

Conservation genetics of Australasian sailfin lizards: Flagship species threatened by coastal development and insufficient protected area coverage



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ABSTRACT

Despite rampant coastal development throughout Southeast Asia and the Pacific, studies of conservation genetics and ecology of vulnerable, coastal species are rare. Large bodied vertebrates with highly specialized habitat requirements may be at particular risk of extinction due to habitat degradation and fragmentation, especially if these habitats are naturally patchily distributed, marginal, otherwise geographically limited, or associated in space with high human population densities or heavy anthropogenic disturbance. Particularly telling examples of these conservation challenges are large Australasian reptiles with obligate habitat requirements for lowland, coastal and mangrove forests. Plagued by habitat destruction due to high human densities along coastlines, sprawling rural development, and rapidly developing estuarine fisheries industry, coastal forest reptiles are experiencing rapid declines. And yet studies of population biology, genetics, and habitat requirements of species depending on these environments are few. We undertook the present study in order to take a multifaceted approach to understanding a poignant conservation problem. We identify significant evolutionary units for conservation in large-bodied sailfin lizards (genus *Hydrosaurus*), model suitable habitat in the Philippines from extensive occurrence data and evaluate the efficacy of the current protected area network, and identify the source of hydrosaurus in the illegal pet trade. We determine that the extent of the species' habitat coincident with protected areas is low. Our forensic evaluation of the illegal pet trade in the Philippines determines the existence of a natural population that is at risk of systematic exploitation by traders. Together, this integrative study characterizes a conservation urgency of particular significance: the genetically distinct sailfin lizards of the Bicol faunal region, with suitable habitat virtually unprotected, and clear evidence of heavy exploitation for illegal trade. To the best of our knowledge, our study is the first conservation genetic study to evaluate the potential effectiveness of the protected landscape coverage in the Philippines, a Megadiverse nation and Biodiversity Hotspot.

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1. Introduction

Protection of species with obligate requirements of specific, patchily distributed, marginal, or heavily fragmented habitats represents a special challenge for government agencies, wildlife managers, and conservation biologists. Species unable to survive outside of very specific or highly restricted ecological conditions are, by definition, immediately imperiled if their required habitats are altered, degraded, or destroyed by the activities of humans. Celebrated examples of taxa threatened—or even driven to extinction—by anthropogenic destruction of their required habitats

include Proboscis Monkeys (Jeffrey, 1982), Northern Spotted Owls (Franklin et al., 2000), Dugongs (Preen and Marsh, 1995), and Ivory Billed Woodpeckers (Schock, 2005).

Lowland and coastal forests, and the species that depend on them, represent poignant conservation challenges of particular concern (Mumby et al., 2004; Millennium Ecosystem Assessment, 2005; Duke et al., 2007), and nowhere is this concern more evident than in the highly degraded littoral zone mangroves and beach or coastal forests of Asia and islands of the Pacific (for review: Polidoro et al., 2010). Throughout the edge of the Asian continent and the adjacent Australasian archipelagoes, coastal and mangrove forests have been systematically cleared for brackish water aquaculture ponds, firewood and timber, or residential and urban development (e.g., Walters, 2000; Blasco et al., 2001). Globally, mangrove biodiversity is highest in the Australasian region (Polidoro et al., 2010), yet in some countries, mangrove and dry

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coastal forest removal has been near complete (Primavera et al., 2004; Walters, 2004; Samson and Rollon, 2008).

At the same time, the critical importance of coastal forests has been well documented (Millennium Ecosystem Assessment, 2005; Duke et al., 2007; Polidoro et al., 2010). Mangroves and beach forests are recognized to possess a unique flora, which acts at the critical interface between terrestrial, estuarine, and near-shore marine ecosystems (Polidoro et al., 2010). Coastal forests and mangroves buffer against erosion, protect inland communities from damage by inclement weather (Dahdouh-Guebas et al., 2005; Barbier et al., 2008; Das and Vincent, 2009), and represent critical habitat for terrestrial, estuarine and marine species (Robertson and Duke, 1987; Luther and Greenburg, 2009). Finally, mangroves serve as source and sink for nutrients and sediments for inshore marine habitats (i.e., seagrass beds and coral reefs; Dorenbosch et al., 2004; Duke et al., 2007).

In some archipelago nations, the near complete loss of coastal forests may have already occurred. For example in the Philippines, in just the last 75 years, the destruction of the coastal forests and mangroves has been extensive (Primavera, 2000; Walters, 2000, 2004; Primavera et al., 2004; Lewis, 2005; Samson and Rollon, 2008). The archipelago has lost more than 75% (>337,000 ha) of original mangrove forests (Bacongus et al., 1990; Walters, 2000; Samson and Rollon, 2008), with >66% (or 278,657 ha) lost between 1950 and 1990 (Primavera, 2000). The elimination of this unique coastal ecosystem is primarily attributed to urbanization along the coasts and construction of brackish water fishponds (~60%; Samson and Rollon, 2008) and yet its impacts are largely unknown. Despite the extensive documentation of the effects of habitat loss in inland ecosystems (for review: Posa and Sodhi, 2006; Rickart et al., 2011), few, if any, studies have measured the direct effects of habitat destruction on coastal forest obligate species. Due to the paucity of such studies, there is an immediate need for attention to coastal and mangrove forest obligate species in studies of species persistence, habitat availability and suitability, exploitation, and studies of genetic variation in obligate resident species (e.g., conservation genetics).

One such group for which almost no information is known for conservation status assessment is the spectacularly colorful and morphologically distinctive sailfin lizards of the genus *Hydrosaurus*; *Hydrosaurus pustulatus* is already considered vulnerable (A2acd + 4acde; IUCN, 2012) as a result of habitat loss. Sailfin lizards have a Wallacean distribution, occurring from Sulawesi and the Philippines to Papua New Guinea (Fig. 1B), and inhabit vegetation and coastal forests immediately adjacent to beaches, or surrounding low-lying rivers (less than a few hundred meters in elevation), on the banks of estuarine areas, deltas, river mouths, and in mangroves. Tightly linked to riparian habitats in lowland coastal and mangrove forests, hydrosaurids occur in moderate to high densities in suitable habitats but are conspicuously absent when their specific habitats are removed (*personal observations*). With their required habitat severely threatened, sailfin lizards represent an urgent need for conservation genetics studies.

Two additional concerns accentuate the conservation urgency for members of the genus *Hydrosaurus*. First, the taxonomy of the group is unresolved and has never been the subject of a systematic study using genetic data or modern phylogenetic methods. Originally described in the 1800s, the species' original descriptions are brief, based on specimens that were immature at the time of original preservation, and are non-diagnostic by modern standards, further hindering efforts to determine species boundaries and taxonomic management units. Finally, with their striking dorsal crests, conspicuous caudal sail-like structure, and brightly colored, aesthetically pleasing ornate coloration (Fig. 1A), hydrosaurids are heavily exploited in the local and international pet trade (Gaulke, 1998; Welton et al., 2012, 2013a; E. Sy, *personal communication*). This exploitation creates a potentially exacerbating situation given the already tenuous prospects for continued survival of these species.

We undertook the present study in order to provide more information for conservation planning and to characterize the conservation status and urgency for these largely unstudied species of suspected high conservation importance. We (1) screened multilocus genetic data for divergent lineages (likely conservation targets)

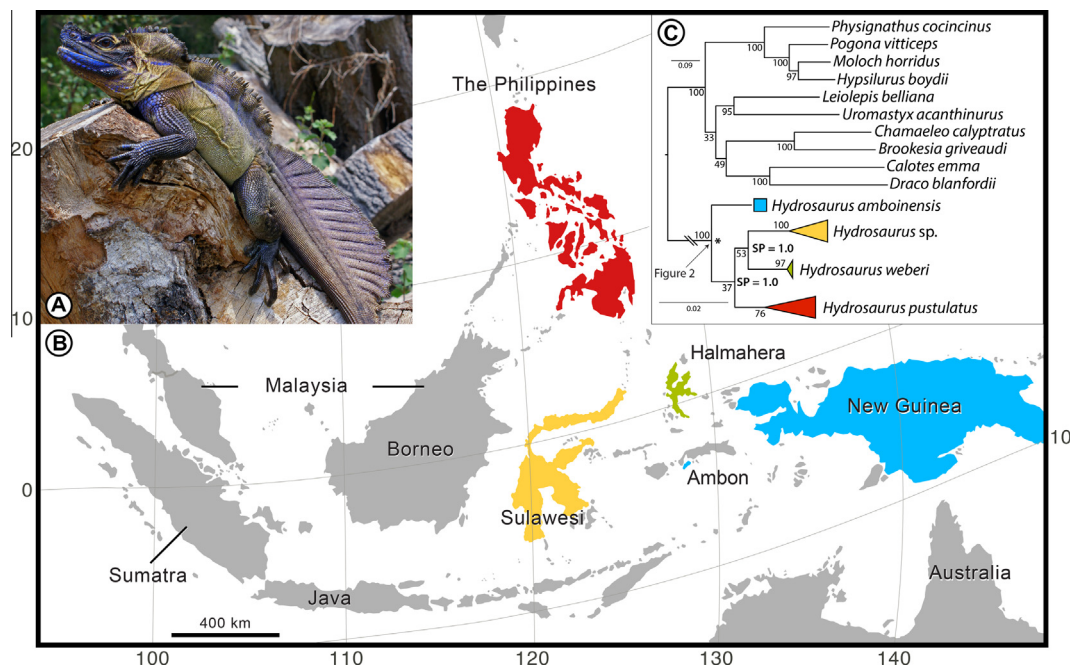


Fig. 1. (A) Photograph of *Hydrosaurus* sp. provided by Scott Corning. (B) The known distribution of sailfin lizards. (C) Simplified phylogenetic estimate inferred from the analysis of one mitochondrial and three nuclear genes, and summary of Bayesian species delimitation (BPP) analyses for the genus *Hydrosaurus* (with BPP speciation probability values on representative nodes). No nuclear data are available for the unvouchered sample of *Hydrosaurus amboinensis*, and therefore, this species was not included in BPP analyses (node highlighted with asterisk). *Hydrosaurus* sp. refers to the sampled population on Sulawesi.

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