



HOKKAIDO UNIVERSITY

Title	Epidemiological and immunological study for intractable infectious diseases in livestock [an abstract of dissertation and a summary of dissertation review]
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Degree Grantor	北海道大学
Degree Name	博士(獣医学)
Dissertation Number	甲第12842号
Issue Date	2017-09-25
Doc URL	https://hdl.handle.net/2115/67858
Rights(URL)	https://creativecommons.org/licenses/by-nc-sa/2.1/jp/
Type	doctoral thesis
File Information	OCHIRKHUU_NYAMSUREN_abstract.pdf, 論文内容の要旨



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)

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学位論文題名

The title of the doctoral dissertation

Epidemiological and immunological study for intractable infectious diseases
in livestock

(家畜の難治性感染症の疫学的および免疫学的研究)

The occurrence of infectious diseases caused by viruses, bacteria, and parasites in animals has been increasing in recent years, and causing great economic loss in livestock industry. Therefore, the surveillance of infectious diseases in livestock is very important for their control but the information on the prevalence of infectious diseases in livestock is extremely limited in the Philippines and Mongolia due to the shortage of financial capacity and inconvenient condition of laboratory facilities. In this study, molecular epidemiological survey of several pathogens that cause intractable infectious diseases in livestock in the Philippines and Mongolia was performed. In addition, the immunoinhibitory molecules in Mongolian native cattle and yak were characterized because immune response of the host is an important factor for the outcome of infectious diseases. The brief summary of these studies was described in below.

CHAPTER I: Molecular epidemiological surveys of several vector-borne pathogens were performed with 339 samples from cattle in Luzon island, the Philippines. High prevalence of *Anaplasma marginale*, *Babesia bigemina*, *B. bovis* and *Theileria* species were observed, whereas low prevalence of *Trypanosoma evansi* was detected. In addition, the mixed infections were detected in the most of the samples. The molecular characterization

of the *16S rRNA* gene for *A. marginale*, *RAP-1* gene for *B. bovis*, *AMA-1* gene for *B. bigemina*, and *MPSP* gene for *Theileria* spp. showed that their pathogens were genetically close to those from other Asian countries including Cebu island of the Philippines.

CHAPTER II: Several bacterial and viral pathogens were surveyed in 928 samples from cattle, yak, sheep and goats in 5 different areas in Mongolia. Seroprevalence of *Mycobacterium avium* subspecies *partuberculosis* was low in cattle. In contrast, the infection rate of *A. ovis* was high in sheep, goats, cattle and yak, and sequencing analysis identified that *A. ovis* isolates were genetically unique. Bovine leukemia virus (BLV) was detected from dairy breed cattle, and the nucleotide sequences of BLV were closely related to those of Russian isolates, suggesting that the BLV was transported from Russia into Mongolia. Ovine gammaherpesvirus 2 (OvHV2) was detected from sheep and cattle and the OvHV2 sequences from Mongolia were identical to the isolates from India, Turkey and Egypt. Bovine viral diarrhea virus (BVDV) was also detected in dairy breed cattle and yaks, and the Mongolian BVDV sequences were classified into genotypes 1a and 2a.

CHAPTER III: Immunoinhibitory molecules including programmed cell death 1 (PD-1), programmed cell death-ligand 1 (PD-L1), T-cell immunoglobulin and mucin domain 3 (TIM-3), galectin 9 (GAL-9), lymphocyte activation gene 3 (LAG-3), and cytotoxic T-lymphocyte-associated protein 4 (CTLA-4) are expressed on various immune cells, and play an important role in the down regulation of the immune system. These immunoinhibitory molecules in Mongolian native cattle and yak showed high homologies to those of other bovine species. These results suggest that the immunoinhibitory molecules in Mongolian native cattle and yaks may have similar functions as previously reported in other bovine species.

Molecular epidemiological survey of intractable infectious diseases in cattle in the Philippines and livestock in Mongolia, and molecular characterization of immunoinhibitory molecules in Mongolian native cattle and yak were performed in this study. These finding provides new information for planning and execution of effective control measures for infectious diseases in the livestock in each the countries.