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Are there limits in phylogeny reconstruction in gobioid fishes?

Multilocus phylogenies are increasingly used to reconstruct the Tree of Life. However, there is also a realization that some nodes in the Tree of Life remain unresolved even using multilocus approaches, and that adding more data in some cases can result in an increased level of systematic error leading to a convergence on erroneous phylogenies with strong statistical support. An important factor regarding the prospects of accurately reconstruct a phylogeny is stemminess, the relative length of internal versus external nodes. It is thought that accurate phylogeny reconstruction of trees that show short internal branches and long terminal branches due to ancient speciation events closely spaced in time may be extremely hard or impossible due to a combination of two factors: (a) the presence of short internal nodes supported by few synapomorphies and (b) long terminal branches showing a high frequency of homoplastic characters. The percomorph order Gobiiformes (sensu Wiley and Johnson 2010) comprises over 2200 species worldwide that are found in most freshwater, brackish, and marine environments, and show a spectacular variety in morphology, ecology, and behavior. The accuracy of previous phylogenetic studies might have been affected by episodes of ‘explosive radiations’ in some parts of the tree characterized by exceedingly short internal branches, e.g., Thacker (2009) for Gobiiformes based on mitochondrial DNA (see also Rüber and Agorreta (2010)) and Thacker and Roje (2011) for Gobiidae based on mitochondrial and nuclear data. We have assembled a large data matrix of three mitochondrial and three nuclear genes for representatives of the major lineages of gobies (about 250 terminal taxa) to ask whether episodes of rapid radiation obscure phylogeny reconstruction in this group.

Ecological diversification, range and Grinnellian niche evolution in a lizard radiation

Diversification and fast radiation is well documented in lacertid lizards. In the framework of this study, we investigated the relationship between niche evolution and phylogeny in a wide spread clade of Green Lizards of the Lacerta media - and trilineata -groups. A fossil-calibrated, dated phylogeny, based on three mitochondrial genes including all species of Lacerta s. str., identified several evolutionary lineages within this clade. These are in concordance with current subspecies taxonomy in case of the L. media -group, whereas the L. trilineata -group (including L. pamphylica ) consists of only three major lineages. Species distribution models were generated for each lineage and combined with the phylogeny to reconstruct ancestral climate niches. All extant lineages (i.e. species) are associated with humid climates, but there is extensive variation in their climatic niches implying pronounced shifts in climatic niche dimensions. Basically, the studied taxa are adapted to two kinds of main climatic conditions. While L. (m.) media , L. (m.) ciliciensis , L. (m.) isaurica , and to some extent L. (t.) dobrogica are occurring in mountainous or continental climates, they are missing in the Mediterranean climatic zone, where the remaining species are distributed. Taking into account the divergence time between taxa and geological events in Anatolia, it appears that first mountain formation caused the fragmentation of the hypothesized
ancestral species and later the process of cladogenesis was completed by the Quaternary climate oscillations. Phyloclimatic reconstructions based on each species’ available climate space transformed in orthogonal principal components (PCs) indicate divergent evolution within subclades and convergent evolution among clades and less niche conservatism. However, this pattern was not evident in each major niche axis. For example, PC2 was dominated by precipitation of the coldest quarter and the phyloclimatic reconstruction based on this PC exhibits greater differences among clades than within clades. This indicates a higher degree of niche conservatism and reflects especially the adaptation of the sister species L. (m.) media and L. (m.) ciliciensis to continental climates with cold winter temperatures and relatively moderate precipitation occurring mostly in summer.

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Mimicry in Cemophora coccinea

Batesian mimicry occurs when a palatable species mimics the color pattern of a dangerous species and thereby benefits from a predator’s instinctual avoidance of the mimicked color pattern. The non-venomous scarlet snake, Cemophora coccinea, is presumed to be a Batesian mimic based on the fact that its red, white, and black body bands closely resemble the red, yellow, and black body bands of the eastern coral snake, Micrurus fulvius, and the Texas coral snake, Micrurus tener, with which it co-occurs. Previous research on another putative Batesian mimicry complex (Scarlet Kingsnake, Lampropeltis elapsoideus, and M. fulvius) shows that the resemblance between models and mimics is highest at the edge of the model's range (edge sympatry), lower in regions where the model is abundant (deep sympatry), and lowest where the mimic occurs in the absence of the model (allopatry) as predicted by Batesian mimicry theory. To determine whether C. coccinea varies in its resemblance to M. fulvius and M. tener in a similar manner, a morphometric analysis of all three species was conducted. Photographs of preserved C. coccinea (665), M. tener (324), and M. fulvius (242) collected throughout the geographical range of each species were taken. Measurements of the width of each band on the dorsum of each snake from the snout to the cloaca were taken. These measurements were then used to compute the proportion of the snake’s dorsum that is red, black, and white/yellow. Over the entire geographical range, the color pattern of C. coccinea was more variable than the local models. However, when specific pattern characteristics (proportion of color, band number, band width, etc.) were compared between C. coccinea and their local model (either M. tener or M. fulvius), there was weak overlap between most pattern characteristics. Contrary to previous research on other putative Batesian mimicry complexes, the results suggest the possibility that the color pattern of C. coccinea may not be mimetic.

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Postmating isolation among six species of three genera (Hoplobatrachus, Euphlyctis and Fejervarya) from the family Dicroglossidae (Anura), with special reference to spontaneous production of allotriploids

The nature of species evolution and speciation process is an important step to evaluate species delimitation, contemporary integrative taxonomy and other biological aspects. According to biological
Evolutionary ecophysiology of lacertid lizards. Do preferred temperatures and water loss rates trade-off in Podarcis?

Studies on thermal ecology undoubtedly dominate the research on lizard ecophysiology. This is especially true for the Old World family Lacertidae. Within this group, preferred body temperatures (Tp) are well known to correlate with several physiological optima but also to carry substantial phylogenetic inertia. In contrast, much less is known on their water ecology traits, although some studies in other families suggest that body temperature and evaporative water loss (Wl) may trade-off. Both aspects, together with their evolutionary trajectories, needed to be investigated to wholly understand the phenotypic evolution and biogeography of these lizards. By integrating thermal and water ecology data, mechanistic models of potential distribution could be elaborated for current species and their ancestors. Here, we analyse both ecophysiological traits in the lacertids of the genus Podarcis, a taxonomically complex group whose phylogenetic relations and divergence times have been recently assessed. For a total of 15 lineages + 3 outgroups, mostly from Iberian Peninsula and North Africa, two laboratory tests were performed: 1) the classic Tp experiment using a photothermal gradient during 10 time intervals; and 2) the determination of Wl rates in sealed chambers during 12 hours. Significant interspecific differences in mean values and temporal patterns were detected either for thermal or for hydric parameters even between sympatric species. Uncorrected results for thermal and hydric traits were inversely related suggesting a trade-off between Tp and Wl. However, phylogenetically distant groups deviated from the common trend advising for phylogenetic correction. In a phylogenetic context, predominant ecophysiological shifts dated back to the Miocene-Pliocene rather than more recent geological times. The importance of these results in terms of current and past ecological modelling and future conservation is discussed.

Satellite tagging of juvenile thresher sharks (Alopias vulpinus) in the Southern California Bight

The common thresher shark is a large, wide-ranging coastalpelagic species. In the eastern Pacific, it ranges from Baja California, Mexico to British Columbia, Canada. Throughout its range it is harvested commercially, and it constitutes the largest shark fishery in California waters. Nevertheless, many aspects of its biology are poorly known, particularly as regards early life history. In the present study, juvenile thresher sharks (i.e., fork length < 120 cm) were tagged with pop-up satellite archival tags (Microwave Telemetry X-tags) to investigate their long-term movement patterns, habitat preferences, and geographic range. All sharks were tagged in southern California waters. Tag deployments ranged from three to six months, and tags archived light level, depth and temperature information. In total, data were successfully acquired from 23 juvenile threshers; eight tags were physically retrieved and produced high resolution archival data sets. 89% of pop-off locations were over the continental shelf. The furthest southward movement was to Bahia Sebastian Vizcaino, Baja California, Mexico, and the furthest northward
species separately, the number of individuals recorded was consistently higher at dusk and night for most species. Our study evidence a trend for crepuscular and nocturnal activity for most Atlantic Rainforest frogs, with few species having primarily diurnal habits. Those results may favor future studies of autoecology and conservation with specific species.

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Allopatric speciation with gene flow and peripheral isolation in Damselfishes (genus Stegastes)

Stegastes is a diverse genus of damselfishes associated to coral and rocky reefs in tropical oceans. Most species are solitary territorial herbivores that aggressively defend their feeding grounds, but a few are gregarious and feed on plankton. Juveniles are usually brightly colored and common in the aquarium trade. We sampled all 38 nominal species while scuba diving or snorkeling and preserved tissue samples in ethanol. Standard laboratory procedures were used to obtain sequences of one ribosomal RNA gene (16s) and one mitochondrial DNA gene (ATPase). As part of the phylogenetic analysis, we performed maximum parsimony, maximum likelihood and Bayesian analyses. The monophyly of the genus was rejected in all analyses. The genus appears to be split into two main groups, one clade (clade I) containing all Atlantic and eastern Pacific (indicating that this radiation originated from a single invasion of the Atlantic before the closure of the Isthmus of Panama) as well as some Indo-Pacific species, and a second clade (clade II) containing only Indo-Pacific species. Species of the genus Microspathodon form the base of clade II, whereas species of Plectroglyphidodon are present in both clade I and II. Additional taxon sampling is necessary to revise the current nomenclature. Cryptic speciation was also detected within many widely distributed species, the most notable case being Stegastes fasciolatus, which seems to be comprised of four different species. Even though ongoing speciation seems to follow an allopatric pattern, several instances of gene flow were detected between incipient and or young species. There is also an apparent pattern of peripheral speciation, with all populations in isolated islands or archipelagos belonging to separate clades.

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Inferring the effects of past climate fluctuations on the distribution pattern of Iranolacerta (Reptilia, Lacertidae): evidences from mitochondrial DNA and species distribution models

A variety of different methods are available for investigating the effects of past climate fluctuation on biota. Among them, molecular phylogeographic and species distribution modeling approaches have been shown to be especially useful tools to trace past climate induced modifications of species' geographic distributions. Comparing the results of both analytical approaches are here combined to better understand the influences of past climate changes on the fragmented distribution pattern of the lizard genus Iranolacerta, that currently ranges the northwest and central Zagros Mountains of Iran. While I. zagrosica is restricted to few localities and cannot be modeled, the distribution modeling of I. brandti suggested a large region of unfavorable habitat between Azerbaijan and the central Zagros Mountains.
populations. For the phylogenetic perspective, both species display deep genetic separation predating likely the Pleistocene. However, limited genetic diversity across this divided range of *I. brandtii*, imply that the current separation is recent. Deeper genetic divergences were, nevertheless, uncovered within Azerbaijan. Since no recent geological events explain these results, the most likely explanation for such a distribution pattern is due to past climate fluctuations. Both sources of evidence suggest that during the last glaciation the Azerbaijan and Zagros populations of *I. brandtii* were connected, and the current pattern was shaped with their disconnection in the early Holocene. Further studies may identify potential glacial refugia for other species in this biodiverse region.

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**Niche stasis in invasive herps? The role of accessible climate space in invasion success**

Several amphibian and reptile species have successfully established invasive populations around the globe and successful management often requires estimates of invasion risk for a given region. The use of species distribution models (SDMs) to predict potential distributions of species including invasion potentials is steadily increasing. A necessary assumption when projecting such models throughout space or time is that climatic niches do not change, at least in contemporary time frames. However, recent findings of niche shifts during biological invasion of particular plant and animal species have indicated that this assumption is not categorically valid. One reason for the detected niche shifts may relate to the selection of predictive variables used for modeling. Another reason may be related to evolutionary responses. In this talk, I provide examples of studies addressing differences in climatic niches in the native and invasive ranges of amphibians and reptiles. I highlight which variables are more ‘conserved’ in comparison to more ‘relaxed’ variables (i.e. subject to niche shift) and how they influence transferability of SDMs through space and time. Using quantifications of available climate spaces I discuss whether these niche shifts are likely to represent methodological artifacts or evolutionary responses. Most studies indicate that the degrees of niche similarity and conservatism vary greatly among the predictive variables. Some shifts can be attributed to active habitat selection, whereas others apparently reflect variation in the availability of climate conditions or biotic interactions between a species native and invasive ranges. Patterns suggesting active habitat selection also vary among variables. These findings evoke considerable implications on the transferability of SDMs over space and time, which is strongly affected by the choice and number of predictors. The incorporation of ‘relaxed’ predictors not or only indirectly correlated with biologically meaningful predictors may lead to erroneous predictions when projecting SDMs - and ultimately to unreliable assessments of invasion risk. I recommend thorough assessments of invasive species’ ecology for the identification biologically meaningful predictors facilitating transferability.

**Rödel, Mark-Oliver** (Museum fuer Naturkunde Berlin);

**West African amphibians: diversity, threats and future**

Globally the biodiversity of the Afrotropics is probably among the least well known. West Africa is no exception from that rule. Although amphibians of this region were intensively studied, in particular since the 1960s, we continuously added new and spectacular discoveries throughout the last 20 years. This process is still far from being completed. In the first part of the talk I will summarize our findings and pinpoint on the major gaps that still exist. Unfortunately, biodiversity in the region suffers from a constantly increasing exploitation of natural resources (i.e. conversion of habitats to agricultural land, logging, mining, bush meat trade), as well as from changing climatic conditions. To uncover the potential