

## Abstract of Thesis/Dissertation

## Applicant

Doctoral Program in Animal and Food Hygiene

Graduate School of Animal Husbandry

Obihiro University of Agriculture and Veterinary Medicine

Student ID: 17360007Name of Applicant: Yongchang LiSignature of Applicant: Yongchang Li

Title : Molecular investigation of tick-borne pathogens in cattle, horses and sheep in Xinjiang Uygur Autonomous Region, China

(中国新疆ウイグル自治区におけるウシ、ウマ、ヒツジのマダニ媒介病原体の分子疫学調査)

## Abstract

Ticks carry and transmit a wide range of pathogens (bacteria, viruses and protozoa) which are of importance to humans and animals globally. Xinjiang Uygur Autonomous Region (XUAR) is located in the northwest part of China, which occupies one-sixth of the country's land area and borders eight countries including Russia, Mongolia, Kazakhstan, Kyrgyzstan, Tajikistan, Afghanistan, Pakistan and India. Livestock production is known as a main industry in XUAR. Additionally, this region is located in halfway along the old Silk Road between eastern Asia and Europe, therefore, the international livestock trade is frequent. Although several studies focusing on tick-borne pathogens (TBPs) of ticks in XUAR have been reported, prevalence and molecular investigation of these TBPs in livestock are still limited. Therefore, the present study is to investigate tick-borne pathogens of cattle, horses and sheep in XUAR, China.

In chapter 1, TBPs were identified in cattle in XUAR. Nested polymerase chain reaction (nPCR) assays and gene sequencing were used to detect *Babesia bovis*, *B. bigemina*, *Coxiella burnetii* and

*Anaplasma bovis* infections in cattle in XUAR. Out of 195 samples tested, 67 (34.4%), 40 (20.5%), 24 (12.3%) and 10 (5.1%) were positive for *B. bigemina*, *C. burnetii*, *B. bovis* and *A. bovis*, respectively. Mixed infections involving 2-3 pathogens were observed in the present study. The most common dual infections were *B. bigemina* + *C. burnetii* while the most frequent triple infections were *B. bigemina* + *B. bovis* + *C. burnetii* with co-infection rates of 6.2% (12/195) and 1.0% (2/195), respectively. Although clinical cases were not observed, it is possible that cattle infected with multiple pathogens may have more pronounced clinical signs or hematological abnormalities than those infected with single pathogens. It suggests that *B. bovis*, *B. bigemina* and *C. burnetii* were co-infection of pathogens in cattle in XUAR. This study revealed the existence and genetic diversity of *B. bigemina*, *B. bovis*, *C. burnetii* and *A. bovis* in cattle in XUAR. The current data determined the infection rates of detected pathogens in cattle in that region and suggest the possible emergence of tick-borne diseases in animals in XUAR.

In chapter 2, TBPs were investigated in horses in XUAR. Molecular survey of *C. burnetii*, *Rickettsia* spp., *B. caballi* and *T. equi* were investigated in horses in XUAR by using nPCR assays and gene sequencing. Out of 200 samples tested, 114 (57.0%), 79 (39.5%), 79 (39.5%) and 49 (24.5%) were positive for *Rickettsia* spp., *C. burnetii*, *T. equi*, and *B. caballi*. Mixed infections involving 2-4 pathogens were observed in the present study. The most common dual infections were with *Rickettsia* spp. + *T. equi* while the most frequent triple infections were *C. burnetii* + *Rickettsia* spp. + *T. equi* with co-infection rates of 11.0% (22/200) and 8.5% (17/200), respectively. In addition, 11 (5.5%) samples were infected with the 4 TBPs (*Rickettsia* spp.+ *C. burnetii* + *T. equi* + *B. caballi*) among these co-infection. The current findings are expected to provide a basis for better TBPs (*B. caballi*, *T. equi*, *C. burnetii* and *Rickettsia* spp.) control in the region. These results also suggest that the persons associated with horses in the region should pay attention for preventing zoonotic

tick-borne pathogen (*B. caballi*, *T. equi*, *C. burnetii* and *Rickettsia* spp.) from horses.

In chapter 3, TBPs were identified in sheep in XUAR. Nested PCR assays and gene sequencing were used to detect *Babesia* spp., *Theileria* spp. and *Anaplasma* spp. in sheep from the bordering area in XUAR. Out of 323 samples tested in this study, 206 (63.8%), 60 (18.6%), 54 (16.7%), 51 (15.8%), 32 (9.9%), 19 (5.9%), 16 (5.0%) were positive for *A. ovis*, *B. motasi*-like, *A. bovis*, *T. uilenbergi*, *A. phagocytophilum*, *T. luwenshuni* and *B. motasi*-like Xinjiang, respectively. Mixed infections involving 2-3 pathogens were observed in the present study. The most common dual infections were *A. ovis* + *B. motasi*-like while the most frequent triple infections were *A. ovis* + *B. motasi*-like + *T. uilenbergi* with co-infection rates of 17.0% (55/323) and 5.0% (16/323), respectively. Meanwhile, only 1 sheep was dually infected with *A. phagocytophilum* + *T. luwenshuni*. These findings provide important data for understanding the distribution of *Babesia*, *Theileria* and *Anaplasma* in sheep from the bordering area in XUAR.

Overall, molecular detection of TBPs in livestock (cattle, horses, sheep) were investigated were analyzed. These results provide important data for understanding the distribution of TBPs, and is expected to improve the approach for control of tick-borne diseases in XUAR, China.

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