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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：中村　有紀子
Name

学位論文題名
The title of the doctoral dissertation

Estimating the Genetic Diversity and Population Structure of Tsetse Flies and African Trypanosomes in Zambia and Malawi
(ザンビア、マラウイにおけるツェツェバエとアフリカトリパノソーマ原虫の遺伝的多様性と集団構造の推定)

Human African trypanosomiasis (HAT) and African animal trypanosomiasis (AAT) are transmitted between mammalian hosts via the blood sucking activity of tsetse flies (*Glossina* spp.). HAT in East Africa (rHAT) is caused by *Trypanosoma brucei rhodesiense*, whereas AAT is mainly caused by *T. congolense*, *T. vivax*, and *T. b. brucei*. rHAT has a zoonotic nature, which complicates the disease ecology and makes the complete elimination of rHAT unfeasible. The aim of this thesis was to elucidate the genetic diversity and population structure of both the tsetse fly vector and the trypanosome parasite, to suggest effective control strategies against rHAT and AAT.

Tsetse control is considered to be the most feasible control strategy against rHAT. Since most of the failures in tsetse control is due to population rebound, it is crucial to understand the population structure before control implementation. The aim of chapter one was to estimate the population structure of *G. morsitans morsitans* in Zambia and Malawi, the two representative countries endemic for rHAT in south-eastern Africa. Mitochondrial CO1 sequence and 10 microsatellite loci of *G. m. morsitans* collected from three locations of Zambia and two locations from Malawi were analyzed. As a result, restricted gene flow was observed between Nkhotakota Wildlife Reserve (NWR) in Malawi and the other four locations. In addition, NWR had a small effective population size. Therefore, population rebound is unlikely to occur in NWR, and is suggested to be a potential target for area-wide tsetse control. On the other hand, free gene flow was suggested to be occurring between the other four locations. In the

aspect of tsetse and disease control, further fine-scale analysis is needed, to assess the degree and direction of migration into adjacent areas.

To understand the complex disease ecology of rHAT and AAT, it is important to elucidate the prevalence and genetic diversity of the *Trypanosoma* spp. found within the same ecosystem. In chapter two, comprehensive methods targeting the ITS1 and the CATL region was used to elucidate the prevalence and genetic diversity of *Trypanosoma* spp. in cattle and tsetse flies from the Kafue ecosystem, Zambia. As a result, high prevalence of *T. vivax* was found in cattle and tsetse flies. Further sequencing of the CATL region detected varying diversity between cattle and tsetse flies, and between the tsetes fly species. Furthermore, *T. vivax*-positive cattle had significantly lower packed cell volume compared to negative cattle, suggesting that *T. vivax* is the main cause of anemia in this area. Since *T. vivax* can be mechanically transmitted, epidemiological studies and AAT control should expand their target to other biting flies. In addition, *T. b. rhodesiense* was detected in 5.42% of the cattle, presenting the risk of cattle acting as a reservoir of rHAT in the community. Altogether, the combination of molecular methods was useful in assessing the *Trypansoma* spp. diversity.

In conclusion, extending these molecular methods across geographic areas, potential vectors, and mammalian hosts will expand the knowledge against the disease ecology of both rHAT and AAT.