Estimating seroprevalence and variation to four tick-borne infections and determination of associated risk factors in cattle under traditional mixed farming system in Mbeere District, Kenya

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Abstract

A cross-sectional study of serum antibody responses of cattle to tick-borne disease (TBD) parasites (Theileria parva, Theileria mutans, Anaplasma marginale and Babesia bigemina) was conducted on traditional smallholder mixed farms in Mbeere District in Kenya. The objective was to estimate the infections' seroprevalence and variation and identify associated risk factors. A total of 440 cattle in 80 farms, selected by stratified random sampling from the four divisions in the district, were surveyed. Information on animal and on each farm's management practices, particularly on tick control practices, was obtained by personal interview using a standardized questionnaire. Prevalences of serum antibodies were determined using the enzyme-linked immunosorbent assay (ELISA) technique. The relationship between TBDs seroprevalence and the risk factors was assessed by multivariable analysis using standard logistic regression models and mixed models using the farm as a random effect. Overall estimation of seroprevalences and their 95% confidence limits were: T. parva (19% [14%, 25%]), T. mutans (25% [20%, 29%]), A. marginale (58% [52%, 64%]) and B. bigemina (19% [15%, 23%]). Analysis in presence of extra-binomial variation under Analysis Of Variance (ANOVA) yielded relatively larger intra-farm correlation coefficient (ICC) (0.3) and variance-inflation factor (VIF) (2.35) values for T. parva than for the other parasites [range, 0.05–0.07 (for ICC) and 1.02–1.32 (for VIF)]. Both farm- and area-level variables had variably significant and large effects on all infections, but these were more pronounced on T. parva seroprevalence. Inclusion of farm random effect resulted in substantially higher estimate of farm variance component for T. parva infection (1.73) compared to other infections [range, 0.29–0.56], comparable ICC values with those under ANOVA analysis [range, 0.08–0.35] and a substantially better fit than the standard multivariable logistic regressions. The above results serve as possible indicators of existence of endemic instability for the studied TBD infections in the district. A probable differential ecological and climatic variability in vector suitability habitats, particularly for T. parva vector, was likely in Mbeere District and this was suggested to influence farm tick control management across the area. Implications of the design-based sampling and analyses on the above results are also discussed.