Sri Lankan Society for Microbiology
12th Annual conference and scientific sessions 2023

SLJID 2023 Vol 13 (Supplement) S5:
DOI: https://doi.org/10.4038/sljid.v13i5.8634

Phylogenetic analysis of spotted fever causing rickettsiae in humans

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Introduction and Objective(s): Spotted fever (SF) group rickettsioses is caused by rickettsial species. This meta-analysis aimed to gather all confirmed pathogens that cause spotted fever rickettsioses in humans and evaluate their taxonomic relationships.

Methods: A systematic review was conducted on all types of articles that report on spotted fever in humans available in the electronic databases PubMed and ScienceDirect and published in the English language from 2000 to 2023. Grey literature and reference lists of the selected studies were manually examined for relevant articles. All retrieved abstracts were collated, and duplicates removed using Rayyan Intelligent Reviews web software. Titles and abstracts were screened according to the inclusion criteria. (ie: experimental research based on the topics, systematic reviews, meta-analysis, retrospective case–control studies, and case reports that mentions spotted fever causing pathogens up to species level). In vitro studies and studies conducted on animals were excluded. Year of publication, species or strains of SF causing organisms, and country, were extracted from selected studies. The nucleotide sequences of the 16s rRNA and OmpA genes of the species identified in the search were obtained from the National Center for Biotechnology Information database. A multiple sequence analysis was performed using Clustal W, and a phylogenetic tree was constructed using MEGA version 7.

Results: A total of 1276 articles were initially identified, of which 68 duplicates were removed, leaving 1208 unique articles. Following the study criteria, 870 articles were excluded by screening title and abstract. By in-depth review of the remaining 338 articles, 43 strains responsible for causing spotted fever group rickettsiosis were identified. Of these 43 strains, 16s RNA nucleotide sequences were available for 37 strains and OmpA gene sequences were available for 38 strains. The sequence logos and phylogenetic trees were constructed. The rickettsia strains responsible for SF were found to belong to four clades based on the analysis of phylogenetic trees.

Conclusion: The analysis of 16s rRNA and OmpA gene sequences revealed that the strains responsible for causing spotted fever are closely related and belong to four clades.

Keywords: Spotted fever group rickettsiosis, Human infection, Causative organisms, Phylogenetic tree

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