SNAKES OF THE WORLD

Recent Discoveries & Research Perspectives

Abstracts of the First World Congress on Snakes

1-4 October 2026

Kandy, Sri Lanka

Compilers

Anslem De Silva

Muhammad Rais

Nimal D. Rathnayake

Suranjan Karunarathna

Kanishka D.B. Ukuwela

WCS 2026 SRI LANKA

boundaries. I also discuss more broadly in how this approach reframes snakes as a powerful system for investigating macroevolutionary patterns, showing how integrating legacy collections with genomic data enables more accurate inferences of biodiversity through time.

Keywords: Snakes, Historical DNA, Ancient DNA, Phylogenomics, Australasia, Lycodon, Stegonotus

A 30 - Ryabov *et al*.

Mitophylogeny of the Genus *Boiga* Reveal Hidden Diversity of *B. cyanea* from Southeast Asia

*S. A Ryabov[1], M. Matsiushova[1,2], O.S. Bezman-Moseyko[2], A.O. Svinin[3], N.B. Ananjeva[2]

[1] Moscow Zoo, Moscow, Russia
[2] Zoological Institute, Russian Academy of Sciences, St. Petersburg, 199034, Russia
[3] Institute of Cytology, Russian Academy of Sciences, St. Petersburg, 194064, Russia

sergryabov@mail.ru

The genus *Boiga* includes 37 species with high species diversity in South-East Asia. One of them, the green cat snake, *Boiga cyanea*, occurs in Bhutan, Cambodia, China, India, Laos, Peninsular Malaysia, Myanmar, Nepal, Thailand, and Vietnam. Several phylogenetic reconstructions suggest that *B. cyanea* may comprise multiple cryptic species. Despite the availability of a complete genome, genetic data are represented by only a few sequences. A total of four *B. cyanea* specimens from Vietnam: Côn Sơn and Hòn Cầu Islands (Con Dao archipelago), Nghệ An Province and mainland Southern Vietnam were examined using molecular methods. The Bayesian inference (BI) and Maximum likelihood (ML) phylogenetic analyses were performed based on mitochondrial DNA sequences (*cytb* and *COI*). Mitophylogeny results support the presence of three distinct genetic lineages. The genetic divergence among these lineages was further supported by uncorrected *p*-distances, which ranged from 6.7% to 7.6% for *cytb* and from 4.2% to 5.5% for *COI.* The first lineage includes specimens from Vietnam (Côn Đảo, Hòn Cầu and MN961964-7); the second comprises those from Nghệ An Province and mainland Southern Vietnam, and the third contains specimens from Myanmar (MT607992-3) and Vietnam (MN961962-3). The genetic distances allow these lineages to be considered as subspecies. However, it must be acknowledged that mitochondrial markers alone provide a limited perspective on evolutionary relationships and further analyses based on nuclear genes will shed light on the taxonomy of the species.

Keywords: Mitophylogeny, Genus *boiga, Boiga cyanea,* Southeast Asia

This research was supported by a grant from the Russian Science Foundation No. RSF-VAST 24-44-04004 (https://rscf.ru/project/24-44-04004).

A 31 - Shanker

Molecular Phylogeny and Multivariate Morphometrics of the King Cobras (Serpentes: *Ophiophagus*) Reveal Multiple Cryptic Allopatric Species

P. Gowri Shanker

Kālinga Foundation, Agumbe, India.

gowrishankar.pogiri@gmail.com