



Morphological and molecular analysis to characterize members of Phlebotomus (Euphlebotomus)

argentipes complex; the potential vector for leishmaniasis in Sri Lanka.

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ABSTRACT

The most vulnerable persons are affected by leishmaniasis. From 2009 to 2016, almost a thousand leishmaniasis cases were reported in the Hambantota and Anuradhapura districts. During this time, more than 500 cases were documented in the districts of Matara, Kurunagala, and Polonnaruwa. The current study looked at the diversity of the *Phlebotomus* (*Euphlebotomus*) argentipes species complex in both endemic and non-endemic locations in Sri Lanka. From 2015 to 2018, samples were collected utilizing a cattle baited hut, cattle baited net, and a mouth aspirator in the districts of Anuradhapura, Hambantota, Puttalam, and Jaffna, as well as the connected islands (Delft and Pungudutivu). The taxonomy proposed by Ilango (2000), which is based on the sensilla chaetica (SC2) and second antennal flagellomere (AF2) ratio, was used to differentiate Sri Lankan male morphospecies. Ilango's most recent classification (2010) was found to be incompatible with Sri Lankan male morphospecies. DNA sequencing data validated the morphospecies identification. Primer sets were created to target a certain COI region. The constructed phylogenetic tree demonstrates that the Argentipes complex has two genetically distinct groupings. One has a SC2/AF2 ratio of less than 0.4, while the other has a ratio of 0.45 and higher. Based on COI sequencing data, it was shown that there are only two genetically distinct groups in the *Phlebotomus* (*Euphlebotomus*) argentipes male species complex, although three morphospecies exist with minor phenotypic differences.

Key words: Morphology analysis, molecular analysis, *Phlebotomus* (Euphlebotomus) argentipes, Argentipes complex, Leishmaniasis.

Recommendation of authorized person

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