

## ABSTRACT

Areas which lie at the border of Mikumi National Park, Tanzania are considered to be the hotspot for the tick species and possibly tick-borne pathogens, although data on ticks and the diversity of the viruses in ticks are non-existing. Herein, identification of ticks into genus level based on morphological characteristics, the tick burden in cattle and goats based on parasitological parameters, genetic diversity of tick species based on mitochondrion 16S rRNA gene, mean and pairwise genetic variation in ticks based on Kimura 2 parameters model, and the diversity of viruses in ticks using viral metagenomic approach were determined. Using the morphological characteristics, two ticks genera; *Hyalomma* and *Rhipicephalus* were identified. Tick burden findings reported the overall proportion of tick-infested animals to be 48.6%; cattle (51.5%) and goats (44.3%) whereas; the overall mean tick intensity and abundance in cattle and goats were  $3.9 \pm 0.01$  and  $1.8 \pm 0.01$  respectively. Based on mitochondrion 16S rRNA gene, six tick species were identified including *Rhipicephalus microplus*, *Rhipicephalus evertsi*, *Hyalomma rufipes*, *Hyalomma truncatum*, *Hyalomma marginatum*, and *Hyalomma turanicum*. The *Hyalomma marginatum* and *Hyalomma turanicum* species are reported for the first time from the study area and Tanzania in general. In the genetic variation analysis data it was observed that, *Hyalomma marginatum* recorded the highest mean ( $0.04 \pm 0.01$ ) and pairwise (0.06) intraspecies distance value whereas, the highest pairwise intragenus value (0.139) was recorded in *Hyalomma* genus. Notably, high values of  $0.11 \pm 0.01$  and 0.23 mean and pairwise genetic distances respectively in the tick community were recorded. Viral groups related to known viral families; *Retroviridae*, *Flaviviridae*, *Rhabdoviridae*, *Chuviridae*, *Orthomyxoviridae*, *Phenuiviridae*, *Totiviridae*, *Rhabdoviridae*, *Parvoviridae*, *Caulimoviridae*, *Mimiviridae*, as well as unknown viral families named as unknown virus 1 and 2 were reported. Therefore; intensification of the surveillance of ticks and tick-borne pathogens in Tanzania is highly encouraged to predict future emerging ticks and tick-borne pathogens.