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Research Article

Enhancing AI-Based Risk Prediction for Animal Disease Outbreaks in Korea Using KAHIS Big Data.

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Abstract

This study presents an integrated framework for predicting and managing animal disease outbreaks in Korea using artificial intelligence (AI) models powered by big data from the Korea Animal Health Integrated System (KAHIS). First introduced during the 2016–2017 highly pathogenic avian influenza (HPAI) epidemic, these deep learning-based models estimate transmission risk by analyzing livestock vehicle movement patterns. The system produces farm- and municipality-level risk scores to guide targeted interventions for transboundary animal diseases such as HPAI, foot-and-mouth disease (FMD), African swine fever (ASF), and lumpy skin disease (LSD). While the models have proven effective in early detection and response, they are constrained by limited outbreak samples, outdated datasets, and the exclusion of environmental and vector-borne transmission variables. To enhance predictive capacity and disease preparedness, future models should incorporate multivariable data inputs and remain adaptable to evolving epidemiological landscapes.

Keywords : Artificial intelligence, transboundary animal disease, KAHIS, big data, Korea.

INTRODUCTION

Artificial intelligence (AI) has emerged as a transformative tool in epidemiology, offering real-time predictive capabilities for infectious disease outbreaks. While traditional mathematical models have long been used to simulate disease transmission, they often fall short in processing large-scale, rapidly evolving data (Yilmaz-Cagirgan and Cagirgan, 2020). AI overcomes these limitations by identifying complex patterns within big data, enabling more flexible and accurate risk prediction (Bajwa et al., 2021).

In response to repeated outbreaks of highly pathogenic avian influenza (HPAI), foot-and-mouth disease (FMD), and African swine fever (ASF), Korea incorporated AI algorithms into its national disease control strategy. The Korea Animal Health Integrated System (KAHIS), launched in 2014, provided the infrastructure for developing AI-based risk models, which were first applied during the 2016–2017 HPAI epidemic (Kim et al., 2018; APQA, 2024a).

This study reviews the structure, application, and performance of AI-based risk prediction models implemented in Korea from 2016 to 2024. It further evaluates their effectiveness across multiple transboundary animal diseases—including HPAI, FMD, ASF, and lumpy skin disease (LSD)—and outlines future directions for improving adaptability, precision, and field utility.

MATERIALS AND METHODS

Korea Animal Health Integrated System (KAHIS)

The Korea Animal Health Integrated System (KAHIS) is a centralized web-based platform that supports nationwide disease control by integrating real-time data on livestock farms, facilities, vehicles, diagnostic results, and biosecurity measures (APQA, 2024a). Operated by the Animal and Plant Quarantine Agency (APQA), the national animal health authorities, the system is accessible via both internal government networks and the internet. KAHIS maintains structured records on various facility types—including farms, feed factories, slaughterhouses, manure treatment plants, hatcheries, and egg packing plants. It also monitors livestock vehicle movements using GPS data and a geographic information system (GIS). Vehicles are classified into 24 types based on transport purpose, such as animals, feed,

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manure, raw milk, eggs, or personnel. These data streams form the basis for epidemiological tracing and AI-driven risk assessment (Yoon et al., 2021a).

Big Data Platform and Analytical Pipeline

The AI-based risk analysis model is integrated into KAHIS and operates on an external big data platform (NDAP®, ktNexR, 2015). This platform uses the Hadoop Distributed File System (HDFS) for parallel storage of high-volume datasets and Apache Hive for distributed querying. A combination of ETL (Extract, Transform, Load) tools and Python-based pipelines preprocess the raw data into structured analytical datamarts. Final analysis results are stored in Tibero® (TmaxTibero, 2015), a relational database management system. Visualizations and reports are automatically generated through the KAHIS interface and made accessible via the "Decision Support" menu for authorized users (APQA, 2022). Robotic Process Automation (RPA) has been deployed since 2022 to streamline repetitive reporting tasks.

Deep Learning Risk Prediction Model

Model Framework and Assumptions

The model is designed to predict the likelihood of disease transmission between livestock farms based on epidemiological vehicle movements. It assumes that transmission risk is influenced by multiple factors, including:

- Livestock species and production type (e.g., breeder, broiler, layer, chicken, duck),
- Farm size (i.e., herd/flock size),
- Frequency, recency, and temporal order of vehicle visits,
- Time intervals between visits to infected and subsequently visited farms,
- Vehicle type (e.g., manure, feed, personnel).

Risk is primarily modulated by the spatiotemporal characteristics of vehicle movement. Specifically, the model tracks vehicles that have visited outbreak farms within a disease-specific tracing window, as stipulated in the Standard Operating Procedure (SOP) for each disease. For example, the tracing period is defined as 21 days for HPAI and ASF, 14 days for FMD, and 28 days for LSD.

Each vehicle visit to a non-infected farm is assigned a risk score based on the above factors. The model then calculates a cumulative farm-level exposure score by summing the time-weighted risk contributions of all relevant vehicle visits as follows:

$$Exposure_j = \sum_{i=1}^{N_j} R_{ij} \cdot e^{-\lambda \Delta t_{ij}}$$

Where,

- *$Exposure_j$*: Total exposure score for farm j_j, representing its cumulative risk of infection.
- N_j: Number of relevant vehicle visits to farm *j* by vehicles that previously visited outbreak farms within the applicable SOP-defined tracing window.
- R_{ij}: Risk weight for the *i*-th visit to farm *j*, incorporating vehicle type, farm type, and farm size.
- Δt_{ij}: Time interval (in days) between the vehicle's visit to the outbreak farm and its visit to farm *j*.
- λ: Decay rate parameter representing reduction in transmission probability over time.
- $e^{-\lambda \Delta t_{ij}}$: Temporal decay function modeling virus survivability on fomites such as vehicle surfaces.

This modeling framework allows for quantifying indirect farm-to-farm transmission potential and supports the prioritization of high-risk farms for targeted disease control interventions (Yoon et al., 2020).

Data Processing and Model Training

Raw KAHIS data are processed through ETL routines and transformed into modeling-ready datamarts. Records are cleaned, deduplicated, and normalized. Time-series features such as visit frequency, interval lag, and cumulative exposure count are engineered from vehicle movement logs. Meteorological and environmental variables were excluded due to a lack of validated correlation at the time of development.

The predictive model is a supervised binary classifier implemented using a multi-layer perceptron (MLP) artificial neural network. The input layer accepts engineered features, which are fed into three hidden layers with 10 nodes each and hyperbolic tangent (tanh) activation functions. The output node produces a probability value (between 0 and 1), representing the predicted risk of disease occurrence at a farm. Model training uses mini-batch stochastic gradient descent with backpropagation to minimize the sum of squared errors. A dropout rate of 0.5 is applied during training to mitigate overfitting. Hyperparameters were tuned using stratified cross-validation, and model selection was based on the highest F1-score on the validation set.

Output and Reporting Structure

The final risk score is a continuous value from 0 to 1 and is classified into four levels:

+ [0-0.2), ++ [0.2-0.5), +++ [0.5-0.8), ++++ [0.8, 1.0), where [] includes the boundary and () excludes it.

Results are exported as Excel files with four sheets:

- Sheet 1: Municipality-level summary of high-risk farm counts
- Sheet 2: Farm-level list with exposure scores
- Sheet 3: Vehicle metadata (type, ID, route history)
- Sheet 4: Network map of outbreak-to-farm transmission

These outputs support targeted disinfection, surveillance, and communication by regional authorities.

Vehicle Tracking and Epidemiological Relationships

Vehicle visit events are registered when GPS signals remain within the predefined geofenced boundaries of livestock facilities for more than two minutes. Since 2021, the geofencing system has been enhanced by introducing an inner geofence to more accurately determine whether a vehicle has entered the premises (i.e., crossed the fence or gate), rather than merely stopping at or near the entrance. This improvement in spatial resolution enables the model to distinguish between actual entries and pass-by events, thereby enhancing the accuracy of epidemiological linkage (Son et al., 2022).

RESULTS

HPAI Risk Prediction Model

Risk Assessment for Outbreaks in Poultry Farms

Korea's first AI-based risk prediction model for HPAI was developed in early 2016 using outbreak data from January to November 2015 and launched as a pilot in the first half of that year. In 2017, it was enhanced with a larger dataset of 804 outbreak farms from 2014 to 2017 (Kim et al., 2018). The model analyzed 9,094 livestock vehicle visits to outbreak farms within 21 days prior to disease onset, resulting in 90,264 secondary visits to other facilities. Notably, 96.6% (87,173 visits) were to poultry farms, highlighting the importance of vehicle movement in HPAI transmission. To reflect seasonal patterns, data were stratified into four periods: early 2014, and the winters of 2014/15, 2015/16, and 2016/17. Training, validation, and test sets were drawn accordingly to capture time-dependent transmission dynamics.

The final model was a multi-layer perceptron (MLP) with three hidden layers of 10 nodes each, using a hyperbolic tangent activation function and 0.5 dropout. It trained for 140,000 epochs, converging near 40,000. On a test set of 34,733 records, it achieved a recall of 0.90, precision of 0.54, and F1-score of 0.65, correctly identifying 3,030 of 3,361 outbreak-related cases, with 2,867 false positives. Validation showed significantly higher predicted risk scores for outbreak farms (mean 0.20 ± 0.31) than non-outbreak farms (0.18 ± 0.30, $P < 0.001$). In the 2017/18 winter, the model also predicted higher risk for outbreak farms (0.25 ± 0.17 vs. 0.17 ± 0.29), though the difference was not statistically significant ($P = 0.21$) (Yoon et al., 2020).

High-risk scores were typically linked to vehicles visiting outbreak farms shortly before other poultry farms, and to farms with frequent vehicle traffic. Early risk signals were associated with vehicles used for culling and manure transport. As more data accumulated, the model increasingly reflected risks related to epidemiological links between farms of the same integrator, similar production types, and confirmed direct vehicle entries (Yoon et al., 2020; Yoon et al., 2022; APQA, 2024c).

Risk Assessment for Detection of H5/H7 Avian Influenza Viruses in Wild Birds

When H5 or H7 avian influenza viruses (AIVs), which are known for their potential high pathogenicity, are detected in wild birds (e.g., feces, captured birds, carcasses), livestock vehicle movement data within a 3 km radius of the detection point is retrieved from KAHIS. The data covers vehicle movements from one day before the sampling date to the analysis date, accounting for the possible delay between viral contamination and the discovery of infected feces or carcasses in the environment (Yoon et al., 2021b). The visit history of these vehicles to poultry farms is traced to assess potential risk.

A Python-based program was developed to calculate the risk for each poultry farm visited by these vehicles, as well as for the municipalities where the farms are located. The model classifies farms, vehicles, and migratory bird habitats into six infection stages based on their contamination status with AIV at time t. Infection dynamics are simulated using an individual-based stochastic model, repeated 3,000 times per scenario and replicated 50 times. The number of times each farm is predicted to be infected is summarized into a statistical distribution, which is modeled using a Gaussian mixture model. Farm-level risk is categorized into four tiers: ++++, +++, ++, and + (APQA, 2019). These values are aggregated at the municipal level, and K-means clustering is applied to classify municipalities into four risk levels: ++++, +++, ++, and + (Yoon et al., 2021a; Yoon et al., 2021b). The final output includes a choropleth map showing municipality-level risk, along with statistics on the number and types of vehicles and the number of poultry farms visited in each area. Since January 2022, this entire process—from data extraction to report generation—has been automated using robotic process automation (RPA), reducing the processing time from over 3 hours to under 15 minutes (Yoon et al., 2022; Cho, 2022).

Epidemiological analysis showed that approximately 80% of related vehicle movements involved livestock transport, feed delivery, and consulting services. When AIVs were detected in the capital region, related farms were widely dispersed nationwide, primarily due to the movement of these vehicles. The highest predicted risks were consistently observed in the detection areas and adjacent municipalities (Son et al., 2022).

FMD Risk Prediction Model

The risk prediction model for FMD in cloven-hoofed animal farms was developed using the same algorithmic framework as the HPAI model for poultry farms. The initial model was trained in 2016 using data from 180 pig farms and five cattle farms with confirmed FMD cases between December 2014 and April 2015. However, due to the limited number of cattle cases in the training dataset, the model's predictive performance for cattle farms was suboptimal. To improve accuracy, the model was retrained using additional data from nine outbreaks that occurred during the 2017 epidemic. A total of 1,698 livestock vehicle visits to outbreak farms within 14 days prior to the onset of outbreaks were analyzed. These visits resulted in 53,011 subsequent movements to livestock facilities, of which 50,045 (94.4%) were to farms raising cloven-hoofed animals.

The final model architecture consisted of three hidden layers using sigmoid activation functions and no dropout. It was trained over 700 epochs, with the loss function stabilizing after approximately 300 epochs. In a test dataset comprising 15,951 samples, the model correctly identified 124 true positives out of 133 actual cases, yielding a high recall of 0.93. However, the model also produced 771 false positives, resulting in a precision of 0.14 and an F1-score of 0.24 (Internal report, unpublished).

The model's predictive performance varied by species. For swine farms, high-risk predictions were frequently associated with visits by vehicles transporting livestock manure. In contrast, for cattle farms, visits by feed transport vehicles were more commonly linked to elevated risk (APQA, 2024d).

ASF Risk Prediction Model

Risk Assessment for ASF Outbreaks on Swine Farms

At the time of the AI-based model's development in 2017, no outbreak data on ASF was available, as the first confirmed case in South Korea occurred in 2019 (MAFRA, 2024a). As a result, the model was not initially designed to predict ASF outbreaks. Instead, it was adapted by calibrating the existing FMD risk prediction model to focus specifically on swine farms and vehicle movements related to swine operations.

Since the initial outbreak in 2019, the calibrated model has been utilized to assess the risk of epidemiologically linked swine farms. High-risk predictions are typically associated with farms visited by a variety of epidemiological vehicles, including those used for feed transport, animal transport, manure transport, veterinary pharmaceuticals, veterinary services, consultancy, and artificial insemination semen delivery (APQA, 2024b).

Epidemiological Analysis for ASF Virus Detection in Wild Boars

Upon detection of ASF virus in wild boars, livestock vehicle movements within a 3 km radius of the detection site are examined, reflecting the possible movement range of the infected wild boars before detection. For carcasses, vehicles are traced from the estimated date of death to the analysis date; for hunted or captured wild boars, tracking begins from the date of capture. After identifying the relevant vehicles, their visit histories to pig farms are comprehensively analyzed. Unlike farm outbreaks, farm- or municipality-level risk categories are not publicly disclosed for ASF detections in wild boars. Instead, municipalities are classified based on the number of epidemiologically linked pig farms within their boundaries. A detailed epidemiological report is generated, including information on the detection location, vehicle movements, and related farms. As with AIV detections in wild birds, this report is produced using robotic process automation (RPA) (Cho, 2022).

Feed transport vehicles account for the majority of epidemiological vehicle movements linked to wild boar detections, followed by animal transport and consultant vehicles. During the initial ASF outbreaks in 2019–2020 in northern Gyeonggi-do and Gangwon-do, related farms were primarily concentrated near detection areas due to strict movement controls. However, as the outbreak progressed, epidemiologically related farms became more geographically dispersed nationwide. This expansion was largely attributed to the limited movement restrictions imposed on most livestock vehicles—except manure transport vehicles—which were subject to strict monitoring within designated control zones (MAFRA, 2024b).

Epidemiological Analysis for LSD Outbreaks on Cattle Farms

Unlike FMD, HPAI, or ASF, LSD is primarily transmitted by blood-sucking insects acting as biological vectors, rather than through mechanical transmission via contaminated vehicles. It is hypothesized that such insects may attach to vehicles, enabling indirect transmission between farms rather than direct vehicular spread (Bianchini et al., 2023).

Considering this unique transmission pathway, vehicles that passed within a 3 km radius of an outbreak farm (outbreak area) from 28 days before the outbreak to the outbreak date are identified. Their subsequent visits to cattle farms are then traced. Although the existing FMD risk model is applied to LSD outbreaks for analytical purposes, no farm- or municipality-level risk scores are generated. Instead, epidemiological information linking outbreak areas, vehicle movements, and related farms is disclosed.

During the 2023 LSD epidemic, vehicles passing near 107 outbreak farms and subsequently visiting other cattle farms were predominantly animal transport vehicles (31.8%), followed by feed transport vehicles (23.3%) and consultant vehicles (9.8%). These vehicles accessed cattle farms across 159 municipalities (epidemiological areas), including 34 with confirmed outbreaks. In municipalities with outbreak farms, animal transport vehicles accounted for 30.9% of movements, followed by feed transport (25.3%) and consultant vehicles (12.5%). In contrast, in municipalities without outbreaks, feed transport vehicles were most prevalent (39.5%), followed by animal transport (18.3%) and consultant vehicles (9.1%).

Risk Information by Disease

Table 1 summarizes key risk assessment parameters for each disease, including the geographic radius used to identify passing vehicles, the timeframe for vehicle data extraction and tracking, the year in which risk assessments began, and the total number of services delivered (as of 27 December 2024).

Publicly accessible risk categories for farms and municipalities are available on the official website of the Animal and Plant Quarantine Agency (APQA) for HPAI (APQA, 2024c), FMD (APQA, 2024d), and ASF (APQA, 2024b).

Table 1. AI-Based Risk Analysis for HPAI, ASF, FMD, and LSD in Livestock Farms in Korea.

Disease	**HPAI**		**ASF**		**FMD**	**LSD**
Items	**Farm**	**Wild bird**	**Farm**	**Wild boar**		
Geographic scope for identifying passing vehicles	Farm	3km-radius	Farm	3km-radius	Farm	3km-radius
Timeframe for vehicle extraction and tracking (before the outbreak date)	21 days	2 days	21 days	Estimated date of death (for carcasses) or date of capture (for live boars)	21 days	28 days
Starting year for providing risk	2016	2019	2019	2020	2017	2023
Yearly service delivery totals (as of 27 December 2024)						
2016	419	-	-	-	-	-
2017	18	57	-	-	-	-
2018	22	64	-	-	2(+ NSP 1)	-
2019	-	32	14	33	4(+ NSP 2)	-
2020	109	407	2	1,211	NSP 3	-
2021	47	147	5	964	-	-
2022	90	326	7	965	-	-
2023	42	126	10	936	11	107
2024	20	130	11	934	-	24

Note: *NSP = Non-Structural Protein*

DISCUSSION

AI-based risk analysis for livestock farms has become an essential tool for animal health management in Korea. The model has demonstrated its value by accurately identifying high-risk farms, enabling targeted preventive measures and reducing the impact of animal diseases. However, limitations in data availability for certain diseases and the constraints of the current model highlight the urgent need to improve its predictive capabilities. Looking ahead, it is critical to prepare for potential outbreaks of emerging diseases. Lessons learned from ASF and LSD outbreaks emphasize the need for a flexible and scalable prediction model that can adapt to new diseases, even when initial data is limited. Enhancing the AI-based prediction system will not only improve disease prevention and response but also strengthen the resilience and sustainability of Korea's livestock industry. In contrast, evaluation of the FMD model was limited by a small number of outbreaks—only nine in 2017 and two in 2018—restricting robust statistical validation. Nevertheless, both the HPAI and FMD models benefited from proper parameter tuning and model selection based on the highest F1-scores, partially addressing concerns regarding overfitting, which are common in machine learning applications (Slob et al., 2021).

At the time of model development in 2017, disease transmission in Korea was primarily attributed to farm-to-farm spread, especially via livestock vehicles (APQA, 2015; APQA, 2016; Yoon et al., 2015; Lee et al., 2021). In response, Korean authorities enforced strict biosecurity regulations, requiring livestock vehicles to undergo multi-stage disinfection, including mandatory stops at designated disinfection facilities and on-farm sanitation using high-pressure spraying equipment (MAFRA, 2023; 2024c–e). However, more recent outbreaks of HPAI and ASF suggest a shift in transmission patterns. Environmental sources and indirect routes—such as contaminated equipment or human-mediated spread—are now considered more prominent than direct vehicle-borne pathways (APQA, 2023; APQA, 2024e). These findings highlight the need to expand the current model's scope beyond vehicle movement. Incorporating environmental variables, human traffic, and biosecurity compliance metrics would allow for multivariable risk modeling that more accurately reflects present-day transmission dynamics (Rees et al., 2021; Han et al., 2022; Min and Yoo, 2023).

Another major limitation is the lack of model updates since 2017. Although the ASF model was first applied in 2019, it remains based on the epidemiological assumptions of earlier diseases and does not reflect significant shifts in ASF transmission patterns observed since 2020 (Yoo et al., 2021; APQA, 2022–2024). Similarly, the model for LSD does not currently generate risk scores; it only provides epidemiological tracing outputs. These gaps reinforce the need for dynamic, disease-specific models that are regularly updated and capable of rapid adaptation to emerging pathogens.

Despite these limitations, field-level feedback supports the model's practical value. A nationwide survey conducted in June 2024 showed that 100% of the 46 respondents—animal health officials across 218 jurisdictions—found the AI-based risk assessments helpful for disease control. The reports were used to inform administrative units and farmers, enabling preventive actions such as vehicle disinfection, serological testing, and clinical surveillance tailored to regional conditions (Internal report, http://www.open.go.kr).

CONCLUSION

AI-based risk prediction models have played a critical role in Korea's efforts to manage transboundary animal diseases, particularly by enabling early warnings and targeted interventions. However, the current systems face clear limitations, including outdated data, an overemphasis on vehicle-based transmission, and insufficient flexibility to adapt to new or evolving disease patterns. To remain effective, future models must integrate diverse data sources—such as environmental and meteorological factors—and support continuous updates tailored to each disease. Building such flexible and scalable AI systems will be essential not only for enhancing outbreak preparedness and response, but also for strengthening Korea's long-term livestock biosecurity and sustainability.

Data Availability

The internal report referenced in this study is available upon request from the corresponding author. Risk analysis results for HPAI, ASF, and FMD outbreaks on livestock farms are publicly accessible on the APQA website (https://www.qia.go.kr).

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Declaration of Competing Interest

The authors declare that there are no known financial conflicts of interest or personal relationships that could have influenced the work reported in this paper.

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