

Introduction: *Phlebotomus argentipes* is the vector of *Leishmania donovani* which causes the disease leishmaniasis, a neglected tropical disease and a growing health problem in Sri Lanka. A proper understanding of the population genetic structure of sand fly vectors is considered important prior to planning and implementation of a successful vector control program. Thus, the present study was conducted to determine the population genetic structure of sand fly vectors in Sri Lanka.

Methods: DNA was extracted from individual sand flies ($n \leq 10$ per site) followed by PCR amplification using two mitochondrial genes namely Cytochrome c oxidase subunit 1 (Cox 1) and Cytochrome b (Cytb), and the internal transcribed spacer 2 (ITS2) region from the nuclear ribosomal DNA and sequencing. Analyses included maximum likelihood method, network analysis and DNA polymorphisms.

Results: The outcome revealed that the cox 1 gene had a relationship with sand flies isolated previously from Sri Lanka, India and Israel. The sequences from cytb gene of 4 sand flies that aligned with those isolated earlier from Sri Lanka and 3 from Madagascar. Furthermore, cox 1 gene and ITS 2 region analyses based on F_{ST} values indicated a possible gene flow between the study sites whereas cytb gene analysis favoured the existence of genetically distinct populations of *P. argentipes* in each of the study sites.

Conclusion: Poor population differentiation of *P. argentipes*, a possible consequence of a gene flow, is indeed of concern due to the risk imposed by promoting the spread of functionally important phenotypes such as insecticide resistance across the country, making future vector control efforts challenging.