Effect of a Wildlife-Livestock Interface on the Prevalence of Intra-Erythrocytic Hemoparasites in Cattle

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ABSTRACT

We conducted a cross-sectional study to establish the effect of proximity of livestock to a wildlife-livestock interface on the relative abundance of intra-erythrocytic hemoparasites in cattle. Blood samples were obtained from 131 randomly-selected cattle raised around Queen Elizabeth National Park. Cattle-farm location was determined by using Global Positioning System device from an arbitrarily reference point. Giemsa-stained blood smears were examined microscopically for intra-erythrocytic hemoparasites. Correlational analysis was used to examine the relationship between farm location and prevalence, whereas risk ratios were used to determine the strength of mixed hemoparasitic infections among cattle, using a significant level of $\alpha = 0.05$. The location of a cattle farm significantly predicted the prevalence of Anaplasma (rs = 0.33, p < 0.05) and Theileria (rs = 0.57, p < 0.01) but, farm's proximity to QENP did not explain the variation in the prevalence of Babesia (rs = 0.14, p < 0.2). Although mixed infections occurred in 15% of sampled cattle, concurrent infection of cattle with *A. marginale* and *B. bigemina* [RR = 36; 95% CI (7.191); p < 0.001] was the only statistically significant mixed infection which was recorded. This study demonstrated that unlike the prevalence of *B. bigemina*, the prevalence of *T. parva* and *A. marginale* in livestock significantly increased with close proximity to a wildlife-livestock interface.

Keywords: Wildlife-Livestock Interface; Geographical Information System; Proximity; Ankole Long-Horned Cattle; Intra-Erythrocytic Hemoparasites

1. Introduction

Wildlife-livestock interfaces are characterized by conflict between livestock keepers and wildlife conservation authorities especially as it relates to the transmission and prevention of diseases common to both wildlife and domesticated animals [1].

Livestock keepers living within the wildlife-livestock interface mostly practice pastoral farming as a sustainable management system [2]. This management system is characterized by bidirectional movement of domesticated cattle and wild herbivores in search of water and pasture with little regard to defined boundaries, limited access to veterinary services, use of local plant species for prophylaxis and chemotherapy, and if inadequate at all any record keeping [2,3]. Such characteristics of the wildlifelivestock interface are fundamentally responsible for patterns of distribution of ticks and tick borne diseases (TTBDs) between livestock and wildlife [2,4]. Cattle keepers raising animals around wildlife national parks have identified Theileriosis (East coast fever) caused by *Theileria parva* and vectored by *Rhepicephalus appendiculatus*; Anaplasmosis caused by *Anaplasma margi-*



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nale and vectored by *R. evertsi evertsi* and Babesiosis (Red water) caused by *Babesia bigemina* and vectored by *Boophilus decoloratus* as priority diseases [3,5-7].

In an effort to find solutions to conflicts which occur as a result of these diseases, as well as to better understand the effect of the wildlife-livestock interface on the transmission dynamics of intra-erythrocytic hemoparasites, Ankole-long horned cattle raised around Queen Elizabeth National Park (QENP) were sampled and tested with the aim of investigating whether proximity of livestock to a wildlife-livestock influenced the relative abundance of intra-erythrocytic hemoparasites. Nonintra-erythrocytic hemoparasites are beyond the scope of this study.

2. Materials and Methods

2.1. Study Area and Design

With permission from the Uganda Wildlife Authority (UWA) and Uganda National Council for Science and Technology, a cross sectional survey was performed around QENP between June, 2005 and March, 2006. QENP covers an area of over 2000 sq km and lies in the Western region of Uganda (0°23'S Latitude 29°58'E Longitude). Katunguru Bridge was arbitrarily selected a reference point and farms located east to this point were included in the study. Geographical information system (GIS) coordinates of the kraal were taken for each farm using a global positioning system (GPS) device (Garmin eTrex[®] Legend C). Inclusion criteria considered farms with 10 - 30 indigenous Ankole long-horned cows aged between 1 month and 7 years. Cattle with evidence of clinical disease were excluded from the study but, appropriate treatment protocols with anti-protozoa agents were instituted. Because of confidentiality concerns, as well as the purpose of the study, all farms were coded with unique identification numbers.

2.2. Sampling and Sample Size Determination

An established prevalence (10%) of mixed hemoparasite infection in adult cattle [8] and a 20% tolerable error were assumed when determining the number of cows to be randomly selected into the study [9]. About 3 mls of blood were obtained by venipuncture of the jugular or tail veins of each cow sampled and placed in EDTA (Becton-Dickinson, vacutainer system, USA), labeled and stored at 6°C until further processing. Thin blood smear were prepared and stained with May-Grunwald-Giemsa and microscopically examined under oil immersion.

2.3. Data Analysis

Cattle were classified as positive or negative for intra-

erythrocytic hemoparasites based on microscopic evaluation of the blood smear. Data were coded and statistical analyses were performed using EPIINFO (version 7, CDC, Georgia, Atlanta USA) at a significant level of α = 0.05. We used a Spearman's rank correlation co-efficient to test for the effect of livestock proximity to a wildlifelivestock interface and risk ratio (RR) to determine the strengths of associations of mixed infection. Distances from the reference point, Katunguru Bridge, determined by GIS coordinates was calculated using GIS Arc View 3.2a.

 $Prevalence = \frac{No of animals with parasite}{Total number of animals sampled} \times 100$ $RDP = \frac{Number of specific parasite}{Total number of parasites identified} \times 100$

RDP: Relative diagnostic percentage.

3. Results

The target population was 139 cows but, blood samples were randomly obtained from only 131 cows located on 13 farms giving a response rate of 94.2% (131/139). Failure to collect blood samples from 8 cows was due to a lack of adequate handling facilities. The nearest farm was 2.7 miles whereas farthest farm included in the study was 20.8 miles away the reference point. The prevalence of all intra-erythrocytic hemoparasite infections combined was 55.7% (73/131) with varying between-farm prevalence (**Table 1**).

The prevalence of *T. parva* and *A. marginale* increased significantly with close proximity of livestock to the wildlife-livestock interface ($r_s = 0.57$, p < 0.01) and ($r_s = 0.33$, p < 0.05) respectively but, the prevalence of Babesia did not vary significantly with closeness to the wild-life-livestock interface ($r_s = 0.14$, p = 0.2). Mixed intraerythrocytic hemoprotozoan infections were detected in 15% (11/73) of cows and the number of hemoparasites identified ranged from 0 - 3 per cow but, the only statistically significant mixed infection was recorded between *A. marginale* and *B. bigemina* [RR = 36; 95% CI (7.191); p < 0.001] (**Table 2**).

4. Discussion

This study is unique that it utilized proximity of the indigenous Ankole long-horned breed of cattle to QENP as a model for investigating the consequences of increasing interaction of domestic cattle with wildlife on the distribution of intra-erythrocytic hemoparasites in cattle.

In spite of the fact that intra-erythrocytic hemoparasites routinely cause fatal disease in cows [10] and that their prevalence was high, the cows used in this present study did not have evidence of clinical disease. This

Table 1. Prevalence (%) of intra-erythrocytic hemopara-sites in cattle stratified by farm proximity.

			Prevalence % (95% CI)		
Farm i.d	n	Distance (miles)	T. parva	A. marginale	B. bigemina
1	11	2.7	55 (23, 83)	36 (11, 69)	9 (0, 41)
2	9	3.9	89 (52, 99)	0 (0, 36)	0 (0, 34)
3	10	4.8	60 (26, 88)	60 (26, 88)	10 (0, 45)
4	9	6.0	78 (40, 97)	22 (3, 60)	11(0, 49)
5	11	7.1	73 (39, 94)	9 (0, 41)	22 (3, 52)
6	9	7.8	78 (40, 97)	22 (3, 60)	22 (3, 60)
7	9	9.0	11 (0, 11)	11 (0, 48)	0 (0, 37)
8	10	10.6	50 (19, 81)	0 (0, 31)	0 (0, 31)
9	10	11.5	40 (26, 87)	20 (3, 57)	10 (0, 44)
10	11	12.4	64 (31, 89)	18 (2, 51)	18 (0, 31)
11	10	14.6	0 (0, 31)	0 (0, 31)	0 (0, 29)
12	11	18.3	18 (3, 52)	0 (0, 29)	0 (0, 29)
13	11	20.8	0 (0, 29)	0 (0, 29)	0 (0, 29)

i.d = identification; n = number of cows sampled.

 Table 2. Overall prevalence and relative diagnostic percent of intra-erythrocytic hemoparasites.

	Prevalence 95% CI	Relative diagnostic percent %
Theileria parva	51% (95% CI 49, 62);	68% (66/97)
Anaplasma marginale	15% (95% CI 9, 21)	21% (20/97)
Babesia bigemina	8% (95% CI 4, 15)	11% (11/97)

finding indicates that this indigenous cattle breed has adapted mechanisms to regulate the growth and development of hemoprotozoa in their blood which has led to endemic stability [11]. This desirable characteristic makes the Ankole long-horned breed apt for mixed livestockwildlife production systems; hence it lessens some of the conflicts in this wildlife-livestock interface.

With the highest prevalence and highest relative frequency of detection (RDP), *T. parva* appears to be of primary importance within the QENP wildlife-livestock interface. This suggests that wildlife, especially the Cape buffalo, which is a keystone species in QENP, is a natural reservoir, and therefore a fundamental source of vectors and hemoparasites for cattle [12].

T. parva and *A. marginale* infections were significantly higher in cattle raised closer to QENP wildlifelivestock interface. The zonal differences in prevalence may be directly correlated with the distribution of the specific vectors involved. *Babesia bigemina* had the lowest prevalence and proximity of cows to QENP was not significantly associated with the prevalence of *B. bigemina* in farmed cows. This finding is in accordance with previous research findings, which demonstrated that trends of *B. bigemina* across different ecological zones were similar [13]. Mixed *A. marginale* and *B. bigemina* infections were common and statistically significant, and likewise a high farm prevalence of *A. marginale* was matched by a high farm prevalence of *B. bigemina*. Similar mechanisms of transmission or cross-transmission may be possible explanations for the coexistence of *A. marginale*, and *B. bigemina* in cows [8,14].

The effects of confounding factors such as use of acaricides (concentration and frequency of application) or the method of acaricide application (spraying versus dipping) was not assessed in this study. Future studies using serological and molecular diagnostic tools are encouraged and may be performed concurrently with hemoparasites in wildlife herbivores.

5. Conclusion

In conclusion, this study finds evidence that proximity of livestock to a wildlife-livestock interface explains a significant proportion of the variation in the prevalence of *T. parva* and *A. marginale* infection in cattle but, it does not explain the variation in the prevalence of *B. bigemina* infection in cattle.

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