

DIVERSITY OF THE SERPENT FAUNA IN CENTRAL AFRICA: FROM FIELD SURVEYS TO INTEGRATIVE SYSTEMATICS

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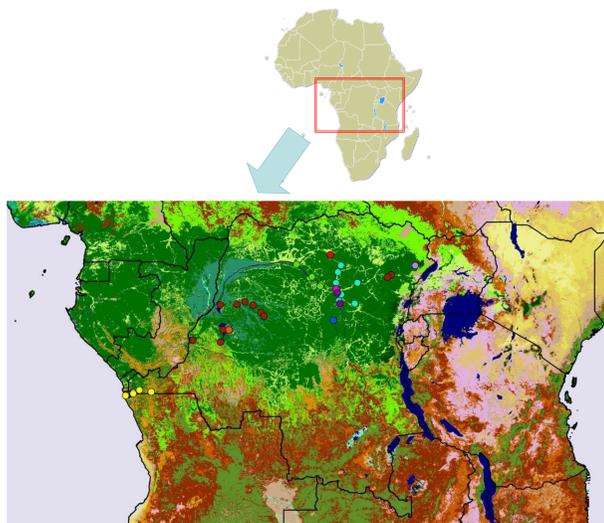


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Context

The Congo Basin hosts the second largest continuous tropical rainforest on Earth. The largest country in Central Africa, the Democratic Republic of the Congo (DRC), has 14 ecoregions according to WWF and hosts over 330 species of non-avian reptiles, including ca. **180 species of snakes**. Until recently, however, the exploration of the Congo was hindered due to its inaccessibility. Hence, its herpetofauna remained poorly explored in an integrated way including genetic methods. In this context, in 2010 we started herpetofaunistic surveys, a DNA barcoding campaign and integrative taxonomic studies focusing on the serpent fauna of this intriguing region.

Material, methods and aims

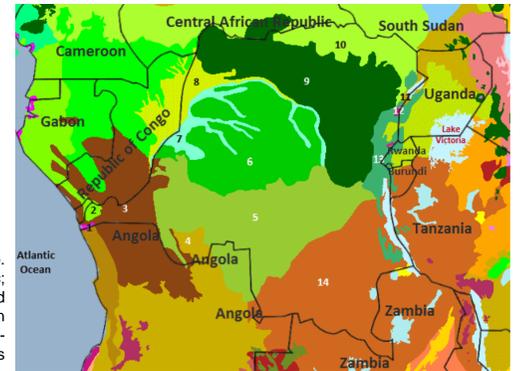


- Ecoregions of the Democratic Republic of the Congo.
1. Central African mangroves; 2. Atlantic Equatorial coastal forests; 3. Western Congolian forest-savannah mosaic; 4. Angolan Miombo woodlands; 5. Southern Congolian forest-savannah mosaic; 6. Central Congolian lowland forests; 7. Eastern Congolian swamp forests; 8. Western Congolian swamp forests; 9. Northeastern Congolian lowland forests; 10. Northern Congolian forest-savannah mosaic; 11. East Sudanian savannah; 12. Ruwenzori-Virunga montane moorlands; 13. Albertine Rift montane forests; 14. Central Zambebian Miombo woodlands

Snakes were collected at various localities across the country (see map left; different colors represent different surveys). We established a large collection of preserved voucher specimens. In addition, tissue samples and DNA extracts are available for genetic studies. So far, we analyzed **>700 specimens** of ca. **90 species** of snakes. First, we completed a large-scale **DNA barcoding** study to assess genetic divergence of Congolese reptiles, including snakes.

Second, we analyzed the **phylogeographic structure** of some widespread species.

Third, we started to reconstruct **higher-level phylogenies** of selected African snake lineages using genomic data.

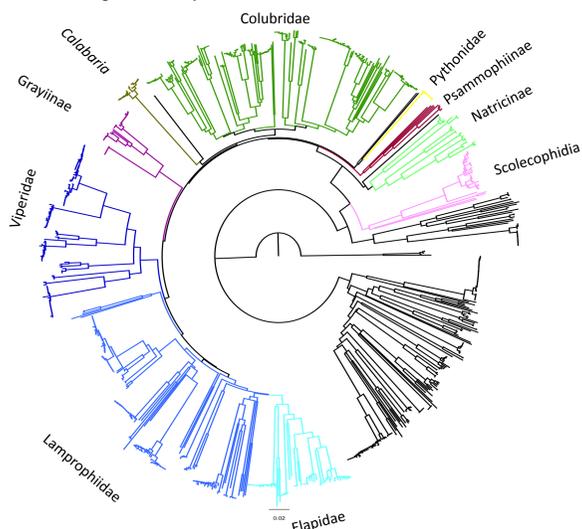


Above: *Naja melanoleuca* (Elapidae); Top right: *Bothrophthalmus lineatus* (Lamprophiidae); middle right: *Thelotornis kirtlandii* (Colubridae); bottom right: *Calabaria reinhardtii* (Calabariidae)

Results

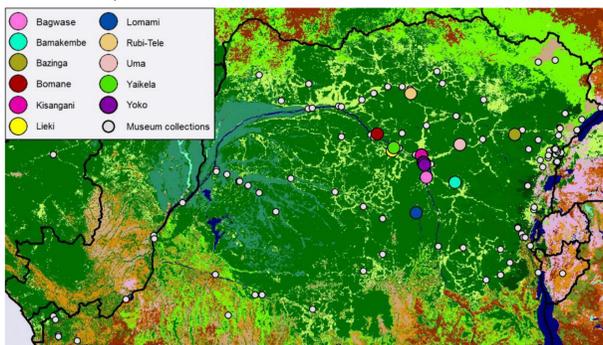
1) DNA barcoding

- ca. 900 samples of reptiles from Central Africa sequenced
- Snakes are marked in colors
- Lineages are easy to delineate

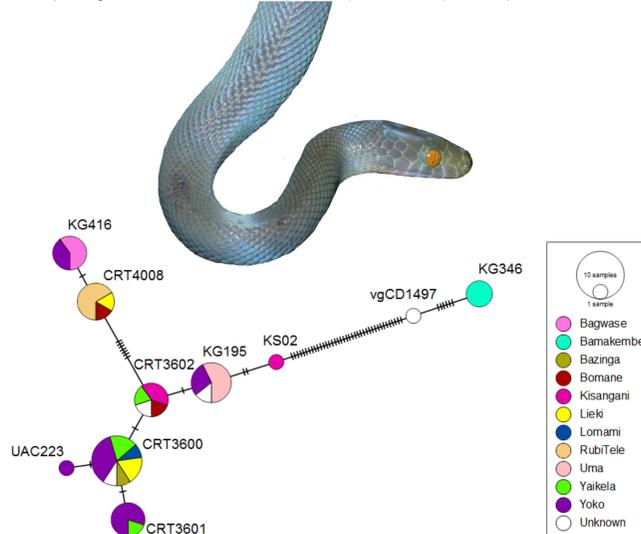


2) Phylogeography

- An example of a common African species: *Boaedon olivaceus* (Olive house snake), Lamprophiidae
- We sequenced the mitochondrial COI marker



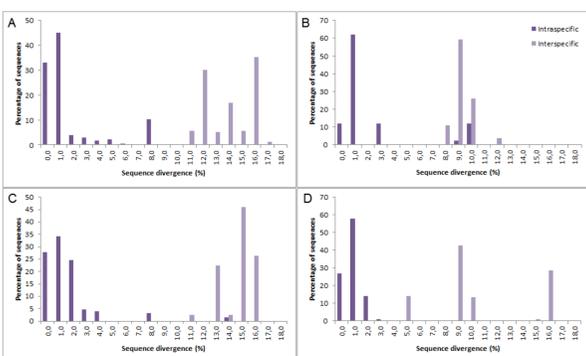
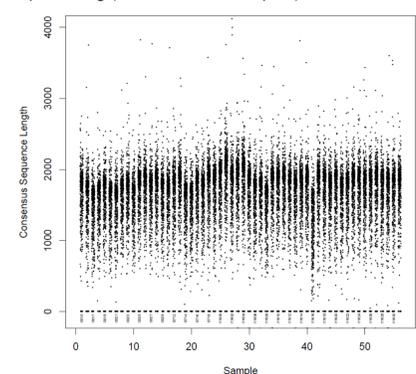
Geographical distribution of the *Boaedon olivaceus* specimens in our COI dataset. Small grey circles indicate historical voucher specimens deposited in the herpetological collections of RBINS (Brussels) and RMCA (Tervuren).



COI haplotype network of *Boaedon olivaceus*

3) Phylogenomics

- Four studies are in progress, all relying on anchored phylogenomics *sensu* Lemmon et al. (2012): phylogenomics of African Natricinae, African Colubridae, Lamprophiidae and water cobras
- Even more degraded DNA samples yield good results; capture, library prep and sequencing seem to work well
- Preliminary results of sequence assembly are promising (see below, 56 samples):



Intraspecific (dark purple) and interspecific (light purple) genetic distances in different snake families. A: Colubridae (n=25 species, 195 sequences), B: Elapidae (n=6 species, 48 sequences), C: Lamprophiidae (n=18 species, 146 sequences), D: Viperidae (n=7 species, 105 sequences)

Conclusions

According to our results, most snake species are easy to distinguish with mitochondrial sequences, and intraspecific divergences appear modest. However, some common and widespread serpent species showed unexpectedly high divergence. Selected snake taxa should be further analyzed in an integrative systematic context, benefiting from novel approaches of species tree inference and phylogenomics. Our results may lead to alter current classification and challenge the biogeographic interpretation of apparently widespread Afrotropical taxa.

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