

environments, and possibly played a role in the radiation of *Quercus* into Mexico the region with the highest species diversity.

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Phylogenomic heterogeneity and attempts to identify noise and signal in evolution

Before the wide-spread availability of large genomic datasets, researchers worked under the assumption that recalcitrant nodes would be resolved with the collection of more data. The development of new sequencing technologies made large datasets a reality, though recalcitrant nodes remain. The last decade of genomic sequencing and phylogenetic reconstruction has demonstrated that with the collection of more data has come an increase in the heterogeneity underlying those data. In this presentation, I will discuss some of the sources of heterogeneity and how we might distinguish signal from noise. I will also argue that, instead of discarding conflict, phylogenetic conflict serves to present a more complete picture of the processes underlying lineage diversification.

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Homology in the age of phylogenomics

Homology is arguably the most central concept in phylogenetic biology. Molecular systematists have traditionally paid diligent attention to the homology statements that are implied by their sequence alignments, but manual gene-by-gene curation has gone by the wayside in the phylogenomics era. Here, we show that a variety of phylogenomic data sets are compromised by homology errors that negatively impact the integrity of these data. We also outline multiple approaches to efficiently screen for and detect homology errors in phylogenomic data. Application of these screening approaches shows that some phylogenomic data sets are replete with homology errors including alignments of different exons to each other, alignments of introns to exons, and alignments of paralogous sequences to each other. The extent of these homology errors weakens the conclusions of these studies. Despite advances in automated phylogenomic pipelines, the sometimes tedious work of systematics is still required to guard against pervasive homology errors. This conclusion is underscored by recent studies that show that just a few outlier genes can impact phylogenetic results at short, closely spaced internodes that are deep in the Tree of Life. The view that widespread DNA sequence alignment errors are not a major concern for rigorous systematic research is not tenable. If a primary goal of phylogenomics is to resolve the most challenging phylogenetic problems with the abundant sequence data that are now available, researchers must employ effective procedures to screen for and correct homology errors prior to performing phylogenetic and other downstream analyses.

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Unraveling Ross' classification of Anisembiidae (Embioptera)

The Southamerican family Anisembiidae appears as a monophyletic group in the first to the last published cladistic analyses of the Embioptera Order. However, half of the genera

described by Edward S. Ross – the specialist of order - appear as paraphyletic or polyphyletic groups (e.g. *Bulbocerca*, *Dactylocerca*, *Pelorembia*, *Stenembia*). The Anisembiidae, had - at the end of the 90 - a handful of genera (4-5) and around 40 species. Between 2001 and 2004, Ross published six compendia on Embioptera in the journal Occ. Paper of California Academy. One of them is a review of the family Anisembiidae, where he describes about 70 new species and 15 new genera (half of them monotypic), as well as groups like tribes and subfamilies. In this compendium is clear the conflict between the specialist's point of view and the basic principle in systematics: achieve a stable classification; taxonomic groups should be supported by the evidence. As a result of this particular interpretation of the systematics, there are new genera grouping autapomorphic species of other well known genera and, geography as a criterion to define genera (e.g. the genus *Mesembia* exclusive for Cuba). Therefore, in this work we propose to analyze the whole group (around 110 species) and try to untangle Ross' classification in a phylogenetic context.

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Biogeographic and diversification patterns of squamate reptiles across North Africa and Arabia

Desert areas comprise an important part of the world's land surface. In spite of their harsh conditions, deserts can harbor a high diversity of fauna and flora. This offers the opportunity of investigating how the geographic and climatic history of these areas have affected the evolutionary history of their biodiversity. In this study, we focus on some of the largest arid regions of the world, the north of Africa and the Arabian Peninsula, to study large-scale biogeographic and diversification patterns of squamate reptiles, one of the most successful groups inhabiting the deserts. Evolutionary history has been explored and discussed independently for several groups of reptiles from north Africa and the Arabian Peninsula, but a study integrating a large number of groups is still lacking. Here, we assemble a comprehensive dataset including most of the squamate genera present both in Africa and Arabia with the objective of investigating large-scale biogeographic and diversification patterns in a comparative framework. We reconstruct phylogenetic relationships among 550 species with 5 mitochondrial and 6 nuclear loci, and estimate divergence times with eleven calibration points, including fossils and biogeographic events. With this broad dataset, we are able to reconstruct and compare the evolutionary history of 22 genera of squamate reptiles across north Africa and Arabia. By applying statistical biogeographic models, we can associate diversification dynamics with paleogeographic events affecting these regions. As a result, we can describe the effect of the Afro-Arabian geologic and climatic history on the diversity and evolution of desert-dwelling squamates.

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Gene tree incongruence is a major predictor of the differences between parsimony and maximum likelihood in phylogenomics

In previous studies we found a high congruence between the results of Maximum Parsimony (MP) and Maximum Likelihood (ML) for 149 phylogenomic datasets (average of 3.5