

CONSERVATION RESEARCH REPORTS

New Pacific Iguana

The Pacific iguanas of the Fijian and Tongan archipelagos are a biogeographic enigma in that their closest relatives are found only in the Western Hemisphere. These iguanas were thought to comprise two genera and four species of extinct and extant taxa. The two currently recognized extant species, *Brachylophus fasciatus*, from Fiji, Tonga, and Vanuatu, and *Brachylophus vitiensis*, from western Fiji, are of considerable conservation concern, with *B. vitiensis* listed as critically endangered. In a recent molecular study, KEOGH ET AL. (2008. *Philosophical Transactions of the Royal Society B (Biological Sciences)* 363:3413–3426) showed that *Brachylophus* comprised three evolutionarily significant units. To test these conclusions and to reevaluate the phylogenetic and biogeographic relationships within *Brachylophus*, the authors generated a mitochondrial DNA dataset for 61 individuals from 13 islands, representing both currently recognized species of *Brachylophus*. The data rejected the monophyly of specimens previously believed to comprise *B. fasciatus*, instead demonstrating that *Brachylophus* includes three distinct species: *B. fasciatus* from the Lau group of Fiji and Tonga, a new species, *B. bulabula*, from the central regions of Fiji, populations which until now were considered



Top predators such as Nile Monitors (*Varanus niloticus*) may be at risk of reduced fitness and population declines due to cumulative effects of persistent environmental contaminants to which they are exposed over long life spans.

to be *B. fasciatus* or *B. vitiensis*. These molecular and taxonomic results have important implications for future conservation initiatives for Pacific iguanas.

Emerging Threats to Long-lived Vertebrates

Persistent contaminants are ubiquitous in the environment, often present at concentrations that may jeopardize reproductive fitness only after long periods of exposure. As the duration of exposure is largely regulated by life span, long-lived species of high trophic status, such as many reptiles, birds, and mammals, may be at risk of reduced fitness and population decline. ROWE (2008. *BioScience* 58:623–631) suggested that delayed maturation and iteroparity (repeated production of offspring at intervals throughout the life cycle) confer the potential for cumulative effects to be expressed prior to reproduction, and large parental investments in yolk and milk may threaten offspring because of exposure during critical developmental periods. Long generation times may delay emergence of obvious effects on populations, perhaps eluding early intervention, while constraining rates at which populations may recover if conditions subsequently improve. Life history theory thus suggests that the suite of traits that optimized reproductive fitness throughout long-lived species' evolution-

ary histories may ultimately put them in peril in the modern anthropogenically altered environment.

Frogs with Disease-resistance Genes May Escape Extinction

As frog populations die off around the world, researchers have identified certain genes that can help the amphibians develop resistance to harmful bacteria and disease. The discovery may provide new strategies to protect frog populations in the wild. New research examines how genes encoding the major histocompatibility (MHC) complex affect the ability of frogs to resist infection by a bacterium that is commonly associated with frog population declines.

“In the short term, captive management of frogs with complementary disease-resistance genes may offer the best hope for saving species from extinction,” says Bruce Waldman, a biologist at Lincoln University in New Zealand and one of the paper's authors. “Management practices that maintain or enhance diversity in MHC genes may prove the key to safeguarding frog populations in the wild.” “Massive die-offs of frogs may indicate environmental problems that ultimately will affect other species, including humans,” Waldman says. “But, despite the concern, little is known about factors that make individuals susceptible to disease.”



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Populations from central regions of Fiji, formerly assigned to *Brachylophus fasciatus*, were shown to represent a new species, *B. bulabula*.



ERIC BSELEE

A study of tadpoles of African Clawed Frogs (*Xenopus laevis*) indicated that some individuals with disease resistant genes grew more slowly.

BARRIBEAU ET AL. (*PLoS One* 3: e2692, <www.plosone.org/article/info:doi/10.1371/journal.pone.0002692>) exposed African Clawed Frog tadpoles to several doses of the bacterium *Aeromonas hydrophila* and examined the number of tadpoles that survived and measured how fast they grew. Certain genes allowed tadpoles to survive bacterial infection but at a cost, as these tadpoles sometimes grew more slowly. Among siblings, patterns of disease resistance corresponded to tadpoles' MHC genes rather than other genes that they shared, demonstrating that the MHC genes conferred immunity.

Programs currently are underway to rescue frogs from declining wild populations and breed them in captivity to ensure that species are not lost to extinction. This study suggests that selective breeding of individuals with known disease-resistance genes might produce frogs that can survive infection by pathogens, even after the frogs are reintroduced into the wild.

The research team studied the African Clawed Frog because its immune system already had been well characterized, but as most frogs and toads have similar immune systems, they believe that their results will be generally applicable to all threatened and endangered amphibians.

New Approach to Conserving Amphibians

The global extinction crisis demands immediate action to conserve species at risk. However, if entire groups such as superfamilies are at risk due to shared evolutionary history, a shift towards conserving such groups rather than individual species may be needed. Using phylo-

genetic autocorrelation analysis, COREY AND WAITE (2008. *Diversity and Distributions* 14:614–629) demonstrated that multiple kinds of extinction threat clump within the amphibian tree of life. Their study provided insight into how these threats might collectively influence the extinction risk of whole groups, consistent with the supposition that related species, with similar traits, share an intrinsic vulnerability to common kinds of threat. Most strikingly, they found a significant concentration of 'enigmatic' decline and critically endangered status within families of the hyloid frogs. This phylogenetic clumping of risk is also geographically concentrated, with most threats found in Central and South America, and Australia, coinciding with reported outbreaks of chytridiomycosis. They speculated that the phylogenetic clumping of threat represents, in part, shared extinction proneness due to shared evolutionary history. However, even if the phylogenetic clumping of threat were simply a by-product of shared geography, this concordance between phylogenetic and geographical patterns represents a prime opportunity. Where practical, conservation plans should focus on biogeographical regions where threatened groups occur, thereby improving the capacity for conserving species. This approach could outperform the usual triage approach of saving individual species after they have become critically endangered.



A clumping of threats to groups of frogs, especially the hyloid frogs such as this Red-eyed Treefrog (*Agalychnis callidryas*), might represent, at least in part, a shared extinction proneness due to shared evolutionary history.

Surveying Herpetofaunal Mortality on Rural Highways

Road mortality can contribute to local and regional declines in amphibian and reptilian populations. Consequently, accurately and efficiently identifying hotspots of road-mortality is necessary for hazard assessment and mitigation. In 2002, LANGEN ET AL. (2007. *Journal of Wildlife Management* 71:1361–1368) conducted walking and driving surveys throughout an extensive rural highway network in northern New York to evaluate survey methods and to quantify spatial and temporal patterns of herpetofaunal road-mortality. In 2004, they repeated the surveys at a subset of locations to quantify interannual repeatability. Reptilian and amphibian species had different peak periods of road-mortality because they differed in the causes of movements that resulted in crossings.



CHUCK SCHAEFER

Reptilian and amphibian species had different peak periods of road-mortality because they differed in the causes of movements that resulted in crossings. Spatial locations of herpetofaunal road-mortality were concentrated at a limited number of hotspots, such as those used by female turtles moving to nesting areas.

Spatial locations of herpetofaunal road-mortality were concentrated at a limited number of hotspots. Hotspots overlapped across species and were located at consistent locations across years. Results of walking and driving surveys were highly repeatable among survey teams, but driving surveys underestimated the density of road-mortality because many animals were missed. Detection failure was higher in some taxa (e.g., frogs) than others (e.g., turtles). Their results indicated that designing a valid, efficient methodology for locating hotspots of reptilian and amphibian road-mortality along a road network is possible, thus pinpointing priority sites for mitigation.