

Epidemiology of ticks and tick-borne protozoan and rickettsial infections of cattle in Karamoja region, Uganda

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Abstract

Livestock production is the main source of social and economic livelihoods for communities in Karamoja region. However, tick-borne Protozoan and Rickettsia infections pose a major threat to livestock production and lead to significant economic losses, which impact the livelihoods and the social setup of the Karimojong. To improve livestock production, efforts to address animal health are required; therefore, vector and parasite control is of vital significance. Standardised vector and parasite surveys are essential in providing up-to-date data to guide in the formulation and implementation of these programmes. To this end, a cross-sectional survey was undertaken to determine the prevalence, distribution and diversity of the major tick-borne haemoparasites / pathogens (TBH) infecting cattle, and the tick species infesting cattle in the Karamoja region as well as to understand the knowledge, attitudes, and preventive practices of the Karimojong towards ticks and tick-borne diseases (TTBD). This study involved the collection of ticks and blood samples from 3,540 cattle drawn from a total of 59 villages in the wet and dry seasons in six districts of Karamoja. In addition to the tick and blood surveys was a qualitative survey to understand the perceptions of the pastoralist towards TTBD. The pastoral communities perceived tick-borne diseases, especially anaplasmosis and ECF, as among the most important diseases, based on the case fatality rates, morbidity and costs of treatment. Livestock production was perceived as the most important contributor to household income, and livestock disease and their vectors were considered the single most important constraint to livestock production. The preventive practices perceived to be most effective against ticks and TBD were acaricide application and curative treatment, respectively. Other control practices, including bush burning, handpicking, pricking ticks and vaccination, were said not to be so effective by the respondents in all the study areas. The key constraints to the control of TTBD were shortage of money to buy veterinary inputs, unavailability of veterinary services, drugs and inputs, inadequate knowledge of the pastoralist in disease diagnosis/treatment and insecurity. The cost of the preventive practice and a high case fatality /morbidity rate of the disease were ranked as the most significant influencers for undertaking the prevention and or control of TBD. A total of 15 tick species from three genera (10 Rhipicephalus; three Amblyomma; two Hyalomma species) were identified. Rhipicephalus appendiculatus was the most dominant (37.9%) tick species, followed by Amblyomma variegatum (32.3%); A. lepidum (17.3%); R. evertsi evertsi (7.8%); and R. (Boophilus) decoloratus (1.4%). The distribution of the tick species was not uniform across the study districts. The proportion of tick-infested cattle was similar in the wet and dry season ($\chi^2 = 0.5077$, $n = 1385/1534$, $p = 0.476$). Cattle were predominantly infested by five tick species, namely A. variegatum (55%), R. appendiculatus (53%), A. lepidum (41%), R. evertsi (22%), and R. (Boophilus) decoloratus (8%). In total, 46 R. (Boophilus) microplus ticks were found infesting cattle in five study sites in the districts of Amudat, Kaabong and Napak. Rhipicephalus (Boophilus) decoloratus co-existed with R. (Boophilus) microplus however R. (Boophilus) decoloratus was the most dominant (76.1%; $n=179$) of the three Rhipicephalus (Boophilus) tick species recorded in the region. At least 39.2% (95% CI: 37.6-40.9; $n=1,387/3,540$) and 39.0% (CI: 37.3-

40.6; n=1,380/3,540) of the screened cattle were positive for at least one of the screened TBH in the dry and wet seasons, respectively, a difference that was not statistically significant ($p > 0.05$). The overall prevalence of infection with the individual TBH in the dry season in descending order was: - *B. bigemina* 11.8% (CI: 10.8-12.9), *B. bovis* 11.8% (CI: 10.8-12.9), *A. marginale* 9.2% (CI: 8.2-10.2), *E. ruminantium* 5.1% (CI: 4.4-5.8) and *T. parva* 1.3% (CI: 1.0-1.8). In the rain season, the prevalence of different TBH was: - *T. parva* 22.6% (CI: 21.3-24), *A. marginale* 13.6% (CI: 12.5-14.8), *B. bigemina* 12.7% (CI: 11.6-13.8), *E. ruminantium* 1.4% (CI: 1.1-1.9) and *B. bovis* 0.3% (CI: 0.1-0.5). Geospatial location, increasing age, sex, overnight stay in cattle kraals and cattle breeds were significant predictors for testing positive for at least one of the TBH during the survey. Mixed infections with *B. bovis* and *B. bigemina* (2.74%; CI: 2.23-3.33) were more encountered while mixed infections with *E. ruminantium* and *T. parva* (0.14%; CI: 0.05-0.33) were the least encountered during the dry season. On the other hand, mixed infections with *A. marginale* and *E. ruminantium* (1.64%; CI: 1.25-2.11) were more encountered while mixed infections with *B. bovis* and *E. ruminantium* (0%; CI: 0-0.1) were the least encountered during the wet season. The sequences of TBH clustered closely within the individual species indicative of a high degree of similarity. The MSP4 gene sequences of *A. marginale* were grouped into two clusters with other published sequences with limited branching in the tree, and showed minimal nucleotide variation with other published sequences. These findings highlight limited regional divergence, likely shaped by ecological similarities or shared vector species. The p104 gene sequences of *T. parva* were grouped into four clusters, illustrating the diversity of isolates from different regions. Four sequences from this study clustered closely together, forming a distinct subgroup within Clade 4 alongside previously published sequences and exhibited minimal pairwise nucleotide differences. The rap-1a gene sequences of *B. bigemina* were grouped into two clusters. The isolates clustered closely with published sequences from cattle in Uganda, Tanzania and India exhibiting zero nucleotide differences. The sbp2 gene sequences of *B. bovis* clustered into one highly conserved group. The isolates were identical to the Chinese *B. bovis* T2Bo strain (XM_001610444.2), indicating no nucleotide differences and suggesting a shared origin of infection. Minimal variation of 2-6 nucleotide differences was observed among the isolates. Haplotype diversity analysis of the msp4 gene across 24 sequences including those from this study and those in the GenBank showed a high haplotype diversity ($h = 0.859 \pm 0.066$) and moderate nucleotide diversity ($\pi = 0.0047 \pm 0.00074$). For the p104 gene, seven haplotypes were identified, demonstrating considerable nucleotide diversity among the isolates. Haplotype diversity analysis of the rap-1a gene across 38 sequences, including those from this study and GenBank, revealed low haplotype diversity ($h = 0.401 \pm 0.091$) and nucleotide diversity ($\pi = 0.00197 \pm 0.00049$). Interestingly, sbp2 exhibited substantial global diversity, with nine unique haplotypes reported. The findings from this study provide knowledge on the perceptions, vector quantitative indices and epidemiology of TTBD, which can be used in animal health advocacy, design and implementation of control strategies, and to support diagnosis. More effort should be placed in the control of TTBD in the region. There is a need to sensitize livestock farmers on the epidemiology of TTBD and improve on the regulation of livestock movement.

Description

A dissertation submitted to the Directorate of Research and Graduate Training for the award of the Degree of Doctor of Philosophy of Makerere University.

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