

environmental and skin contaminants; however, *Brevundimonas nasdae* was detected in 3 out of the 6 FPLIs (50%), in addition to all of the aforementioned flora using the single assay detection protocol. Overall, the distribution of flora in ulcers of severe ($n=2$) and non-severe phenotypes ($n=4$) did not differ ($p=1.000$).

Conclusion: CL ulcers with a secondarily-infected phenotype are universally treated with broad-spectrum antibiotics, often without microbiological confirmation of presence of bacterial pathogens. Therefore, understanding the presence and complement of bacterial potential pathogens in ulcers of CL has implications for antimicrobial stewardship and evidence-based management strategies. WGS enables detection and identification of the full range of organisms present in the microbiome of the CL ulcer. Further prospective analysis, including additional WGS studies of CL ulcers, is necessary to determine the role of empiric antibiotic therapy in CL ulcers with an inflammatory phenotype.

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Risk factors for Crimean-Congo hemorrhagic fever virus infection in Livestock in Pakistan



K.K. Kasi^{1,*}, M.A. Sas², C. Sauter-Louis¹, J.M. Gethmann¹, M.H. Groschup², F.J. Conraths¹

¹ Friedrich-Loeffler-Institut, Greifswald- Insel Riems, Germany, Institute of Epidemiology, Greifswald/DE
² Friedrich-Loeffler-Institut, Greifswald - Insel Riems, Germany, Institute of Novel and Emerging Infectious Diseases, Greifswald/DE

Purpose: Crimean-Congo hemorrhagic fever (CCHF) is a severe, often lethal viral disease in humans caused by the arbovirus Crimean-Congo hemorrhagic fever virus (CCHFV). It is mainly transmitted to humans and animals by Ixodid ticks of the genus *Hyalomma*. The epidemiological situation regarding CCHFV in livestock is important for assessing the potential risk of exposure of the human population to this virus.

Methods & Materials: A cross-sectional study was conducted to study potential risk factors for CCHFV infections in livestock animals of the region Balochistan, Pakistan. Blood samples were collected from 1600 sheep and goats in Quetta, Sibi and Zhob divisions of Balochistan from July to September 2016. Farm and animal-related information was collected in interviews using a standardized questionnaire. Pools containing five serum samples each were tested for CCHFV genome fragments by reverse transcription quantitative real-time polymerase chain reaction (RT-qPCR). For serological analysis, two indirect CCHFV-IgG-Enzyme-Linked Immunosorbent Assays (ELISA) were used. In case of divergent results, an adapted commercial immunofluorescence assay (IFA) was also performed.

Results: RT-qPCR identified 8 (5%, CI: 2%-10%) out of 160 sheep serum pools positive for the CCHFV genome fragments, while all goat serum pools (0%) were negative in this assay. In the serological analysis, 149 (19%, CI: 16%-21%) out of 800 sheep serum samples and 37 (5%, CI: 3%-6%) out of 800 goat serum samples were positive for CCHFV-specific IgG antibodies. The open type of housing (OR=3.76, CI: 1.57-9.56, $p=0.003$), grazing (OR=4.18, CI: 1.79-10.37, $p=0.001$), presence of vegetation in/around the farm (OR=3.13, CI: 1.07-10.15, $p=0.043$), lack of treatment against ticks (OR=3.31, CI: 1.16-10.21, $p=0.029$), absence of rural poultry (OR=2.93, CI: 1.41-6.29, p -value=0.004), sheep with age > 2 years (OR=2.72, CI: 1.36-6.22, $p=0.008$), sheep infested with ticks (OR=2.11, CI: 1.38-3.29, $p<0.001$), and goats infested with ticks (OR=2.68, CI: 1.23-6.72, $p=0.02$) were identified as statistically

significant risk factors associated with the occurrence of CCHFV infections in livestock.

Conclusion: Risk factors identified in this study might elevate the probability of CCHFV infection in livestock. Humans who are in close contact with these animals may consequently also at a higher risk of infection with this virus.

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The species diversity of ticks that attack human hosts in Eastern Siberia (Russian Federation) and prevalence of tick-borne pathogens



M. Khasnatinov*, A. Liapunov, E. Manzarova, N. Liapunova, I. Solovarov, V. Salchak, G. Danchinova

Federal state public science institution "Scientific center for family health and human reproduction problems", Irkutsk/RU

Purpose: The purpose of this work was to characterize the population of ticks that attack humans in the Eastern Siberia and analyze the dynamics of tick-borne infections in the region.

Methods & Materials: Ticks were delivered to the laboratory by bitten people between 25.03.2007 and 17.10.2017. The developmental stage and species of ticks were identified morphologically using appropriate key guides. Four tick-borne pathogens, i.e. tick-borne encephalitis virus (TBEV), *Borrelia burgdorferi sensu lato*, *Anaplasma phagocytophilum*, *Ehrlichia muris*/E. *chaffeensis* were detected in ticks using the range of laboratory diagnostic methods, including direct light microscopy, ELISA and real-time PCR.

Results: Total of 46357 tick specimens detached from bitten people were identified and tested individually during 10 consecutive years. The majority (85.4%) of victims was bitten by *I. persulcatus*; 14.55% of attacks on humans were caused by *D. nuttalli* and *D. silvarum*; whereas *H. concinna* was documented only in 25 cases (0.05%). Among all studied ticks, several unconventional species i.e. *Rhipicephalus sanguineus*, *D. reticulatus* and *Amblyomma americanum* were identified. In 2017, besides two cases of *R. sanguineus* bites, the bite of *A. testudinarium* was registered. Analysis of tick bite histories indicates that five cases have local origin whereas other five ticks are imported from endemic regions.

Mean prevalence of infection in *I. persulcatus* comprised $12 \pm 6.5\%$, $7.8 \pm 2.7\%$, $4.6 \pm 1.5\%$ and $1 \pm 0.7\%$ for *B. burgdorferi sensu lato*, *A. phagocytophilum*, *Ehrlichia sp.* and TBEV respectively. The dynamics of the prevalence of TBEV and *B. burgdorferi s.l.* in *I. persulcatus* indicate the significant increase of infection rate during 2014 – 2017. In *Dermacentor sp.*, the prevalence of every infection was below 5%, with the highest rate for *A. phagocytophilum* ($4.2 \pm 3.7\%$). No pathogens detected in *H. concinna*.

Conclusion: *I. persulcatus* remains the most important vector of tick-borne diseases to humans in Eastern Siberia with highest attack rate and with about 25% of ticks being infected with at least one of four pathogens. The *H. concinna* does not play any significant role as a disease vector. The regular events of invasion of non-endemic tick species are discovered.

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