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Genome structure sharing by reptiles and avians as of *Isospora* from bearded dragon and black throated laughing thrush

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The complete mitochondrial genome of *Isospora amphiboluri* and *Isospora sp. n.* (Eimeriidae, Coccidia, *Apicomplexa*) were sequenced. These coccidia infect the bearded dragon, *Pogona vitticeps* (Sauria: Agamidae) and black throated laughing thrush *Garrulax chinensis* (Aves: Passeriformes) respectively. PCR was performed post DNA extraction and protein estimation by Nanodrop. The Whole Genome was achieved in fragments and assembled. Genome organization and gene content was conventional. The circular-mapping mt genome of *Isospora amphiboluri* is 6264bp and *Isospora* sp. n. 6158bp in length consisting of 3 protein coding genes (*cox1, cox3 and cytb*), 19 gene fragments encoding large subunit (*LSU*) *rRNA* and 14 gene fragments encoding small subunit (*SSU*) *rRNA*. Like other Apicomplexan, no *tRNA* was encoded. The comparable mitochondrial genome sequences and structures of *Isospora* and *Eimeria* species confirm the close relationship between these eimeriid genera of apicomplexan parasites. Investigation of *Eimeria* genes intricate the basic biology and host-parasite interaction and highlights adaptations to a comparatively simple developmental life cycle. The purpose of this study was to sequence and annotate the complete mitochondrial genomes of *Isospora amphiboluri* and *Isospora* sp. n that commonly infect bearded dragon and black throated laughing thrush.

Biography

Mian A Hafeez has completed his Doctor of Veterinary Medicine (DVM), MPhil and his PhD from University of Agriculture, Faisalabad, Pakistan. He did his Post-doctoral studies from University of Guelph, Ontario Veterinary College, Canada and continued working for seven years as Diagnostic Molecular Parasitologist. Currently, he is working as Associate Professor (visiting, on leave from Ontario Veterinary College) in University of Veterinary & Animal Sciences, Lahore, Pakistan. He has published more than 35 papers in reputed journals and has been serving as an Editorial Board Member of repute.

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