Blindsnake evolutionary tree reveals long history on Gondwana

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They feed on small social insects (ants, termites and their larvae), and do so on a frequent basis (Cundall & Greene 2000). They include the smallest snakes and rarely exceed 30 cm in length (Hedges 2008). Most species have greatly reduced eyes and head scalation, a pinkish or brownish, tubular-shaped body with smooth scales, and are frequently mistaken for earthworms by non-scientists. Scolecodophiids are distributed on all continents except Antarctica, but most species inhabit the southern continents and tropical islands (Uetz et al. 2010).

Scolecodophiids include approximately 400 species divided into three families: Anomalepididae (anomalepidids, approx. 17 species), Leptotyphlopidae (threadsnakes, approx. 120 species) and Typhlopidae (blindsnakes, approx. 260 species) (Adalsteinnsson et al. 2009; Uetz et al. 2010). All three occur in the New World tropics, with the anomalepidids restricted to that region. Threadsnakes also occur in Africa, Arabia and southwest Asia, whereas blindsnakes are even more broadly distributed, occurring in Africa, Madagascar, southeastern Europe, southern Asia and Australia (Adalsteinnsson et al. 2009). Remarkably, for a lineage of terrestrial vertebrates, only two higher level scolecodophid phylogenies are available. The first one is an unpublished PhD dissertation based on an analysis of mostly internal anatomy (Wallach 1998). The second is a recent molecular study of threadsnakes using sequences of nine mitochondrial and nuclear genes (Adalsteinnsson et al. 2009).

Snakes in general and scolecodophidians in particular have a Gondwanan origin (Vidal et al. 2009). Threadsnakes originated on West Gondwana (Africa and South America), as did anomalepidids (Adalsteinnsson et al. 2009). The wide distribution of blindsnakes on Gondwana, and their fossorial (burrowing) habits, suggests that continental drift influenced the early evolutionary history of this family as well. However, they lack a significant fossil record and therefore details are unclear. Did oceanic dispersals also occur? If so, which continents were occupied by blindsnakes ancestrally and which ones were colonized later by dispersal? These are questions that we address here with a new molecular dataset.

2. MATERIAL AND METHODS

We constructed a molecular dataset for 96 scolecodophid species from the three recognized families, with detailed sampling of the largest family, Typhlopidae. The dataset comprised of five nuclear protein-coding genes (recombination-activating gene 1: RAG1, amelogin: AMEL, brain-derived neurotrophic factor: BDNF, neurotrophin 3: NT3 and bone morphogenetic protein 2: BMP2) for 101 taxa (85% of the sequences were newly determined, i.e. 402 sequences that have been deposited in GenBank under accession numbers GU902304–GU902705). Phylogenies were built using probabilistic approaches (maximum-likelihood (ML) and Bayesian inferences) and dating analyses were performed according to the Bayesian relaxed molecular clock approach (figure 1; electronic supplementary material).

3. RESULTS AND DISCUSSION

The resulting ML and Bayesian phylogenetic trees show remarkable consistency. Among Scolecodophia, five main clades diverged in the Jurassic and Cretaceous, between 159 (154–167) and 97 (112–81) Myr ago: these are (i) anomalepidids; (ii) threadsnakes; (iii) Typhlops hedraeus (Philippines) and Typhlops mirus...
Figure 1. (Caption opposite.)
The earliest divergence in the typhlopoid tree (figure 1). The subsequent split of East and West Gondwana. The putative origin of the East Gondwanan typhlopoids can be inferred from the palaeolandmass of Indigascar, it can be inferred that the split between typhlopoids and Gerrhopilidae occurred on this landmass. Myr ago (this study). Because West Gondwana drifted from East Gondwana (Antarctica, Madagascar, India and Australia) 166—116 Myr ago (Ali & Atchison 2008) and the basal typhlopoid lineages are present on Indo-Madagascar (163–136) Myr ago (Vidal et al. 2009). Within this group, the Australian radiation is relatively recent, 28 (19–39) Myr ago, and apparently reached Australia by oceanic (flotsam) dispersal from Southeast Asia or Indonesia. Another insular radiation occurred in the West Indies, originating by dispersal from South America during the mid-Cenozoic, 33 (44–23) Myr ago, as did the vast majority of West Indian terrestrial vertebrates (Hedges 2006). Finally, because all major splits among typhlopids are more recent than 63 (49–78) Myr ago, and because Africa broke from South America 100 Ma, only westward—not eastward—transatlantic dispersal can explain the presence of blindsnakes in South America. Until now, only six or seven transatlantic events were known in terrestrial vertebrates, all following the prevailing westward water currents (Vidal et al. 2008; Adalsteinsson et al. 2009). Transatlantic journeys during the Cenozoic would have taken at most six months (Houle 1999), not an insurmountable task for vertebrates with a low food requirement and most likely travelling along with their invertebrate prey. Our molecular timing results support the conclusion that oceanic dispersal should not be dismissed as a possible biogeographical mechanism for organisms that otherwise appear to be poorly adapted for an overseas journey (Vidal et al. 2008). Thus, blindsnakes—and scolecophidians in general—have had a long evolutionary history that has been influenced by both continental drift and ancient ocean currents.

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