

BOOK OF ABSTRACTS
10TH WORLD CONGRESS OF HERPETOLOGY
5–9 August 2024

Compiled by
Indraneil Das



World Congress of Herpetology (WCH)



Institute of Biodiversity and Environmental Conservation
Universiti Malaysia Sarawak

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94300 Kota Samarahan
Sarawak, Malaysia

2024

COMPILER'S NOTES

The 10th World Congress of Herpetology is being held at the Borneo Convention Centre Kuching, in the State of Sarawak, Malaysia, 5–9 August 2024. The Congress is organised by the World Congress of Herpetology (<https://www.worldcongressofherpetology.org>) and the Institute of Biodiversity and Environmental Conservation (<https://www.ibec.unimas.my>), Universiti Malaysia Sarawak. The event is supported by Business Events Sarawak, Ministry of Tourism, Creative Industry and Performing Arts Sarawak, Sarawak Forestry Corporation, Sarawak Biodiversity Centre, AGARK DGHT, the Institute of Agriculture, University of Tennessee (UT AgResearch) and the Society for the Study of Amphibians and Reptiles.

A total of 1,481 abstracts of oral and poster papers were received at the website of the Congress (<https://2024wch10.com>), through an online conference management system (KonferenceX Content Management System), or came in via email. Only those submitted by registered delegates were included in this book of abstracts. Poster presentations include the full spectrum of herpetological topics, including subject material corresponding to Symposia. Also included are abstracts of Plenary Lectures, Special Presentations and Official Side Events.

Abstracts were formatted and lightly edited for content and style but did not undergo a full peer review. Any new taxon descriptions or other nomenclatural acts contained in this book of abstracts and programme should not be considered published in the sense of Article 8 of the International Code of Zoological Nomenclature (1999).

We welcome all delegates to the beautiful city of Kuching, Sarawak and to the 10th World Congress of Herpetology.



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tissue samples that were either stranded or caught by accident to determine the genetic composition, genetic diversity, and the origins of these two sea turtle species by using Mixed Stock Analysis (MSA). Based on our genetic analyses, it appears that the Korean sea turtle population shares a significant number of haplotypes with nesting populations in Japan. Moreover, their genetic diversity is comparable to that of other feeding grounds in Japan. Based on these results and MSA results, it is likely that the majority of *C. mydas* and *C. caretta* in Korean waters originate from Japan's nesting grounds. However, some *C. mydas* may come from the Indo-Pacific nesting areas. These results are in line with previous satellite tracking studies of these species in South Korea. To conserve these sea turtle species effectively, it may be crucial to establish international cooperation with the countries where their nesting populations are located. This study was supported by grants from the National Marine Biodiversity Institute of Korea (2024M00300 and 2024E00300) funded by the Ministry of Oceans and Fisheries.

A-0296 (Poster)

Some like it Hot: Past and Present Phylogeography of a Desert Dwelling Gecko across the Arabian Peninsula

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Deserts represent dynamic ecosystems that support communities of endemic and often specialised species. We analysed the role of present and past climatic conditions in shaping the distribution of the widespread *Bunopus* geckos in the Arabian and south-west Asian deserts. We studied their phylogeographic and demographic history to test whether the geckos colonised Arabia from Asia or, vice versa, Asia from Arabia and to identify migration corridors that have historically enabled the dispersal of *Bunopus* geckos. We generated sequence data for four genes and performed Maximum Likelihood, Bayesian Inference and time-calibrated phylogenetic analyses and ancestral area reconstruction to infer the phylogenetic and biogeographic history of the genus. We modelled the species' distribution and projected it to several past time periods spanning from mid-Pliocene to the present. We analysed contemporary landscape connectivity across the peninsula to identify dispersal corridors that enable migration and promote gene flow among *Bunopus* populations in Arabia.

A-0297 (Poster)