

Distribution of Spotted Fever Group in Ixodid Ticks, Domestic Cattle and Buffalos of Faisalabad District, Punjab, Pakistan

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Abstract : Rickettsiosis, caused by a Spotted Fever Group Rickettsiae (SFGR), is considered as an emerging infectious disease from public and veterinary perspective. The present study reports distribution of SFGR in the host (buffalo and cattle) and vector (ticks) population determined through gene specific amplification through PCR targeting outer membrane protein (ompA). Tick and blood samples were collected using standard protocols through convenient sampling from district Faisalabad. Ticks were dissected to extract salivary glands (SG). Blood and tick SG pools were subjected to DNA extraction and amplification of ompA using PCR. Overall prevalence of SFGR was reported as 21.5% and 33.6 % from blood and ticks, respectively. *Hyalomma anatolicum* was more prevalent tick associated with SFGR as compared to *Rhipicephalus* sp. Higher prevalence of SFGR was reported in cattle (25%) population as compared to that of buffalo (17.07%). On seasonal basis, high SFGR prevalence was recorded during spring season (48.1%, 26.32%, 17.76%) as compared to winter (27.9%, 21.43%, 15.38%) in vector and host (cattle and buffalo respectively) population. Sequencing analysis indicated that rickettsial endo-symbionts were associated with ticks of the study area. These results provided baseline information about the prevalence of SFGR in vector and host population.

Keywords : Rickettsia, livestock, polymerase chain reaction, sequencing, ticks, vectors

Conference Title : ICE 2018 : International Conference on Entomology

Conference Location : Paris, France

Conference Dates : October 29-30, 2018