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Taxonomic revision of the semi-aquatic skink *Parvoscincus leucospilos* (Reptilia: Squamata: Scincidae), with description of three new species

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Abstract

We review the recent discovery of multiple populations of the enigmatic, semi-aquatic Sphenomorphus Group skink, Parvoscincus leucospilos Peters, and investigate the morphological and genetic diversity of isolated, allopatric populations of this unique skink. Our investigations support the recognition of four unique evolutionary lineages distributed across Luzon Island in the Philippines, three of which are herein described as new species (*P. tikbalangi* sp. nov., *P. manananggalae* sp. **nov.**, and P. duwendorum sp. nov.). All four recognized species are genetically divergent in both mitochondrial and nuclear DNA sequences, and morphologically distinct. The description of three new Luzon Island endemic species adds to the growing body of literature suggesting that mechanisms driving the accumulation of vertebrate diversity in the Philippines may vary regionally across the archipelago.

Key words: biodiversity, conservation, cryptic diversity, endemism, lizard, Luzon Island, riparian, Southeast Asia, Sphenomorphus group

Introduction

Recent studies have revealed that our understanding of amphibian and reptile diversity in the Philippines is vastly underestimated (Brown et al., 2013a). Phylogeny-based studies focused on species delimitation have identified and revised numerous species complexes within the Philippines (Brown and Guttman, 2002; Brown et al., 2009, 2010; Siler et al., 2010a,b, 2011a,b, 2012; Siler and Brown, 2010; Welton et al., 2009, 2010a,b; Linkem et al., 2010a,b; Linkem and Brown, 2013); many of these complexes were once considered by taxonomists to be widely distributed species (e.g., Leviton, 1963; Brown and Alcala, 1970, 1980). More recent studies, fueled with evidence documenting high levels of genetic divergence between isolated evolutionary lineages repeatedly have found that few endemic Philippine reptiles actually possess broad distributions spanning regionally recognized faunistic boundaries (Brown and Diesmos, 2009; Brown et al., 2013a; Linkem and Brown, 2013). Although molecular data have had a tremendous impact on the discovery and identification of unique biodiversity in the archipelago, extensive survey work has resulted in the rediscovery of several enigmatic reptile species (Eutropis bontocensis Taylor [Barley et al., 2013], Brachymeles elerae Taylor [Siler, 2010], B. pathfinderi Taylor [Siler et al., 2011c], Hologerrhum philippinum Günther (McLeod et al., 2011; Brown et al., 2013b), Platymantis polillensis Taylor and P. cornutus Taylor (Siler et al., 2011c; Brown et al., 2012, 2013b). These rediscoveries have resulted in a better understanding of the ecology and distribution of these putatively rare species, and in many cases, revealed that they are not in fact rare, simply misunderstood or with previously unappreciated microhabitat preferences. The rediscovery and phylogenetic assessment of the Philippine endemic, semi-aquatic skink Parvoscincus leucospilos Peters, 1872 (Brown et al., 2000, 2013; Linkem et al., 2011; McLeod et al., 2011; Siler et al., 2011d) is exactly one such situation.

still vastly underestimate reptile diversity in this geographically dynamic island nation. Not only will future studies undoubtedly discover and describe additional species of skinks, but, as we approach a more accurate understanding of the country's taxonomic diversity for various species groups, researchers will be able to begin questioning broad-scale mechanisms of diversification (Brown *et al.*, 2013a). For example, what are the mechanisms driving the disparate accumulation of biodiversity in different regions of the archipelago? Considering scincid lizards alone, why does the Luzon faunal region possess by far the highest species richness in the archipelago (Linkem and Brown, 2013; Davis *et al.*, in press)? Studies focused on the mechanisms driving the assembly and evolution of vertebrate communities are poignant topics for future investigation (Brown *et al.*, 2013a).

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