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

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学位論文題名
The title of the doctoral dissertation

Characterization of genetic diversity of bovine trypanosomes in African and Middle Eastern countries

（アフリカおよび中近東におけるウシ感染性トリパノソーマ原虫の遺伝的多様性に関する研究）

Bovine trypanosomiasis has long been known to hamper agriculture and farming productions in many countries. Despite its significance, bovine trypanosomiasis is still considered as neglected disease in livestock. The present study was intended to provide information on the prevalence and genetic diversity of *T. evansi* in Syria and African trypanosomes in Malawi.

Syria is geographically located in the “gate”, where *T. evansi* started to spread worldwide from its origin in Africa. Therefore, Syria can be a key place to know the evolution of *T. evansi*, where the parasite moved out of its origin and started to spread worldwide. However, there is no literature on the molecular study of *T. evansi* in Syria. In this study, 207 samples of blood DNA collected from Holstein Friesian crossbred cattle in the central region of Syria in May 2010 were screened for *T. evansi*, aiming to determine the prevalence of the parasite. *T. evansi* was screened by PCR targeting the internal transcribed spacer (ITS) 1 region, and 27 samples were found positive out of 207 (13%), which is relatively high considering that no clinical symptoms were observed. The ITS1 amplicons were later subjected to *RoTat1.2*-PCR for detection of *T. evansi* type A. Genetic diversities were revealed in the sequence analysis of *ESAG6* from the Syrian samples. The obtained genotype did not have association with regions, countries, or animal host. This is the first report of molecular detection of *T. evansi* in Syria. This study emphasizes the necessity of advanced investigations in cattle and other domestic animals are necessary in Syria.

The identification of trypanosomes infecting cattle in Malawi was also conducted in order to understand the importance of cattle in the transmission dynamics of human African trypanosomiasis (HAT) and animal African trypanosomiasis (AAT). A total of 446 DNA

samples from cattle blood from three regions of Malawi were screened for African trypanosomes by ITS1 PCR. The obtained amplicons were sequenced using a portable next-generation sequencer, MinION, for validation. Comparison of the results from ITS1 PCR and MinION sequence showed that combining the two methods provided more accurate species identification than ITS1 PCR alone. Further PCR screening targeting SRA gene was conducted to detect *Trypanosoma brucei rhodesiense. T. congolense* was the most prevalent *Trypanosoma* sp., which was found in Nkhotakota (10.8%; 20 of 185), followed by Kasungu (2.5%; 5 of 199). Notably, the prevalence of *T. b. rhodesiense* detected by SRA PCR was high in Kasungu and Nkhotakota showing 9.5% (19 of 199) and 2.7% (5 of 185), respectively. This is the first study to assess the presence of animal African trypanosomes and *T. b. rhodesiense* from cattle at the human–livestock–wildlife interface in Malawi. According to the results, it is confirmed that animal trypanosomes are important causes of anemia in cattle and that cattle are potential reservoirs for HAT in Malawi. The trypanosomes detection system used in this study has the potential to be applied in the future research for genetic diversity of parasite, and characterization of the trypanosomes up to sub-species.