# Theileria parva genetics, prevalence and vaccination practices in Zimbabwe and the African region and the prospects for vaccine development: a systematic review

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## Abstract

### Introduction

January disease causes the deaths of over 55,000 cattle valued at approximately US$ 17 million annually in Zimbabwe. The locally developed Boleni stabilate vaccine is in use for controlling the disease. In the present review, we show the current knowledge of the genetic variation and population structure of Theileria parva parasite and its implications on the epidemiology and control of the parasite in eastern and southern Africa, with a major emphasis on Zimbabwe.

### Methods

A systematic review was conducted to analyse the reports available in literature in order to map the Theileria parva genetic diversity profile. A total of 103 studies met the criteria for analysis and were included in the review.

### Results

The reports retrieved in this study show that East Coast fever and Corridor disease have been extensively sequenced to establish the parasite population genetic structure. One report described genetic diversity in January disease, with no sequencing tools included. The live sporozoite stabilate administered as infection without concurrent treatment remains the vaccination approach of choice in January disease.

### Discussion

The adoption of population genetics led to the determination of genotypes that were employed in the development of the Muguga cocktail vaccine. To date, vaccination against East Coast fever is reported to reduce mortality rate. The Boleni isolate remains in use for vaccination against uncharacterized populations of January disease in spite of increased mortality rates extensively reported from 2015 to date. There is need to adopt comparative genomics in vaccine development for a more effective vaccine.