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A Phylogenetic Analysis of the *Anolis pentaprion* species group

The lizard genus *Anolis* is the largest amniote genus with 371 species spanning North America, Central America, Central America, South America, and the Caribbean. *Anolis* has been a model system for a variety of studies from behavioral, ecological, and morphological research to studies of biogeography, adaptive radiation, and character displacement. Despite decades of work, the phylogeny of *Anolis* has been difficult to elucidate. The relationships of mainland forms are especially poorly understood. The *Anolis pentaprion* species group is found from southeastern Mexico to northwestern Colombia from sea level to approximately 2000 m. These small to medium-sized *Anolis* have short limbs and tail and a distinctive lichenous dorsal color pattern. Here I present a phylogenetic analysis of the *pentaprion* group, hereby defined to include *A. beckeri*, *A. charlesmeyersi*, *A. cristifer*, *A. fungosus*, *A. ortonii*, *A. pentaprion*, *A. salvini*, *A. utilensis*, and *A. sulcifrons*. I use molecular and morphological data and Bayesian and likelihood-based approaches to examine the evolutionary history of the *pentaprion* group and test its monophyly.

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Reproductive Isolation in *Anolis* lizards

Although speciation is defined as the evolution of reproductive isolation, our knowledge of how various forms of reproductive isolation accumulate during speciation remains rather limited. Detailed multi-generation experimental studies with a small number of representatives from several major clades - including plants, invertebrates, fish, amphibians, birds, and mammals - suggest that the evolution of reproductive isolation is often characterized by four general patterns: (1) heterogametic hybrids disproportionately suffer the consequences of barriers (Haldane's Rule), (2) asymmetric sterility and/or inviability of hybrids (Darwin's Corollary to HR), (3) prezygotic isolation evolves before postzygotic isolation and (4) hybrid sterility evolves before hybrid inviability.

Here we report the results of a multi-generation reproductive isolation experiment designed to test these patterns with two closely-related species of *Anolis* lizards. Our work is among the largest and most detailed study of its kind on any squamate reptile, a group that accounts for nearly 30% of tetrapod species. Our work is also among the first studies to investigate intrinsic reproductive isolation between closely-related and morphologically cryptic species diagnosed by recent surveys of geographic genetic variation among populations in nature.

Levi Gray, Robbie Burger

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Do allometries reveal evolutionary constraints in *Anolis* lizards?

Adaptive radiations can offer unique insights to the evolutionary and macroecological processes shaping morphological diversification. *Anolis* lizards exhibit evolutionary radiations in both mainland and island environments, resulting in comparable ranges in body size. Given that selection pressures are expected to vary greatly in the diverse environments inhabited by anoles, it seems unlikely that universal patterns of allometry would emerge. Here, using data from 292 species of anoles, we demonstrate universal scaling in two ecologically relevant traits: head

length and hindlimb length. These allometries reveal statistically identical slopes and intercepts for both island and mainland groups, regardless of ecomorph status or environment. These shared patterns suggest fundamental evolutionary constraints to morphology and thus ecology in the *Anolis* radiations.

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Colonization and Differentiation in the Honduran Bay Islands Populations of *Anolis allisoni*

Anolis allisoni Barbour occurs throughout Islas de Bahia off Honduras, and was originally described from Roatan, Bay Islands. This species also occurs throughout much of Cuba where it was previously considered conspecific with *A. porcatatus* but was separated based mainly on ear morphology (elongate in *A. allisoni*, round in *A. porcatatus*; Ruibal and Williams, 1961). Populations of *A. allisoni* inhabiting the Bay Islands are geographically isolated from populations inhabiting Cuba by approximately 1,100 km of open ocean. The geographic barriers between Bay Islands populations, and especially between these populations and Cuba, should perpetuate genotypic and phenotypic divergence. We use morphological and molecular analyses of fresh specimens and tissues from the type locality of *A. allisoni* to address the following questions in Bay islands *A. allisoni*: whether the invasion of *A. allisoni* to the Bay Islands was the result of single or multiple dispersal events from Cuba; whether populations of *A. allisoni* from the Bay Islands are morphologically and/or molecularly differentiated from Cuban populations; if so, whether this variation warrants species distinction.

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Habitat Use in Naturalized *Anolis* Lizard Communities

Human-mediated introductions of species have resulted in novel combinations of species in communities worldwide. Non-indigenous species may have negative impacts on their new environments, but they also provide unique opportunities to study patterns of community assembly and habitat partitioning. Shared patterns among natural and naturalized communities may suggest universal rules for community assembly and maintenance.

Anolis lizards form natural communities of at least 12 species and naturalized communities of up to six species. *Anolis* has been a model system for study of community patterns and processes in native communities, but little is known about communities of naturalized *Anolis*. We collected habitat use, body size, and abundance data for communities in Florida and Bermuda that include naturalized species of *Anolis*. We compared our data on naturalized communities to existing data on natural communities.

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Estimation of phylogeny of the *Anolis cupreus* (Squamata: Dactyloidae) species group

The *Anolis cupreus* species group of Savage and Guyer (1989) includes *Anolis cupreus* (Hallowell 1860), which encompassed *A. c. hoffmani*, *A. c. spilomelas* (Hallowell 1860), *Anolis c. dariense* (Fitch and Seigel 1984), and *Anolis c. macrophallus* (Werner 1917) at that time; *Anolis dollfusianus* (Bocourt 1873) and *Anolis villai* (Fitch and Henderson 1976). Two of the four subspecies (*A. c. dariense* and *A. c. macrophallus*) have been elevated to species status

(Köhler, Günther and Kreutz 1999). We add *A. yoroensis*, which, subsequent to the Savage and Guyer treatment, was diagnosed relative to *A. cupreus* due to its similarity with this species. The members of this species group are distinguished by male dewlap color, the condition of the nasal scale, dorsal coloration, and scale counts (Hallowell 1860; Fitch, Echelle and Echelle 1972; Savage 2002; Kohler 2008). Species of the *A. cupreus* species group are found in Costa Rica, Honduras, Nicaragua, El Salvador, parts of southern Mexico, and southeastern Guatemala (Stuart 1955; Fitch, Echelle and Echelle 1972; Fitch and Seigel 1984; Nicholson, McCranie and Kohler 2000). Previous authors have evaluated the relationships of *A. cupreus* to other anoles in Central America based on morphological data (Fitch, Echelle and Echelle 1972; Poe 2004) and molecular techniques (Nicholson 2002; Nicholson et al. 2005), but no other *cupreus* group species have been included in phylogenetic analyses. We use mitochondrial and nuclear gene sequence data to estimate relationships among the *Anolis cupreus* species group of Central America and test the monophyly of this previously informally recognized group.

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Biogeography of *Norops capito*: Second Example of a Contradictory Pattern

Previous literature has posited that the genus *Norops* originated in the Caribbean after the separation of North and South America, left members in Cuba and Jamaica, and disbursed overwater to Mexico, subsequently giving rise to a monophyletic clade that distributed themselves southwards until they invaded South America, presumably after the closure of the Panamanian Portal. However, a recent paper proposed a contradictory hypothesis suggesting that entire genus *Norops* originated prior to the separation of North and South America. It was suggested that perhaps *Norops* was widespread prior to the separation of North and South America, and that perhaps some mainland *Norops* lineages were separated on the mainland when the proto-Greater Antilles moved eastward. We present evidence from *Norops capito*, an arboreal species, and the second anole species to show a distinct south to north biogeographic pattern in contrast to previous hypotheses positing a north to south distribution. Our analysis of DNA sequence data from samples throughout the range of *N. capito* show this south to north distribution, in agreement with previously presented data for the *N. limifrons* group, but in contrast to data we presented previously for the *N. humilis* group, which shows a north to south distribution. A picture is emerging suggesting support for widespread *Norops* distribution prior to the separation of North and South America.

Steven Poe

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Identification Key for *Anolis* Lizards

Anolis lizards are notoriously difficult to identify. In 1995 Ernest Williams and collaborators published a landmark paper describing their "computer approach" to identification of *Anolis*. This work employed the program Hypercard to produce an application that matched a set of character scores from an unknown specimen to scores in Williams' vast database of *Anolis* lizards. This "*Anolis* Handlist" had obvious advantages over its paper dichotomous counterparts. In matching keys, accurate identification is not dependent on correct decisions on early couplets, as it is in dichotomous keys, and a set of similar and possible species rather than a single final verdict may be rendered.

The Williams et al. approach was ahead of its time. Today such electronic matching-based keys are commonplace. The Lucid platform has become the commonest means to present such keys, probably due to its widespread availability, functionality, and ease of use. Here I apply the Lucid platform to produce a key to all species of *Anolis* lizards.

Steven Poe

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Phylogeny of *Anolis*

We present new DNA sequence data from two mitochondrial (ND2, COI) and one nuclear gene (ecl) to elucidate the phylogeny of *Anolis*. We combine these data with morphological data and published DNA data to produce a comprehensive phylogenetic estimate of *Anolis*. We use this estimate to assess taxonomic and biogeographic issues in *Anolis*.

Bradley Truett, Steven Poe

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Revisiting the Aquatic Anole Ecomorph

We use both nuclear and mitochondrial genes (NDAH2, CO1, and ECEL1) to build a phylogeny and identify evolutionary relationships between aquatic anoles (*Anolis barkeri*, *A. robinsoni*, *A. riparius*, *A. aquaticus*, *A. lionotus*, *A. poecilopus*, *A. vermicularis*, *A. eugenegrahami*, and *A. maculagula*) and a potential new aquatic anole species from Monte Verde Costa Rica. Aquatic lifestyle among anoles appears to have multiple origins, with no phylogenetic basis of adaptation to aquatic conditions. I measured 24 morphological characters to evaluate aquatic ecomorphology. Using these measurements, the ancestral traits of non-aquatic sister species were predicted in order to identify potential intermediate aquatic traits.

Kristin Winchell

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Phenotypic shifts in urban populations of the tropical lizard, *Anolis cristatellus*

Urbanization is widespread and intensifying globally, altering environments and imposing unique pressures on animal species that live in urban areas. Prior studies have revealed adaptive responses to urbanization in a range of plant and animal species, although relatively few have involved reptiles. We investigated morphological adaptation in the tropical lizard, *Anolis cristatellus*, in three paired urban and natural sites in Puerto Rico. Our preliminary results show that urban populations have longer hindlimbs and forelimbs, more subdigital lamellae, and higher body temperatures. Lizards in urban areas were captured on broader surfaces and nearly 50% of urban captures were on manmade substrates such as metal fence posts and painted concrete. We hypothesize that phenotypic differences between urban and natural populations may be due to selection for improved locomotor performance on the wider and smoother artificial substrates typical of urban habitats. Genetic analyses of neutral markers show high gene flow between paired populations, suggesting that differences between populations are not likely to be due to genetic drift. In future research we will directly measure selection in urban habitats as well as test for the genetic basis of the phenotypic trait shifts found in the present study using common-garden rearing experiments. Understanding the novel selective pressures faced by *A. cristatellus* in urban areas, along with how this species may be adaptively responding to these challenges, has the potential to provide considerable insight into the mechanism of rapid microevolution and has implications for conservation of urban-persistent species.