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Data descriptor

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A high-resolution emission inventory of veterinary antibiotics in China

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Abstract

From a One Health perspective, the excessive use of veterinary antibiotics poses a significant risk to human health. As a leading global producer of livestock and aquaculture, China requires rigorous assessment and management of veterinary antibiotics use and emissions. However, such efforts are often constrained by emission data scarcity and inaccuracy. By integrating official statistics on livestock populations and aquaculture indicators (products and farming areas) with empirical concentrations of veterinary antibiotic residue in feces and aquaculture water from peer-reviewed literature, an Excretion–Removal–Emission (ERE) framework was established to construct a refined 2020 emission inventory for veterinary antibiotics in China. The inventory quantifies county-level emissions of ten categories of veterinary antibiotics from livestock and aquaculture, to soil, freshwater, and seawater. To account for uncertainty, we developed low-, best-guess- and high-emission scenarios based on policy compliance and key parameter variations, providing a robust assessment of potential outcomes. The inventory development framework established here provides a transferable methodological foundation for constructing veterinary antibiotic emission inventories in other countries worldwide. The resulting dataset can serve as a foundational input for subsequent multimedia fate modeling, environmental and human health risk assessments. Furthermore, it provides a critical basis for antibiotic stewardship and pollution control management strategies.

Keywords: Veterinary antibiotics, Emission inventory, Livestock, Aquaculture, Data description

Highlights

- A high-resolution (county-level) inventory of ten veterinary antibiotic categories is presented, covering emissions to soil, freshwater, and seawater.
- The dataset provides a scientific basis for mitigating antibiotic pollution.
- A transferable framework is established for constructing emission inventories in regions lacking antibiotic usage data.

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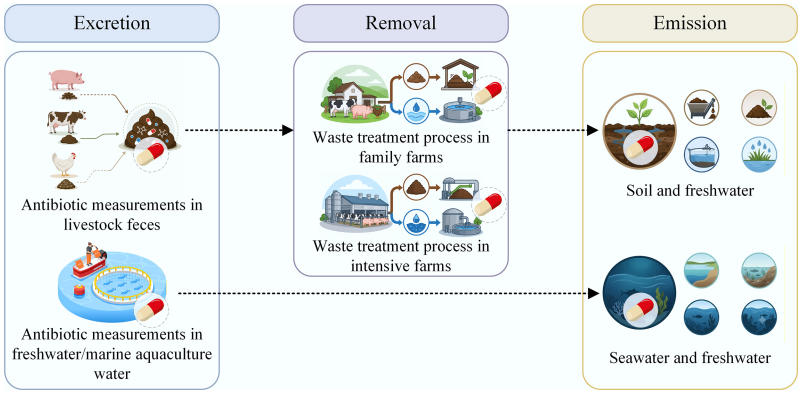
Graphical abstract



Introduction

Livestock farming accounts for over 70% of global antibiotic use, with veterinary antibiotics consumption projected to reach 143,481 tonnes by 2040, a 29.5% increase from 2019 levels[1–3]. These compounds are released into the environment through livestock farming and aquaculture, driving the emergence and spread of antibiotic resistance[4–7]. Antibiotic resistance now poses a critical global health threat, contributing to 1.27 million deaths in 2019[8]. These risks highlight the urgent need to quantify veterinary antibiotic emissions to inform interventions within the One Health framework.

In low- and middle-income countries (LMICs), the close interaction between livestock and human populations, coupled with a scarcity of veterinary resources, increases the risk of antibiotic resistance transmission from animals to humans[6]. As the world's largest consumer of veterinary antibiotics, China faces a serious and growing problem of antibiotic resistance in livestock farming[9,10]. Therefore, accurately quantifying antibiotic environmental discharge from livestock farming and aquaculture in China is vital for risk management and the effective implementation of control policies. High-resolution emission inventories have thus become an essential data basis for identifying resistance risks[11].

Recent studies have quantified the usage and environmental release of veterinary antibiotics in China. Global-scale studies including China have primarily focused on antibiotic consumption rather than emissions[12,13]. Initially, early foundational studies in China did not adequately account for antibiotic removal during waste treatment processes in different types of livestock farming systems, introducing high uncertainties[11]. While subsequent research has incorporated removal rates during waste treatment processes, it remains constrained by incomplete veterinary antibiotic coverage. The most recent emission inventory has expanded the range of antibiotics considered, yet the spatial resolution of national-scale emission inventories for China remains as limited as in previous studies[11,14,15]. Consequently, a publicly available, high-quality national emissions inventory covering multiple veterinary antibiotic categories is still lacking.

To address these limitations, we developed a nationwide, high-resolution (county-level) emission inventory for ten categories of veterinary antibiotics. The framework accounts for regional differences in livestock populations and the variable removal efficiencies of antibiotics across waste treatment practices. It also integrates emissions from both terrestrial livestock and aquaculture, the latter yet being an increasingly critical contributor to the risk of antibiotic resistance[16,17]. By improving spatial granularity, broadening antibiotic coverage, and applying a detailed approach to evaluate antibiotic removal across different regions and waste treatment processes, this inventory provides a more reliable basis for quantifying environmental emissions than previous national-level assessments.

This veterinary antibiotic emission inventory provides essential input for environmental fate modeling to assess subsequent environmental risks. Its high spatial resolution allows for the precise identification of geographic hotspots and strengthens the application of quasi-experimental approaches to evaluate the causal effects of policy interventions. Developing a comprehensive veterinary antibiotic emission inventory for China not only addresses domestic needs but also provides a replicable methodological framework that can be applied in other countries facing similar environmental and public health challenges. Ultimately, this work enables local governments to identify high-risk farming areas and implement targeted regulatory measures, thereby advancing the goal of safeguarding public health.

Methods

In this study, an Excretion–Removal–Emission (ERE) framework was employed to quantify veterinary antibiotic emissions, with the detailed procedure presented in Section 2.3. Figure 1 illustrates the detailed methodological approach for constructing the emission inventory. The inventory construction procedures for aquaculture and livestock farming were designed separately according to data availability and farming characteristics. For aquaculture, emissions were primarily calculated based on the aquaculture water volume associated with different aquaculture types, including freshwater and marine aquaculture, and the residual concentrations of antibiotics in aquaculture water. The aquaculture inventory was developed through a stepwise downscaling procedure: emissions were first calculated at the provincial level and then allocated to the municipal and county levels using different allocation weights. In contrast, livestock antibiotic emissions were estimated by considering three livestock categories. Antibiotic excretion was first calculated based on feces production and antibiotic residue concentrations in feces. Then, according to the proportions of intensive and family farming, different waste treatment processes were applied, and final antibiotic emissions were estimated by accounting for the corresponding antibiotic removal rates during these waste treatment processes. Since county-level livestock population data were directly available, livestock inventories could be calculated directly at the county scale, without the need for additional spatial allocation.

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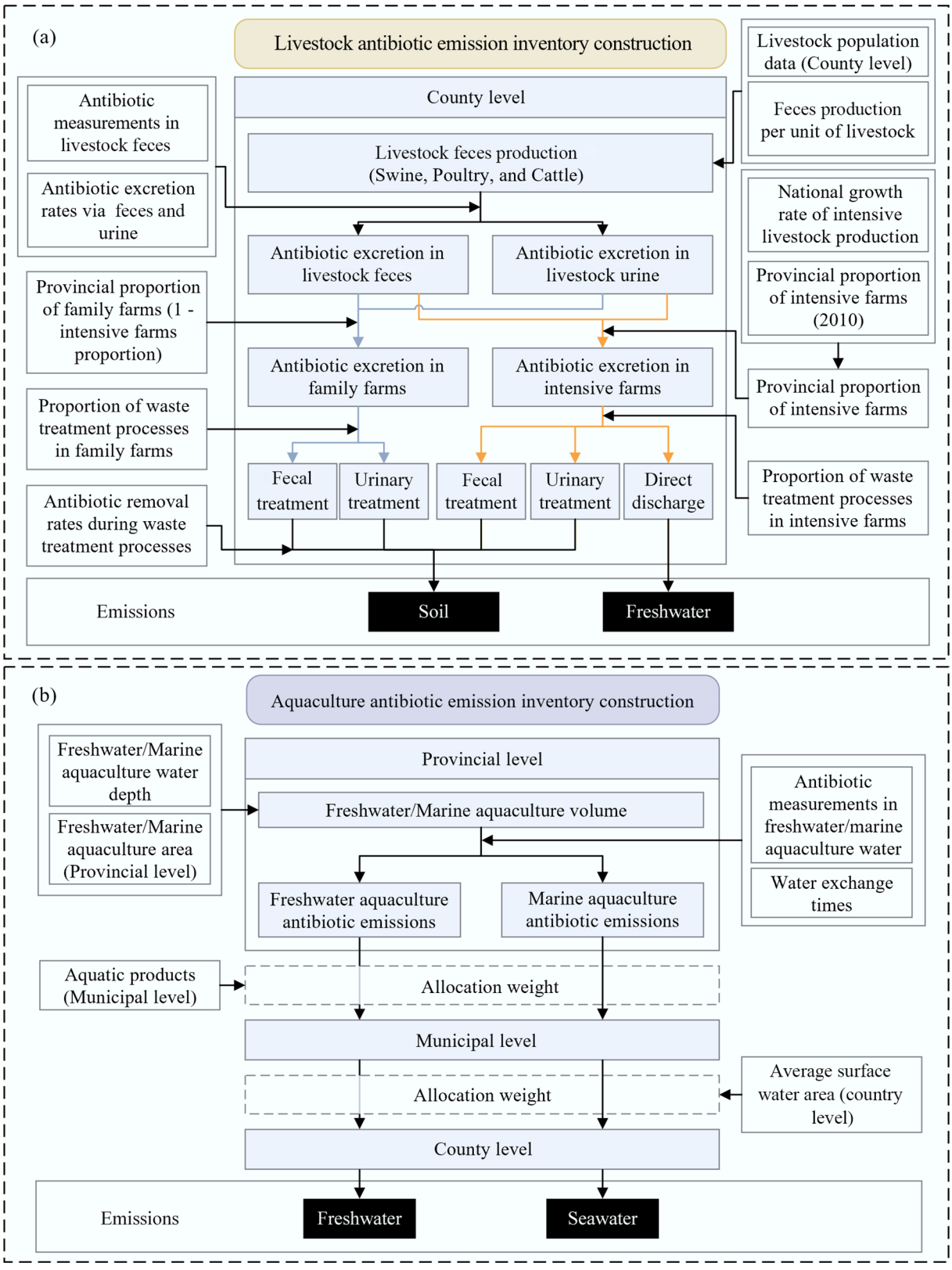

Fig. 1 Methodology for estimating veterinary antibiotic emissions from (**a**) livestock and (**b**) aquaculture.

Data acquisition

Empirical measurement data on veterinary antibiotics in livestock feces (including swine, cattle, and poultry) and aquaculture water were compiled through a comprehensive literature review. The specific search terms and data-filtering strategy were detailed in the previous study[18]. The nationwide concentration data for ten categories of veterinary antibiotics were finally collated from 55 studies. The categories of veterinary antibiotics are as follows: sulfonamides,

tetracyclines, quinolones, macrolides, β-lactams, lincomycins, chloramphenicols, aminoglycosides, polypeptide, and others.

Livestock population and aquaculture indicators (products and farming areas) were primarily obtained from official statistical yearbooks. Remaining data gaps were addressed through direct inquiries with local statistical bureaus and formal information requests to regional government agencies. Table 1 provides an exhaustive list of the yearbooks and parameter sources employed in this study.

Data processing

Processing of residual concentration data in feces and aquaculture water

Antibiotic residual concentrations in livestock feces and aquaculture water were collated from the 55 studies. Provincial antibiotic residue levels were determined by averaging the empirical concentrations reported across different studies within each province. For provinces without measured data, the national average was adopted.

Processing of livestock population data

Although livestock population data were obtained from official departments and statistical yearbooks, some data gaps persisted at the county level. For counties lacking livestock population data, values were estimated by multiplying the county's three-year average share by the city's livestock total for the same year. This is based on the assumption that breeding scales remain relatively stable over short durations.

Processing of aquaculture data

County-level veterinary antibiotic emissions data for aquaculture were estimated following the methodology described in Section 2.4. Notably, our calculations encompassed a wide variety of systems, including pen culture, cage culture, and industrialized culture in freshwater aquaculture, as well as pond culture, cage culture, deep-sea cage culture, raft culture, hanging culture, and industrialized culture in marine aquaculture. The volume for each aquaculture system was calculated by multiplying the aquaculture area (sourced from statistical yearbooks) by the aquaculture water depth. Remaining gaps were filled using municipal statistical bulletins or proxies from adjacent years. In this study, a uniform depth value was applied to each aquaculture system across all regions, assuming no significant variations between provinces.

Table 1 Data composition and sources

Parameter indicator	Data source
Concentration of antibiotic residues in livestock feces and aquaculture water	Data from previous studies[1]
Livestock population data (county-level)	China Statistical Yearbook or local statistical bureaus[19]
Aquaculture area data (provincial-level)	China Fishery Statistical Yearbook[20]
Aquatic products data (municipal-level)	China Statistical Yearbook[19]
feces production per unit livestock	Dong, 2019[21]
Aquaculture water depth parameters	Food and Agriculture Organization report[22], Occupational standard and local standard[2]
Average depth and area of surface water	Zhu et al., 2016[23]
Veterinary antibiotic removal rates during waste treatment processes	Data from previous studies[1]
Provincial proportion of intensive farms (2010)	China Animal Husbandry and Veterinary Yearbook[24]
Proportion of waste treatment process in intensive and family livestock farms	Data from previous studies[1]
Antibiotic excretion rates via feces and urine	Data from previous studies[1]

[1] Data can be found in our previous study[18].[2] The following standards are included: SC/T 1006–92 and NY/T 3616–2020 (occupational), DB35/7 1708–2017 and DB 3302/T 152–2018 (local).

Method for calculating veterinary antibiotic emissions from livestock at the county-level

Calculation of proportions of provincial-level intensive and family livestock farms

Intensive and family livestock farming systems adopt different livestock waste treatment practices, which in turn influence the removal efficiency of veterinary antibiotics[25]. To distinguish between the two types of livestock farming systems, we referred to the criteria of the Ministry of Agriculture and Rural Affairs of China, which define intensive farms based on annual inventory and slaughter thresholds for swine, cattle, and poultry[26]. Farms below these thresholds were considered family farms in this study. As provincial-level proportions of intensive livestock farming were unavailable after 2010, the national growth rate of intensive livestock farming was used to extrapolate provincial proportions from the 2010 baseline data for subsequent years. Due to the lack of county-level data, the estimated provincial proportion was assumed to apply uniformly to all counties within the same province. Accordingly, the proportion of intensive farming was calculated according to Eqs. (1–4), with the proportion of family farming calculated as the complement to 100%.

$$\alpha_{\mathrm{in,pr},y+1} = \frac{Sl_{\mathrm{in,pr},y} \times \left(1 + I_{\mathrm{in,n},y+1}\right)}{Sl_{\mathrm{all,pr},y+1}} \tag{1}$$

$$Sl_{\mathrm{in,pr},y} = \alpha_{in,\mathrm{pr},y} \times Sl_{\mathrm{all,pr},y} \tag{2}$$

$$I_{\mathrm{in,n},y+1} = \frac{\left(Sl_{\mathrm{in,n},y+1} - Sl_{\mathrm{in,n},y}\right)}{Sl_{in,n,y}} \tag{3}$$

$$Sl_{\mathrm{in,n},y} = \alpha_{\mathrm{in,n},y} \times Sl_{\mathrm{all,n},y} \tag{4}$$

where in and all represent intensive livestock farms and all farm types, respectively; pr and n represent provincial and national, respectively. The base year y_0 is 2010. y and $y+1$ represent the current year and the subsequent year, respectively. α represents the proportion of intensive farming, and Sl denotes the slaughter number of livestock. I represents the national growth rate of livestock slaughter numbers from intensive farms. $\alpha_{in,pr,y+1}$ denotes the proportion (%) of intensive livestock farms for each province in the subsequent year; $Sl_{\mathrm{in,pr},y}$ represents the intensive slaughter numbers at the provincial level for the current year; $I_{\mathrm{in,n},y+1}$ denotes the national growth rate (%) of intensive livestock production in the subsequent year; and $Sl_{\mathrm{in,n},y}$ refers to the national intensive slaughter volumes for the current year. To ensure that the estimated proportion of intensive farming remained within a physically meaningful range, the calculated value of $\alpha_{in,pr,y+1}$ was constrained to 0–100%.

Calculation of livestock feces production at the county level

The calculation of feces production from livestock was shown as Eq. (5).

$$F = \begin{cases} \mathrm{N_{sl}} \times p_{\mathrm{sl}} + N_{\mathrm{st}} \times p_{\mathrm{st}} \times \alpha_{\mathrm{in,pr},y+1}, \text{intensive farms} \\ N_{\mathrm{sl}} \times p_{\mathrm{sl}} + N_{\mathrm{st}} \times p_{\mathrm{st}} \times (1 - \alpha_{\mathrm{in,pr},y+1}), \text{family farms} \end{cases} \tag{5}$$

where F refers to the annual amount of feces produced by livestock at the county level (kg/year). sl and st represent slaughter and in stock, respectively. N_{sl} and N_{st} denote the county-level number of livestock slaughtered and in stock, respectively. p_{sl} and p_{st} represent feces production per unit of slaughtered livestock and livestock in stock, respectively (kg/unit/year). The specific emission factors adopted in this study were primarily derived from previous research[21].

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Livestock populations were categorized according to their distinct growth cycles and functions, since fecal production rates vary significantly between stock and slaughter cohorts. For the swine sector, populations were disaggregated into two groups: pigs intended for slaughter (representing meat production) and sows intended for breeding. Following the biomass estimation guidelines of the World Organization for Animal Health (WOAH), boars were excluded from the calculations due to their negligible contribution to the total population[27]. Similarly, cattle populations were classified by utility: slaughtered cattle primarily represent beef production, while livestock herds include dairy and draft cattle. In the poultry sector, a distinction was made between egg-producing layers and meat-producing slaughtered broilers. This categorical approach takes into account the substantial differences in growth periods and fecal production volumes across different animal sub-sectors, thereby ensuring a more accurate calculation of total veterinary antibiotic environmental loading.

Calculation of antibiotic excretion from livestock at the county level

The calculation of the excretion for individual veterinary antibiotics from livestock was shown as Eq. (6).

$$E_{\mathrm{ex}} = \begin{cases} F \times C_{\mathrm{f}} \times \theta, & E_{\mathrm{ex},f} = \text{excretedin feces} \\ F \times C_{\mathrm{f}} \div RX_{\mathrm{f}} \times RX_{\mathrm{u}} \times \theta, & E_{\mathrm{ex,u}} = \text{excretedin urine} \end{cases} \tag{6}$$

where E_{ex} represents the amount of antibiotics (tonnes/year) excreted in urine ($E_{\mathrm{ex,u}}$) and feces ($E_{\mathrm{ex,f}}$) at the county level; C_{f} represents the concentration (μg/kg) of antibiotics residues in livestock feces (f); RX_{f} and RX_{u} represent excretion rates (%) of antibiotics through feces (f) and urine (u), respectively, from livestock; θ is the unit conversion factor for converting the calculated antibiotic excretion from μg/year to tonnes/year, with $\theta = 10^{-12}$.

Calculation of antibiotic emission from livestock at the county level

This study calculated antibiotic emissions based on the size of livestock farms, distinguishing between intensive farms and family farms. The calculations for the discharge of individual veterinary antibiotics from livestock farming into soil and water were shown as Eqs. (7) and (8).

$$E_{\mathrm{s}} = \begin{cases} E_{\mathrm{ex,f}} \times P_{\mathrm{f}} \times (1 - RE_{\mathrm{f}}) + E_{\mathrm{ex,u}} \times P_{\mathrm{u}} \times (1 - RE_{\mathrm{u}}), \text{intensive farms} \\ E_{\mathrm{ex}} \times P_{\mathrm{f}} \times (1 - RE_{\mathrm{f}}), \text{family farms} \end{cases} \tag{7}$$

$$E_{\mathrm{w}} = E_{\mathrm{ex,u}} \times P_{\mathrm{d}} \times (1 - RE_{\mathrm{d}}), \text{ intensive farms} \tag{8}$$

where E_{s} and E_{w} represent the amount (tonnes/year) of veterinary antibiotics released into soil and freshwater, respectively, at the county level. The proportion (%) of the fecal and urinary treatment process in livestock farms is represented by P_{f} and P_{u}, while P_{d} represents the proportion (%) of direct discharges (d) for livestock. Antibiotic removal rates (%) are denoted by RE_{f} (fecal treatment process), RE_{u} (urinary treatment process), and RE_{d} (direct discharge). For direct discharge, RE_{d} is assumed to be 0%. The corresponding category-level emissions were subsequently obtained by summing the calculated emissions of the antibiotics belonging to the same category.

This study considered both fecal and urinary pathways of livestock waste treatment processes. fecal treatment includes agricultural utilization, composting, and anaerobic digestion, while urinary treatment encompasses agricultural utilization and anaerobic digestion. In intensive livestock farming, the amount of veterinary antibiotics excreted in feces and urine was calculated separately before integration into the respective manure treatment processes. Untreated and directly discharged urine was considered to be released into the freshwater. Conversely, on family farms, crop cultivation and livestock rearing were usually combined. The resulting excreta were used as organic fertilizer and applied to the soil. In contrast to swine and cattle waste, poultry excreta (a mixture of feces and urine) was assumed to be discharged entirely into the soil[28].

Method for calculating veterinary antibiotic emissions from aquaculture

Calculation of provincial antibiotic emissions from aquaculture

Both freshwater and marine aquaculture were considered in this study, and the calculation methods for them were consistent. Since aquaculture effluent is frequently discharged untreated, the removal process is typically excluded from aquaculture veterinary antibiotic discharge calculations[29]. Emission was calculated using Eq. (9), which is a formula for calculating emissions at the provincial level.

$$E_{\mathrm{pr,a}} = C_{\mathrm{pr,a}} \times A_{\mathrm{pr}} \times D \times T \times \gamma \tag{9}$$

where $E_{\mathrm{pr,a}}$ represents the quantity of antibiotics discharged (tonnes/year) in aquaculture (a) by province (pr); $C_{\mathrm{pr,a}}$ denotes the concentrations of antibiotics residues in aquaculture by province (ng/L). $A_{\mathrm{pr}} \times D$ is used to denote aquaculture water volume; A_{pr} represents the aquaculture area of each province (m^2); D represents the water depth in the designated aquaculture area (m); T represents the water exchange times between aquaculture area and surrounding waters in aquaculture per year; and γ is the unit conversion factor for converting the calculated antibiotic emissions from ng/L × m^3 to tonnes, with $\gamma = 10^{-12}$. Freshwater aquaculture systems were treated as an open system, and marine aquaculture can also be divided into pond culture and other open systems. Water quality management requires pond culture renewal and water exchange. Based on the infrequent water exchange in winter and the 15–30 day intervals during the peak season (May–September), an average annual water exchange rate of ten times was assumed for pond culture, primarily to enhance pond water quality and increase dissolved oxygen levels[30]. As open aquaculture systems are situated in expansive water bodies, continuous water exchange was assumed on a year-round basis (365 days)[29].

Calculation of municipal antibiotic emissions from aquaculture

Regions with a high prevalence of aquatic products tend to have higher antibiotic emissions in aquaculture[13]. To improve the spatial resolution of the emission inventory in aquaculture, antibiotic discharges were downscaled from the provincial to the municipal level. This allocation process utilized the aquatic production-based weighting method. Specifically, the ratio of a city's aquatic product output to the total provincial output, as recorded in the provincial statistical yearbook, served as the spatial allocation proxy. By applying these scaling factors to the provincial emission totals, we derived the estimated antibiotic discharge for each city. The estimation of municipal emissions was expressed in Eqs. (10) and (11).

$$E_{\mathrm{m,a}} = E_{\mathrm{pr,a}} \times w_{\mathrm{m}} \tag{10}$$

$$w_{\mathrm{m}} = Y_{\mathrm{m}} / Y_{\mathrm{pr}} \tag{11}$$

where $E_{\mathrm{m,a}}$ denotes the antibiotic emissions (tonnes/year) in aquaculture (a) at the municipal level (m); w_{m} represents the allocation weight for the city; Y_{m} and Y_{pr} represent the aquatic products (tonnes) in the city and its province, respectively.

Calculation of county-level antibiotic emissions from aquaculture

The amount of aquaculture is closely related to surface water resources[31]. Using the surface water area of each county as a weight,

the municipal-level aquaculture discharge was accurately allocated to the county level. Furthermore, all aquaculture facilities included in this study had a water depth of ≥ 2 meters. Based on county-level surface water depth data, we believed that areas that did not meet this requirement were not engaged in aquaculture activities. The main calculation formulas were as follows in Eqs. (12) and (13).

$$E_{c,a} = \begin{cases} 0, d < 2 \\ E_{m,a} \times \chi_c, d \geq 2 \end{cases} \quad (12)$$

$$\chi_c = M_c / M_m \quad (13)$$

where $E_{c,a}$ denotes the antibiotic emissions (tonnes/year) in aquaculture (a) at the county level (c); d represents the average surface water depth in the county (m); χ_c represents the allocation weight for the county; M_c and M_m represent the surface water areas (m^2) of the county and the city where it is located, respectively.

Data records

The comprehensive inventory encompasses three distinct tables: "Emi livestock soil.xlsx", "Emi livestock freshwater.xlsx", and "Emi aquaculture.xlsx". The sheets in each file are divided by livestock category (swine, cattle, poultry) and aquaculture water (freshwater, seawater). The rows represent the antibiotic emissions of the relevant county, and the columns correspond to the ten categories of veterinary antibiotics. The unit is labeled as tonnes.

Emi livestock soil.xlsx and Emi livestock freshwater.xlsx: These two documents contain data on the discharge of ten categories of veterinary antibiotics into soil and freshwater in Chinese counties in 2020.

Emi aquaculture.xlsx: This document contains data on the discharge of ten categories of veterinary antibiotics into freshwater and seawater in Chinese counties in 2020.

Data overview

In 2020, the total discharge of veterinary antibiotics in China was estimated to be 23,110 tonnes. Approximately 85% of total veterinary antibiotics were discharged into soil, while the remainder was released into aquatic environments, including freshwater and seawater. Among livestock sectors, swine was the largest contributor to soil emissions (13,986 tonnes), followed by poultry (3,279 tonnes) and cattle (2,381 tonnes). In addition, veterinary antibiotic discharge into seawater was estimated at 3,007 tonnes, approximately 6.6 times higher than the total discharge into freshwater. Notably, considerable regional differences were observed in veterinary antibiotic emissions. Detailed data stratified by antibiotic class, animal category, aquaculture water type, environmental compartment, and region are provided in the inventory.

Technical validation

Uncertainty analysis

To quantify methodological uncertainties, we estimated lower bound and upper bounds of total emissions alongside the best-guess scenario by applying extreme values for parameters with uncertainties and considering policy effects, which could provide a potential range of environmental discharge in China. The parameter uncertainty analysis centered on the variability of key production metrics (livestock feces volume and aquaculture water depth) and encompassed the removal efficiency of veterinary antibiotics during waste treatment. According to Zhu et al.[32], we applied the variability-based sensitivity coefficient (SCV) to perform a global sensitivity analysis of key model input parameters. The input parameters were assumed to follow normal and log-normal distributions. Parameters with an SCV index greater than 0.1 were considered highly influential on the model output. Detailed results are presented in the Supplementary Data (Supplementary Table S1). In the low-emission scenario, minimum values for farming production parameters were applied, and strict compliance with national prohibitions was assumed, resulting in zero emissions for banned veterinary antibiotics after implementation[33,34]. The best-guess-emission scenario assumed general policy adherence unless residues were detected in 2020, utilizing mean parameter values. In contrast, the high-emission scenario assumed complete non-compliance with the ban and applied maximum parameter values. Notably, the high-emission scenario assumed that all waste treatment processes are ineffective, with all associated veterinary antibiotics being released into the environment without any removal. The uncertainty ranges and sources of the key parameters under the three scenarios are provided in the Supplementary Data (Supplementary Table S2–S5). The resultant emissions for these ten veterinary antibiotic categories across the three scenarios are illustrated in Figure 2.

By comparing the resultant discharge across these three scenarios, we identified that the key production metrics, policy implementation effectiveness, and the removal of veterinary antibiotics during waste treatment are the primary drivers of variability in total veterinary antibiotic loads. Our analysis indicates that policy implementation effectiveness is the predominant driver of the overall variance for chloramphenicols. The divergence between the low and high scenarios defines the upper and lower bounds of potential environmental discharge, effectively capturing the uncertainties stemming from parameter stochasticity, regulatory implementation, and waste treatment efficiency. These validation results underscore the reliability of the best-guess-emission scenario as a representative estimate of China's veterinary antibiotic landscape.

Limitations

Despite its comprehensive scope, this emission inventory can be further improved. First, antibiotic residue concentrations were compiled from published studies, and national averages were used for provinces lacking data. Collecting more site-specific monitoring data would improve the spatial accuracy of the estimates. In addition, because provincial-level proportions of intensive livestock farming were unavailable after 2010, provincial proportions were extrapolated using the national growth rate of intensive livestock farming. This approach may not fully capture regional differences in farming systems and could therefore introduce uncertainty into the estimates. Nevertheless, given the currently available data, it represents the most feasible approach. Future studies could further improve these estimates as more comprehensive and spatially resolved data become available. The provincial-level intensive farming proportions were applied without distinguishing between slaughtered livestock and livestock in stock, which may introduce uncertainty in the allocation of emissions between intensive and family farms. However, the overall impact is likely limited because intensive swine farms are defined only by slaughtered swine and dominate total livestock emissions. Second, the antibiotic removal rates in the model were derived from the literature, but actual operational efficiencies in waste treatment processes can fluctuate based on local management practices. Field-based measurements would help align modeled parameters with real-world conditions. Third, the inventory does not assess future emission trends. Incorporating livestock population projections would enable evaluation of long-term changes in emissions. Notwithstanding these limitations, the inventory represents the most comprehensive assessment currently feasible given available data. It provides a solid

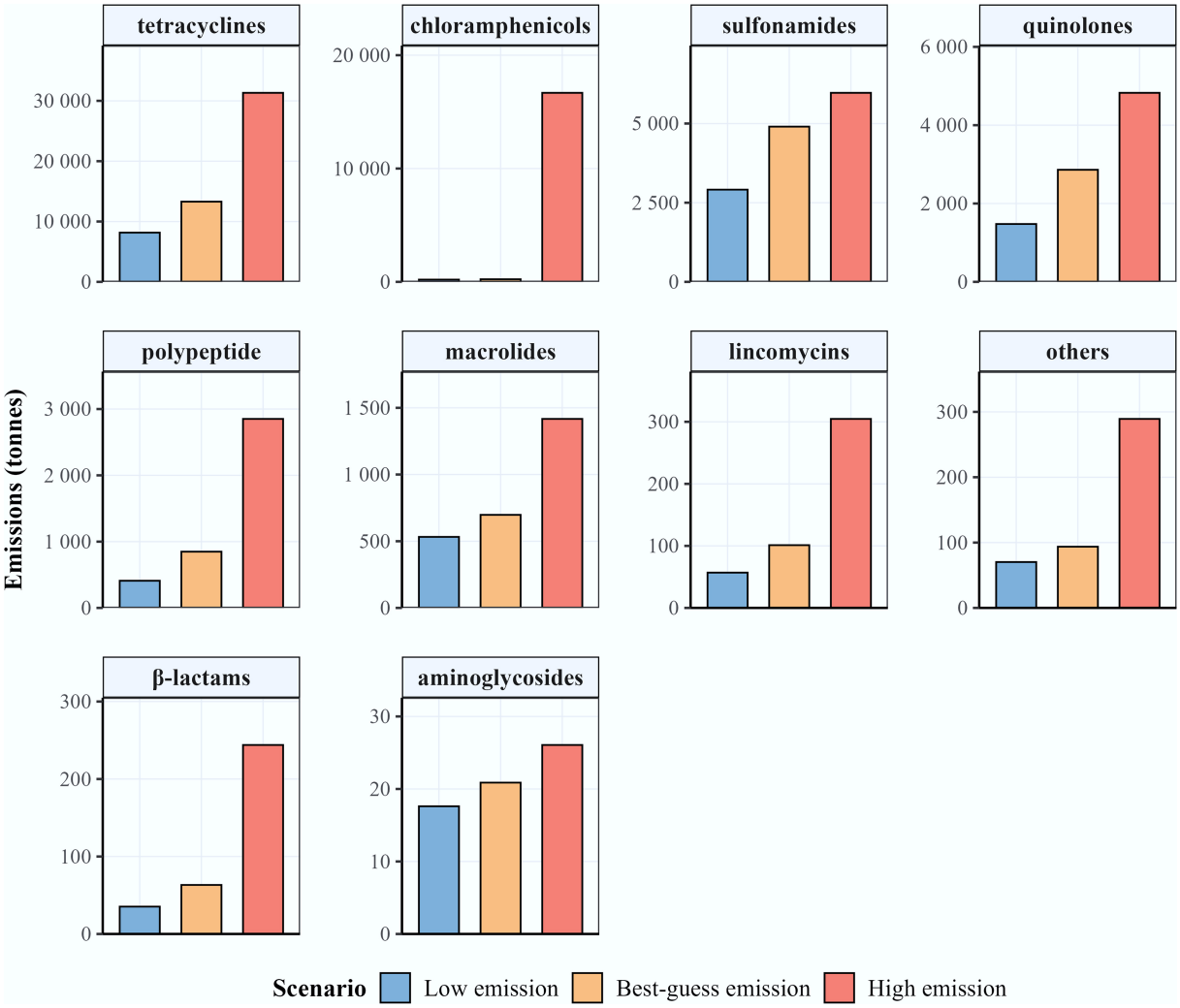

Fig. 2 Comparison of emissions of ten veterinary antibiotic categories under three scenarios.

foundation for evaluating the environmental risks of veterinary antibiotics and offers valuable evidence to inform targeted mitigation policies.

Code availability

No custom code was developed for this study. Microsoft Excel, Visio, and RStudio (2024.04.2) were employed for data processing and figure preparation.

Supplementary information

It accompanies this paper at: https://doi.org/10.66178/aie-0026-0014.

Ethical statements

Not applicable.

Author contributions

The authors confirm their contributions to the paper as follows: Shuaiqi Li: Data curation, writing – original draft; Ying Zhu: Conceptualization, supervision, funding acquisition, writing – review & editing.

Data availability

The datasets generated during this study are available from the link https://doi.org/10.6084/m9.figshare.31829449.

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Declarations

Competing interests

The authors declare that they have no conflict of interests.

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