Abstract of Thesis/Dissertation

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Title : The molecular epidemiology of bovine *Babesia* species in livestock animals

in Mongolia

(モンゴルの家畜動物における牛バベシア種の分子疫学研究)

Abstract

Infectious diseases are a direct threat to cattle farming around the world. Among them, bovine babesiosis caused by the species of genus *Babesia* has a global distribution. In host animals, *Babesia* parasites invade red blood cells (RBCs), reproduce asexually, and egress from the infected RBCs, causing severe intravascular hemolysis, which results in fever, anemia, icterus, and hemoglobinuria. If the treatment is delayed, the affected cattle may die as a result of hypoxia-related causes. Several *Babesia* species infect cattle, but only four of them cause clinical babesiosis: *Babesia bovis*, *Babesia bigemina*, *Babesia naoakii*, and *Babesia divergens*. Bovine babesiosis causes a significant economic loss due to the costs of control and prevention, production losses, and animal deaths. As a result, control of bovine babesiosis is critical for sustainable cattle farming. However, the currently available methods for controlling bovine babesiosis are limited by a number of factors, including a lack of commercially available vaccines, low efficacy and adverse side effects of anti-babesial drugs, the development of acaricide resistance in ticks, and a lack of adequate epidemiological data in the endemic countries. A lack of understanding about the role of non-cattle livestock animals in the epidemiology of bovine *Babesia* species may also render the control methods ineffective.

Mongolia is an agriculturally rich country with large livestock populations. However, the profit from livestock farming remains low, because the country is unable to export livestock animals and their products to developed countries due to infectious diseases of veterinary and public health importance. According to a recent serosurvey, cattle across Mongolia were exposed to *B. bovis* and *B. bigemina* infections. However, molecular surveys to detect active *B. bovis* and *B. bigemina* infections were only conducted in a few Mongolian provinces. In addition, *B. naoakii*, a recently discovered *Babesia* species capable of causing clinical bovine babesiosis, has not been surveyed in Mongolia. Moreover, non-cattle livestock animals, which are grazed together with cattle in Mongolia, have never been surveyed for bovine *Babesia* species. As a result, the current status of the epidemiology of bovine *Babesia* species remains unclear in Mongolia.

Therefore, I designed a series of studies with the objective of surveying cattle and non-cattle livestock reared throughout Mongolia for bovine *Babesia* species with clinical significance. The specific objectives were to survey Mongolian cattle for *B. bovis*, *B. bigemina*, and *B. naoakii* using PCR assays and to survey Mongolian Bactrian camels and yaks for the *Babesia* species detected in cattle.

For the cattle survey, I prepared blood DNA samples from 725 cattle in 16 of the 21 Mongolian provinces and screened them using PCR assays specific to *B. bovis*, *B. bigemina*, and *B. naoakii*. As a result, I detected *B. bovis* and *B. bigemina* in cattle from all 16 provinces surveyed and *B. naoakii* in cattle from 11 provinces. The overall positive rates of *B. bovis*, *B. bigemina*, and *B. naoakii* infections were 27.9%, 23.6%, and 5.4%, respectively. This is the first report of *B. naoakii* in Mongolia. These findings highlight the need for monitoring cattle throughout Mongolia for clinical bovine babesiosis, as I found that *B. bovis*, *B. bigemina*, and *B. naoakii*, which can cause severe clinical bovine babesiosis, are widespread in Mongolia.

As the cattle in Mongolia were infected with *B. bovis*, *B. bigemina*, and *B. naoakii*, I surveyed the Bactrian camels for these three *Babesia* species. I collected blood samples from 305 Bactrian camels in six Mongolian provinces (Bayan-Ulgii, Govi-Altai, Khovd, Uvs, Zavkhan, and Bayankhongor) and extracted the DNA samples. Using the parasite-specific PCR assays, I screened these DNA samples for *B. bovis*, *B.*

bigemina, and *B. naoakii* infections. Similar to cattle, all three surveyed *Babesia* species were detected in the Bactrian camels in Mongolia. The overall positive rates of *B. bovis*, *B. bigemina*, and *B. naoakii* infections were 32.1%, 21.6%, and 24.3%, respectively. These infection rates were comparable to those observed in cattle. The findings of this study suggest that Bactrian camels are a well-adapted host for bovine *Babesia* species. Therefore, future research should look into the clinical significance of bovine *Babesia* species in Bactrian camels. Tick species that infest Bactrian camels also infest cattle in Mongolia. As a result, there is a possibility that bovine *Babesia* species might be transmitted from cattle to Bactrian camels and vice versa. Therefore, minimizing *Babesia* infections in Bactrian camels is critical for managing bovine babesiosis in Mongolia.

Similar to Bactrian camels, yaks are also grazed together with cattle in Mongolia. Therefore, I have conducted a survey to investigate whether yaks in Mongolia were infected with the *Babesia* species that infect cattle. For this study, I surveyed 375 yaks in eight Mongolian provinces, including Bayankhongor, Bayan-Ulgii, Khovd, Khovsgol, Omnogovi, Ovorkhangai, Uvs, and Zavkhan. Blood DNA samples from these yaks were screened for *B. bovis*, *B. bigemina*, and *B. naoakii* infections, using the specific PCR assays. I found that the Mongolian yaks were infected with *B. bovis* and *B. bigemina*, but not with *B. naoakii*. *Babesia bovis* infection was widespread, with 238 (63.5%) of 375 yaks tested the positive across all provinces, while only eight (2.1%) tested positive for *B. bigemina* in three provinces (Bayankhongor, Bayan-Ulgii, and Omnogovi). Additional research into the clinical significance of *Babesia* infections is now required in yaks, as a previous study demonstrated that yaks are susceptible to bovine babesiosis. The current study, the first to report *Babesia* infection in Mongolian yaks, emphasizes the importance of controlling *Babesia* infections in yaks for managing bovine babesiosis in this country.

To summarize, my findings show that the infections with *Babesia* species capable of causing clinical bovine babesiosis are common in cattle, Bactrian camels, and yaks in Mongolia. This observation, combined with the facts that all livestock are grazed together and that tick species infesting one animal type also infest others, suggests that *Babesia* infections might be transmitted by ticks among the cattle, Bactrian camels, and

yaks in Mongolia. My research results suggest that cattle throughout Mongolia are at a risk of bovine babesiosis and that minimizing the *Babesia* infections in cattle, as well as Bactrian camels and yaks, is critical for managing bovine babesiosis in this country. In addition to monitoring cattle for bovine babesiosis, future studies should investigate the clinical significance of *Babesia* infections in Bactrian camels and yaks in Mongolia.