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Assessing the impact of biosecurity compliance on farmworker and livestock health within a one health modeling framework

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ABSTRACT

Biosecurity compliance refers to adherence to protocols aimed at preventing infectious disease outbreaks and controlling antimicrobial resistance (AMR) across human, animal, and environmental interfaces. While many models focus solely on animal health, this study develops a One Health modeling framework to assess the impact of different compliance levels on both animal and farmworker health. The model integrates Ordinary Differential Equations (ODE) for pathogen transmission in animals and the environment with Stochastic Differential Equations (SDE) for disease spread among farmworkers. The next-generation matrix approach estimates the basic reproduction number $\left(R_0^{[i]}\right)$ specific to each pathogen strain *i*, identifying thresholds for outbreaks or elimination of infection. Using literature-derived data on *Salmonella* transmission dynamics, the model is validated, and key parameters values are estimated. Using the calibrated model, we examine infection transmission in dairy cattle and zoonotic spillover to farmworkers with a focus on five key biosecurity measures: (1) animal movement control and quarantine, (2) disease monitoring and reporting, (3) hygiene and disinfection, (4) feeding and watering practices, and (5) antimicrobial stewardship. Simulations reveal that compliance with biosecurity measures that reduce host-to-host transmission in the animal population has the highest impact on the reduction of infection both in animal and farmworker populations. Further ODE-SDE model analysis indicates that full compliance with the other biosecurity measures is insufficient to prevent outbreaks in a dairy farm. These results are consistent with the local and global sensitivity analyses of the model. The One Health modeling framework developed in this study can also be applied to other zoonotic diseases as a guiding tool for decision making and optimal resource allocation to reduce the likelihood of spillover.

1. Introduction

Antimicrobial resistance (AMR) is a growing global health threat, affecting both human and animal populations. Intensive animal farming has significantly contributed to the emergence and spread of resistant pathogens, particularly *Escherichia coli* and *Salmonella* [1]. The overuse and misuse of antibiotics in livestock, agriculture, and human medicine accelerate AMR, leading to difficult-to-treat infections and increased public health risks [2–4]. According to the Centers for Disease Control and Prevention (CDC), *Salmonella* bacteria are responsible for approximately 1.35 million foodborne infections annually in the U.S., leading to 26,500 hospitalizations and 420 deaths [5]. Rising antibiotic resistance in nontyphoidal *Salmonella* strains, approaching 10 % for ciprofloxacin, underscores the urgent need for stricter AMR control measures [3,4,6].

Over 75 % of emerging infectious diseases originate from animals, with intensive farming, deforestation, and environmental disturbances creating favorable conditions for pathogen spillover and the evolution of AMR [8]. The One Health approach is essential for tackling AMR and zoonotic spillover (i.e., the transmission of pathogens from animals to humans), recognizing the deep interconnection between human, animal, and environmental health [7]. Poor biosecurity measures on farms exacerbate zoonotic transmission, allowing AMR pathogens to spread between livestock, farmworkers, and surrounding communities [9].

Biosecurity measures, including hand hygiene, sanitization, and the use of personal protective equipment (PPE), play a crucial role in limiting zoonotic pathogen transmission within farms. However, the effectiveness of these interventions varies based on implementation, monitoring, and enforcement strategies, highlighting the need for more

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robust evidence of their impact on human health outcomes [10]. Inconsistent implementation and monitoring of biosecurity measures remain significant challenges in farm settings, affecting the control of zoonotic pathogens and AMR. Studies have shown that while biosecurity protocols exist, their effectiveness depends on proper enforcement and adherence, which varies widely across farms. The lack of standardized assessment tools and data-sharing mechanisms further complicates efforts to evaluate and improve biosecurity compliance, potentially increasing the risk of pathogen spillover into human populations [11]. Biosecurity implementation in dairy farms is often hindered by inconsistent veterinary guidance and poor communication between stakeholders, leading to distrust and reduced compliance. Additionally, regulatory enforcement tends to emphasize penalties over educational support, further complicating adherence to effective biosecurity measures [12].

Despite the emphasis on biosecurity, many models focus on pathogen spread within livestock, often prioritizing intra-animal dynamics while giving limited attention to human exposure pathways [13,14]. Morgan et al. (2023) [15] highlight this gap, emphasizing the need for models that integrate human exposure pathways and targeted interventions to mitigate public health risks. The present study aims to fill this gap by constructing and analyzing a hybrid animal-environment-farmworker model of zoonotic spillover.

Biosecurity measures are essential for mitigating AMR and zoonotic spillover, most studies assessing their effectiveness have relied on qualitative approaches rather than quantitative modeling. Expert evaluations highlight that while measures like herd movement control and hygiene protocols are considered effective, their implementation remains inconsistent due to economic and logistical barriers [16]. A survey of 56 cattle farms in North-West England further revealed that biosecurity adherence varies significantly, often due to financial constraints and the lack of proven efficacy [17]. Additionally, a study across five European countries found that farmers' risk perception and sense of responsibility toward public health strongly influence compliance [18]. While these studies provide valuable behavioral insights, they do not quantify how biosecurity compliance impacts the dynamics of disease transmission, particularly in the case of *Salmonella*. This study integrates biosecurity measures into a One Health modeling framework to assess their direct influence on *Salmonella* transmission dynamics and farmworker health risks.

We develop a mathematical modeling framework to assess the impact of biosecurity compliance on disease transmission risks in farm environments. By employing both deterministic and stochastic modeling approaches, we aim to (i) identify key biosecurity interventions that significantly reduce zoonotic spillover, (ii) quantify how farmworker compliance influences pathogen persistence and transmission, and (iii) provide data-driven insights to improve One Health biosecurity policies. This research contributes to a more comprehensive understanding of human-animal interactions in disease control and highlights the role of biosecurity and antimicrobial stewardship in mitigating zoonotic risks in livestock settings.

2. Material and methods

2.1. Modeling zoonotic spillover

Zoonotic pathogen transmission occurs through multiple interconnected pathways, involving livestock, the environment, and farmworkers. As shown in Fig. 1. We assume that disease progression in the cattle population follows a Susceptible-Infected-Recovered (SIR) model with two pathogen strains. Specifically, the cattle population consists of susceptible animals S_a, animals infected with drug-susceptible and drug-resistant strains (I_{a1} and I_{a2}, respectively), and recovered animals R_a which may gradually lose immunity over time. Infected animals may be isolated or culled, while unidentified cases may contribute to continued pathogen circulation. Disease transmission in the farmworker

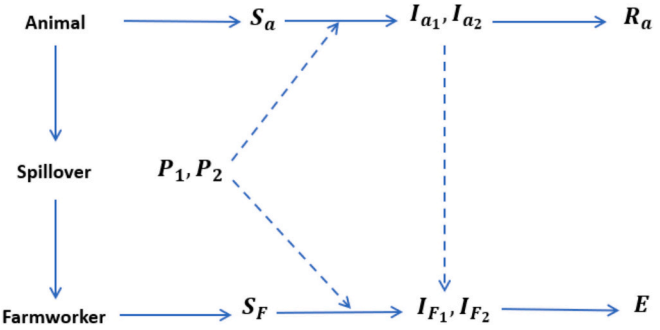

Fig. 1. A conceptual framework of zoonotic spillover. Zoonotic spillover takes place from infected animals I_{a1}, I_{a2} and pathogens in the environment P_1 and P_2 to susceptible.

population follows a structured compartmental model. Susceptible farmworkers (S_F) may become infected with either drug-susceptible (I_{F1}) or drug-resistant strains (I_{F2}) through direct contact with infected animals or indirect exposure to contaminated environmental reservoirs. Once infected, farmworkers may exit the farm due to illness (E), reducing the risk of further transmission within the workforce.

Pathogen spillover occurs through both direct and indirect transmission pathways. Direct transmission arises from close contact between farmworkers and infected livestock, while indirect transmission results from exposure to contaminated environmental reservoirs containing drug-susceptible (P_1) or drug-resistant (P_2) pathogens. The importance of direct zoonotic transmission has been highlighted in models such as Allen & Nandi (2021) [19], which describe spillover dynamics between infected animals and humans without explicitly modeling environmental reservoirs. Meanwhile, environmental contamination plays a critical role in sustaining pathogen circulation in livestock populations [20], which in turn may contribute to human exposure through indirect pathways.

The progression of infection in the cattle population is modeled using a system of Ordinary Differential Equations (ODE), which assumes homogeneous mixing and follows mass action principles [21], making it suitable for large populations. In contrast, disease spread in farmworker population is modeled using Stochastic Differential Equations (SDE) to account for the greater randomness in disease transmission within a small population. This hybrid ODE-SDE approach allows us to incorporate both deterministic and stochastic effects in pathogen transmission, providing a more realistic representation of disease spread under varying biosecurity compliance levels. The following two sections provide a detailed formulation of each model and its underlying assumptions.

2.2. Model of disease transmission in cattle population

The cattle population is structured into six compartments: animals susceptible to infection $S(t)$, animals infected with the drug-susceptible strain I_1(t), animals infected with drug-resistant strain $I_2(t)$, recovered animals $R(t)$, and two compartments in the environment that measure the density of drug-susceptible pathogen $P_1(t)$ and the density of drug-resistant pathogens $P_2(t)$ at time t. The total cattle population at any given time is the sum of these groups: $N(t) = S(t) + I_1(t) + I_2(t) + R(t)$.As shown in Fig. 2 (a), susceptible animals can become infected through contact with infected animals or contaminated environment, and infected animals can maintain the survival of pathogens in the environment by shedding pathogens. In the ODE model, we do not consider reverse transmission from infected farmworkers to animals (reverse zoonosis), as existing epidemiological evidence suggests that such events are extremely rare. A portion of animals, which experience development of drug resistance due to either inadequate treatment or misuse of primary drugs [22,23] will move from the drug-susceptible

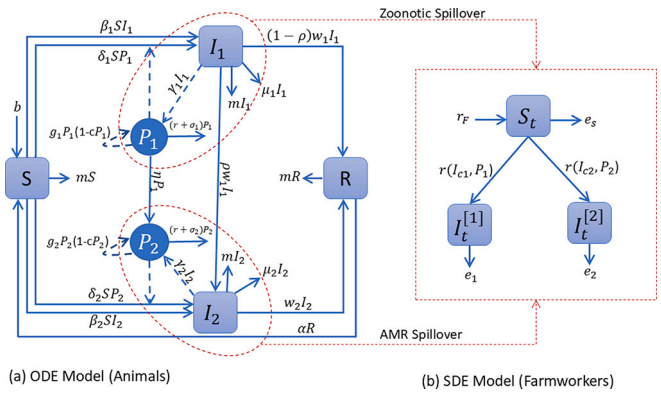

Fig. 2. Compartmental diagram of the hybrid ODE-SDE model connecting (a) the SIRSP ODE model of disease spread in animal population to (b) SI SDE model of disease spread in farmworker population. The solid lines represent movement from one compartment to another, whereas dashed lines represent pathogen transmission, replication, survival, and shedding. Red dashed lines indicate the spillover from animals and contaminated environment to farmworkers. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

group, I_1, to the drug-resistant group, I_2. Furthermore, some pathogens in the environment evolve from drug-susceptible (P_1) to drug-resistant (P_2) [24,25].

In the ODE model we assume that (i) there is a homogeneous mixing of the animal population, where each animal has an equal chance of contact with others, and uniform susceptibility to infection; (ii) there is an inconsiderable or no latent period between an animal's infection and its infectiousness, (iii) transmission can occur directly, from adequate contact with an infected animal, or (iv) indirectly, through exposure to a sufficient concentration of environmental pathogens. The ODE set representing the SIRSP model of disease spread in animal population is formulated as follows:

$$\frac{dS}{dt} = b - (\beta_1 I_1 + \beta_2 I_2)S - (\delta_1 P_1 + \delta_2 P_2)S + \alpha R - mS \tag{1}$$

$$\frac{dI_1}{dt} = \beta_1 S I_1 + \delta_1 S P_1 - (\mu_1 + m + w_1) I_1 \tag{2}$$

$$\frac{dI_2}{dt} = \beta_2 S I_2 + \delta_2 S P_2 + \rho w_1 I_1 - (\mu_2 + m + w_2) I_2 \tag{3}$$

$$\frac{dR}{dt} = (1-\rho) w_1 I_1 + w_2 I_2 - (\alpha + m) R \tag{4}$$

$$\frac{dP_1}{dt} = \gamma_1 I_1 + g_1 (1 - c P_1) P_1 - (r + \sigma_1) P_1 - \eta P_1 \tag{5}$$

$$\frac{dP_2}{dt} = \gamma_2 I_2 + \eta P_1 + g_2 (1 - c P_2) P_2 - (r + \sigma_2) P_2 \tag{6}$$

where all parameter values $b, m, \beta_1, \ldots$ are positive constants. Indexes 1 and 2 correspond to drug-susceptible and drug-resistant strains, respectively. Parameters δ and β are respectively the transmission coefficients for environment-to-host and host-to-host contacts, μ is the natural per-capita death rate across the entire dairy cow herd, w is the per-capita recovery rate, $1/\alpha$ is the average duration of immunity for recovered cows, ρ is the proportion of animals that develop resistance to drug during the treatment, η is the proportion of pathogens that evolve from the drug-susceptible to drug-resistant, γ is the shedding rate to the environment, r is the pathogen removal rate in the environment due to cleaning, σ is the pathogen natural decay rate, g represents the pathogen replication rate, and $1/c$ is the carrying capacity of the pathogen in the environment. In this study, we utilize parameter values specific to *Salmonella* for simulation purposes. However, the model is adaptable to a wide range of infectious diseases. Table 1 provides a summary of the model parameters, units, descriptions, ranges, and values.

2.3. Model of disease transmission in farmworkers

To model disease spread in the farmworker population we assume that (i) the farm managers maintain a consistent supply of workers; (ii) the number of farmworkers varies around a constant value of K; (iii) all active farmworkers are healthy but susceptible to the infection; (iv) farmworkers stop working from the time that they become infectious; (v) the latent period is negligible, and (vi) the farmworkers become

Table 1
Description of the parameters, values, ranges and units used the SIRSP model describing *Salmonella* transmission dynamics on a cattle farm.*

Symbol: Description (Remarks)	Unit	Value	Range	Refs
b : animal birth/ purchase rate	$cow\ day^{-1}$	1.6	1–3	E
m : mortality/culling rate	day^{-1}	0.00055	0.0002–0.001	E
η: rate of drug resistance development in environment	$cow\ day^{-1}$	0.15	0.05–0.9	A
ρ: rate of within host drug resistance development	—	0.15	0.05–0.9	A
r: pathogen removal rate	day^{-1}	0.9	0–4.6	E
α: rate of loss of immunity	day^{-1}	0.01	0.005–0.2	[20]
$1/c$: carrying capacity of pathogen in the environment	$cells$	10^6	$\frac{2}{3}\times 10^6 - 2\times 10^6$	[20]
Parameters associated with the drug-susceptible strain				
β_1: host-to-host transmission rate	$day^{-1}\ cow^{-1}$	4×10^{-5}	$0 - 4\times 10^{-4}$	V [13,26]
δ_1: environment-to-host transmission rate	$cells^{-1}\ day^{-1}$	5×10^{-6}	$10^{-7} - 5\times 10^{-5}$	V [13,14]
γ_1: pathogen shedding rate	$cells\ day^{-1}\ cow^{-1}$	4×10^8	$10^8 - 10^9$	[14]
g_1: pathogen growth rate	day^{-1}	0.6	0.2–1.0	V [20]
σ_1: pathogen natural decay rate	day^{-1}	0.25	0.05–0.78	V [27]
w_1^*: recovery rate	day^{-1}	0.11	0.08–0.16	V [20]
μ_1: mortality rate due to the infection	day^{-1}	0.011	0.006–0.016	V [28]
Parameters associated with the drug-resistant strain				
β_2: host-to-host transmission rate	$day^{-1}\ cow^{-1}$	3×10^{-5}	$0–3\times 10^{-5}$	A
δ_2: environment -to-host transmission rate	$cells^{-1}\ day^{-1}$	4×10^{-6}	$10^{-7} - 4\times 10^{-5}$	A
γ_2: pathogen shedding rate	$cells\ day^{-1}\ cow^{-1}$	4×10^8	$10^8 - 10^9$	A
g_2: pathogen growth rate	day^{-1}	0.6	0.2–1.0	A
σ_2 pathogen natural decay rate	day^{-1}	0.25	0.05–0.78	A
w_2^*: recovery rate	day^{-1}	0.09	0.05–0.12	A
μ_2: mortality rate due to the infection	day^{-1}	0.013	0.01–0.02	A

* The parameter value may vary and is not necessarily derived from empirical data. Abbreviations: A: Assumed, E: Estimated, V: Varies. See supplementary document S-Doc 5 for detailed parameter estimation.

infected either by contacting infectious animals or pathogen in the environment. Fig. 2 (b) provides a schematic representation of the SDE model. Let $S(t)$ be the number of susceptible farmworkers at time t. Then using the logistic growth model, we have

$$\frac{dS(t)}{dt} = r_F S(t)\left(1 - \frac{S(t)}{K}\right), \tag{7}$$

where K is the average number of farmworkers required to operate the farm and r_F is the recruitment rate of the farmworkers. Given that the number of farmworkers can change on a daily basis, it is more realistic to use the stochastic logistic equation given by

$$dS_t = r_F S_{t-1}\left(1 - \frac{S_{t-1}}{K}\right) dt + \sigma S_{t-1}\sqrt{dt}\,\epsilon, \tag{8}$$

where dS_t is the change in the number of farmworkers over the time increment dt, $\sqrt{dt}\,\epsilon$ is an approximation for each increment of the Brownian motion process, ϵ is the random noise and σ is the standard deviation parameter. The rate of healthy farmworks who quit working, e_s is equal to $r_F S^2(t)/K$.

It is important to note that farmworkers who contract the infection will promptly be substituted with healthy individuals and regarded as newly recruited personnel. Hence the infection does not influence the numbers of active farmworkers as governed by Eq. (8). Contacts with the contaminated environment or infected animals can make a portion of farmworkers infected. Let $I_t^{[j]}$ be the number of farmworkers infected with strain j of the pathogen at time t, where $j = 1$ is the drug-susceptible and $j = 2$ is the drug-resistant strain. Then the change in the number of infected farmworkers can be stochastically modeled by:

$$dI_t^{[j]} = r(I_{cj}, P_j)\, I_{t-1}^{[j]}\left(1 - \frac{I_{t-1}^{[j]}}{S_{t-1}}\right) dt + \sigma I_{t-1}^{[j]}\sqrt{dt}\,\epsilon \tag{9}$$

where $r(I_{cj}, P_j) = \mu I_{cj} + qP_j$ is the infection growth function with animal-to-farmworker and environment-to-farmworker infection transmission rates μ and q, respectively. The cumulative incidence of animals infected with strain j, denoted as I_{cj}, is obtained by simulating the SIRSP Eqs. (1)–(6) describing disease spread in the animal population. Given the lack of direct estimates for μ and q in the literature, these values were determined based on expert opinion and iterative model simulations.

Specifically, μ was set to a small value $(\mu = 0.0005)$ to reflect the high compliance of farmworkers with biosecurity measures, thereby minimizing direct animal-to-human transmission risk. Likewise, q was considered negligible $(q \approx 0)$ due to the routine use of head-to-toe protective equipment, which substantially reduces environment-to-human transmission. The stochastic nature of farmworker infections is further captured by the volatility parameter σ, representing random exposure events that contribute to infection risk. These parameter assumptions align with expert assessments and ensure biologically plausible infection dynamics within the farm setting.

Additionally, S_{t-1} *is* the total number of healthy farmworkers at the time step t-1, acting as a carrying capacity in the logistic growth term in Eq. (9). The rate of infectious farmworks who will permanently quit working, e_j,is given by $r(I_{cj}, P_j)\frac{(I_{t-1}^{[j]})^2}{S_{t-1}}$. Table 2 provides a detailed summary of the parameter values used in the stochastic differential equation (SDE) model for disease transmission among farmworkers.

2.4. Empirical data and model validation

Empirical data for model validation was extracted using Web Plot Digitizer v4.6 [29] from published literature. Animal prevalence data was obtained from commercial dairy farms in New Mexico [30] and a Michigan dairy herd [31], while environmental contamination data, including soil and water samples, was sourced from studies in southwestern dairy farms and commercial agricultural facilities [32,33].

All datasets, including their sources, formats, and descriptions, are summarized in Supplementary Document S-Doc 2 (Table S1), along with an external link to the full dataset. Model calibration was performed using the least squares method with MATLAB's fmincon applied to Eqs. (1)–(6), ensuring the model accurately replicates observed prevalence patterns.

Table 2
Parameters of the stochastic model of disease transmission in farmworker population.

Parameters	Description	Value (unit)
r_F	average recruitment rate of farmworkers	0.1 (1/Day)
μ	infection rate of animal-to-human infection spread	0.0005 (1/Day)
q^*	rate of environment-to-human infection spread	0 (1/Day)
K	The maximum number of farmworkers	60 (N/A)
σ	volatility or magnitude of the stochasticity	0.3 $(1/\sqrt{Day})$
N_0	Initial farmworker population size	50 (N/A)
I_0	The initial number of infected farmworkers	1 (N/A)
T	Study period	180 (Day)

* The rate was considered negligible, assuming head-to-toe protection of farmworkers on a daily basis. N/A: Not Applicable - Dimensionless

2.5. Biosecurity measures

Biosecurity measures prevent and control infectious disease spread, with farmworker adherence crucial for minimizing zoonotic risks. Table 3 summarizes key biosecurity measures in dairy farms and their influence on parameters of Eqs. (1)–(6).

In this study, biosecurity compliance was classified into four levels: *Excellent*, where farmworkers rigorously adhered to all biosecurity measures with continuous monitoring and veterinary consultation; *Good*, where most measures were followed with minor lapses and timely veterinary oversight; *Marginal*, where adherence was inconsistent, with occasional veterinary involvement; and *Low*, where biosecurity practices were largely neglected, with minimal monitoring and slow responses to health issues.

2.6. Transparency and reproducibility

We have developed our computational tools using Matlab and Python environments. To ensure transparency and reproducibility of results obtained in this study, we have made all codes accessible for the

Table 3
Summary of key biosecurity measures in dairy farms and their corresponding effects on parameters in Eqs. (1)–(6).

Biosecurity Measures	Key Practices	Affected Parameters
Animal Movement Control and Quarantine	Controlling animal movements, quarantine sick or new animals and visitor restrictions.	β
Disease Monitoring and Reporting	Regular disease testing, timely reporting, and regular involvement with a vet.	β, δ
Hygiene and Disinfection	Regular cleaning and disinfection of tools, equipment, and environment.	δ
Feeding and Watering Practices	Maintaining clean feed and water supplies, using pasteurized milk or treated waste milk for calves, avoiding raw milk consumption.	δ
Antimicrobial Stewardship	restricting and optimizing antimicrobial use, education and training farmworkers.	ρ, η
Manure and Contamination Management	Regular cleaning of watering and feeding areas and equipment, and using separate manure-handling equipment for feeding cows	r

research community to examine, adapt, and use. These resources are available in the GitHub repository: https://github.com/AArjcode/Biosecurity-Compliance-One-Health-Modeling-Framework.

3. Model performance and analysis

3.1. Model performance

As mentioned in Section 2.4, to assess the validity of Eqs. (1)–(6), we employed six distinct datasets to determine if the model can accurately conform to the underlying data patterns. Model performance was assessed by comparing simulated outputs with observed data from six datasets. A summary of model fit and goodness-of-fit measures is provided in Supplementary Document S-Doc 3 (Figure S2, Table S2). Table S2 shows that SIRS models better fit herd infection data (R^2 = 0.78–0.81), while SIRSP models (i.e., models that include contaminated environment) reasonably capture environmental contamination (R^2 = 0.62–0.69). The AIC and AICc values further supported the goodness of fit. To further assess model validity, we show that all solutions remain biologically meaningful, ensuring positivity and boundedness (see section S-Doc 4.1 of the supplementary document).

3.2. Model analysis and basic reproduction numbers

The basic reproduction number, R_0 is defined as the average number of secondary infections that one infected animal or pathogen in the environment generates in a herd that is entirely susceptible [19]. To estimate R_0, we applied the Next Generation Matrix (NGM) approach to Eqs. (1)–(6). This involves linearizing the system at the Disease-Free Equilibrium (DFE) and calculating the spectral radius of the next generation matrix. Environmental contamination influences disease transmission in three distinct ways, leading to different formulations of R_0. As described in [20], there are three possible roles of the environment in transmission of infection: *(I) Transition:* the environment can act as a temporary host for pathogens; (II) *Transition–Reservoir*: the environment is a reservoir for pathogens until they are transmitted to susceptible cows; and (III) *Reservoir*: the environment solely acts as a permanent reservoir of pathogens supporting their growth and survival [22]. Each of these cases leads to a different R_0 expression (see the Supplementary Document S-Doc 4.2 for details). Nevertheless, all three R_0 estimates converge on the threshold value of 1 such that R_0 values for case (II) are always bounded by cases (I) and (III). Given that the model incorporates two pathogen strains, R_0 will be determined by the maximum value corresponding to each strain [45,46]. Specifically,

$$R_0 = max\left\{R_0^{[i]}, i = 1, 2\right\}, \tag{10}$$

where $R_0{}^{[i]}$ represents the strain-specific basic reproduction number, i = 1 corresponds to the drug-susceptible and $i = 2$ to the drug-resistant strain. As shown in the Supplementary Document S-Doc 4.2, $R_0^{[i]}$ is expressed as a function of $R_{0_d}^{[i]}$ and $R_{0_{in}}^{[i]}$, which are the average numbers of new infections transmitted directly from an infectious host and indirectly from the contaminated environment to susceptible hosts, respectively. The value of $R_{0_{in}}^{[i]}$ is regulated by pathogen growth-decay ratio $R_{0_e}^{[i]}$ in the environment.

Analysis of the model shows that there are up to four equilibrium solutions: Disease-Free Equilibrium (*DFE*)**:** No infection persists in the system, Drug-Susceptible Dominant Equilibrium (E_1): Only the drug-susceptible strain is present, Drug-Resistant Dominant Equilibrium (E_2): Only the drug-resistant strain is present and Coexistence Endemic Equilibrium (E_{12}): Both strains are present. The conditions for stability and existence of these equilibria are determined by specific threshold conditions. Formal theorems outlining these conditions are provided in sections S-Doc 4.3 and 4.4 of the Supplementary Document.

3.3. Baseline parameter values

The baseline parameter values used in Eqs. (1)–(6) are specific to *Salmonella* infection and summarized in Table 1. A few values were assumed based on expert opinion and calibrated through model simulations to ensure biologically meaningful outcomes. A full explanation of parameter estimation, including transmission rates, pathogen decay, and the impact of antibiotic resistance on fitness, is provided in Supplementary Document S-Doc 5. We hypothesized that antibiotic-resistant bacteria may have slower growth, reduced competition, or lower virulence, leading to decreased transmissibility [51,52]. Hence, we set and values slightly lower than to account for this fitness cost. The range of parameter values used for numerical simulations are provided in Tables S3-S7 section S-Doc 6.

3.4. Local and global sensitivity analyses

To assess parameter influence on model dynamics, we conducted Local Sensitivity Analysis (LSA) and Global Sensitivity Analysis (GSA). For LSA, we computed the Elasticity Index $Y_k^{R0} = \frac{\partial R0}{\partial k} \times \frac{k}{R_0}$, which measures how small perturbations in parameter k affect R_0 Results [34].

Fig. 3(a) and 3(b) indicate that parameters $b, m, \mathrm{w}, \beta, \delta$ *and* γ have the most substantial impact on R_0values. Also, the parameters b and m are inversely related to disease persistence.

For GSA, we employed the Random Forest (RF) machine learning approach to rank parameter importance based on its predictive power. The RF was chosen due to its ability to handle nonlinear interactions efficiently. A 5-fold cross-validation ensured robustness, yielding an accuracy of 99 % across test runs. The most influential parameters for both drug-susceptible and drug-resistant strains were β, δ, m *and* b (Fig. 3 (c) and 3(d)). The remaining 17 parameters had minimal impact and are collectively represented as parameter x. To derive these rankings, 2500 random samples were generated across the parameter ranges. In addition to RF we employed other machine learning models to ensure that the GSA results consistent (see section S-Doc 6).

4. Impacts of biosecurity compliance

4.1. Outbreak risk management

We used the estimated R_0 values to assess the impact of biosecurity measures on outbreak risk. The parameters β (direct transmission rate), δ (indirect transmission rate), r (pathogen removal rate), and η (rate of drug resistance development in environment) were selected due to their strong association with biosecurity measures (Table 3, Fig. 2). These parameters directly influence disease control strategies, making them critical for optimizing biosecurity protocols. Birth rate (b) and mortality rate (m), though significant, were excluded as they pertain more to farm management than biosecurity. Additionally, deviations in b and m would invalidate the assumption of a stable 3000-cattle population.

We evaluated eight biosecurity compliance scenarios to assess their impact on disease outbreaks. The first four (S1–S4) vary a single parameter: S1 (direct transmission β_1, β_2), S2 (indirect transmission, δ_1, δ_2), S3 (pathogen removal, r), and S4 (drug resistance development, η). The remaining scenarios combine these factors: S5 (S1 and S2), S6 (S1 and S3), S7 (S2 and S3), and S8 (S1, S2 and S3). Our simulations indicate that η (drug resistance development in the environment) has minimal impact on R_0. To streamline the analysis, we excluded combinations involving η, focusing instead on the most influential biosecurity parameters.

Our simulations ran for 180 days, with initial conditions set as S_0 = 2998, $I_1 = 1, I_2 = 1$,

$R = 0, P_1 = 10^8, P_2 = 0.5 \times 10^8$. All parameters followed a normal distribution, except the host-to-host transmission rate, which followed a gamma distribution [40]. We conducted 2500 simulations per

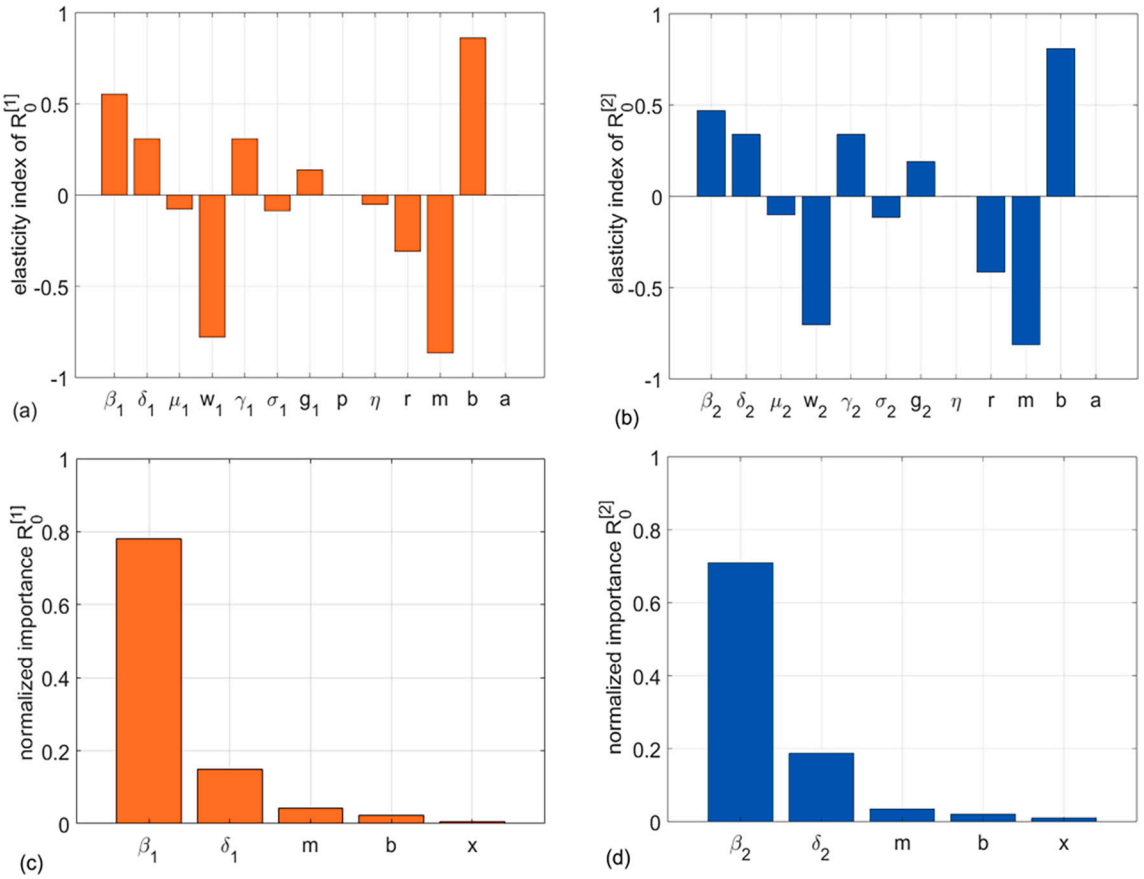

Fig. 3. Local and global sensitivity analyses of Eqs. (1)–(6). (a) Local sensitivity index of $R_0^{[1]}$ with different parameters, (b) Sensitivity index of $R_0^{[2]}$ with different parameters. The global sensitivities with respect to (c) $R_0^{[1]}$, and (d) $R_0^{[2]}$.

compliance level for single-parameter scenarios (S1 —S4), ensuring β_1, and β_2 changed together for consistency. Combined scenarios (S5 – S8) involved two or three parameters varying simultaneously. Scenarios S5 – S7 generated 16 sub-scenarios, while S8 contained 64, but we focused on the worst-case scenario (low compliance across all parameters). To evaluate compliance levels, we divided parameter ranges into four interval: Excellent (strictest biosecurity), Good, Marginal, and Low (most relaxed biosecurity). This classification quantifies the effect of compliance on R_0,and prevalence and incidence of infection. Details for scenarios S1–S8 are provided in Supplementary Document S-Doc 6 (Tables S3-S7).

The primary objective of outbreak risk management is to reduce the basic reproduction number below one. Fig. 4, Fig. S3 and Fig. S4 in the Supplementary Document illustrate the impact of biosecurity compliance on R_0 under different scenarios. Simulations of scenarios S1–S4 indicate that host-to-host transmission rates (β) have the most significant impact on R_0. In scenarios S1 and S2, improving compliance from low to good leads to a sharp decline in R_0, indicating that reducing direct (β_1, β_2) and indirect (δ_1, δ_2) transmission is highly effective in controlling disease spread, specially host-to-host transmission rate (See Fig. S3). However, further improvement from good to excellent results in only a marginal reduction, suggesting diminishing returns at higher compliance levels. Box plot representations of Scenarios 5–7 are provided in Fig. 4. Note that compliance with biosecurity measures in Scenario 7 is less effective, primarily due to insufficient emphasis on reducing direct transmission rates β_1, β_2.

4.2. Compliance with antibiotic stewardship program

Simulations of the two-strain SIRSP model demonstrate that the rate of within host drug resistance development (ρ) plays a critical role in pathogen dynamics. As shown in Fig. 5, our results identify a threshold value near $\rho = 0.15$, below which drug-susceptible strains dominate. However, once ρ exceeds this threshold, drug-resistant strains become increasingly prevalent. This finding highlights the importance of managing antimicrobial use to prevent surpassing this critical resistance threshold and limiting the emergence of drug-resistant pathogens.

4.3. Animal and farmworker health

Details of calculating cumulative incidence in animal population is provided in section S-Doc 7. As shown in Figure S5, the cumulative incidence of drug-susceptible infections is much higher than drug-resistant ones in cattle, particularly in scenarios involving direct transmission coupled with marginal or low compliance to biosecurity measures. An analysis of 66 sub-scenarios within the farmworker population indicates that marginal or low biosecurity compliance can result in a high infection prevalence, particularly when direct host-to-host transmission is not effectively minimized (Figure S6). A detailed explanation of results is provided in Supplementary Document S-Doc 7.

5. Discussion

The proposed ODE-SDE hybrid model introduces a novel One Health framework for evaluating the impact of biosecurity compliance on zoonotic spillover. While the ODE model captures the large-scale transmission dynamics in livestock and the environment, the SDE model incorporate the uncertainty of disease spread among farmworkers, reflecting the stochastic nature of human interactions with infected animals and contaminated environments.

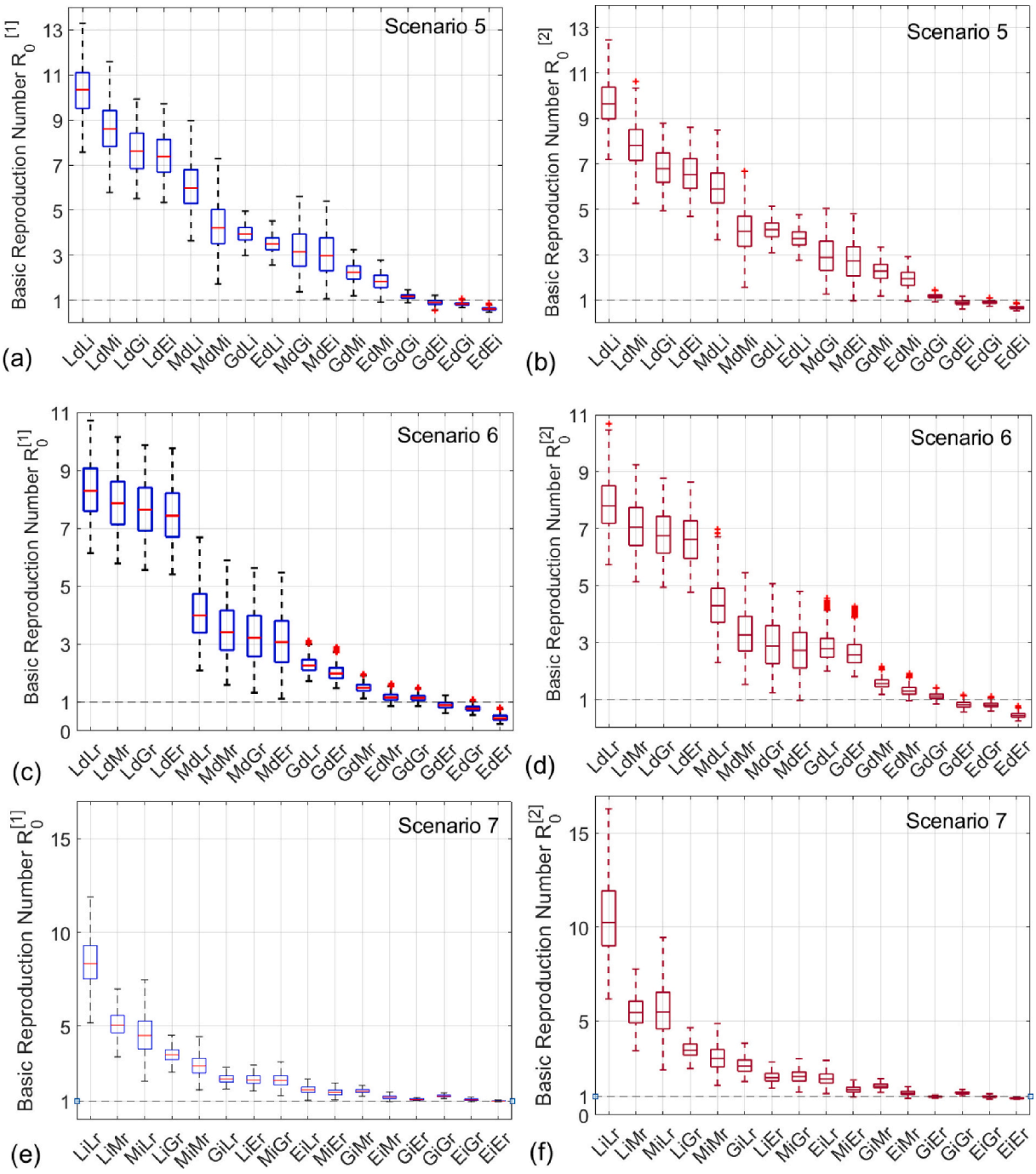

Fig. 4. Boxplots of the basic reproduction numbers and for various combinations of biosecurity measures at levels of Low (L), Marginal (M), Good (G), and Excellent (E) across different parameters values of direct and indirect transmission rates, denoted by (d) and (i), and pathogen removal rate denoted by (r) on each panel. It can be seen that increased levels of compliance with biosecurity measures associated with direct transmission and indirect transmission (i.e., scenarios 5 and 6) can significantly reduce the risk of outbreaks.

Our findings indicate that a single biosecurity measure is insufficient to prevent zoonotic spillover, and a combination of measures with high compliance is necessary. Specifically, preventing direct transmission between herds is essential for reducing bacterial infections in both livestock and farmworkers. Studies on dairy farms in the UK have also demonstrated that maintaining closed herds and implementing strict quarantine protocols are key strategies for infection control [16]. These results emphasize that minimizing close contact among animals is a critical biosecurity approach to protecting both livestock and human health.

Moreover, compliance with biosecurity measures is a major determinant of outbreak dynamics [35–39]. Several empirical studies suggest that farmworker education and behavioral change programs can significantly reduce pathogen transmission within and between farms [40–43]. However, there is still a lack of systematic quantification of the relative effectiveness of different biosecurity measures, making risk assessments difficult. This study addresses this gap by applying a model-driven approach to rank biosecurity measures based on compliance levels.

By focusing on the transmission of *Salmonella* on dairy farms, our simulations demonstrate that low compliance with certain biosecurity measures can counteract the effectiveness of all others. For example,

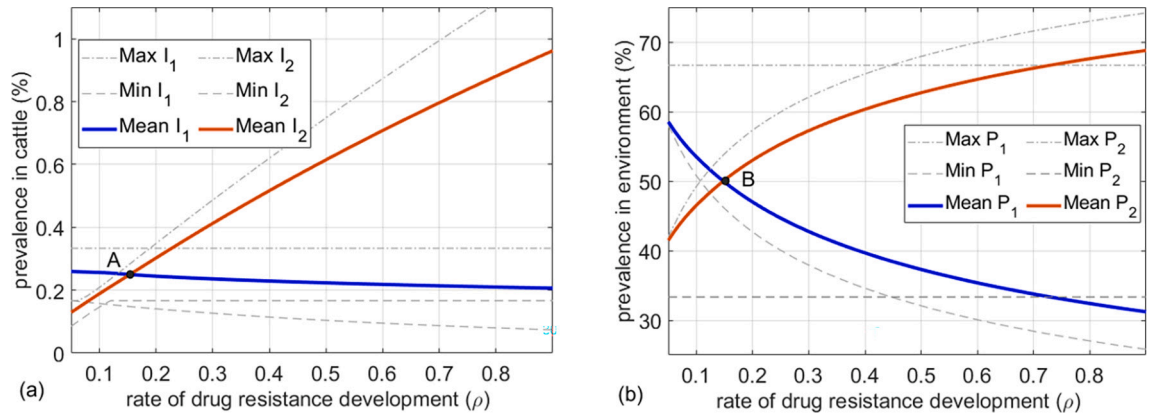

Fig. 5. The impact of rate of drug resistance development on the prevalence of infection. (a) Impact of rate of within host drug resistance development (ρ) on prevalence of drug-susceptible and drug-resistant *Salmonella* in cattle, (b) impact of rate of within host drug resistance development (ρ) on prevalence of drug-susceptible and drug-resistant pathogens in the environment.

poor compliance with animal movement control and quarantine negates the protective effects of feeding, watering, and hygiene measures (Fig. 4). Similarly, increased antibiotic use can reshape the infection ecology in both livestock and the environment (Fig. 5). Another key finding is that infection prevalence among farmworkers is directly linked to compliance levels. Low compliance can increase the cumulative prevalence of infection in farmworkers to over 50 % in six months (Fig S5), highlighting the role of human behavior in zoonotic spillover.

Unlike previous studies that focus solely on livestock infection dynamics [44–46], this research integrates a One Health framework that explicitly models human-environment-pathogen interactions. While prior work has analyzed the impacts of individual biosecurity measures, our approach demonstrates how interactions between different measures influence overall disease control effectiveness. Additionally, our negative feedback loop framework accounts for the long-term consequences of low biosecurity compliance, offering a more comprehensive risk assessment than traditional deterministic models [47–50].

Despite these contributions, certain limitations remain. Future studies should incorporate qualitative data on farmworker perceptions and behavioral compliance, expand the model to interconnected farm networks, and integrate real-time monitoring of biosecurity adherence. Nevertheless, our research establishes a quantitative foundation for evaluating farm biosecurity policies and highlights the pivotal role of farmworkers in mitigating zoonotic spillover risks.

In conclusion, this study provides an innovative modeling approach that emphasizes the interconnectedness of human, animal, and environmental health. Our findings reinforce the importance of multi-layered biosecurity strategies and the need for sustained compliance efforts to prevent antimicrobial-resistant pathogen spillover.

Availability of data and materials

All data used are publicly available.

CRediT authorship contribution statement

Arash Arjmand: Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Methodology, Formal analysis, Data curation, Conceptualization. **Majid Bani-Yaghoub:** Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Software, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization. **Kiel Corkran:** Writing – review & editing. **Pranav S. Pandit:** Writing – review & editing, Conceptualization. **Sharif S. Aly:** Writing – review & editing, Conceptualization.

Consent for publication

Not applicable.

Ethical approval

Ethical approval and consent to participate are not applicable.

Code availability

https://github.com/AArjcode/Biosecurity-Compliance-One-Health-Modeling-Framework

Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work the authors used Grammarly and ChatGPT to improve the writing style. After using these tools, the authors reviewed and edited the content as needed and took full responsibility for the content of the publication.

Declaration of competing interest

The authors (Arjmand, A., Bani-Yaghoub, M., Corkran, K., Pandit, P., Aly, S.) of this paper titled " Assessing the Impact of Biosecurity Compliance on Farmworker and Livestock Health within a One Health Modeling Framework" declare that there are no conflicts of interest regarding this research study. We have received no financial support or other benefits that could potentially influence the outcome or interpretation of the findings presented in this paper. All sources of funding and support for this research are acknowledged, and there are no competing interests to disclose.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.onehlt.2025.101023.

Data availability

No data was used for the research described in the article.

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