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学位論文内容の要旨  
Abstract of the dissertation

博士の専攻分野の名称：博士（獣医学）

氏名：CHATANGA ELISHA

Name

学位論文題名  
The title of the doctoral dissertation

Molecular detection and characterisation of tick-borne pathogens of domestic animals in  
Malawi

（マラウイの家畜におけるマダニ媒介性病原体の  
分子学的解析）

Tick-borne diseases (TBDs) remains a major challenge to the improvement of livestock production in the tropics where the vector ticks are widespread. The commonly diagnosed TBDs of domestic animals are anaplasmosis, babesiosis, ehrlichiosis, hepatozoonosis and theileriosis. In Malawi, there has been no study conducted to characterise the tick-borne pathogens (TBPs) of domestic animals. This thesis aimed at detecting and characterising the TBPs in cattle, sheep, goats and dogs in Malawi using molecular techniques.

In chapter I, screening for TBPs in 191 cattle DNA samples showed that 177 (92.7%) of the samples were positive for at least one TBP species. Co-infection of different species was observed in 152 (79.6%) of the samples analysed. *Anaplasma bovis*, *Anaplasma marginale*, *Anaplasma platys*-like, *Anaplasma* species, *Babesia bigemina*, *Ehrlichia* species, *Theileria mutans*, *Theileria parva*, *Theileria taurotragi* and *Theileria velifera* were detected in cattle in Malawi.

In chapter II, the genetic diversity and sequence polymorphism of two genes encoding *Theileria parva* was investigated. The study showed extensive genetic diversity in *Tp2* gene compared to *Tp1* gene. Most sequences were either identical or similar to *Theileria parva* Muguga, Kiambu 5 strains and Serengeti transformed, the components of Muguga cocktail (MC) vaccine. This study provides information that support the use of MC vaccine to control East Coast fever (ECF) in Malawi.

The study in chapter III, extended the study in chapter II to further investigate the population structure of *Theileria parva* in Malawi using 100 *Theileria parva*-PCR positive samples. A total of 9 satellite markers were employed in this study. There was sub-structuring among the samples into two clusters based on the principal coordinate analysis (PCoA). Majority of the isolates clustered with the Muguga reference strain, suggesting that the isolates in Malawi are closely related to the MC vaccine component.

In chapter IV, molecular detection and characterisation of TBPs in 8 sheep and 99 goats samples from Malawi showed that 77 (72.5%) of the samples analysed were positive for at least one TBP species. *Anaplasma ovis*, *Babesia gibsoni*-like strain, *Ehrlichia ruminantium*, *Ehrlichia canis*, *Theileria ovis*, *Theileria* spp. MSD like, *Theileria mutans* and *Theileria separata* were detected in sheep and goats in Malawi.

In chapter V, molecular detection and characterisation of TBPs in 209 dogs in Malawi showed that 93 (44.5%) of the samples analysed were infected with at least one TBP species. This study has provided molecular evidence that dogs in Malawi are infected with *Anaplasma platys*, *Babesia rossi*, *Babesia vogeli*, *Ehrlichia canis* and *Hepatozoon canis*.

The studies in this thesis have shown that domestic animals in Malawi are infected with a wide range of TBPs. These studies have also shown that domestic animals do not always present clinical symptoms even when infected with certain TBPs and serve as reservoirs of TBPs, which could be the source of TBP infections to other susceptible domestic animals. The molecular epidemiological data generated in these studies are important in monitoring the control measures currently in place and conceiving novel methods to control ticks and TBDs in Malawi.