East Coast fever (ECF) and prospects of using efficient vaccines for integrated control strategy in Uganda

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Present undesirable situation

- East Coast fever (ECF) causes high mortality of up to 100% among exotic and crossbred cattle which impedes the development of the dairy industry and poverty reduction among smallholder farmers.
- ECF control greatly depends on acaricides used to kill ticks. Prolonged acaricide use has resulted into environmental contamination and emergence of acaricide resistant ticks (Vudriko et al 2016).
- The Muguga cocktail vaccine which uses the Infection and Treatment Method (ITM) does not protection against buffalo-derived ECF (Corridor disease) (Sitt et al 2015) .



The African buffalo habours Corridor disease

Desirable situation



- Formulate efficacious vaccines based on local *T. parva* strains especially in areas where buffalo and cattle (Sitt et al 2015) share grazing pastures for example in southwestern Uganda
- An effective vaccine will save about 100,000 head of cattle per annum in Uganda.

CURRENT RESEARCH EFFORTS TO ACHIEVE DESIRED TARGETS

The distribution of *T. parva* in Uganda

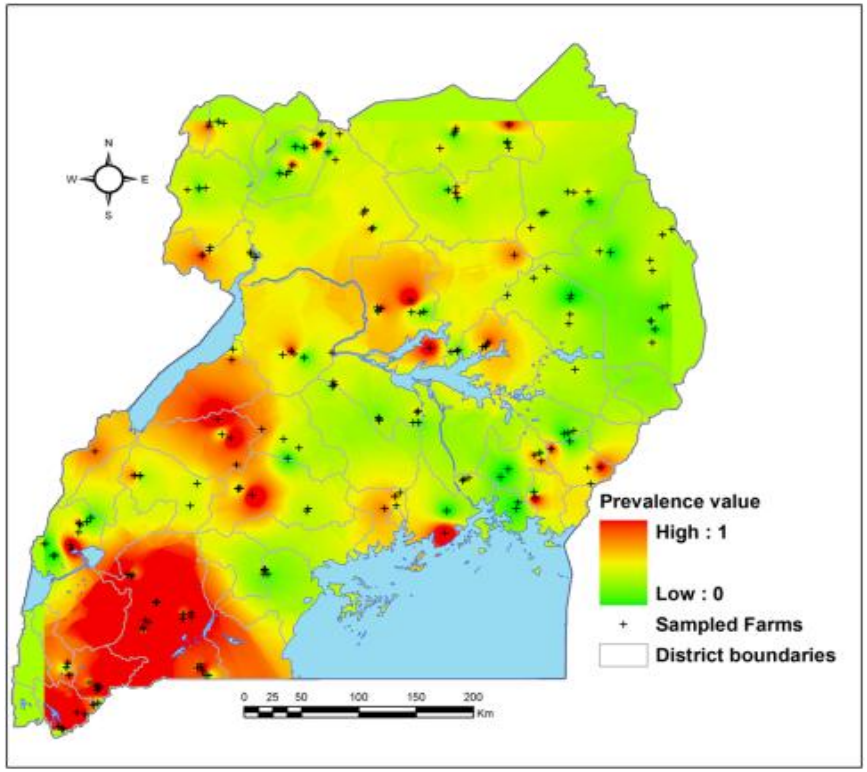


Figure 1: The spatial distribution of *T. parva* in Uganda: (2011 – 2012)

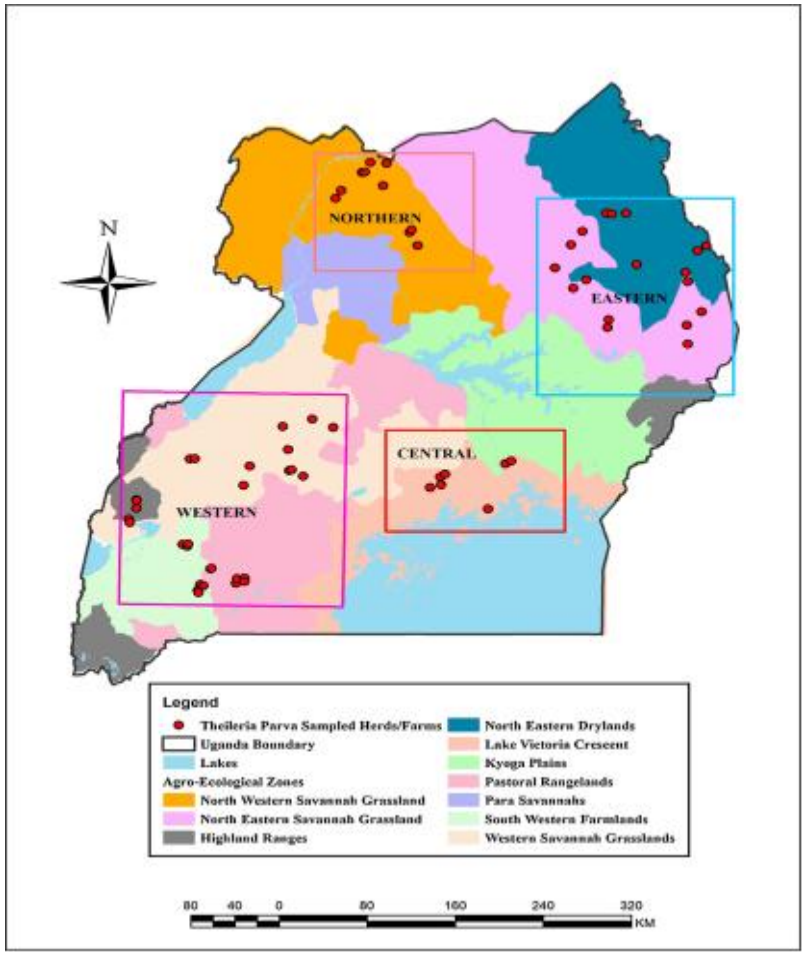
Methods:

- Samples were randomly collected from 925 cattle in 209 herds spread out in 10 agro-ecological zones (AEZs). A nested PCR assay was used determine their ECF status. The influence of AEZ, breed, age and farmers' perception of ECF importance were interrogated using a logistic regression model at 95% confidence interval.

- **Results:** ECF prevalence ranged from 17% to 43% in the North Eastern Savannah Grasslands (NESG) and Western Highland Ranges (WHR), respectively. The prevalence was 18% and 35% among the East African shorthorn Zebu (EASZ) and Ankole cattle respectively. The likelihood of ECF outbreak is 35.5% greater in the western highlands compared to the northeastern semi-arid AEZs among naïve cattle.

- **Conclusion: The distribution of ECF is influenced by AEZ, Breed and presence of wild reservours like buffaloes**

Genetic variation of *Theileria parva* strains in Uganda



- *Theileria parva* strains obtained from the different Agro-ecological zones were genotyped to determine the level of genetic differences using mini - and microsatellite markers (Oura et al. (2003).

Table 1 Pairwise comparisons of *T. parva* genetic populations from the different obtained from AEZs

N = 78	Western	Northern	Central	Eastern
Western (n = 30)	-	0.001**	0.001**	0.001**
Northern (n = 19)	0.154	-	0.009**	0.020*
Central (n = 11)	0.160	0.085	-	0.002**
Eastern (n = 18)	0.173	0.048	0.101	-

Above the diagonal: - p values for significant differences between populations, ** highly significant, * significant. Below the diagonal:- Wrights F_{ST} values indicating differences between populations

Conclusions:

1. *Theileria parva* strains from the different AEZs are genetically diverse.

2. The use of a vaccine as an integral component of ECF control should be tailored to specific genotype strains to achieve maximum protection

References: 1. Muwanika, V., Kabi F., Masembe C. (2015) Population genetic structure of Theileria parva field isolates from indigenous cattle populations of Uganda. Ticks Tick-borne Dis. Sitt, T., Poole, E., Ndambuki, J et al 2015. Exposure of vaccinated and naive cattle to natural challenge from buffalo-derived T. parva. Int. J. Parasitol. Parasites Wildl. 4, 244–251