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Abstract of the dissertation

博士の専攻分野の名称：博士（感染症学）

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Molecular Characterization and Serological Epidemiology of Viral
Diseases of Humans and Animals in Zambia

(ザンビアにおけるウイルス感染症の血清疫学および分子疫学解析)

Viral infectious diseases pose socio-economic and public health implications. Over the last decade, a number of viral pathogens have emerged, causing deadly disease outbreaks globally. Zoonotic diseases, which are transmitted from animal to humans, pose a major public health risk. In contrast, epizootics threaten global food security. The impact of zoonoses and epizootics is disproportionately high in sub-Saharan Africa. In Zambia, the epidemiology of most viral diseases is poorly understood. Moreover, the high incidence of HIV and Tuberculosis has led to disease prioritization. This has resulted in a number of endemic diseases being neglected. In order to mitigate emerging and re-emerging infectious diseases in high burden, resource limited countries like Zambia, public and animal health systems encompassing a multidisciplinary “One Health” approach are needed.

In chapter I, the epidemiology of rift valley fever (RVF) in Zambia was investigated. RVF virus antibodies (20.1%; 112/557) were detected in wild (33.7%; 96/285) and domestic (5.9%; 16/272) ruminants. This finding was suggestive of a role wildlife play in the epidemiology of RVF in Zambia. Retrospective analysis of RVF epizootics revealed a positive correlation between high precipitation and RVF emergence, intimating that past outbreaks were influenced by high precipitation. On risk mapping, the northern and eastern parts of Zambia were at high risk, however, the domestic ruminant population density was low (< 21 animals/km²) in these areas. This observation could be attributed to the long inter-epizootic period in Zambia. In summary, this study highlights the probable risk of RVF emergence in Zambia. Chapter II describes first evidence of Hepatitis E virus (HEV) infection in domestic pigs in Zambia. Besides the observed high seroprevalence (47.7%) of HEV antibodies in domestic pigs in Zambia, zoonotic genotype 3 HEV was detected in slaughtered pigs. Taken together, these findings highlight the presence, and risk of zoonotic

transmission of HEV.

Chapter III explored the epidemiology of African swine fever (ASF) in endemic and non-endemic regions in Zambia. ASF virus (ASFV) genome was detected in asymptomatic pigs, providing first evidence of ASF 'tolerant pigs' in Zambia. Similarly, the high seroprevalence (65.7%) to ASFV antibodies in indigenous pigs was suggestive of exposure to, and recovery from ASF. Furthermore, eight ASFV lineages were detected based on sequence analysis of the CD2v gene. This findings was indicative of high genetic diversity among ASFV in Zambia. Chapter IV reports on first evidence of bluetongue (BT) in Zambia. Sequence analysis of segment 2 of BT virus (BTV) revealed presence of serotypes 3, 5, 7, 12 and 15, with five nucleotypes (B, E, F, G and J) being identified. This finding was suggestive of co-circulation of multiple BTV serotypes. Segment 10 phylogeny showed Zambian BTV sequences clustering with Western topotype strains from South Africa, intimating likely transboundary spread of BT. The high seroprevalence in cattle (96.2%) and co-circulation of multiple serotypes showed that BT is widespread, underscoring the need to formulate prevention and control strategies. Lastly, it is anticipated that the findings from this study will be used to formulate effective disease prevention and control strategies.