

Research Statement

Simon Scarpetta

When did various lizard groups evolve, where did they live in the past, what are their closest relatives, and how do we know? I leverage the fossil record, genetic data, and geological data to answer those questions in my research. I am interested in holistic approaches that consider all relevant data and that combine methods and ideas from multiple scientific fields, including evolutionary biology, paleontology, and geology. My main research focus is the evolutionary history of lizards inhabiting North America across both short and long timescales, but I am also interested in other organisms, including salamanders, snakes, and voles. My research is grounded in phylogenetic methods, and I have used phylogenetic analyses of genetic, morphological, and combined-evidence datasets in my research. I am also very compelled by the power of statistical biogeographic methods to address questions related to modern and past species and clade distributions. I have also pursued projects related to tooth pathology and development, species descriptions of *Anolis* lizards, and Pleistocene reptile and amphibian faunas from eastern North America.

Modernization of lizard fauna in North America

I am interested in understanding the climatic and geologic events that precipitated the assembly of the modern lizard biota in North America. I have investigated the appearance of extant species groups, and the extinction or extirpation of groups that are no longer found in North America. I recorded the last appearance of a large-bodied and heavily armored lizard group, Glyptosaurinae. Glyptosaurine lizards likely became extinct during a middle Oligocene cooling event, after having dominated North America for much of the Mesozoic and early Cenozoic. Through discovery and description of new fossils and divergence time analyses (see below), I found that several extant groups first appeared during the Miocene, including fringe-toed lizards and alligator lizards.

Not all lizards exhibited the same ecological behavior in the past that we associate with them today. For example, I found and described the first known fossil of a North American fringe-toed lizard, a group that known is in the modern biota for occupation and specialization to fine-grained sand dunes. The depositional environment that the lizard fossil occurred in suggests that the animal inhabited an environment lacking fine-grained sand, and divergence time analyses demonstrated that the first appearance of the group preceded the formation of large dune fields in the southwestern USA.

Divergence times

I have several active research projects that aim to determine divergence times for a variety of lizard groups. I am largely focused on North American sand and spiny lizards, whiptails, collared and leopard lizards, and alligator lizards. I have worked extensively in museum collections across the United States to find and identify fossils that might represent early occurrences of those groups, and that could be used to calibrate rates of molecular evolution in Bayesian divergence time analyses. I recently produced a revised chronology of North America sand lizard evolution, using a large dataset of protein-coding nuclear genes (exons) and mitochondrial genes, calibrated with multiple fossil occurrences. I will soon begin a project addressing divergence times of all sand and spiny lizards, using fossils that I described, previously described fossils, and targeted sequence capture data.

Phylogeny of alligator lizards

In collaboration with my advisor and a former mentee in the UT Biology department, I am producing a new morphological phylogeny of alligator lizards that is grounded in recently published molecular hypotheses. Convergent evolution and excessive variation among alligator lizards complicates the use of morphology as a phylogenetic dataset. However, a morphological perspective is required in order to identify fossils. We created a new phylogenetic dataset specific to alligator lizards, and are using that dataset to identify and describe a new species known from a well-preserved skull fossil.

Practice and philosophy for fossil identification

During my dissertation, I developed a strong interest in the practice and philosophy of fossil identification. In recent years, many vertebrate paleontologists have moved away from fossil identifications based on stratigraphy, geography, or overall similarity, towards a fossil identification approach that assesses the presence or absence of evolutionarily derived features, or apomorphies. Identifications made using an evolutionarily explicit approach can be accomplished quantitatively via a phylogenetic analysis or qualitatively with an apomorphy-based diagnosis. That gradual shift has improved the reproducibility and objectivity of the field. Little attention has been devoted, however, to assessing the effects of alternative evolutionary hypotheses on fossil identifications made in a phylogenetic context. In a recent publication, I described a new iguanian lizard from the Eocene. I found that accounting for alternative phylogenetic hypotheses drastically changed the relationships of the new species. The corresponding biogeographic, divergence time, and paleoecological interpretations from the fossil vary widely based on its identification. That finding has broad ramifications for all paleontologists would identify fossils with a phylogenetically explicit approach.

Combining genomic data with morphological and fossil data in phylogenetic analyses

Combining paleontological and molecular data in combined-evidence phylogenetic analyses has been a relatively common practice for several years. The recent proliferation of larger genomic datasets produced via next-generation sequencing has created methodological issues for such analyses, because larger molecular datasets swamp other data when analyzed simultaneously. Several recent studies have addressed that problem by subsampling genomic datasets to decrease their size. I recently published the first combined-evidence analysis with a next-generation genomic dataset that was not drastically subsampled and a morphological dataset. I found that by increasing the weight of the morphological data, a more synthetic result was achieved that accounted for both data types, and that subsampling is not strictly necessary.

Future work

I am currently writing postdoctoral fellowships to pursue a project incorporating many of my research interests. The overarching goal of the project is to estimate an integrative biogeographic history of iguanian lizards. I intend to collect genomic data, including ultraconserved elements and exons, and morphological data from extant and fossil iguanians. Those data will be used to estimate a combined-evidence phylogeny, which will be dated via divergence time analyses incorporating a broad sample of fossil ages. The result will be incorporated into a dynamic statistical biogeographic model that accounts for origination, extinction, and changing dispersal probabilities in response to global and local tectonic and climatic events.