Molecular identification of potential leishmaniasis vector species within the Phlebotomus (Euphlebotomus) argentipes species complex in Sri Lanka

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Abstract

Background: Leishmaniasis is an emerging vector-borne disease in Sri Lanka. Phlebotomus (Euphlebotomus) argentipes sensu lato Annandale and Brunette 1908 is suspected to be a potential vector. Three sibling species have been reported in the species complex based on analysis of morphological data. A study was carried out in different parts of Sri Lanka including cutaneous leishmaniasis prevailing localities to characterise the sibling species of Phlebotomus (Euphlebotomus) argentipes sensu lato and to establish their possible role in Leishmania transmission. Methods. Sandflies were collected using cattle baited trap nets and mouth aspirator. They were identified based on existing taxonomic keys. Sequences of amplified cytochrome oxidase subunit I (CO I), cytochrome oxidase b (cyt b), internal transcribed spacer 2 (ITS2), 18s and 28s rDNA regions were analysed to confirm the number of sibling species. Vectorial capacity of the sibling species was checked by detecting human and Leishmania DNA. Results: Sandflies collected using different techniques were processed for identification, parasite detection and molecular characterization. The 18s, 28s rDNA and cytochrome oxidase subunit I (CO I), internal transcribed spacer 2 (ITS2) and cytochrome b oxidase (cytb) sequences confirmed that the species belonged to the Argentipes complex. 18s and 28s sequences did not show any variation among the proposed sibling species. The phylogeny created from mitochondrial CO I and cytochrome b data and from the nuclear ITS2 region supports the existence of only two groups of flies (termed A and B) from Phlebotomus (Euphlebotomus) argentipes complex instead of the previously proposed three. The Leishmania mini-circle kinetoplastid, heat shock protein 70 (hsp70) and internal transcribed spacer I DNA along with human blood were detected from sibling species A only, which has not previously been considered to be a vector. Conclusions: The taxonomy of the Sri Lankan Argentipes species complex is reassessed based on the molecular data. The existence of two sibling species is proposed; sibling species A has a long sensilla chaetica (> 50% length of the second antennal flagellomere) and sibling species B has a short sensilla cheatica (< 50%). Sibling species A is incriminated as a vector for leishmaniasis in Sri Lanka.

Author keywords

Argentipes complex; Leishmaniasis; Sibling species; Sri Lanka; Vector

Indexed keywords

EMTREE drug terms: cytochrome b; cytochrome c oxidase; DNA 18S; DNA 28S; heat shock protein 70; internal transcribed spacer 2; oxidoreductase; ribosome DNA; unclassified drug

EMTREE medical terms: amino acid sequence; article; controlled study; gene sequence; Kinetoplastida; Leishmania donovani; nonhuman; parasite identification; Phlebotomus argentipes; phylogeny; sibling; skin leishmaniasis; species identification; taxonomy

Species Index: Bos; Kinetoplastida; Phlebotominae; Phlebotomus argentipes