**INTRODUCTION**

Antimicrobial resistance (AMR) is one of the largest threats to human health, with a growing number of key antibiotic therapeutics being rendered ineffective by resistant bacterial pathogens. Antibiotic usage in livestock has been identified as a potentially important driver of AMR in human populations, with transmission of resistant bacteria and resistance determinants potentially occurring at the livestock/human interface [1]. This has led to efforts to curtail the usage of antibiotics in livestock. Examples include bans on usage of antibiotics for both growth promotion and for prophylaxis of livestock diseases [2-4]. The aims of these curtailment strategies are to safeguard the efficacy of clinical antibiotics and reduce the potential for transmission of resistant pathogens to human populations.

Curtailment of antibiotic usage in livestock has resulted in desired reductions to AMR, with an example being reductions to faecal *Enterococci* resistance rates in Denmark and Germany resulting from the 2006 growth promotion ban [5-7]. These reductions in usage have also been associated with transient increases in the carriage of other resistant pathogens, increases in livestock carriage of foodborne pathogens and increases in therapeutic antibiotic usage in livestock [8-10]. However, arguments have been made that these negative consequences can be largely attributed to increases in livestock productivity [11-13].

The uncertainty surrounding the consequences of curtailing antibiotic usage in livestock highlights the risks of introducing interventions into highly complex and poorly understood population/microbial level systems that have been built up through decades of antibiotic use as part of a “precautionary principle” based approach [10]. The need to better understand the potential long-term impacts of future AMR policy is also likely to increase, with EU legislation strictly controlling the use of antibiotics in livestock for metaphylaxis or prophylaxis in 2022 [4]. Therefore, there is a need for an increased understanding into the potential human health consequences following curtailment of antibiotics in livestock, especially when placed into a “one health” context.

One approach to better understand the complexities of antibiotic usage in livestock includes the use of mathematical models. These models can help by testing uncertainties, especially regarding the potential effects of antibiotic usage in livestock on human health and the extent of AMR transmission at the livestock/human interface. However, there is a dearth of models which quantitatively explore these uncertainties [14]. Existing frameworks include predictive risk assessment models and a small number of generalised deterministic models [15-21]. Nevertheless, significant knowledge gaps still exist, including a lack of understanding of the potential outcomes resulting from curtailment of antibiotic usage in livestock and the impact of different mitigating scenarios on altering these outcomes [22].

To address gaps in AMR modelling literature, a deterministic mathematical model was developed to explore the effects of antibiotic curtailment in livestock on *Salmonella* spp. infections in humans. Salmonellosis was explicitly chosen as a case study due to the clear zoonotic link between livestock carriage of *Salmonella* spp. and human infections. By explicitly modelling both livestock/human populations and various assumptions regarding the effects of antibiotic usage in livestock, we explore the potential long-term consequences of antibiotic curtailment in livestock, including alterations to the overall incidence of human salmonellosis and the antibiotic-resistant fraction of infections. Additionally, we explore the effects and feasibility of introducing interventions to mitigate the potential negative consequences of antibiotic curtailment in livestock.

**METHODOLOGY**

**Model Structure and Description**

A compartmental model was developed to describe the transmission of antibiotic-resistant and antibiotic-sensitive *Salmonella* spp. within and between livestock and human populations (Figure 1) [23]. Each host population can be stratified based on their respective infection status: susceptible humans (SH), humans infected with antibiotic-sensitive bacteria (ISH) or antibiotic-resistant bacteria (IRH), susceptible livestock food-animals (SA) and livestock food-animals infected with antibiotic-sensitive bacteria (ISA) or antibiotic-resistant bacteria (IRA). For simplicity, we considered “infected” states in livestock to also include asymptomatic carriage.

Transmission is simplified into four transmission routes: animal-to-animal (βAA), human-to-human (βHH), animal-to-human (βHA) and human-to-animal (βAH) transmission, with each β parameter describing both indirect and direct transmission between compartments for model tractability.

A background rate of transmission in the livestock population was also modelled (ζ). This represents infection/contamination of livestock hosts from sources other than livestock or humans, including the environment or new introductions from other (non) considered populations. This background transmission rate was scaled by a factor of 0.5 to ensure an equal influence of ζ on both antibiotic-sensitive and resistant transmission routes. This value was chosen due to a lack of *a priori* information on potential differences in background livestock contamination rate for antibiotic-sensitive/resistant strains. Natural recovery from antibiotic-sensitive/resistant infection/carriage occurs in both human/livestock populations at rate rH and rArespectively. Per capita birth/death rates are represented by µA in livestock and µH in human populations.

Antibiotic usage was modelled as a rate (τ) and was assumed to have a combined therapeutic and selective pressure effect on antibiotic-sensitive *Salmonella* spp infection/carriage. This therapeutic effect was assumed to both shorten the duration of carriage and clear carriage of antibiotic-sensitive bacteria. However, as there is currently an unclear relationship between antibiotic usage and clearance of *Salmonella* spp. in livestock species, a scaling parameter was also included to describe the efficacy of antibiotic mediated recovery in livestock (κ). As an illustrative example, lower values of κ correspond to a lower ability of antibiotic usage in livestock to shorten the duration of carriage or clear *Salmonella* spp. in livestock. Antibiotic usage was also modelled to have a selective pressure converting livestock between antibiotic-sensitive to resistant states. This could be interpreted as an implicit majority-minority relationship in each infected state, with livestock in each infected compartment possessing a small proportion of bacteria belonging to the other susceptibility class. Subsequent antibiotic usage may therefore clear antibiotic-sensitive bacteria (ISA) and allow the minority antibiotic-resistant (IRA) strain to proliferate and dominate, leading to “conversion” [15].

A reversion rate (φ) was also used to encompass a range of different biologically plausible phenomena that may cause reversion of antibiotic-resistant (IRA) to sensitive (ISA) carriage/infection. For example, this rate may describe growth-mediated competition within-host, where antibiotic-sensitive strains may outcompete antibiotic-resistant strains in the absence of antibiotics. This is assumption is captured through the antibiotic treatment rate (τ), with this rate implicitly assuming that while some livestock are treated and exposed to antibiotics, others may not be.

Transmission-related fitness costs associated with antibiotic-resistance were included and assumed to reduce the rate of transmission for antibiotic-resistant bacteria as a scaling factor (α). This parameter can be interpreted as a decrease in capacity for resistant strains (relative to sensitive strains) to establish infectious carriage in new hosts due to changes in important cellular machinery to facilitate resistance to antibiotics [24-26].

**Primary outcome measures**

Two primary outcome measures were considered in this study: 1) the daily incidence of human non-typhoidal human salmonellosis per 100,000 population in the EU, defined as the sum of the daily incidence of antibiotic-sensitive and resistant infections at the long-term non-zero steady state. This was calculated directly from model output as the daily proportion of newly infected humans multiplied by the EU population size of 446.8 million and then scaled by 100,000 [27]. 2) The fraction of antibiotic-resistant human non-typhoidal salmonellosis (I\*­RHProp) (defined as IRH / (ISH+IRH) at the long-term non-zero steady state.

The long-term non-zero steady state of the two previously defined quantities was calculated using the “rootSolve” package. Although we note that it is likely that the current “real-world” dynamics of AMR are in flux due to the influence of interventions, population dynamics etc., studying it at equilibrium is a useful indication of the long-term dynamics of the AMR and where the system is heading. This is especially the case for resistant *Salmonella* spp. infections, with a short duration of infectious human carriage (1/rH), facilitating a rapid approach to equilibrium. This approach is also justified with temporal surveillance data suggesting the proportion of antibiotic resistance in livestock populations has stabilised at roughly constant levels in recent years (Figure S1-4).

**Case Studies and Datasets**

As a key part of our model is to assess dynamics following a withdrawal of antibiotic usage in livestock, it is critical that the model is able to reproduce the relationship between antibiotic usage in livestock and fraction of antibiotic-resistant livestock infection. Therefore, this livestock portion of the model was fitted using an approximate Bayesian computation sequential Monte-Carlo (ABC-SMC) to the relationship between antibiotic usage and the resistance using resistance/treatment surveillance data. Detailed methodology for the ABC-SMC approach can be found in Toni et al, (2009) [28].

Phenotypic resistance data was obtained from the European Food Safety Authority (EFSA) summary reports. The proportion of isolates resistant to the specific antibiotic class from carcasses of broiler poultry/fattening pigs was extracted from the respective EFSA datasets [29-34]. Antibiotic sales data was obtained from European surveillance of veterinary consumption (ESVAC) reports [35-39]. ESVAC antibiotic sales data are averaged for all livestock species in each country in the original surveillance report. A scaling calculation was therefore required to convert the generic antibiotic sales to a value specific to the modelled livestock host with sales described as grams per population correction unit, g/PCU (Table S1). Note that due to a lack of accurate country-level antibiotic usage data, sales were assumed to be a proxy for usage. Mentions of “usage” are therefore in reference to the ESVAC sales data. Details of the raw datasets and data manipulation of the ESVAC and EFSA datasets can be found in the supplementary information.

Four case studies were chosen to aid model parameterisation and to ground the model with EU epidemiological surveillance data. These case studies were: 1) ampicillin-resistant non-typhoidal salmonella in broiler poultry from 2014-2018, 2) tetracycline-resistant non-typhoidal salmonella in broiler poultry from 2014-2018, 3) ampicillin-resistant non-typhoidal salmonella in fattening pigs from 2015-2018 and 4) tetracycline-resistant non-typhoidal salmonella in fattening pigs from 2015-2018.

These four case studies were chosen due to the high level of usage (both historical and current) of tetracycline and ampicillin in broiler poultry and fattening pigs, and the availability of resistance data for these two livestock species [35-40]. However, it is acknowledged that more relevant case studies regarding direct clinical relevance and drug/bug combination may exist in literature but cannot be modelled to lack of adequate surveillance data. As a preliminary test for a relationship between usage and resistance before simulating the dynamics of this relationship, we identified an observed statistically significant relationship between usage and resistance for three out of four included case studies (Figure S5, Table S2).

**ABC-SMC Model Fitting Procedure**

A simulated dataset for each case study was generated by modelling the fraction of antibiotic resistant livestock infections for each country/year observation, for each of the observed levels of antibiotic sales included in the dataset. A sum of squared errors distance function was then used to calculate the distance between the simulated and observed fraction of antibiotic-resistant livestock infection for each country/year data point for use in the ABC-SMC inference process. In accordance with the EFSA methodology, countries with <10 isolates in the respective EFSA dataset for a particular year were omitted from the dataset [29, 30, 33, 34].

Two additional summary statistics were also used for ABC-SMC model fitting: 1) minimise the difference between the modelled daily EU incidence of human salmonellosis at baseline antibiotic usage and the observed ECDC daily EU incidence of human salmonellosis currently observed (0.593 per 100,000), 2) minimise the difference between the model estimated proportion of resistant human salmonellosis at baseline antibiotic usage and the EFSA averaged European proportion of resistant human salmonellosis specific for each case study.

The baseline antibiotic usage for each case study was considered the unweighted average tetracycline/ampicillin usage across each included antibiotic country/year data point. 1) Ampicillin-resistant *Salmonella* spp. in broiler poultry (0.314 at 0.0049 g/PCU), 2) tetracycline-resistant *Salmonella* spp. in broiler poultry (0.316 at 0.0069 g/PCU), 3) ampicillin-resistant *Salmonella* spp. in fattening pigs (0.345 at 0.0125 g/PCU) and 4) tetracycline-resistant *Salmonella* spp. in fattening pigs (0.340 at 0.01305 g/PCU).

**Fitted Parameters**

The ABC-SMC approach was used to estimate the marginal posterior probability distribution for six model parameters (θ) given the data [28, 41]. Other model parameters were not fitted as estimates with high levels of certainty were available (rH, rA, μA and μH), or due to the relative nature of other transmission parameters with respect to βAA, βHA and ζ (βHH and βAH). βHH and βAH were instead held at values of 0.0001. These low values were chosen due to the negligible impact of these transmission routes on *Salmonella* spp. transmission [42]. Prior distributions and fitted model values can be found in the supplementary material (Table S3).

**Sensitivity Analyses**

A Fourier amplitude sensitivity test (FAST) approach was used to conduct a sensitivity analysis of the model system to the model parameters with regards to two outcome measures [43]: 1) the daily incidence of human foodborne infection and 2) proportion of resistant human infection. The parameter space range chosen for the sensitivity analysis was limited to an order of magnitude above and below the parameterised values.

The FAST approach was also used to identify the sensitivity of the model system to two additional intervention related outcome measures: 1) Relative changes in daily incidence when antibiotic usage in livestock were curtailed (*τ* = 0 g/PCU), compared to daily incidence at mean baseline antibiotic usage across the four case studies (*τ* = 0.00934 g/PCU) and 2) Relative changes in daily incidence under antibiotic curtailment (0 g/PCU) relative to the observed daily incidence with current levels of antibiotic usage (0.593 per 100,000). An in-depth description of this sensitivity analysis can be found in the supplementary material.

**RESULTS**

Curtailment of antibiotic usage (τ → 0 g/PCU) in the fattening pigs case studies resulted in the largest increase in the daily incidence with a 1.11-fold (0.668 per 100,000) increase relative to baseline levels, and a 1.20-fold (0.72 per 100,000) for the ampicillin and tetracycline case studies respectively (Figure 2). In contrast, increases in daily incidence for the broiler poultry case studies ranged from a zero-fold change below 3 significant figures (0.598 per 100,000) for the ampicillin case study and a 1.02-fold (0.617 per 100,000) increase in the daily incidence for the tetracycline usage case study.

Increases in antibiotic usage in livestock above baseline usage levels in the four case studies resulted in the opposite phenomenon, with decreases in overall human foodborne disease and increases in the proportion of resistant infection (Figure 2).

A Fourier amplitude sensitivity test (FAST) was next performed to identify the parameters which had the greatest influence on the relative increase in the daily incidence when antibiotic usage in livestock was curtailed (τ → 0 g/PCU) (Figure 3). Briefly, FAST analyses are a type of global sensitivity test using periodic sampling and Fourier transformations to decompose variance in a model outcome measure to individual model parameters. Therefore, influential model parameters in this specific FAST analysis can be interpreted as parameters that lead to case studies with large relative changes in daily incidence compared to baseline antibiotic usage under antibiotic curtailment.

The model outcome measure used to explore relative increases in daily incidence under curtailment was defined as the relative change in the daily incidence at mean baseline antibiotic usage in livestock (τ = 0.00934 g/PCU) when compared to incidence under antibiotic curtailment (τ = 0 g/PCU) across the four case studies (Figure 3A). As each parameter combination explored by the FAST search curve will result in a different daily incidence at baseline antibiotic usage (τ = 0.00934 g/PCU), this can be interpreted as exploring case studies and scenarios other than the specific drug/livestock/pathogen combinations used as baseline scenarios in this study.

Transmission related fitness costs associated with antibiotic-resistance (α), the per capita rate of background transmission to livestock populations (ζ) and efficacy of antibiotic-mediated livestock recovery (κ) were found to be the most influential parameters in determining the relative increase in daily incidence from baseline antibiotic usage in livestock when antibiotics where curtailed. (Figure 3A). Specifically, lower κ and α, and higher ζ parameter values resulted in lower relative increases in daily incidence when antibiotic usage in livestock was curtailed (τ = 0 g/PCU) (Figure S16).

A follow up sensitivity analysis was performed to identify parameters that could best *mitigate* increases in daily incidence under antibiotic curtailment for the particular ampicillin/tetracycline in broiler poultry/fattening pigs case studies used in this study (Figure 3B). This was identified by comparing increases in daily incidence under antibiotic curtailment (τ → 0 g/PCU) to a fixed daily incidence at baseline antibiotic usage of 0.593 per 100,000 population (average τ = 0.00934 g/PCU), as this is the baseline daily incidence of salmonellosis relevant for our case studies. Influential model parameters are therefore those that cause the greatest relative change in daily incidence from the *fixed* baseline value of 0.593 per 100,000. By extension, interventions targeting these identified parameters will be more capable of reducing levels of daily incidence back down to these baseline levels currently observed for the modelled case studies.

The per capita rate of animal-to-human transmission (βHA) was identified as the key parameter to mitigate increases in daily incidence (Figure 3B). Intuitively, decreasing βHA leads to a non-linear decrease in the daily incidence observed (Figure S16). This therefore represents the best parameter to target to mitigate potential increases in daily incidence due to curtailment of antibiotic usage in livestock.

Due to the importance of targeting the animal-to-human transmission route to control increases in daily incidence, we next quantified the alterations in βHA required to mitigate increases in daily incidence under antibiotic usage curtailment (0 g/PCU), below a threshold of 0.593 per 100,000 population (Figure 4). This threshold represents a removal of antibiotic selection pressure in livestock (0 g/pCU) and a prevention of increases in daily incidence above what is currently observed for human salmonellosis (0.593 per 100,000). Alterations to βAA and ζ parameters were also chosen as potential intervention targets, due to their relevance in agricultural biosecurity strategies to promote livestock health and mitigate livestock disease/AMR [44, 45]. Limited transmission parameter reductions were explored for βHA (0% - 25%), but with alterations to βAA and ζ parameters allowed to vary from 0-100%**.**

Only reductions to βHA were capable of mitigating increases to daily incidence below baseline levels across all considered case studies in the explored parameter space, with a reduction of 1%, 4%, 12% and 18% required for each case study (Figure 4). Isolated or even combined reductions to βAA or ζ were only capable of reducing daily incidence below baseline levels with strong reductions below ~50%, or if the initial increase in daily incidence is negligible upon antibiotic curtailment, as seen with the ampicillin usage in broiler poultry case study (Figure 4A).

**DISCUSSION**

A mathematical modelling approach was used to identify changes in the daily incidence of non-typhoidal human salmonellosis, as well as changes in the proportion of resistant human salmonellosis following curtailment of antibiotic usage in livestock. This was explored across four relevant antibiotic/livestock specific case studies. Scenarios with high transmission-related fitness costs of resistance (α), high efficacies of antibiotic-mediated livestock recovery (κ) and low background transmission rates of *Salmonella* spp. in livestock (ζ) were found to result in large increases in the daily incidence of human salmonellosis upon antibiotic curtailment. However, interventions to decrease animal-to-human transmission (βHA) were found to effectively mitigate increases in the daily incidence of human salmonellosis following curtailment of antibiotic usage in livestock.

These reductions to βHA could take the form of interventions to increase awareness from workers in the farm-to-fork pathway to maintain good hygiene, reducing microbial contamination on carcasses, as well as comprehensive public information campaigns to promote safe handling of food products [44, 46]. Many of these interventions have already been implemented, with legislation requiring businesses to comply with stringent hygiene standards [47]. This could be a promising signal that current business-as-usual approaches or small improvements to the current situation, could be sufficient to control increases in foodborne disease following future antibiotic usage stewardship interventions [22, 48, 49].

However, despite these improvements to farm-to-fork hygiene and farm-level biosecurity, it is important to note that *Salmonella* incidence/prevalence has plateaued in certain regions [50, 51]. This may be an indication that further reductions to incidence, if not already reduced by current interventions to reduce transmission, may be difficult to achieve. It is also worth noting there will also likely be large heterogeneity in the impact of different interventions to improve hygiene at the farm-to-fork pathway to reduce βHA [52]. Further work must be done to quantify the exact contribution of these individual interventions on the animal-to-human transmission route to improve future predictions [53]. This could include the integration of dynamic epidemiological models with explicit microbial risk-assessment models detailing the farm-to-fork pathway [22, 54, 55]. Additionally, incorporating economic models into future dynamic modelling could also assess the economic feasibility of introducing hypothetical interventions in the food production chain [56].

Curtailment of antibiotic usage in livestock was found to have varying impacts across the modelled livestock host species, with negligible changes in the daily incidence in the broiler poultry case studies and with the largest increases in incidence observed with the fattening pig case studies (Figure 2). These differences across broilers and pigs can be attributed to the large differences in transmission-related fitness costs associated with antibiotic resistance between species (α = 0.084 and 0.416 for broiler poultry and fattening pigs respectively). Difference in fitness cost between species may reflect heterogeneity in the distribution of *Salmonella* spp. serotypes colonising poultry and pig hosts [57]. Heterogeneity in fitness cost across hosts could also be attributable to distinct plasmid types in chickens and pigs, with studies in *E.coli* identifying differences in fitness cost across these resistance-encoding plasmids [58].

In addition to α, differences in the relative increase in daily incidence of salmonellosis between modelled case studies can also be attributed to ζ and κ parameters (Figure 3A). The effects of changes in these parameters on the impact of curtailment are twofold: Firstly, treatments which have a greater therapeutic impact on the duration of antibiotic-sensitive carriage, , will intuitively result in larger increases in prevalence when withdrawn (high κ) (Figure S17). Secondly, as antibiotic-sensitive strains are the only *Salmonella* spp. strains impacted by treatment, if the proportion of antibiotic-sensitive relative to antibiotic-resistant strains is higher, then we will observe a greater increase in overall disease when treatment is withdrawn. This tendency for antibiotic-sensitive strains to dominate occurs when there are greater transmission-related fitness costs associated with antibiotic-resistance (high α), as sensitive strains will have an even greater relative fitness advantage over resistant strains. Additionally, a constant source of antibiotic-resistant bacteria from external sources such as the environment (high ζ) may also reduce the proportion of antibiotic-sensitive to resistant strains (Figure S18).

The importance of the therapeutic effect of antibiotic usage (τκ) in determining the relative increase in incidence of salmonellosis also has important implications when considering the assumptions used in this study. Antibiotic usage in livestock was modelled to be a proxy for all modes of application (meta-phylaxis, prophylaxis etc.) and therefore by extension, our model implicitly assumes that all types of antibiotic usage have a therapeutic effect in livestock. This assumption can be considered an edge-case, highly positive interpretation of antibiotic usage in livestock, considering that the impact of antibiotic exposure to *Salmonella* carriage in livestock is likely highly variable and dependent on the antibiotics used [59, 60]. However, the fact that increases in human incidence are still relatively minor under an assumption that curtailment is occurring to antibiotic usage with a highly therapeutic effect in livestock, further reinforces the message that the real-life impact of antibiotic curtailment on human salmonellosis will likely be minimal.

It is worth highlighting that bacteria species such as *Listeria* spp. and *E.coli* (i.e. VTEC) will likely have different dynamics upon curtailment of antibiotic usage in livestock, with both being commonly found in the intestinal flora of immunocompetent individuals and only causing disease as opportunistic infection [61, 62]. Therefore, it is likely that there will be a less clear link between improvements in farm-to-fork hygiene and the incidence of opportunistic infections of *Listeria* spp. and *E.coli*.

It is important to note that the aim of this study was not to specifically explore the evolutionary dynamics underlying the coexistence of sensitive and resistant strains. Instead, we implicitly acknowledge that this phenomenon exists, simplifying the mechanisms underlying coexistence and instead concentrating on the impact of host heterogeneity and zoonotic transmission on livestock AMR interventions. Additionally, the primary result of this study, increases in the prevalence of disease following antibiotic curtailment, is robust across models that explicitly incorporate population and within-host level mechanisms that drive coexistence [63]. However, we note that the existence of the ζ parameter prevents the model from being considered a neutral-null model due to the presence of “immigration infections”, that is infections that cannot be traced back through a chain of infection events back to initial infectives [64]. However, it is worth noting that the exclusion of ζ resulted in a poorer model fit compared to where the parameter is present (Figure S8). Further exploration into the dynamics of curtailment of antibiotic usage in livestock may benefit from explicitly modelling this general background transmission rate as an environmental reservoir of infection.

Large variability exists in both literature and the explored case studies regarding the relationship between livestock/human antibiotic usage and resistance, ranging from non-significant to significant across the four explored case studies (Figure S5, Table S2). Due to the historical lack of high-quality AMR surveillance and presence of confounding factors, it is difficult to disentangle whether observed significant relationships are due to a genuine relationship between usage and resistance or due to the inherent noise associated with AMR surveillance data [65]. This is important to recognise, as the extent of increases in the daily incidence of salmonellosis upon curtailment of antibiotic usage in livestock is determined through fitting modelled livestock dynamics to a presumed direct relationship between usage and resistance.

However, our key message, specifically that potential increases in the daily incidence are likely to be low and potentially controllable through interventions targeting the farm-to-fork pathway, is robust to these uncertainties and variations in the data. To highlight the robustness of our results to uncertainty in the surveillance data, we describe two hypothetical scenarios concerning the “real” relationship between antibiotic usage and resistance. Firstly, if the true relationship between usage and resistance is not real, then we would expect to see negligible increases in the daily incidence of foodborne disease in humans. This is due to the effects of transmission-related fitness costs (α) being an important parameter in driving both relative changes in resistance and increases in the daily incidence of foodborne disease upon curtailment (Figure 4A, S17). Therefore, if there is a weak/no association between antibiotic usage and resistance due to negligible fitness costs, then increases in incidence will also be unimportant and of limited public health concern. Secondly, if a significant relationship between usage and resistance was observed, then we have also demonstrated in this study that the associated increases in daily incidence of salmonellosis following antibiotic curtailment can be controlled through ensuring good biosecurity at the farm-to-fork-pathway (Figure 4).

The results from this study suggest that curtailment of antibiotic usage in livestock may have unforeseen effects, with a reduction in both livestock and human antibiotic resistance, but with increases in the livestock carriage and onwards transmission of foodborne pathogens such as *Salmonella* spp. to humans. However, potential increases in the daily incidence of salmonellosis range from negligible to preventable through interventions that target animal-to-human transmission routes. The efficacy of these interventions suggests that a one-health approach with a focus on improving farm-to-fork hygiene to minimise human disease is essential when considering potential strategies to tackle the AMR crisis.