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：Jesca Nakayima
Name

学位論文題名

Molecular epidemiological study of protozoan and other zoonotic diseases from two countries in Africa

（アフリカ２カ国における原虫ならびにその他の人獣共通感染症の分子疫学的研究）

Human African trypanosomiasis (HAT), also known as sleeping sickness, is a neglected tropical disease that impacts 70 million people distributed over 1.55 million km^2 in sub-Saharan Africa. *Trypanosoma brucei gambiense* accounts for almost 90% of the infections in central and western Africa, the remaining infections being from *T. b. rhodesiense* in eastern Africa. Furthermore, the animal diseases caused by trypanosomes inflict major economic losses to countries already strained. The parasites are transmitted to the mammalian hosts through the bite of an infected tsetse fly. Additionally, zoonoses are infections or diseases that can be transmitted directly or indirectly between animals and humans. This study assessed the molecular epidemiology of human and animal trypanosomes, in addition to zoonotic pathogens in non-human primates in Zambia.

The first chapter of this thesis describes results of molecular epidemiological study on trypanosomiases which were carried out in two tsetse-infested areas of Ghana. The samples included tsetse flies, and cattle and pig blood, and were analyzed by using multiple polymerase chain reaction tests. *Trypanosoma vivax* was the most prevalent trypanosome species, followed by *T. congolense* and *T. brucei brucei*. Two subspecies causing HAT, *T. b. gambiense*, and *T. b. rhodesiense* were not detected in animals and flies in this study, which confirms that the country having been formally a HAT focus has been free of HAT since 2000. The results in this study may be reflected by the fact that *T. vivax* can be mechanically transmitted by biting flies in addition to biological transmission by tsetse fly, hence its distribution outside the tsetse fly belt of Africa.

The second chapter describes results on the genetic characterization of *T. vivax* strains from different geographical regions based on sequence comparison of Cathepsin L-like gene. *T. vivax* from Ghana clustered with West African and South American strains while *T. vivax* from Zambia clustered with East and Southern African strains. These results revealed genetic diversity of *T. vivax* in Africa.

In the third chapter, molecular epidemiological studies on zoonotic pathogens in non-human primates in Mfuwe in South Luangwa National Park, Zambia were carried out. This area is a HAT endemic focus with wildlife-livestock-human interface, hence the risk for zoonotic disease transmission is very high. Three species of zoonotic pathogens, *Rickettsia africae*, *Anaplasma phagocytophilum* and *Babesia microti* were detected among 9 pathogenic species/genera tested by PCR. These zoonoses detected in Zambia could be endemic in Zambian primates and possibly transmitted to humans but simply misdiagnosed as malaria due to their febrile nature.

Zoonoses in Africa are not just an African problem, since recent studies reveal an increase in these zoonotic infections in non endemic countries, especially in returning tourists from African national parks. Therefore, zoonotic disease control requires a multi-sectoral approach involving participants from the health, veterinary, entomology and environment professions because zoonosis transmission involves interaction between the pathogen, host, vector and environment.