

**POSTGRADUATE INSTITUTE OF SCIENCE
UNIVERSITY OF PERADENIYA
SRI LANKA**



PGIS RESEARCH CONGRESS 2020

PROCEEDINGS

26th - 28th November 2020

MOLECULAR PHYLOGENY AND TAXONOMY OF GENERA *Argyrodus* AND *Rhomphaea* (ARANEAE: THERIDIIDAE) IN SRI LANKA

M. Tharmarajan, N. Athukorala and S.P. Benjamin*

National Institute of Fundamental Studies, Kandy, Sri Lanka

**suresh.benjamin@gmail.com*

Comb-footed spiders are highly diverse from the perspective of species richness, morphological diversity, web architecture and behavioural repertoires. The genera *Argyrodus* and *Rhomphaea* are part of the subfamily Argyrodinae. Genus *Argyrodus* is known for their kleptoparasitism and *Rhomphaea* are solitary. A large number of endemic species from both genera remains undiscovered and unrecorded in Sri Lanka. The diversity and phylogeny of Sri Lankan species, in relation to other Asian and American species, were investigated. Field work was conducted in 40 localities representing 12 districts in Sri Lanka. One hundred and seventy (170) spiders from both genera were collected by hand or by beating vegetation. Samples were preserved in 70% ethanol for morphological study or 100% for molecular genetic analysis. Morphological identification was carried out using a stereomicroscope and published descriptions of species from the surrounding region. This was followed by detailed drawings of genitalia. Geometric morphometric analysis was conducted only for *Argyrodus* spp. Digital images of male carapace were taken and processed using tps Util and tpsDig2. Principal Component Analysis (PCA) and Canonical Variance Analysis (CVA) were conducted for digital images of male carapace using MorphoJ v 1.05 to track shape changes of male carapace. A Molecular Phylogeny of 43 Sri Lankan species from both genera with 53 Asian and American species representing six recognised genera of the subfamily Argyrodinae (32 taxa from *Argyrodus*, 17 taxa from *Rhomphaea*, 6 taxa from *Faditus*, 3 taxa from *Neospintharus* and 3 taxa from *Ariamnes*) were sequenced. The matrix of 2152bp length included fragments of three genes: two mitochondrial genes 16S rRNA (primers NIJ-12581 and LRN-12945R~536bp), COI (LCO1-1490 and HCO-2776~1067bp) and one nuclear gene 28S rRNA (28Sc and 28So~544bp). DNA sequences were edited and aligned using Genious 11.1.5 and Mesquite v 3.51. Partition finder was used to determine appropriate model for each partition. Maximum-likelihood (ML) tree was inferred with RaxML and Bayesian analysis on MrBayes. Consensus trees of both Bayesian and ML analysis supported the monophyly of *Rhomphaea*, while *Argyrodus* was paraphyletic. Sri Lankan *Argyrodus* species were recovered in five clades. Morphometric analysis of carapace shape also supported to distinguish the corresponding clusters of *Argyrodus*. Species level identification of both genera was strongly supported by the drawings of their genitalia. Under genus *Argyrodus* five species were diagnosed, and among them, three species (*A. antipodinus*, *A. flavescens*, *A. nasutus*) were previously described by Pickard O. Cambridge in 1880 while the other two were new species. Further, the present study records the genus *Rhomphaea* for the first time in Sri Lanka with four new species.

Financial assistance from the National Institute of Fundamental Studies is acknowledged.

Keywords: *Argyrodus*, Molecular, Phylogeny, *Rhomphaea*, Sri Lanka