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Distribution of spotted fever group in ixodid ticks, domestic cattle and buffalos of Faisalabad District, Punjab, Pakistan

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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% and 17.76%) as compare to winter (27.9%, 21.43% and 15.38%) in vector and host (cattle and buffalo, respectively) population. Sequencing analysis indicated that rickettsial endosymbionts were associated with ticks of the study area. These results provided baseline information about the prevalence of SFGR in vector and host population.

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