A PRELIMINARY STUDY ON THE PHYLOGENY OF TWO CLOSELY RELATED CRAB SPIDER GENERA IN SRI LANKA (ARANEAE: THOMISIDAE)

I.S. Ileperuma Arachchi, N. Athukorala and S.P. Benjamin*

National Institute of Fundamental Studies, Hantana Road, Kandy, Sri Lanka
**suresh.benjamin@gmail.com*

Thomisidae is the sixth largest family of spiders with 2155 species worldwide placed in 175 genera (World Spider Catalog 2017). Thirty six species of crab spiders are currently recorded from Sri Lanka. Members of the Genera *Tmarus* and *Peritraeus* are morphologically very similar and difficult to identify without thorough observation. *Peritraeus* was thought to be endemic to Sri Lanka, while *P. hystrix* is the only species of this genus, recorded from Sri Lanka about 127 years ago. This species was rediscovered from Kandy (its type locality) through this study. *Tmarus* is a specious genus that contains 222 species distributed worldwide and, only 38 species were described in the Asian region. The objective of this study was to assess the monophyly of *Peritraeus* and its relationship to *Tmarus* using a multi locus molecular phylogeny of these two genera, close relatives and representatives of other branches of the thomisid tree of life using a multi-locus molecular approach. Field work was conducted in 80 localities covering 20 districts in Sri Lanka with the aim of maximizing the number of species collected from 2015-2016. Beating and hand collection were used for collection. Specimens were preserved in 70% and/or 100% ethanol. A total of 31 males and 43 females were collected. Two species of *Peritraeus* and two species of *Tmarus* were recorded (*Peritraeus* sp. B: 17, *Peritraeus* sp. C: 21, *Tmarus* sp. A: 27, *Tmarus* sp. E: 19). DNA was extracted from two legs of each specimen. DNA extraction was performed using Qiagen DNeasy Tissue kit. PCR was carried out in total reaction mixture of 20 µL. Partial fragments of nuclear Histone 3(H3) and 28S r DNA (28S) and mitochondrial genes, cytochrome *c* oxidase subunit 1(COI) and a spanning section from 16S to NADH dehydrogenase subunit 1 and (16S-NAD1) were amplified. Twenty six ingroup and eleven outgroup taxa were included in the final analysis. Sequences were edited and assembled using Geneious 6.1.5 software package and further edited manually using Mesquite (version 2.72). Maximum-likelihood (ML) tree was inferred with MEGA ver. 6.06) with GTR+G+I model. The analysis of the combined data set (1833 bp) recovered a monophylectic *Tmarus* (Bootstrap value = 54). Further, the ML analysis suggests that *Peritraeus* is a clade within *Tmarus*. Thus, it is concluded that *Peritraeus* should be transferred to *Tmarus*. Further, three species of *Tmarus* new to science, discovered during this study will be formally described in a future publication.

Financial assistance from National Science Foundation of Sri Lanka (Grant No.: RG/2015/EB/04) is acknowledged.

Keywords: Crab spider, *Peritraeus*, Sri Lanka, Thomisidae, *Tmarus*,