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Applying the Simulation of Inter-Regional Movement of Japanese Dairy and Beef Cows: Estimation of the Surveillance Regions Following the Detection of Chronic Infectious Disease in a Disease-Free Country

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Abstract

Animal movement plays a critical role in the transmission of infectious diseases. The movement of infected cattle is suggested to contribute to the spread of chronic diseases such as bovine brucellosis and tuberculosis. When infected cattle are detected in disease-free countries, follow-up tests are conducted on all cattle with a history of cohabitation with the detected cattle to detect additional cases. Because follow-up tests require considerable human and testing resources, this study simulated the inter-regional movement of dairy and beef cows to identify regions where testing will be required after disease detection. The inter-regional movement probability was estimated from a complete set of cattle movement records in Japan, reflecting the characteristics of Japanese cattle movements between seven categories (Hokkaido, Tohoku, Kanto, Chubu, Kinki, Chugoku/Shikoku, and Kyushu/Okinawa). The results suggest that the possibility of conducting follow-up tests was higher in Hokkaido for dairy cows. In contrast, this possibility was higher for beef cows in Hokkaido and Kyushu/Okinawa, regardless of the region where the infected cows were detected. These findings are beneficial for allocating human and material resources to high-risk regions and developing more efficient disease control programs.

Discipline: Animal Science
Additional key words: brucellosis, cattle movement, movement probability distribution, tuberculosis

Introduction

Animal movement is one of the most important routes of transmission of infectious diseases. For infectious diseases with long latent periods, such as brucellosis (BR) and tuberculosis (TB), the potential movements of infected cattle may contribute to disease spread (Gilbert et al. 2005, Picasso et al. 2017, Stringer et al. 2008). Consequently, disease control measures should be implemented when these diseases are detected in disease-free countries, considering that the outbreak farm may not be the initial case.

In Japan, the detection and culling of cattle for BR and TB have been continuously conducted through periodic whole-herd inspections as part of a national eradication program under the Domestic Animal Infectious Diseases Control Law. Building on the program's success, the Ministry of Agriculture, Forestry, and Fisheries (MAFF) conducted nationwide surveillance from April 2018 to March 2021 to verify the absence of both diseases. Following this surveillance, MAFF submitted a declaration of freedom from BR and TB in bovids to the World Organisation for Animal Health (WOAH). WOAH reviewed and published the declaration on its website, effective from April 1, 2021 (MAFF 2022, WOAH 2022, Yamamoto & Hayama 2022).

Particularly in the case of TB, maintaining surveillance through ante- and post-mortem inspections is encouraged even in disease-free countries (WOAH 2024), and when a chronic infectious disease such as BR or TB is detected in a disease-free country, all cattle with a history of cohabitation with the infected cattle must be

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tested. This testing includes the farms where the infected cattle were identified and those where the infected cattle were previously kept.

Our previous studies revealed significant heterogeneity in cattle movement patterns across Japan, influenced by season, region, and age. These patterns differ between dairy and beef cows. To conduct a proper simulation considering these characteristics of cattle movement, we developed movement probabilities to predict cattle movement at the regional level. These probabilities reflect the characteristics of dairy and beef cows, respectively (Murato et al. 2021, 2023a, 2023b).

When cattle infected with infectious diseases such as BR or TB are detected in Japan, tests targeting cattle with a history of cohabiting with the infected cattle, or follow-up tests (FT), may be conducted on all farms where the infected cattle were raised from birth to detection. These tests aim to identify any additional infected cattle on these farms. Considering the characteristics of cattle movement patterns in Japan, the regional distribution of farms subject to FT varies depending on the region where the infected cattle were initially detected. Suppose farms subject to FT are distributed across multiple regions beyond the detection site or are likely to be located in certain regions regardless of the detection site; disease control strategies must address these assumptions. These include allocating adequate resources, such as testing supplies and human resources, which account for these situations. While earlier research has identified trends in cattle movement, their impact on FT requirements across regions remains insufficiently explored.

This study simulated the inter-regional movement of dairy and beef cows using a probability distribution developed to predict cattle movements at the regional level. Using the simulation results, we estimated the possibility of having a farm with cattle cohabiting with infected cattle for each region. Surveillance will be conducted in these regions when cattle infected with chronic infectious diseases, such as BR or TB, are detected in a disease-free country like Japan.

Material and methods

1. Summary of the simulation

In this simulation, we assumed the presence of a non-specific chronic infectious disease that does not result in death because of the clinical symptoms associated with the infection. We assumed that infected cattle were identified during a clinical inspection conducted during healthy slaughter or after natural death. We defined FT to include all cattle that cohabited with the infected cattle on the same farm for at least one day. Therefore, all regions where infected cattle were kept for at least one day from birth to death would be subjected to FT. Considering that the region where the infection was detected is always known, whereas the region of the infected cattle's birth is often unclear at the time of detection, we estimated the probability of each region being subjected to FT based on the region where the infected cattle were detected.

2. Simulation of inter-regional movement

We simulated the inter-regional movement of cows using a previously developed movement probability distribution (Murato et al. 2023b). The probability distribution represents the likelihood of cattle being kept in each region one month later, given the cattle's age, departure region, and birth region. The regions in the simulation were divided into seven categories (Hokkaido, Tohoku, Kanto, Chubu, Kinki, Chugoku/Shikoku, and Kyushu/Okinawa) as defined in the previous study. The simulation estimated the movement of target cows from birth to death (i.e., the time of infection detection) in a one-month time step. At the beginning of the simulation, the "age" of the target cow was set as zero months, and the "departure region" was set as the birth region. The movement probability corresponding to the given conditions (i.e., departure region, birth region, and age at the time of movement) was selected for each target cow to determine their location for the following month. By iteratively updating the destination region for each month, the entire history of the location from birth (i.e., zero months) to death was estimated. The age at death was assumed to be the average age at the time of disuse of the cows (66 months for dairy and 114 months for beef cows) (Livestock Improvement Association of Japan (LIAJ) 2013, LIAJ 2022). The inter-regional movement of the target cow was simulated 10,000 times for each of the seven birth regions for both dairy and beef cows.

3. Calculating the probability of cumulative stay

The regions where the target cow had been kept at least once since birth were counted for each detection region, that is, where the cattle were kept at the end of their lives, for both dairy and beef cows. For all target cows, the regions in which they had been kept at least once during their lives were identified. The number of corresponding simulations (C_i) was then tabulated for the detection regions (i), the region where the cow had been kept at least once (stayed region [j]), and the region where the cattle were born (birth region [k]).

$$C_i = \begin{pmatrix} C_{i11} & \cdots & C_{i1k} & \cdots & C_{i17} \\ \vdots & \ddots & \vdots & \ddots & \vdots \\ C_{ij1} & \cdots & C_{ijk} & \cdots & C_{ij7} \\ \vdots & \ddots & \vdots & \ddots & \vdots \\ C_{i71} & \cdots & C_{i7k} & \cdots & C_{i77} \end{pmatrix}$$

Although the simulations were iterated 10,000 times for each birth region (k), the number of cattle born in each region varied. Therefore, we weighted C_i using B_k, the proportion of the annual number of cattle born in each region (k), to calculate the weighted number of iterations (S_i) corresponding to the stayed region (j) and detection region (i).

$$S_i = C_i \times B_k = \begin{pmatrix} C_{i11} & \cdots & C_{i1k} & \cdots & C_{i17} \\ \vdots & \ddots & \vdots & \ddots & \vdots \\ C_{ij1} & \cdots & C_{ijk} & \cdots & C_{ij7} \\ \vdots & \ddots & \vdots & \ddots & \vdots \\ C_{i71} & \cdots & C_{i7k} & \cdots & C_{i77} \end{pmatrix} \begin{pmatrix} B_1 \\ \vdots \\ B_k \\ \vdots \\ B_7 \end{pmatrix} =$$

$$\begin{pmatrix} C_{i11} \times B_1 & + & \cdots & + & C_{i1k} \times B_k & + & \cdots & + & C_{i17} \times B_7 \\ \vdots & & \ddots & & \vdots & & \ddots & & \vdots \\ C_{ij1} \times B_1 & + & \cdots & + & C_{ijk} \times B_k & + & \cdots & + & C_{ij7} \times B_7 \\ \vdots & & \ddots & & \vdots & & \ddots & & \vdots \\ C_{i71} \times B_1 & + & \cdots & + & C_{i7k} \times B_k & + & \cdots & + & C_{i77} \times B_7 \end{pmatrix}$$

$$= \begin{pmatrix} S_{i1} \\ \vdots \\ S_{ij} \\ \vdots \\ S_{i7} \end{pmatrix}$$

Consequently, given a certain detection region (i), the probability of being the target of the FT (pFT_i) is obtained by dividing S_i by S_{ii}, or S_{ij}, where j=i.

$$pFT_i = S_i \div S_{ii} = \begin{pmatrix} S_{i1} \\ \vdots \\ S_{ij} \\ \vdots \\ S_{i7} \end{pmatrix} \div S_{ii}$$

Because the detection region, that is, the region at the time of death, is always included in the location history of the target cow, the pFT of the detection region is always 100%. Therefore, the pFT of the detection region was excluded from the evaluation. All analyses were conducted using R (version 4.3.3, R Core Team 2021).

Result

For dairy cows, pFT was highest in Hokkaido (27%-63%) compared to the other regions (0.02%-3%), in all regions except when Hokkaido was the detection region. When the region at death was Hokkaido, pFT was relatively low in other regions (0.01%-0.1%) (Fig. 1). For beef cows, when the detection region was Hokkaido, the pFT was highest in Kyushu/Okinawa (6%). Meanwhile, when the detection regions were Tohoku, Kanto, Chubu, or Chugoku/Shikoku, the pFTs were high in Hokkaido (2%-14%) and Kyushu/Okinawa (11%-16%). For Kinki, pFT was high in Chugoku/Shikoku (2%) and Kyushu/Okinawa (9%). Additionally, for Kyushu/Okinawa, the pFTs were low across all regions but showed slightly higher values in Hokkaido and Chugoku/Shikoku (1% in both cases) (Fig. 2).

Discussion

In this study, we simulated the lifelong movement history of Japanese cows using movement probability distributions generated from actual cattle movement data in Japan. Based on these simulations, we predicted the regions likely to be subjected to FT in case chronic infectious diseases, such as BR or TB, were confirmed in a disease-free country like Japan. For dairy cows, pFT was highest in Hokkaido when the detection region was outside Hokkaido. Conversely, when the detection region was Hokkaido, pFT was relatively low in other regions (Fig. 1). These findings reflect the common practice of outsourcing calf rearing from dairy farms outside Hokkaido to breeding farms in Hokkaido, leading to the congregation of dairy cows from other regions in Hokkaido. As Hokkaido is the largest dairy cow production region and a source of replacement heifers for other regions, many dairy cows move from Hokkaido to other regions. Meanwhile, focusing on the entire between-farm movement of Japanese dairy cows, most of those movements are within the region, especially within Hokkaido, indicating that most cows born in Hokkaido remain in the region for their entire lives (Murato et al. 2021). Our findings align with previously reported inter-regional movement trends of dairy cows. For beef cows, pFT was higher in Hokkaido, Kyushu/Okinawa, or both when the detection region was outside Kyushu/Okinawa (Fig. 2). These results align with those of previous studies identifying Hokkaido and Kyushu/Okinawa as the major sources of beef cows in Japan (Murato et al. 2023a).

This study employed a movement probability distribution based on one-month time steps. It does not consider whether cattle movement at a certain time or where it moves is affected by its past movement. For example, cattle that moved in a given month were less likely to move in the following month than those that did not. However, since the purpose of this study was to evaluate the relative likelihood of conducting FTs across regions by capturing trends in the movement of the cattle population, the impact of this limitation on the findings is unlikely to be significant.

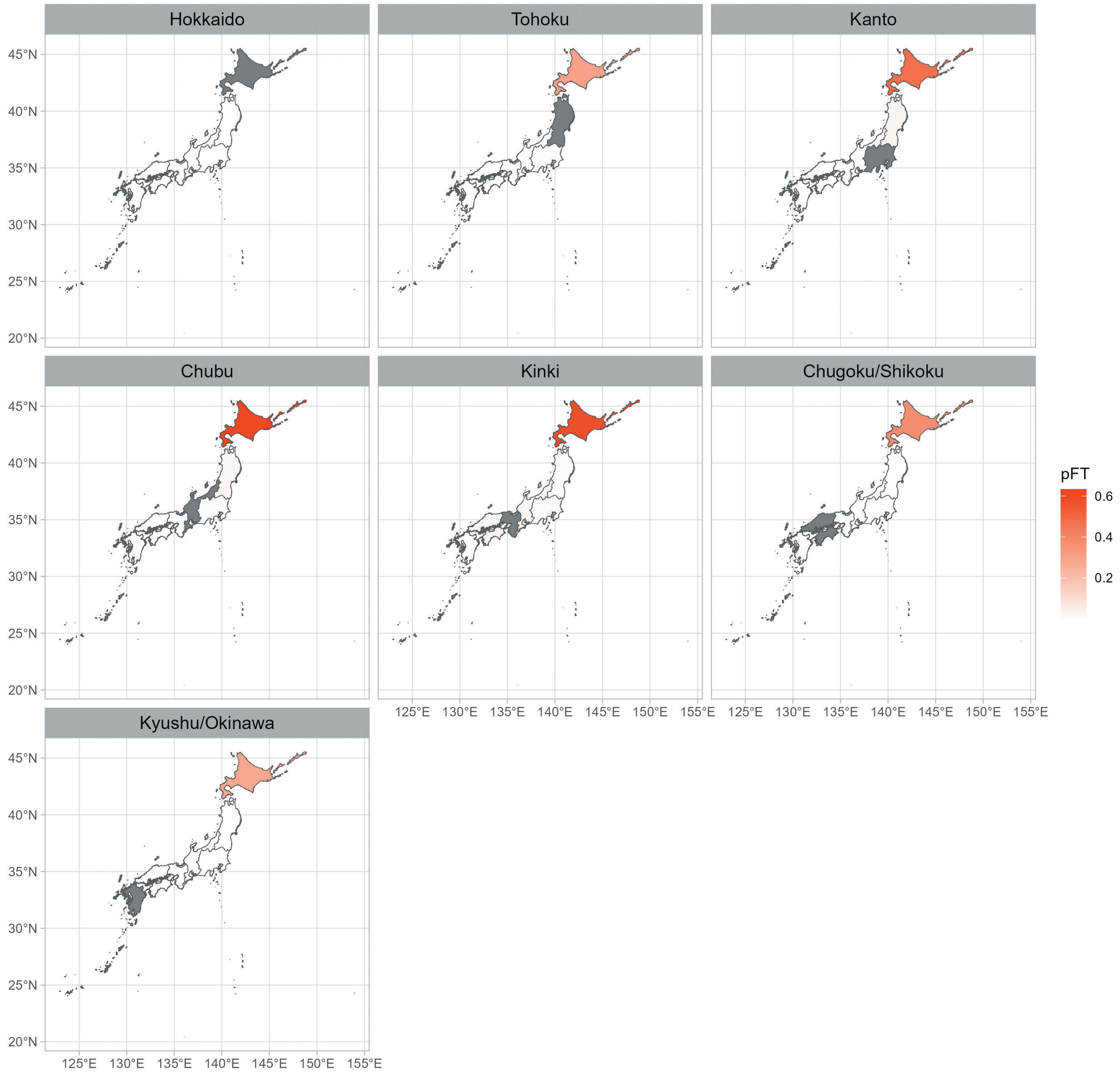

Fig. 1. The pFT for each detection region where the target cattle were located at 66 months old, or at the average time of disuse in dairy cows

The detection region was excluded from the evaluation and filled in gray because its pFT is always 100%.

This study demonstrated that dairy farms in Hokkaido and beef breeding farms in Hokkaido and Kyushu/Okinawa were more likely to be subjected to FT than farms in other regions, regardless of where infected cows are detected. Therefore, in Hokkaido and Kyushu/Okinawa, securing human and material resources and developing a disease control program during normal times will facilitate an effective initial response to disease outbreaks. Further studies should investigate seasonal and temporal variations in cattle movements to capture dynamic trends that may affect disease spread and surveillance strategies.

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References

Gilbert, M. et al. (2005) Cattle movements and bovine tuberculosis in Great Britain. *Nature*, **435**, 491-496.

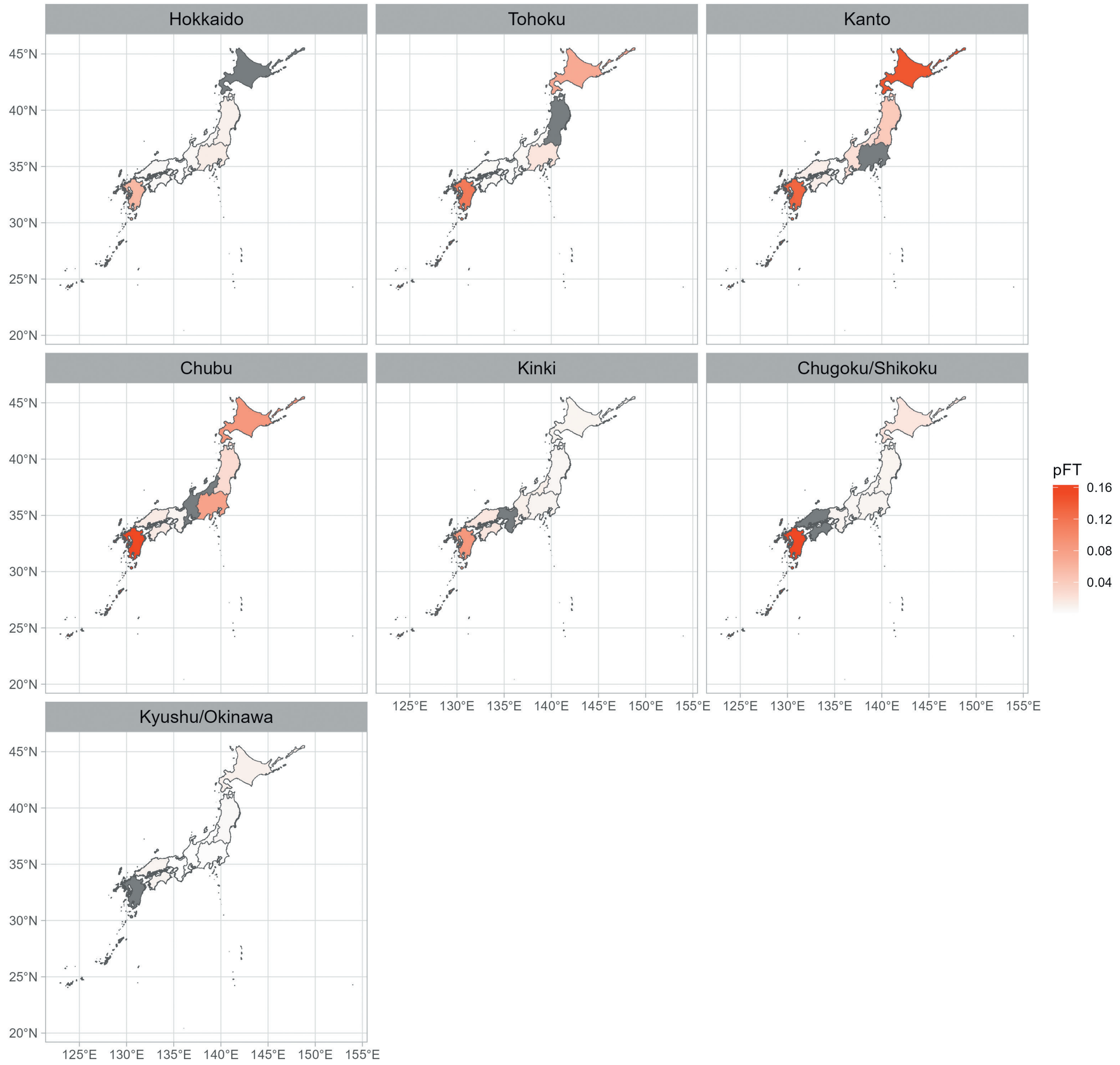

Fig. 2. The pFT for each detection region where the target cattle were located at 114 months old, or at the average time of disuse in beef cows

The detection region was excluded from the evaluation and filled in gray because its pFT is always 100%.

Livestock Improvement Association of Japan (2013) Nikuyougyuu no hanshokuseiseki ni tsuite (The reproductive performance of beef cattle). https://liaj.lin.gr.jp/wp-content/uploads/2023/12/liaj140_01.pdf [In Japanese].

Livestock Improvement Association of Japan (2023) Nyuuyougyuugun nouryokukentei seiseki no matome 2022 nen (Summary of dairy herd performance test results in 2022). https://liaj.lin.gr.jp/wp-content/uploads/2024/03/R04matome.pdf [In Japanese].

Ministry of Agriculture, Forestry and Fisheries (2022) Wagakuni no ushi no buruserashou oyobi kekkaku no seijouka sengen ni tsuite (Declaration of Freedom from Bovine Brucellosis and Tuberculosis in Japan). https://www.maff.go.jp/j/press/syouan/douei/220830.html [In Japanese].

Murato, Y. et al. (2023a) Region-wise analysis of beef cow movements in Japan. *Frontiers in Veterinary Science*, **10**. 1012978.

Murato, Y. et al. (2023b) The probability distributions of the movement of dairy and beef cattle in Japan: a data note. *BMC Res. Notes*, **16**, 153.

Murato, Y. et al. (2021) Region-wise analysis of dairy cow movements in Japan. *BMC Vet. Res.*, **17**, 305.

Picasso, C. et al (2017) Epidemiological investigation of bovine tuberculosis outbreaks in Uruguay (2011-2013). *Prev. Vet. Med.*, **138**, 156-161.

R Core Team (2024) *R: A Language and Environment for*

Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria. https://www.R-project.org/.

Stringer, L. A. et al. (2008) Risk associated with animals moved from herds infected with brucellosis in Northern Ireland. *Prev. Vet. Med.*, **84**, 72-84.

World Organisation for Animal Health (2022) Self-declared Disease Status. https://www.woah.org/en/what-we-offer/self-declared-disease-status/

World Organisation for Animal Health (2024) Terrestrial Animal Health Code. Infection with *Mycobacterium tuberculosis* complex. https://www.woah.org/en/what-we-do/standards/codes-and-manuals/terrestrial-code-online-access/?id=169&L=1&htmfile=chapitre_bovine_tuberculosis.htm

Yamamoto, T. & Hayama, Y. (2022) Recent Initiatives for Improving Animal Health Surveillance System in Japan. *J. Vet. Epidemiol.*, **26**, 116-125 [In Japanese with English summary].