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Detection of carrier state and genetic diversity of *Theileria parva* in ECF-vaccinated and naturally exposed cattle in Tanzania

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Detection of carrier state and genetic diversity of *Theileria parva* in ECF-vaccinated and naturally exposed cattle in Tanzania

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Abstract

Infection and Treatment Method (ITM) has been practiced in Tanzania for over 20 years as a prevention measure against East Coast Fever disease. It is known that ITM, like natural ECF infection, leads to a carrier state, whereby vaccinated cattle become asymptomatic carriers of the parasite. It is expected that ECF vaccination using ITM also leads to generation of combinations of vaccine specific *Theileria parva* and local strains that circulate in the field what contributes to an unknown level of parasite diversity. Moreover, the long term impact of ITM on carrier state and parasite diversity in cattle are largely unknown. To address this question blood was collected from ECF-vaccinated ($n = 239$) and unvaccinated ($n = 97$) cattle from Loiborsoit, Emboreet, Esilalei, Manyara ranch and Mswakini villages in the Maasai steppe of northern Tanzania, as well as Mruazi and Leila farms in Tanga in eastern Tanzania. Screening for *T. parva* using nested PCR revealed an overall prevalence of *T. parva* to be 34.5%, with a significant higher prevalence among ECF-vaccinated cattle. Using three VNTR markers (ms2, ms5 and MS7) higher parasite genetic diversity in terms of higher number of alleles and expected heterozygosity was shown in vaccinated than unvaccinated cattle. These parameters were highest in cattle from Manyara ranch. Nevertheless, the principle component analysis (PCoA) showed no distinct clustering patterns as most *T. parva* alleles clustered together throughout the four quadrants implying parasite homogeneity among the sampled populations. However, some of the parasite alleles closely clustered with Muguga vaccine alleles in two of the quadrants, consistent with closer genetic relatedness between the vaccine strains and the *T. parva* populations from the Maasai steppe. Likewise analysis of molecular variance (AMOVA) revealed most of the genetic variation (93%) being contained within populations with only 7% being among populations. This study therefore confirms the role of ECF vaccination in enhancing carrier state and *T. parva* diversity in vaccinated cattle populations. Higher *T. parva* diversity may play an important role in carrier cattle by way of restricting breakthrough infections from field parasite strains.

Keywords

East Coast fever; Infection and treatment method; Genetic diversity; Tanzania; *Theileria parva*