the main causes for speciation, and therefore biodiversity. So, to understand biodiversity, it is important to study, how and under what circumstances morphological structures evolve. Adhesive toe-pads featuring hair-like microstructures (setae) are well-known traits in geckos and anoles. They have evolved multiple times in geckos and are typically associated with climbing in arboreal or saxicoline (rocky) microhabitats. Although the functional morphology of adhesive toe-pads is well studied, their evolution is poorly understood because of the scarcity of intermediate forms between padless terrestrial and pad-bearing climbing forms. To shed light on the evolution of adhesive pads we assessed the toepad scale morphology of *Heteronotia binoei*. The *H. binoei* species complex comprises several morphologically cryptic but genetically divergent lineages of terrestrial geckos generally lacking pronounced toe-pads. There are two phylogenetically distinct lineages from north-eastern Queensland, associated with saxicoline habitats, which appear to have independently developed enlarged terminal subdigital scales. Analysis of subdigital scale size, and scale microstructures *via* scanning electron microscopy (SEM), reveal that the saxicoline lineages have both larger toe-pads and longer, more fully developed adhesive setae with triangular tips (spatulae) in comparison to their terrestrial sister lineages. Furthermore, setae are found not only on the enlarged terminal subdigital scales but also on the inflection scale (where the toe touches the substrate). Considering that the respective saxicoline lineages have diverged from their terrestrial sister lineages fairly recently, this might represent an early stage in the evolution of fully developed adhesive pads.

Adaptation vs. plasticity in gecko habitat choice, and the influence of predators

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Individuals are expected to adapt quickly to prevailing conditions. Microhabitat choice can offer an opportunity to adapt to differing selection pressures. Mainland populations of the gecko *Mediodactylus kotschy* are found almost exclusively on trees, but on small islets, where trees are absent, they are found under rocks. On larger islands, on which trees grow, *M. kotschy* can be found both under rocks and on trees. We compared microhabitat choice of 10 female-offspring pairs of insular and mainland geckos. We hypothesized that hatchlings will choose the same microhabitat as their mothers, the same microhabitat chosen in the wild. We also hypothesized that geckos will prefer safe microhabitats in the presence of predators. To test our hypotheses, we recorded the microhabitat preference of females and their laboratory hatched hatchlings in an arena containing a tree and a rock with and without the presence of a snake. The proportion of time spent in each microhabitat served as a measure of preference. Females and their hatchlings spent similar time on both substrates, unrelated to the substrate from which the females were caught in nature. The presence of the snake did not change the proportion of time hatchlings spent on trees compared to rocks, but females from both origins spent 35% more time on rocks. Our results suggest that, although habitat preference of hatchlings is similar to that of their mothers, the choice between trees and rocks is plastic. We hypothesize that, hatchlings may not recognize the snake as a threat.

Can a Lizard Bite Induce Changes in Steroid Levels? The gecko *Ptyodactylus guttatus* as a model

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The roles of corticosterone and testosterone as mediators of social behavior are well studied. However, recently the ratio between these hormones *per se* was studied as a mediator. In many vertebrates, the level of testosterone, or corticosterone or their ratio, can be correlated with social status. In many lizards higher number of bite-scars reflects higher social status. We used non-invasive hormone extraction from feces to study the association between bite scars, social status and hormones level. We predicted that higher testosterone levels will be associated with higher social status and thus higher number of bite scars (especially in males) using *Ptyodactylus guttatus* geckos from Israel as our model species. Surprisingly we found that high-status males though they had more bite scars than lower status ones, had lower testosterone levels. We interpreted these results to suggest that high-social status individuals are risk-averse. We hypothesized that lizard's bites may induce a decrease in testosterone level due to the mechanical stimuli of the bite. Thus, it modulates risk aversion, consistent with asset protection.

Does nocturnal activity prolong longevity for gekkotan species, compared to other lizard groups?

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Animal lifespan is determined by extrinsic and intrinsic mortality causes. Geckos are mainly nocturnal, whereas most other lizards are diurnal. Exposure to solar radiation is thought to reduce longevity by increasing metabolic costs and the rate of accumulating harmful mutations through UV radiation. By being nocturnal, species may reduce their intrinsic mortality pressure and thus live longer. We examined the effect of activity time on the lifespan of lizards, by comparing the Gekkota to other clades, and likewise compared longevities of diurnal and nocturnal geckos (and skinks). We assembled a dataset on the maximum longevities of 749 lizard species, of which 188 are geckos, and assigned each species as diurnal or nocturnal (cathebral species were ignored). Correcting for phylogeny and size, we did not find any effect of nocturnality on the lifespans between geckos and other lizards and between nocturnal and diurnal geckos (and skinks). We suggest that, diurnal species may have evolved higher resistance to UV radiation via thicker, more keratinized skin, and that elevated metabolic rates do not automatically equate with faster aging – or that mortality through extrinsic causes (e.g., predation and famine) impose much stronger selective pressures than internal causes.

Biogeography of Arabian Geckos

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The Arabian region is renowned for its harsh, hot and arid climate, with massive deserts spanning across most of the interior, enclosed by mountain ranges on the margins of the peninsula. Geckos (Gekkota) form the most diverse reptile group in Arabia, found in a diverse array of habitats: sandy or gravel areas are occupied by genera such as *Bunopus*, *Pseudoceramodactylus* and *Stenodactylus*, while genera such as *Asaccus* and *Ptyodactylus* are restricted to mountain ranges and rocky surfaces. We present a general overview of the biogeography of geckos in Arabia as inferred via detailed phylogeographical analyses of multiple gecko genera, together with geological and environmental data. We show how the formation of various habitats within Arabia and episodic or continuous connections to Eurasia and Africa, have enabled dispersal and diversification of taxa, while creating biogeographical barriers and endemism hotspots. Two major environmental events are hypothesized to have greatly influenced the distribution and diversification of the local fauna - The tectonic movement of the Arabian plate during the Oligocene, and the dramatic climatic changes that occurred during the Miocene-Pliocene. The former caused high geological instability and the detachment from Africa followed by a collision with Eurasia, while also prompting the orogeny of mountain ranges. The latter influenced the expansion and contraction of sand deserts, serving as a barrier to gene flow between the mountains. These events changed the Arabian landscape over time, creating an interesting composition of species diversity that we encounter today.

Geckos of the world in the Reptile Database

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The current release of the Reptile Database lists 1873 gekkotans in all 7 subfamilies, with the Gekkonidae with 1242 species being the largest group. Gekkotans thus make up 17% of the 10,970 species of reptiles (or 2,083 taxa when subspecies are included, i.e. 16% of all ~13,300 reptile taxa). The database has recently started to document the morphological diversity by collecting diagnoses of both species and the 126 genera, as well as photographic documentation. This includes photos of 676 gekkotan species (36%), corresponding to 104 genera). In order to document all genera in detail we have compiled a global list of reptile type specimens, including those of gekkotans, which are distributed over about 165 collections worldwide (compared to 370 collections that have reptile types). A strategy to collect image data and morphological data is presented.