

Integration of water, sanitation, and hygiene program with biosecurity: A One Health approach to reduce the prevalence and exposure of antibiotic-resistant bacteria in the livestock community

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Abstract

The global spread of antibiotic resistance poses a significant threat to public health and is one of the main causes of this problem. Livestock farming plays a significant role in the horizontal and vertical transmission of treatment-resistant genes and bacteria. These processes involve contact with agricultural products and the environment, raising concerns for public health, and farming communities. The farming community is composed of a staggering 608 million farms worldwide, and their livelihood depends heavily on livestock farming. To address this issue, a multidisciplinary One Health approach focusing on integrated monitoring and intervention for humans, animals, and the environment is essential. Water, sanitation, and hygiene (WaSH) programs have the potential to significantly reduce the risk of exposure to antibiotic-resistant bacteria, particularly extended spectrum beta-lactamase (ESBL) *Escherichia coli*, by obstructing the transmission route between humans and animals. Additional risk reduction measures for ESBL *E. coli* infection in animals include vaccination and biosecurity program implementation. Water, sanitation, and hygiene and biosecurity measures must be combined to maximize the effectiveness of the One Health program. Therefore, this study aimed to describe recent advances in biosecurity and WaSH interventions in the livestock environment, analyze the effects of these interventions on human and animal health, and investigate potential future scenarios within the quantitative microbial risk assessment framework. This study used an integrative literature review through searches of four databases, a review of World Health Organization documents through websites, and an examination of relevant texts from previously obtained reference lists. Although hygiene and sanitation are often combined, there is still a lack of quantitative evaluation of the efficacy of integrating WaSH with biosecurity in livestock. In addition, the integration of the WaSH program with biosecurity has potential as a One Health intervention in the coming years.

Keywords: antibiotic-resistant bacteria, biosecurity, extended-spectrum beta-lactamase *Escherichia coli*, One Health, scenario, water, sanitation, and hygiene.

Introduction

In recent decades, the emergence and spread of antimicrobial resistance (AMR) has become a significant threat to the health of people, animals, plants, and the environment [1]. Antibiotic-resistant bacteria (ARBs) are expected to be responsible for 1.27 million fatalities in 2019 [2], demonstrating the devastating effects of AMR. At present, the transmission of AMR extends beyond clinical and pharmaceutical settings and penetrates the agricultural sector, particularly livestock farming. This sector is of great

concern because the horizontal and vertical transmission of ARB and antibiotic resistance genes (ARGs) occurs through contact with agricultural products and the environment [3, 4], leading to various diseases in humans. The main routes of transmission to the human digestive system include oral, skin, and inhalation [5]. The oral route is predominant, usually facilitated by contaminated livestock manure [6] and water polluted with wastewater [7]. As soon as an ARB enters the human body, subsequent colonization and infection can lead to severe disease. Consumption of antibiotics by livestock was positively correlated with the presence of ARB in humans (1.07 [CI 95% = 1.01–1.13], $p = 0.020$) [8]. Extended Spectrum beta-lactamase (ESBL) *Escherichia coli* is a critically resistant bacterium recommended for in-depth research by the World Health Organization (WHO) [9, 10] due to its ability to cause fatal prolonged diarrhea [11].

The livestock sector accounts for 40% and 20% of developed and developing countries, respectively,

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with 608 million farms worldwide [12]. Therefore, farmers are highly vulnerable to AMR exposure, which can be influenced by risk factors, such as hazards, transmission routes, and other determinants, often applied in the pathogen mapping process [13]. The most frequent risks include improper use of agents, poor water, sanitation, and hygiene (WaSH) infrastructure, and insufficient measures for infection control and prevention [14]. Pathway factors encompass types of agriculture, environmental routes, and antibiotic consumption [15], whereas indirect factors include urbanicity and multidimensional wealth index [16].

The WHO, OIE, FAO, and UNEP have established the One Health policy to combat the spread of AMR. This policy aims to achieve holistic health for humans, animals, and surrounding plants [17] through comprehensive transmission analysis, integrated surveillance, interventions, behavioral changes, and economic policies [18]. Biosecurity measures, including restrictions on antibiotic prescriptions and vaccinations, are currently applied in the livestock sector to reduce the risk of AMR transmission. From a medical point of view, biosecurity encompasses cross-sectoral areas such as the prevention of zoonosis, food safety, plant health, animal and plant biosafety, and invasive species control. In the livestock sector, biosecurity programs are the first line of disease control measures and are usually implemented within specific areas of concern [19]. However, there have been limitations, such as inadequate implementation on large farms and lack of stakeholder engagement opportunities [20].

In the field of environmental engineering, WaSH approaches, such as clean water supply, regular water quality checks, periodic cleaning of animal pens, and handwashing practices, are promising for reducing the risk of AMR. This program has been effectively implemented in domestic environments [21, 22], schools [23], and healthcare facilities [24–26]. The World Health Organization and UNICEF launched a monitoring strategy for the 2030 Agenda for Sustainable Development Goal 6, which aims to provide water for all. However, it has not yet been extended to the livestock industry [27]. In view of the urgency of the One Health program to combat AMR, the integration of WaSH and biosecurity programs has significant potential for infection prevention in livestock areas. In view of the close links between people, animals, and the environment in these places, this integration is crucial.

The proposed WaSH program to minimize the spread of AMR in livestock environments [28] remains largely conceptual. On the other hand, the implementation of biosecurity measures to combat AMR remains limited, especially in developed countries [29, 30], due to their complexity. Recently, integrating WaSH with biosecurity has emerged as a means [20, 31] of enhancing control within the One Health program. This review, based on the principles

of WaSH and biosecurity, aimed to (1) provide an overview of the global prevalence of ARB, specifically ESBL *E. coli*, (2) describe recent advancements in WaSH and biosecurity interventions in livestock environments within the context of One Health, (3) assess the effects of these interventions on human and animal health, and (4) explore potential future scenarios on quantitative microbial risk assessment (QMRA). Moreover, it emphasizes the examination of sanitation and water elements at points (2) and (3), focusing on environmental engineering aspects of livestock that have not been extensively discussed in the previous research.

Review Method

The literature search was limited to 2007–2022, which encompasses extensive studies conducted on ARBs in livestock over the past decade. The keywords “livestock AND hygiene” and “livestock AND sanitation” were used to search the Scopus, EMBASE, PubMed, and AGRIS. In addition, publications on the WHO website featuring the latest developments in antibiotic resistance was examined. To commence text synthesis, the acquired literature was collated in the Zotero library.

Inclusion criteria, including studies published in English pertaining to animal husbandry and an explanation on hygiene, sanitation, and biosecurity aligned with the objectives of the study, were used to facilitate the text synthesis. This review included 67 studies, including research papers and WHO publications.

Each study was subjected to a rigorous review process and data extraction was performed on elements related to the size of the intervention. Subsequently, the data were grouped and synthesized based on categories such as resistance tendency of *E. coli* to antibiotics, quantitative value of existing interventions, and direction of future interventions.

Worldwide Prevalence of ESBL *E. coli* in Livestock

Extended-spectrum beta-lactamase *E. coli* from livestock and the surrounding environment can be transmitted to humans through both horizontal and vertical mechanisms, with the horizontal mode being more common [32]. Complex horizontal transmission through ARGs occurs mostly in humans, animals, and the environment [33]. In addition, vertical transmission includes the spread of ARB in the same agricultural area or between farms. The transfer process facilitated by ARGs is more common in plasmids, such as transposons, gene cassettes, and integrons than in mobile genetic elements (MGEs) [34].

In 2019, the highest number of projected deaths due to AMR was observed in South Asia, reaching 389,000 cases, with a global disease burden of 619 disability-adjusted life year per 100,000 individuals [2]. These projections were calculated using statistical predictive models based on collected

secondary data on sepsis, infection syndromes, case-fatality ratios, pathogen distribution, antibiotic use, resistance prevalence, resistance profiles, relative risk of death, and relative length of hospital stay. Surveillance data are crucial to obtain accurate AMR disease burden values. In livestock environments, AMR surveillance data are primarily obtained through the prevalence of ESBL *E. coli* against one or more antibiotics. Extended Spectrum beta-lactamase *E. coli* testing involves sampling from various sources, including pooled fecal materials, cloacal swabs, feed items, and environmental samples, such as soil, compost products, sewage water, and digester output. Several non-standardized laboratory analysis techniques, such as conventional culture, antibiotic susceptibility testing, microdilution broth, molecular quantitative polymerase chain reaction, whole-genome sequencing techniques, and combinations of conventional and molecular methods, are often employed during the estimation process.

The use of antimicrobials in agricultural activities, such as incorporating antimicrobials into feed, administering antibiotics to animals, and implementing biosecurity measures in the farm area, affects the prevalence of ESBL *E. coli*. As a result, there are differences in the number of ESBL *E. coli* identified on farms between countries [32]. This differs between livestock species, with poultry farms generally having a higher prevalence than ruminants [33].

A comparison of ESBL *E. coli* prevalence between developed and developing countries should be performed with caution. For example, ESBL *E. coli* has been reported at a rate of 39% in Canadian cattle farms [35], whereas pig farms in the United Kingdom reported only 2% [36]. In Italy, the prevalence was 23.3% [37], whereas in France, the prevalence was 5%, and in Japan, it reached 5.2% [38]. In Africa, fecal samples of Ethiopian cattle have a higher prevalence (52%) [39], whereas broiler farms in Zambia have reported lower values [40]. Pig farms in Nigeria recorded 41.2% [41], Cameroon recorded 59.1% [42], and Kenya had the highest value at 81% [43]. In Asia, India reported an occurrence rate of up to 75% [44], whereas Qatar reported 18% [45]. In Indonesia, 35.7% of broiler farms [46] and 52% in Sri Lanka [47] were detected. A study [48] found a greater incidence of ESBL *E. coli* (16.8%) in water samples bathed by buffaloes compared to water used for bathing, washing, and community sanitation.

The prevalence of multidrug-resistant (MDR) *E. coli* has been observed in Asia [49–54], Africa [55–58], and four European countries [59], with varied rates and resistance to more than four types of medicines. Further research is required to understand the transmission mechanism of MDR *E. coli* within agricultural contexts and the risk variables that affect temporal changes.

Water, Sanitation, and Hygiene and Biosecurity Measures in Livestock Environments in the Context of One Health

One Health approach balances human, animal, plant, and ecosystem health. Over the past decade, the implementation of this program has involved cooperation between veterinarians and cross-governmental, multi-sectoral, and environmental experts. In Africa, 21 countries have formed a One Health platform to facilitate resource sharing and evaluate One Health activities [60]. The WHO has developed a Global Action Plan on AMR, which will be implemented in the National Action Plan on AMR by countries worldwide. The effects of NAP on AMR were evaluated every 5 years. For example, Bangladesh NAP study on antimicrobial stewardship (AMS) identified a policy gap in the form of tight operational, monitoring and assessment frameworks, precise funding mechanisms, and guidelines for AMS in the veterinary field [61].

In addition to this collaborative approach, the WHO initiated a surveillance stage to build a database of ARBs in 2015 [62]. Developed countries support developing countries in the implementation of innovative integrated surveillance programs. Cocker *et al.* [63] conducted a longitudinal cohort survey study in rural, peri-urban, and urban areas of Malawi. This study found that the critical risk of ESBL *Enterobacteriales* colonization in humans is closely related to environmental sanitation, urbanization, and the rainy season.

Although the prevalence of infections due to exposure to ARBs in livestock and the human environment tends to be lower than that in humans [64], preventive measures to reduce the transmission of bacterial infections in good animal husbandry need to be continuously applied. It is expected that the WaSH program for reducing environmental impacts combined with a biosecurity program to stop the spread of pathogens in the livestock sector will be one of the most effective intervention tools. According to the WHO definition of WaSH, water refers to the provision of safe drinking water, sanitation involves the safe handling of feces, and hygiene focuses on improving basic hygiene practices. The following are the recent developments in WaSH and biosecurity measures to control the spread of pathogens, addressing ESBL *E. coli* and common pathogenic bacteria in livestock.

Hygiene is often used in large-scale or small-scale intensive and extensive livestock farming worldwide. Hygiene-related efforts include (1) implementing standard procedures [65, 66]; (2) regularly cleaning equipment and maintaining pens [67–74]; (3) using farm clothing and personal protection equipment (PPE) to practice personal hygiene, along with cleaning body parts in contact before and after work [75, 76]; (4) periodically inspecting equipment and PPE [77]; and (5) scheduling the washing of large livestock [78]. Depending on the standard procedures

used, various cleaning techniques were applied. These include a combination of washing, rinsing with water, and disinfectant spraying [67, 70, 71, 73], washing with detergent only [69], washing followed by rinsing with an acidic solution [79], and disinfectant spraying only [74].

Recent developments in sanitation include (1) handling livestock feces [80–84] and (2) application of technology to control fecal contamination in the environment [68, 85–87]. Managing livestock feces involves protecting areas by covering storage containers [68]. Other methods include relocating feces during the summer season [80], transferring the collected samples into specific containers or rooms [81], grinding after naturally drying for 100 days [82], and adding straw and sawdust [83, 84]. Fecal contamination can be controlled through anaerobic digestion processes conducted in slurry pits for conversion into biogas and liquid manure [68, 85, 86], composting to obtain solid manure [87], and the conversion of feces into biochar [88].

The processing of feces usually produces agricultural products, biochar, or liquid fertilizers from biodigesters which are directly applied to the soil. Both ARGs and MGEs in fertilizers increased the abundance of native soil ARGs [89]. The soil ARG profile is significantly influenced by the microbial community structure, MGEs, pH, and heavy metals [90]. A setback distance of up to 40 m around the experimental plots with solid manure applied should be installed to prevent runoff from leaching livestock feces into the soil during rainfall [91]. As the distance approached 40 m, the ARGs and MGEs present in the solid manure were carried by runoff water, reducing their impact on the resistome and mobilome in the surrounding area.

Improving the quantity and quality of water is very important for livestock, farmers, and surrounding communities. Water aspects of WaSH include (1) increasing water quantity for domestic purposes [92], (2) ensuring water quality [75, 76, 83, 84, 93, 94], and (3) separating water sources for livestock and human consumption [73]. The approach to water management differs between developed countries and developing countries because clean water in developing countries can originate from various non-piped sources [95]. In addition, rainwater and groundwater are clean sources for livestock farming. Drinking water for workers on large farms is provided in refillable bottles or bottles. Ensuring water quality involves the addition of chlorine [84] and oxygen peroxide [83] to kill pathogens, as well as the application of antibiotics [96] and organic acids [94] in pipeline systems to maintain health or treat poultry diseases. Further, treatments, such as water heating and iron removal systems [97], are employed for non-piped water sources to promote livestock and human health in surrounding areas.

Biosecurity approaches, as described by Constable *et al.* [98], encompass: (1) checking or isolating newly

introduced livestock species; (2) controlling visitor contact; (3) managing contact between livestock, pets, and wild animals entering the farm; (4) separating sick livestock; (5) cleaning and disinfection practices; (6) disease monitoring and record-keeping; and (7) conducting communication, training, and employee assessment. According to Pinto Jimenez *et al.* [20], biosecurity programs include bioexclusion, biocontainment, and biomanagement programs. Bioexclusion prevents the emergence of new pathogens, biocontainment restricts their entry, and biomanagement includes the control of existing pathogens in the agricultural environment. The discussion on biocontainment [94] aligned with the overlapping hygiene terminology in the WaSH program.

Farmers can monitor the implementation of biosecurity by means of paper-based or software-based checklists. Biocontainment actions based on the collection of biosecurity checklist examination data and farmer interviews include fencing around farm areas [76, 99–101], venting in livestock barns [101–103], and separation and quarantine measures [66, 68, 76, 80–82, 93, 99, 100, 102]. Other methods include restricting visitors and wild animals from entering the farm area [67, 80, 81, 83, 99, 101–103], limiting the number of livestock herds [103, 104], designing secure livestock housing [79, 81, 83, 105], and properly handling dead livestock [66, 106]. Longitudinal research carried out in Germany focused on the management of pigs suspected to be infected with ESBL *E. coli* through herd eradication followed by health examinations of farmers [106]. Sick farmers were monitored for 3 months and replaced with healthy individuals; they could resume work only if they stopped experiencing diarrhea and showed improvement in the nasal swab. Subsequently, farm owners implemented a shift rotation control. This study demonstrates the importance of eradicating ARB-infected livestock and consistently implementing quarantine measures when introducing new or isolated unhealthy livestock from the herd.

One Health research mainly focused on surveillance [107] to understand the transmission process. However, studies on interventions are limited [31]. The WaSH biosecurity program can be integrated into a series of intervention steps to address this gap. As outlined by O’Cathain *et al.* [108], these steps include problem identification, literature review, preparation, feasibility testing through pilot tests, optimization, evaluation, and long-term implementation. In addition, One Health-based WaSH biosecurity intervention program can take the form of managerial, structural, educational/behavioral, biological/chemical, and physical/infrastructural approaches [31].

As a first step in the intervention research offered by the WaSH biosecurity program, integrative WaSH biosecurity scenarios must be tested on an integrated farm. In the course of the test, the risk recipient targets must include humans, animals, and the environment.

One health issue should be considered by optimizing (1) WaSH with human and environmental health targets and (2) biosecurity through livestock health targets.

The Effects of Existing WaSH and Biosecurity Strategies

The odds ratio (OR) of ESBL *E. coli* and common pathogen bacteria in the literature was used to review the function of WaSH and biosecurity applications, representing a comparison between farmers who implemented the interventions and their counterparts (Table-1) [72, 76, 80, 84, 92, 99]. The ORs were derived entirely from interviews with the farmer population who indicated the magnitude of the impact of the implementation of both programs. The higher values suggest a greater expected impact, thereby reducing the risk of ARB infection in farmers and livestock.

An adequate supply of clean water significantly contributes to the operational aspects of livestock farming, with an OR of 1.89 ([CI 95% = 1.1–2.78], $p = 0.05$) [92]. Disinfection efforts for drinking purposes had an OR of 1.96 ([CI 95% = 0.52–7.39], $p = 0.32$) [76]. The OR for hygiene, which includes cleaning followed by disinfection, was 3 ([CI 95% = 1.2–7.5], $p = 0.05$) [72]. Similarly, the

use of PPE had an OR of 3 ([CI 95% = 0.6–15.9], $p = 0.2$) [80]. Sanitation interventions were assessed based on the log removal value (LRV), which indicates the level of ARB reduction in logarithmic units after completion of the sanitation process. Composting, ordinary biodigestion, and biodigestion with a bioslurry pit can achieve bacterial LRVs of 1–2 [87], 1–2 [86], and 6.11, respectively, for ESBL *E. coli* [85]. Another aspect of sanitation, such as the addition of straw to litter [84], has an OR of 0.87 ([CI 95% = 0.57–1.33], $p = 0.53$).

According to Mridha *et al.* [76], the overall implementation of biosecurity has an OR of 3.37 ([CI 95% = 0.71–16.06], $p = 0.12$), whereas another investigation [99] reported a lower OR of 1 ([CI 95% = 0.16–0.94], $p = 0.035$). Moreover, recent biosecurity interventions on poultry farms and slaughterhouses in the Netherlands to address *Campylobacter* spp. (a pathogenic bacterium) have focused on disease occurrence that affects the health of broiler chickens for human consumption [109]. The combined effectiveness of insect control efforts, barn cleanliness, and visitor control resulted in a minimum reduction of 5%–10%.

In Burkina Faso, studies on small-scale chicken farms have used a different approach to disrupt

Table-1: WaSH and biosecurity intervention based on the OR of previous studies.

Reference	Type of intervention	OR
Dohmen <i>et al.</i> [80]	Hygiene intervention: Using gloves when treating piglets	3 (CI 95% = 0.6–15.9), $p = 0.2$
Caudell <i>et al.</i> [92]	Water intervention: Increased water supply for domestic purpose (non-livestock)	1.89 (CI 95% = 1.1–2.78), $p = 0.05$
Mridha <i>et al.</i> [76]	Water intervention: Maintain water quality	1.96 (0.52–7.39 CI 95%; $p = 0.32$)
	Hygiene intervention: Attendants' hand rinse water	0.41 (0.12–1.34 CI 95%; $p = 0.14$)
	Biosecurity intervention: Overall biosecurity on farm application (provision of perimeter fencing, netting of the farm, footwear clean entry in the farm, all-in all-out practice)	3.37 (0.71–16.06 CI 95%; $p = 0.12$)
Adebowale <i>et al.</i> [99]	Biosecurity intervention: Presence of isolation bay for sick animals, Quarantining of new animals on arrivals, Restriction visit to other farms, Access to farms by farm buyers, Access to farms by feed transport vehicles, Ownership of farm equipment, Use of farm equipment from other farms.	1 (0.16–0.94 CI 95%)
Coffman <i>et al.</i> [72]	Hygiene intervention: Conducted any pesticide application or cleaning activity Used any PPE Washed hands at least 8 times per shift	3 (1.2–7.5 CI 95%) 0.3 (0.1–1.5 CI 95%) 0.3 (0.1–0.8 CI 95%)
Sanni <i>et al.</i> [84]	Water intervention: Dug-up well using chlorination	0.42 (0.3–0.58 CI 95%, $p < 0.001$)
	Sanitation intervention: Litter materials for litter management	0.87 (0.57–1.33 CI 95%, $p = 0.53$)

PPE=Personal protection equipment, WaSH=Water, sanitation, and hygiene, OR=Odds ratio

the transmission of pathogens. The experts concerned [110, 111] focused on the children of farmers and provided supervision for hand hygiene, feeding practices, and biocontainment of animal feces. To reduce inadvertent soil and fecal ingestion in children, participatory behavioral change sanitation programs combined with biocontainment were implemented through two-way communication. Similar participatory behavior-based sanitation programs have been practiced in pastoralist communities in Ethiopia [112], raising awareness of the importance of maintaining clean water and sanitation infrastructure. Strengthening WaSH and biosecurity measures in livestock farming disrupts the chain of disease transmission between animals and reduces the risk of exposure in animals and humans. These strategies can reduce the incidence of disease in livestock, leading to a reduction in antimicrobial use, in particular antibiotics, thereby suppressing the possible emergence of ARB.

Research on the combined implementation of WaSH and biosecurity programs over the last 5 years has highlighted the impact of these programs. While there is a significant amount of literature on WaSH or biosecurity, the impact of these interventions has not been analyzed using OR, which is a limitation of this review. Literature on other pathogenic bacteria has also been included due to a lack of literature on ESBL-specific *E. coli*.

Quantitative Microbial Risk Assessment Framework in the Livestock Environment for Farmers

Antibiotic-resistant bacteria in farm areas can originate from feed, antimicrobial use, and medications for sick livestock. Antimicrobials, antibiotics, and feed consumed by livestock are processed in the gut and excreted in the feces. Animal feces are considered hotspots due to the presence of pathogens, both in their original state and in processed forms, such as manure and slurry [113].

Manure or slurry tends to bind to pathogens, antibiotic residues, and chemical stressors compared with raw animal waste. These materials are referred to as hotspots for ARGs and MGEs even though their concentration depends on processing method and storage conditions. Moreover, gene transfer can occur immediately after the application of manure or slurry to the soil, even under unfavorable conditions [114]. feedwater, soil, and feed are potential exchange points for ARGs and ARBs between humans and animals. The resistant pattern of *E. coli* has been found in soils with direct or processed contact with animal feces. In Thailand, Tanzania, Peru, and Bangladesh, they are also observed in humans, cattle, and soil [33]. The risk of exposure to resistant *E. coli* is higher in individuals who maintain animals near their homes than those who separate livestock areas from their living spaces [115].

The risk of human exposure to microorganisms has been evaluated using deterministic or stochastic QMRA method [116]. This model involves hazard identification, exposure estimation, dose-response calculation, and risk characterization through ARB transmission across the oral route. According to QMRA research, individuals can be directly or indirectly exposed to animal feces through airborne, oral, or fomite transmission routes [11]. Inhalation exposure by farmers in direct contact with raw and processed manure and slurry differed from the exposure of workers to the digestive system. Research conducted in Beijing, China, revealed that inhalation exposure due to manure being a hotspot is less than that from drinking water or ingesting waste and soil while working [117]. There are limited specific investigations of AMR indicating which exposure pathway is associated with a higher risk.

Once hazard identification was conducted, the next step in QMRA was to calculate the exposure through hand-to-mouth contact while handling animal feces, which was estimated by multiplying the ARB concentration by the manure ingestion rate. Exposure through soil ingestion when feces were applied to agricultural land was estimated by multiplying the concentration of ARB by the soil ingestion rate. We performed a Monte Carlo simulation to calculate the uncertainty of the parameters and conducted a statistical sensitivity analysis. Ingestion rates in occupational farming are currently limited, and empirical data are mostly based on ingestion rates in the general adult population. Behavioral factors such as hierarchical health and safety interventions (e.g., engineering and administrative controls, PPE use) that can reduce intake or exposure time during hotspot handling are currently unavailable in developing countries [118]. Limited research has been carried out on exposure to ESBL *E. coli* and dose-response assessments for farmers, partly because most studies have focused on non-ARB microorganisms [119, 120], and relevant data on antimicrobial exposure remains lacking. Antimicrobial exposure includes vulnerability, resistance, tolerance, and persistence [121]. Therefore, ingestion rate and dose-response assessments of ESBL *E. coli* in farmers are potential opportunities for future research.

Potential Scenarios for Future WaSH and Biosecurity Interventions within the QMRA Framework

The incorporation of WaSH biosecurity into the QMRA framework can reduce the risk of exposure of farmers to ESBL *E. coli* and reduce the incidence of inadvertent soil and livestock feces ingestion. It is possible to reduce the frequency and duration of farmers' daily interactions with soil and animal waste to reduce the rate of accidental ingestion. Reducing ESBL *E. coli* concentration should consider the WaSH principles outlined in the F-diagram [122], whereas biosecurity principles can be derived from

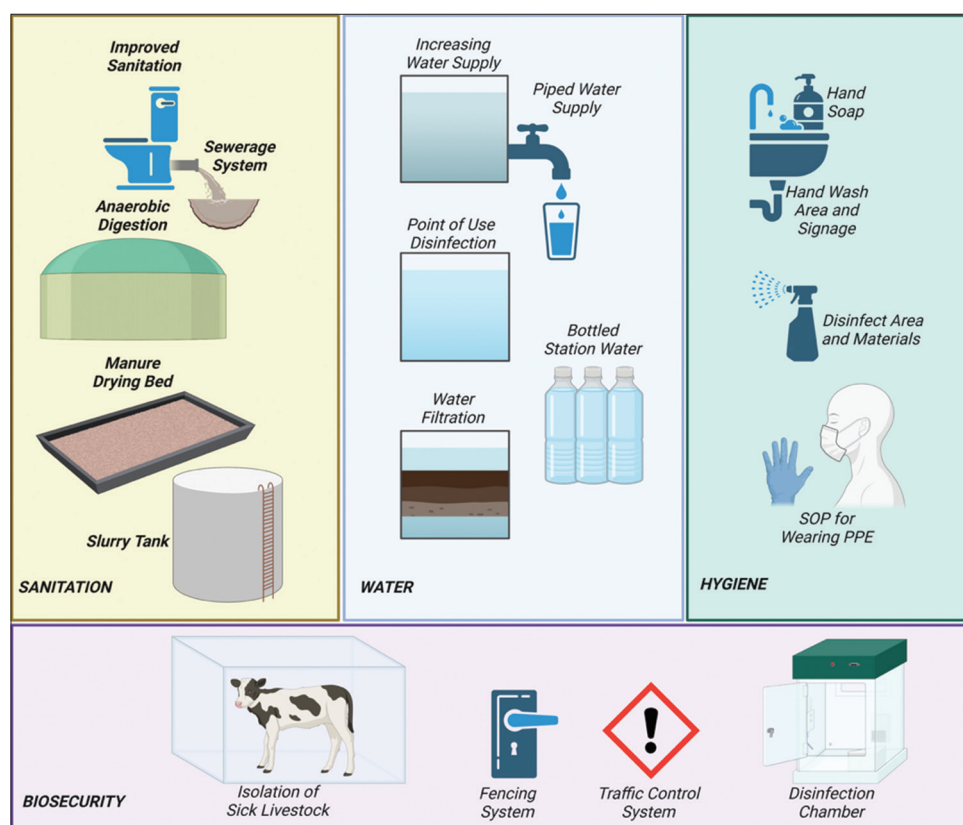


Figure-1: Water, sanitation, and hygiene–biosecurity program framework as an option to reduce extended spectrum beta-lactamase concentrations of *Escherichia coli* in livestock [Source: Prepared by Yudith Vega Paramitadevi using BioRender.com].

biocontainment and biomanagement. Implementing the WaSH biosecurity program involves biocontainment and biomanagement, with water and sanitation components emphasizing fecal management, enhancing drinking water quality, and increasing farmers' cleanliness [31]. Figure-1 alternatives for incorporating WaSH biosecurity to lower the concentration of *E. coli* ESBL.

The WaSH principles in the F-diagram, in sequential order, include: (1) animal and human fecal sanitation, (2) water quality improvement, and (3) personal hygiene, equipment, and food. The measures referred to in points (2) and (3) may be implemented together with biocontainment. Therefore, the combinations to reduce ESBL *E. coli* exposure following environmental engineering disciplines include (a) sanitation-biocontainment, (b) sanitation-water-biocontainment, (c) sanitation-hygiene-biocontainment, (d) sanitation-water-hygiene-biocontainment, and (e) addition of biomanagement to options (a) to (c). Decision analysis can be facilitated by various multicriteria decision-making tools commonly used in conjunction with QMRA using a participatory group discussion approach involving the community or stakeholders.

All available options must be analyzed according to the needs of farmers, farming types, other risk factors such as vaccination programs for livestock, policies restricting the use of antibiotics exclusively for sick animals, and farmers' understanding of

antibiotic use. In addition, indirect factors, such as location and multidimensional wealth index, must be taken into account, especially in the case of farms located in developed or developing countries. The implementation of comprehensive biosecurity measures may be difficult in developing countries where small-scale farms are predominant. Therefore, optimizing the integration of the WaSH program with biocontainment has been proposed as the best practice for reducing the prevalence of ESBL *E. coli*. In developed countries, additional risk factors, such as pathway factors, should be included in the implementation of WaSH biosecurity programs. The adoption of a single health approach through the consistent implementation of WaSH biosecurity activities involving stakeholders will reduce the exposure of ARBs to the farm environment.

Conclusion

The prevalence of critically resistant bacteria such as ESBL *E. coli* varies due to the use of antibiotics in livestock farming. As a result, there are difficulties in comparing developed and developing countries. In the livestock sector, it is essential to maintain high levels of hygiene to ensure the well-being of animals and prevent the spread of diseases. As part of the WaSH program, regular cleaning of equipment and barns is emphasized to maintain optimal hygiene standards. Sanitation involves processing animal feces into manure, biogas, liquid fertilizer, and

biochar to control pollution. The quality of water was ensured by adding chlorine, organic substances, and advanced treatment methods. In addition, biosecurity programs focus on biocontaining or limiting the entry of pathogens into agricultural areas. In this study, we assessed the roles of WaSH and biosecurity based on the intervention effects obtained from interviews with farmers. Technological aspects of sanitation were evaluated using LRV. Water, sanitation, and hygiene and biosecurity programs are often carried out separately; however, both reduce the risk of disease transmission from humans and animals to humans. Several combined WaSH and biosecurity programs exist, but their intervention effects are typically described qualitatively. The development of WaSH biosecurity scenarios within the QMRA framework involved the identification of hazards and estimation of ESBL *E. coli* exposure with a view to reducing its prevalence and minimizing inadvertent soil and fecal ingestion rates. Scenarios should be considered on the basis of associated risk factors.

Authors' Contributions

YVP: Conceptualized the review and drafted the manuscript accordingly. CRP and IR: Edited and revised the manuscript. AR and SSM: Literature search and commented on it. All authors have read, reviewed, and approved the final manuscript.

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Competing Interests

The authors declare that they have no competing interests.

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References

1. Laxminarayan, R. (2022) The overlooked pandemic of antimicrobial resistance. *Lancet*, 399(10325): 606–607.
2. Murray, C.J.L., Ikuta, K.S., Sharara, F., Swetschinski, L., Aguilar, G.R., Gray, A., Han, C., Bisignano, C., Rao, P., Wool, E., Johnson, S.C., Browne, A.J., Chipeta, M.G., Fell, F., Hackett, S., Haines-Woodhouse, G., Hamadani, B.H.K., Kumaran, E.A.P., McManigal, B., Achalapong, S., Agarwal, R., Akech, S., Albertson, S., Amuasi, J., Andrews, J., Aravkin, A., Ashley, E., Babin, F.X., Bailey, F.,

Baker, S., Basnyat, B., Bekker A., Bender, R., Berkley, J.A., Bethou, A., Bielicki, J., Boonkasidecha, S., Bukosia, J., Carvalheiro, C., Castañeda-Orjuela, C., Chansamouth, V., Chaurasia, S., Chiurchiù, S., Chowdhury, F., Donatien, R.C., Cook, A.J., Cooper, B., Cressey, T.R., Criollo-Mora, E., Cunningham, M., Darboe, S., Day, N.P.J., Luca, M.D., Dokova, K., Dramowski, A., Dunachie, S.J., Bich, T.D., Eckmanns, T., Eibach, D., Emami, A., Feasey, N., Fisher-Pearson, N., Forrest, K., Garcia, C., Garrett, D., Gastmeier, P., Giref, A.Z., Greer, R.C., Gupta, V., Haller, S., Haselbeck, A., Hay, S.I., Holm, M., Hopkins, S., Hsia, Y., Iregbu, K.C., Jacobs, J., Jarovsky, D., Javanmardi, F., Jenney, A.W.J., Khorana, M., Khusuwan, S., Kissoon, N., Kobeissi, E., Kostyanov, T., Krapp, F., Krumkamp, R., Kumar, A., Kyu, H.H., Lim, C., Lim, K., Limmathurotsakul, D., Loftus, M.J., Lunn, M., Ma, J., Manoharan, A., Marks, F., May, J., Mayxay, M., Mturi, N., Munera-Huertas, T., Musicha, P., Musila, L.A., Mussi-Pinhata, M.M., Naidu, R.N., Nakamura, T., Nanavati, R., Nangia, S., Newton, P., Ngoun, C., Novotney, A., Nwakanma, D., Obiero, C.W., Ochoa, T.J., Olivás-Martínez, A., Oliario, P., Ooko, E., Ortiz-Brizuela, E., Ounchanum, P., Pak, G.D., Paredes, J.L., Peleg, A.Y., Perrone, C., Phe, T., Phommasone, K., Plakkal, N., Ponce-de-Leon, A., Raad, M., Ramdin, T., Rattanavong, S., Riddell, A., Roberts, T., Robotham, J.V., Roca, A., Rosenthal, V.D., Rudd, K.E., Russell, N., Sader, H.S., Saengchan, W., Schnall, J., Scott, J.A.G., Seekaew, S., Sharland, M., Shivamallappa, M., Sifuentes-Osorio, J., Simpson, A.J., Steenkeste, N., Stewardson, A.J., Stoeva, T., Tasak, N., Thaiprakong, A., Thwaites, G., Tigoi, C., Turner, C., Turner, P., Doorn, H.R., Velaphi, S., Vongpradith, A., Vongsouvath, M., Vu, H., Walsh, T., Walson, J.L., Waner, S., Wangrangsimaikul, T., Wannapinij, P., Wozniak, T., Sharma, T.E.M.W.Y., Yu, K.C., Zheng, P., Sartorius, B., Lopez, A.D., Stergachis, A., Moore, C., Dolecek, C. and Naghavi, M. (2022) Global burden of bacterial antimicrobial resistance in 2019: A systematic analysis. *Lancet*, 399(10325): 629–655.

3. Despotovic, M., de Nies, L., Busi, S.B. and Wilmes, P. (2023) Reservoirs of antimicrobial resistance in the context of One Health. *Curr. Opin. Microbiol.*, 73: 102291.
4. Kim, J. and Ahn, J. (2022) Emergence and spread of antibiotic-resistant foodborne pathogens from farm to table. *Food Sci. Biotechnol.*, 31(12): 1481–1499.
5. Carr, V.R., Witherden, E.A., Lee, S., Shoaie, S., Mullany, P., Proctor, G.B., Gomez-Cabrero, D. and Moyes, D.L. (2020) Abundance and diversity of resistomes differ between healthy human oral cavities and gut. *Nat. Commun.*, 11(1): 693.
6. Marutescu, L.G., Jaga, M., Postolache, C., Barbuceanu, F., Milita, N.M., Romascu, L.M., Schmitt, H., de Roda Husman, A.M., Sefeedpari, P., Glaeser, S., Kämpfer, P., Boerlin, P., Topp, E., Gradisteanu Pircalabioru, G., Chifiriuc, M.C. and Popa, M. (2022) Insights into the impact of manure on the environmental antibiotic residues and resistance pool. *Front. Microbiol.*, 13: 965132.
7. Astuti, M.P., Notodarmojo, S., Priadi, C.R. and Padhye, L.P. (2023) Contaminants of emerging concerns (CECs) in a municipal wastewater treatment plant in Indonesia. *Environ. Sci. Pollut. Res.*, 30(8): 21512–21532.
8. Allel, K., Day, L., Hamilton, A., Lin, L., Furuya-Kanamori, L., Moore, C.E., Van Boeckel, T., Laxminarayan, R. and Jakob, L. (2023) Global antimicrobial resistance drivers: An ecological country-level study at the human-animal interface. *Lancet Planet Health*, 7(4): e291–e303.
9. WHO. (2017) Prioritization of Pathogens to Guide Discovery, Research and Development of New Antibiotics for Drug-Resistant Bacterial Infections, Including Tuberculosis. Available from: <https://www.who.int/publications-detail-redirect/WHO-Emp-Iau-2017.12> Retrieved on 08-11-2023.
10. WHO. (2021) WHO Integrated Global Surveillance on

- ESBL-Producing *E. coli* using a “One Health” Approach: Implementation and Opportunities. Available from: <https://www.who.int/publications-detail-redirect/9789240021402> Retrieved on 08-11-2023.
11. Meier, H., Spinner, K., Crump, L., Kuenzli, E., Schuepbach, G. and Zinsstag, J. (2023) State of knowledge on the acquisition, diversity, interspecies attribution and spread of antimicrobial resistance between humans, animals and the environment: A systematic review. *Antibiotics (Basel)*, 12(1): 73.
 12. Lowder, S.K., Skoet, J. and Raney, T. (2016) The number, size, and distribution of farms, smallholder farms, and family farms worldwide. *World Dev.*, 87: 16–29.
 13. Genter, F., Putri, G.L., Pratama, M.A., Priadi, C., Willetts, J. and Foster, T. (2022) Microbial contamination of groundwater self-supply in Urban Indonesia: Assessment of sanitary and socio-economic risk factors. *Water Resour. Res.*, 58(10):1–21.
 14. WHO. (2015) Global Action Plan on Antimicrobial Resistance. Available from: <https://www.who.int/publications-detail-redirect/9789241509763>. Retrieved on 08-11-2023.
 15. Brunton, L.A., Desbois, A.P., Garza, M., Wieland, B., Mohan, C.V., Häslar, B., Tam, C.C., Le, P.N.T., Phuong, N.T., Van, P.T., Nguyen-Viet, H., Eltholth, M.M., Pham, D.K., Duc, P.P., Linh, N.T., Rich, K.M., Mateus, A.L.P., Hoque, M.A., Ahad, A., Khan, M.N.A., Adams, A. and Guitian, J. (2019) Identifying hotspots for antibiotic resistance emergence and selection, and elucidating pathways to human exposure: Application of a systems-thinking approach to aquaculture systems. *Sci. Total Environ.*, 687: 1344–1356.
 16. Kwong, L.H., Ercumen, A., Pickering, A.J., Arsenaault, J.E., Islam, M., Parvez, S.M., Unicomb, L., Rahman, M., Davis, J. and Luby, S.P. (2020) Ingestion of fecal bacteria along multiple pathways by young children in rural Bangladesh participating in a cluster-randomized trial of water, sanitation, and hygiene interventions (WASH Benefits). *Environ. Sci. Technol.*, 54(21): 13828–13838.
 17. CDC. (2022) What you should know about antibiotics. In: Centers for Disease Control and Prevention. Available from: <https://www.cdc.gov/antibiotic-use/q-a.html>. Retrieved on 08-11-2023.
 18. WHO. (2023) A One Health Priority Research Agenda for Antimicrobial Resistance. Available from: <https://www.who.int/publications-detail-redirect/9789240075924>. Retrieved on 08-11-2023.
 19. Renault, V., Humblet, M.F. and Saegerman, C. (2021) Biosecurity concept: Origins, evolution and perspectives. *Animals (Basel)*, 12(1): 63.
 20. Pinto Jimenez, C.E., Keestra, S.M., Tandon, P., Pickering, A.J., Moodley, A., Cumming, O. and Chandler, C.I.R. (2023) One health WASH: An AMR-smart integrative approach to preventing and controlling infection in farming communities. *BMJ Glob. Health*, 8(3): e011263.
 21. Ghaudenson, R., Priadi, C.R. and Foster, T. (2021) Effectiveness of groundwater boiling as household water treatment in metro and Bekasi cities, Indonesia. *E3S Web Conf.*, 277: 04002.
 22. Imtiyaz, I., Putri, G.L., Hartono, D.M., Zulkarnain, F. and Priadi, C.R. (2021) Effect of boiling and water storage practices on *E. coli* contamination of drinking water in the city of Bekasi (case study: Jatiluhur, Sumur Batu, and Jatirangga Villages). *IOP Conf. Ser. Earth Environ. Sci.*, 633(1): 012016.
 23. Anggraeni, H.E., Paramitadevi, Y.V., Apriliani, F. and Resmeiliana, I. (2023) Assessing students’ “clean and healthy living behavior” in an intervention program. *Int. J. Public Health Sci.*, 12(1): 56–63.
 24. Hosking, R., O’Connor, S.Y., Wangdi, K., Kurscheid, J. and Lal, A. (2022) Acceptability measures of water, sanitation and hygiene interventions in low- and middle-income countries, a systematic review. *PLoS Negl. Trop. Dis.*, 16(9): e0010702.
 25. Piper, J.D., Chandna, J., Allen, E., Linkman, K., Cumming, O., Prendergast, A.J. and Gladstone, M.J. (2017) Water, sanitation and hygiene (WASH) interventions: Effects on child development in low- and middle-income countries. *Cochrane Database Syst. Rev.*, 2017(3): CD012613.
 26. Watson, J., D’Mello-Guyett, L., Flynn, E., Falconer, J., Esteves-Mills, J., Prual, A., Hunter, P., Allegranzi, B., Montgomery, M. and Cumming, O. (2019) Interventions to improve water supply and quality, sanitation and hand-washing facilities in healthcare facilities, and their effect on healthcare-associated infections in low-income and middle-income countries: A systematic review and supplementary scoping review. *BMJ Glob. Health*, 4(4): e001632.
 27. Nadimpalli, M.L. and Pickering, A.J. (2020) A call for global monitoring of WASH in wet markets. *Lancet Planet Health*, 4(10): e439–e440.
 28. Fletcher, S. (2015) Understanding the contribution of environmental factors in the spread of antimicrobial resistance. *Environ. Health Prev. Med.*, 20(4): 243–252.
 29. Nadimpalli, M., Delarocque-Astagneau, E., Love, D.C., Price, L.B., Huynh, B.T., Collard, J.M., Lay, K.S., Borand, L., Ndir, A., Walsh, T.R., Guillemot, D. and Bacterial Infections and antibiotic-resistant diseases among young children in low-income countries (BIRDY) Study Group. (2018) Combating global antibiotic resistance: Emerging one health concerns in lower- and middle-income countries. *Clin. Infect. Dis.*, 66(6): 963–969.
 30. Heckert, R.A., Reed, J.C., Gmuender, F.K., Ellis, M. and Tonui, W. (2011) International biosafety and biosecurity challenges: Suggestions for developing sustainable capacity in low-resource countries. *Appl. Biosaf.*, 16(4): 223–230.
 31. Pinto Jimenez, C.E.P., Keestra, S., Tandon, P., Cumming, O., Pickering, A.J., Moodley, A. and Chandler, C.I.R. (2023) Biosecurity and water, sanitation, and hygiene (WASH) interventions in animal agricultural settings for reducing infection burden, antibiotic use, and antibiotic resistance: A one Health systematic review. *Lancet Planet Health*, 7(5): e418–e434.
 32. Denissen, J., Reyneke, B., Waso-Reyneke, M., Havenga, B., Barnard, T., Khan, S. and Khan, W. (2022) Prevalence of ESKAPE pathogens in the environment: Antibiotic resistance status, community-acquired infection and risk to human health. *Int. J. Hyg. Environ. Health*, 244: 114006.
 33. Swarthout, J.M., Chan, E.M.G., Garcia, D., Nadimpalli, M.L. and Pickering, A.J. (2022) Human colonization with antibiotic-resistant bacteria from nonoccupational exposure to domesticated animals in low- and middle-income countries: A critical review. *Environ. Sci. Technol.*, 56(21): 14875–14890.
 34. Ikhimiukor, O.O., Odih, E.E., Donado-Godoy, P. and Okeke, I.N. (2022) A bottom-up view of antimicrobial resistance transmission in developing countries. *Nat. Microbiol.*, 7(6): 757–765.
 35. Massé, J., Lardé, H., Fairbrother, J.M., Roy, J.P., Francoz, D., Dufour, S. and Archambault, M. (2021) Prevalence of antimicrobial resistance and characteristics of *Escherichia coli* isolates from fecal and manure pit samples on dairy farms in the province of Québec, Canada. *Front. Vet. Sci.*, 8: 654125.
 36. AbuOun, M., O’Connor, H.M., Stubberfield, E.J., Nunez-Garcia, J., Sayers, E., Crook, D.W., Smith, R.P. and Anjum, M.F. (2020) Characterizing antimicrobial resistant *Escherichia coli* and associated risk factors in a cross-sectional study of pig farms in Great Britain. *Front. Microbiol.*, 11: 861.
 37. Mercato, A., Cortimiglia, C., Abualsha’ar, A., Piazza, A., Marchesini, F., Milani, G., Bonardi, S., Cocconcelli, P.S. and Migliavacca, R. (2022) Wild boars as an indicator of environmental spread of ESBL-producing *Escherichia coli*. *Front. Microbiol.*, 13: 838383.

38. Collis, R.M., Burgess, S.A., Biggs, P.J., Midwinter, A.C., French, N.P., Toombs-Ruane, L. and Cookson, A.L. (2019) Extended-spectrum beta-lactamase-producing *Enterobacteriaceae* in dairy farm environments: A New Zealand perspective. *Foodborne Pathog. Dis.*, 16(1): 5–22.
39. Gameda, B.A., Wieland, B., Alemayehu, G., Knight-Jones, T.J.D., Wodajo, H.D., Tefera, M., Kumbe, A., Olani, A., Abera, S. and Amenu, K. (2023) Antimicrobial resistance of *Escherichia coli* isolates from livestock and the environment in extensive smallholder livestock production systems in Ethiopia. *Antibiotics (Basel)*, 12(5): 941.
40. Mwansa, M., Mukuma, M., Mulilo, E., Kwenda, G., Mainda, G., Yamba, K., Bumbangi, F.N., Muligisa-Muonga, E., Phiri, N., Silwamba, I. and Muma, J.B. (2022) Determination of antimicrobial resistance patterns of *Escherichia coli* isolates from farm workers in broiler poultry production and assessment of antibiotic resistance awareness levels among poultry farmers in Lusaka, Zambia. *Front. Public Health*, 10: 998860.
41. Olorunleke, S.O., Kirchner, M., Duggett, N., AbuOun, M., Okorie-Kanu, O.J., Stevens, K., Card, R.M., Chah, K.F., Nwanta, J.A., Brunton, L.A. and Anjum, M.F. (2022) Molecular characterization of extended spectrum cephalosporin resistant *Escherichia coli* isolated from livestock and in-contact humans in Southeast Nigeria. *Front. Microbiol.*, 13: 937968.
42. Ngogang, M.P., Ernest, T., Kariuki, J., Mouliom Mouiche, M.M., Ngogang, J., Wade, A. and van der Sande, M.A.B. (2020) Microbial contamination of chicken litter manure and antimicrobial resistance threat in an Urban Area setting in Cameroon. *Antibiotics (Basel)*, 10(1): 20.
43. Ngaywa, C., Aboge, G.O., Obiero, G., Omwenga, I., Ngwili, N., Wamwere, G., Wainaina, M. and Bett, B. (2019) Antimicrobial resistant *Escherichia coli* isolates detected in raw milk of livestock in pastoral areas of northern Kenya. *Food Control*, 102: 173–178.
44. Tewari, R., Mitra, S., Ganaie, F., Das, S., Chakraborty, A., Venugopal, N., Shome, R., Rahman, H. and Shome, B.R. (2019) Dissemination and characterisation of *Escherichia coli* producing extended-spectrum β -lactamases, AmpC β -lactamases and metallo- β -lactamases from livestock and poultry in Northeast India: A molecular surveillance approach. *J. Glob. Antimicrob. Resist.*, 17: 209–215.
45. Eltai, N., Al Thani, A.A., Al-Hadidi, S.H., Abdifarag, E.A., Al-Romaihi, H., Mahmoud, M.H., Alawad, O.K. and Yassine, H.M. (2020) Antibiotic resistance profile of commensal *Escherichia coli* isolated from healthy sheep in Qatar. *J. Infect. Dev. Ctries.*, 14(2): 138–145.
46. Effendi, M., Faridah, H., Wibisono, F., Wibisono, F., Nisa, N. and Nnabuike, U. (2022) Detection of virulence factor encoding genes on *Escherichia coli* isolated from broiler chicken in Blitar District, Indonesia. *Biodivers. J. Biol. Divers.*, 23(7): 3437–3442.
47. Bamunusinghage, N.P.D., Neelawala, R.G., Magedara, H.P., Ekanayaka, N.W., Kalupahana, R.S., Silva-Fletcher, A. and Kottawatta, S.A. (2022) Antimicrobial resistance patterns of fecal *Escherichia coli* in wildlife, Urban wildlife, and livestock in the eastern region of Sri Lanka, and differences between carnivores, omnivores, and herbivores. *J. Wildl. Dis.*, 58(2): 380–383.
48. Devi, L. and Chattopadhyaya, D. (2022) Possible acquisition of ESBL-mediated antimicrobial resistance by farmers from aquatic reservoir used for bathing and cleaning of water buffalos (*Bubalus bubalis*) with intestinal carriage of ESBL producing *Escherichia coli*. *J. Pure Appl. Microbiol.*, 16(2): 1084–1095.
49. Rafiq, K., Islam, M.R., Siddiky, N.A., Samad, M.A., Chowdhury, S., Hossain, K.M.M., Rume, F.I., Hossain, M.K., Mahbub-E-Elahi, A., Ali, M.Z., Rahman, M., Amin, M.R., Masuduzzaman, M., Ahmed, S., Ara Rumi, N. and Hossain, M.T. (2022) Antimicrobial resistance profile of common foodborne pathogens recovered from livestock and poultry in Bangladesh. *Antibiotics (Basel)*, 11(11): 1551.
50. Nguyen, N.T., Nguyen, H.M., Nguyen, C.V., Nguyen, T.V., Nguyen, M.T., Thai, H.Q., Ho, M.H., Thwaites, G., Ngo, H.T., Baker, S. and Carrique-Mas, J. (2016) Use of colistin and other critical antimicrobials on pig and chicken farms in Southern Vietnam and its association with resistance in commensal *Escherichia coli* bacteria. *Appl. Environ. Microbiol.*, 82(13): 3727–3735.
51. Nguyen, P.T.L., Ngo, T.H.H., Tran, T.M.H., Vu, T.N.B., Le, V.T., Tran, H.A., Pham, D.T., Nguyen, H.T., Tran, D.L., Nguyen, T.P.L., Nguyen, T.T.T., Tran, N.D., Dang, D.A., Bañuls, A.L., Choisy, M., van Doorn, H.R., Suzuki, M. and Tran, H.H. (2022) Genomic epidemiological analysis of mcr-1-harboring *Escherichia coli* collected from livestock settings in Vietnam. *Front. Vet. Sci.*, 9: 1034610.
52. Ström, G., Boqvist, S., Albiñ, A., Fernström, L.L., Andersson Djurfeldt, A., Sokerya, S., Sothyra, T. and Magnusson, U. (2018) Antimicrobials in small-scale urban pig farming in a lower middle-income country - arbitrary use and high resistance levels. *Antimicrob. Resist. Infect. Control*, 7(1): 35.
53. Elmi, S.A., Simons, D., Elton, L., Haider, N., Abdel Hamid, M.M., Shuaib, Y.A., Khan, M.A., Othman, I., Kock, R. and Osman, A.Y. (2021) Identification of risk factors associated with resistant *Escherichia coli* isolates from poultry farms in the east coast of Peninsular Malaysia: A cross sectional study. *Antibiotics (Basel)*, 10(2): 117.
54. Nhung, N.T., Cuong, N.V., Campbell, J., Hoa, N.T., Bryant, J.E., Truc, V.N.T., Kiet, B.T., Jombart, T., Trung, N.V., Hien, V.B., Thwaites, G., Baker, S. and Carrique-Mas, J. (2015) High levels of antimicrobial resistance among *Escherichia coli* isolates from livestock farms and synanthropic rats and shrews in the Mekong Delta of Vietnam. *Appl. Environ. Microbiol.*, 81(3): 812–820.
55. Mtemisika, C.I., Nyawale, H., Benju, R.J., Genchwere, J.M., Silago, V., Mushi, M.F., Mwanga, J., Konje, E., Mirambo, M.M. and Mshana, S.E. (2022) Epidemiological cut-off values and multidrug resistance of *Escherichia coli* isolated from domesticated poultry and pigs reared in Mwanza, Tanzania: A cross-section study. *Animals (Basel)*, 12(7): 835.
56. Kabali, E., Pandey, G.S., Munyeme, M., Kapila, P., Mukubesa, A.N., Ndebe, J., Muma, J.B., Mubita, C., Muleya, W., Muonga, E.M., Mitoma, S., Hang'ombe, B.M., Wiratsudakul, A., Ngan, M.T., Elhanafy, E., Daous, H.E., Huyen, N.T., Yamazaki, W., Okabayashi, T., Abe, M., Norimine, J. and Sekiguchi, S. (2021) Identification of *Escherichia coli* and related *Enterobacteriaceae* and examination of their phenotypic antimicrobial resistance patterns: A pilot study at a wildlife-livestock interface in Lusaka, Zambia. *Antibiotics (Basel)*, 10(3): 238.
57. Hassan, I.Z., Wandrag, B., Gouws, J.J., Qekwana, D.N. and Naidoo, V. (2021) Antimicrobial resistance and mcr-1 gene in *Escherichia coli* isolated from poultry samples submitted to a bacteriology laboratory in South Africa. *Vet. World*, 14(10): 2662–2669.
58. Mulo, D., Kiiru, J., Ward, M.J., Hassell, J.M., Bettridge, J.M., Robinson, T.P., van Bunnik, B.A.D., Chase-Topping, M., Robertson, G., Pedersen, A.B., Fèvre, E.M., Woolhouse, M.E.J., Kang'ethe, E.K. and Kariuki, S. (2019) Epidemiology of antimicrobial-resistant *Escherichia coli* carriage in sympatric humans and livestock in a rapidly urbanizing city. *Int. J. Antimicrob. Agents*, 54(5): 531–537.
59. Mesa-Varona, O., Mader, R., Velasova, M., Madec, J.Y., Granier, S.A., Perrin-Guyomard, A., Norstrom, M., Kaspar, H., Grobbel, M., Jouy, E., Anjum, M.F. and Tenhagen, B.A. (2021) Comparison of phenotypical antimicrobial resistance between clinical and non-clinical *E. coli* isolates from broilers, Turkeys and Calves in four European Countries. *Microorganisms*, 9(4): 678.
60. Nzietchueng, S., Kitua, A., Nyatanyi, T. and Rwego, I.B. (2023) Facilitating implementation of the one health

- approach: A definition of a one health intervention. *One Health*, 16: 100491.
61. Orubu, E.S.F., Zaman, M.H., Rahman, M.T. and Wirtz, V.J. (2020) Veterinary antimicrobial resistance containment in Bangladesh: Evaluating the national action plan and scoping the evidence on implementation. *J. Glob. Antimicrob. Resist.*, 21: 105–115.
 62. Schneider, M.C., Munoz-Zanzi, C., Min, K., Aldighieri, S., Schneider, M.C., Munoz-Zanzi, C., Min, K. and Aldighieri, S. (2019) “One Health” from concept to application in the global world. In: Oxford Research Encyclopedia of Global Public Health. Oxford University Press, Oxford.
 63. Cocker, D., Chidziwisano, K., Mphasa, M., Mwapasa, T., Lewis, J.M., Rowlingson, B., Sammarro, M., Bakali, W., Salifu, C., Zuza, A., Charles, M., Mandula, T., Maiden, V., Amos, S., Jacob, S.T., Kajumbula, H., Mugisha, L., Musoke, D., Byrne, R., Edwards, T., Lester, R., Elvish, N., Roberts, A.P., Singer, A.C., Jewell, C., Morse, T. and Feasey, N.A. (2023) Investigating one health risks for human colonisation with extended spectrum β -lactamase-producing *Escherichia coli* and *Klebsiella pneumoniae* in Malawian households: A longitudinal cohort study. *Lancet Microbe*, 4(7): e534–e543.
 64. Guardabassi, L., Butaye, P., Dockrell, D.H., Fitzgerald, J.R. and Kuijper, E.J. (2020) One health: A multifaceted concept combining diverse approaches to prevent and control antimicrobial resistance. *Clin. Microbiol. Infect.*, 26(12): 1604–1605.
 65. Hille, K., Felski, M., Ruddat, I., Woydt, J., Schmid, A., Friese, A., Fischer, J., Sharp, H., Valentin, L., Michael, G.B., Hörmansdorfer, S., Messelhäuser, U., Seibt, U., Honscha, W., Guerra, B., Schwarz, S., Rösler, U., Käsbohrer, A. and Kreienbrock, L. (2018) Association of farm-related factors with characteristics profiles of extended-spectrum β -lactamase-/plasmid-mediated AmpC β -lactamase-producing *Escherichia coli* isolates from German livestock farms. *Vet. Microbiol.*, 223: 93–99.
 66. Ornelas-Eusebio, E., García-Espinosa, G., Laroucau, K. and Zanella, G. (2020) Characterization of commercial poultry farms in Mexico: Towards a better understanding of biosecurity practices and antibiotic usage patterns. *PLoS One*, 15(12): e0242354.
 67. Kim, T.S., Kim, G.S., Son, J.S., Lai, V.D., Mo, I.P. and Jang, H. (2021) Prevalence, biosecurity factor, and antimicrobial susceptibility analysis of *Salmonella* species isolated from commercial duck farms in Korea. *Poult. Sci.*, 100(3): 100893.
 68. Cao Ba, K., Kaewkungwal, J., Pacheun, O., Nguyen Thi To, U. and Lawpoolsri, S. (2020) Health literacy toward zoonotic diseases among livestock farmers in Vietnam. *Environ. Health Insights*, 14: 1178630220932540.
 69. Gizaw, F., Kekeba, T., Teshome, F., Kebede, M., Abreham, T., Hayishe, H., Waktola, H., Tufa, T.B., Edao, B.M., Ayana, D., Abunna, F., Beyi, A.F. and Abdi, R.D. (2020) Distribution and antimicrobial resistance profile of coagulase-negative staphylococci from cattle, equipment, and personnel on dairy farm and abattoir settings. *Heliyon*, 6(3): e03606.
 70. Heinemann, C., Meyer, I., Bögel, F.T., Schmid, S.M., Hayer, J.J. and Steinhoff-Wagner, J. (2020) Individual training for farmers based on results from protein and ATP rapid tests and microbiological conventional cultural methods improves hygiene in pig fattening pens. *J. Anim. Sci.*, 98(1): skz389.
 71. Kobusch, I., Müller, H., Mellmann, A., Köck, R. and Boelhave, M. (2020) Single blinded study on the feasibility of decontaminating LA-MRSA in pig compartments under routine conditions. *Antibiotics (Basel)*, 9(4): 141.
 72. Coffman, V.R., Hall, D.J., Pisanic, N., Love, D.C., Nadimpalli, M., McCormack, M., Diener-West, M., Davis, M.F. and Heaney, C.D. (2021) Self-reported work activities, eye, nose, and throat symptoms, and respiratory health outcomes among an industrial hog operation worker cohort, North Carolina, USA. *Am. J. Ind. Med.*, 64(5): 403–413.
 73. Fang, J., Gong, G., Yuan, J. and Sun, X. (2021) Antibiotic use in pig farming and its associated factors in L County in Yunnan, China. *Vet. Med. Sci.*, 7(2): 440–454.
 74. Ahmed, A.S., Diab, H.M., Alkahtani, M.A., Alshehri, M.A., Saber, H., Badr, H., Dandrawy, M.K., El-Mansi, A.A., Shati, A.A. and Ezzat Ahmed, A. (2020) Molecular epidemiology of virulent *E. coli* among rural small-scale dairy herds and shops: Efficacy of selected marine algal extracts and disinfectants. *Int. J. Environ. Health Res.*, 32(1): 72–94.
 75. Alam, B., Uddin, M.N., Mridha, D., Akhter, A.H.M.T., Islam, S.K.S., Haque, A.K.M.Z. and Kabir, S.M.L. (2020) Occurrence of *Campylobacter* spp. in selected small scale commercial broiler farms of Bangladesh related to good farm practices. *Microorganisms*, 8(11): 1778.
 76. Mridha, D., Uddin, M.N., Alam, B., Akhter, A.H.M.T., Islam, S.S., Islam, M.S., Khan, M.S.R. and Kabir, S.M.L. (2020) Identification and characterization of *Salmonella* spp. from samples of broiler farms in selected districts of Bangladesh. *Vet. World*, 13(2): 275–283.
 77. Sornplang, P., Aieamsaard, J., Saksangawong, C. and Suayvoo, N. (2022) Risk factors associated with *Salmonella* prevalence, its antibiotic resistance, and egg antibiotic residues in the layer farming environment. *Vet. World*, 15(3): 543–550.
 78. Ndahetuye, J.B., Twambazimana, J., Nyman, A.K., Karege, C., Tukei, M., Ongol, M.P., Persson, Y. and Båge, R. (2020) A cross sectional study of prevalence and risk factors associated with subclinical mastitis and intramammary infections, in dairy herds linked to milk collection centers in Rwanda. *Prev. Vet. Med.*, 179: 105007.
 79. Elmonir, W., Essa, H. and El-Tras, W. (2019) Ecology of *Staphylococcus Aureus* and its antibiotic resistance genes in dairy farms: Contributing factors and public health implications. *Slovenian Vet. Res.*, 56(22 Suppl): 747–54.
 80. Dohmen, W., Dorado-García, A., Bonten, M.J.M., Wagenaar, J.A., Mevius, D. and Heederik, D.J.J. (2017) Risk factors for ESBL-producing *Escherichia coli* on pig farms: A longitudinal study in the context of reduced use of antimicrobials. *PLoS One*, 12(3): e0174094.
 81. Hille, K., Ruddat, I., Schmid, A., Hering, J., Hartmann, M., von Münchhausen, C., Schneider, B., Messelhäuser, U., Friese, A., Mansfeld, R., Käsbohrer, A., Hörmansdorfer, S., Roesler, U. and Kreienbrock, L. (2017) Cefotaxime-resistant *E. coli* in dairy and beef cattle farms-Joint analyses of two cross-sectional investigations in Germany. *Prev. Vet. Med.*, 142: 39–45.
 82. Franceschini, G., Bottino, M., Millet, I., Martello, E., Zaltron, F., Favretto, A.R., Vonesch, N., Tomao, P. and Mannelli, A. (2019) Assessment of the exposure of turkey farmers to antimicrobial resistance associated with working practices. *Vet. Sci.*, 6(1): 13.
 83. García-Sánchez, L., Melero, B., Diez, A.M., Jaime, I., Canepa, A. and Rovira, J. (2020) Genotyping, virulence genes and antimicrobial resistance of *Campylobacter* spp. isolated during two seasonal periods in Spanish poultry farms. *Prev. Vet. Med.*, 176: 104935.
 84. Sanni, A.O., Onyango, J., Usman, A., Abdulkarim, L.O., Jonker, A. and Fasina, F.O. (2022) Risk factors for persistent infection of non-typhoidal *Salmonella* in poultry farms, North Central Nigeria. *Antibiotics (Basel)*, 11(8): 1121.
 85. Islam, M.A., Biswas, P., Sabuj, A.A.M., Haque, Z.F., Saha, C.K., Alam, M.M., Rahman, M.T. and Saha, S. (2019) Microbial load in bio-slurry from different biogas plants in Bangladesh. *J. Adv. Vet. Anim. Res.*, 6(3): 376–383.
 86. Pulami, D., Schauss, T., Eisenberg, T., Wilharm, G., Blom, J., Goesmann, A., Kämpfer, P. and Glaeser, S.P. (2020) *Acinetobacter baumannii* in manure and anaerobic digestates of German biogas plants. *FEMS Microbiol. Ecol.*, 96(10): fiae1176.
 87. Yoshizawa, N., Usui, M., Fukuda, A., Asai, T., Higuchi, H.,

- Okamoto, E., Seki, K., Takada, H. and Tamura, Y. (2020) Manure compost is a potential source of tetracycline-resistant *Escherichia coli* and tetracycline resistance genes in Japanese farms. *Antibiotics (Basel)*, 9(2): 76.
88. Li, Z., Shen, J., Wang, F., Wang, M., Shen, J., Li, Y., Zhu, Q. and Wu, J. (2023) Impacts of organic materials amendment on the soil antibiotic resistome in subtropical paddy fields. *Front. Microbiol.*, 13: 1075234.
89. Wang, F., Han, W., Chen, S., Dong, W., Qiao, M., Hu, C. and Liu, B. (2020) Fifteen-year application of manure and chemical fertilizers differently impacts soil ARGs and microbial community structure. *Front. Microbiol.*, 11: 62.
90. Han, B., Ma, L., Yu, Q., Yang, J., Su, W., Hilal, M.G., Li, X., Zhang, S. and Li, H. (2022) The source, fate and prospect of antibiotic resistance genes in soil: A review. *Front. Microbiol.*, 13: 976657.
91. Mware, N.A., Hall, M.C., Rajendran, S., Gilley, J.E., Schmidt, A.M., Bartelt-Hunt, S.L., Zhang, Y. and Li, X. (2022) Resistome and mobilome in surface runoff from manured soil as affected by setback distance. *J. Hazard. Mater.*, 429: 128278.
92. Caudell, M.A., Mair, C., Subbiah, M., Matthews, L., Quinlan, R.J., Quinlan, M.B., Zadoks, R., Keyyu, J. and Call, D.R. (2018) Identification of risk factors associated with carriage of resistant *Escherichia coli* in three culturally diverse ethnic groups in Tanzania: A biological and socioeconomic analysis. *Lancet Planet Health*, 2(11): e489–e497.
93. Waade, J., Seibt, U., Honscha, W., Rachidi, F., Starke, A., Speck, S. and Truyen, U. (2021) Multidrug-resistant enterobacteria in newborn dairy calves in Germany. *PLoS One*, 16(3): e0248291.
94. Szott, V., Peh, E., Friese, A., Roesler, U., Kehrenberg, C., Ploetz, M. and Kittler, S. (2022) Antimicrobial effect of a drinking water additive comprising four organic acids on *Campylobacter* load in broilers and monitoring of bacterial susceptibility. *Poult. Sci.*, 101(12): 102209.
95. Daly, S.W. and Harris, A.R. (2022) Modeling exposure to fecal contamination in drinking water due to multiple water source use. *Environ. Sci. Technol.*, 56(6): 3419–3429.
96. Hahne, F., Jensch, S., Hamscher, G., Meißner, J., Kietzmann, M., Kemper, N., Schulz, J. and Mateus-Vargas, R.H. (2022) Innovative perspectives on biofilm interactions in poultry drinking water systems and veterinary antibiotics used worldwide. *Antibiotics (Basel)*, 11(1): 77.
97. Hayer, J.J., Heinemann, C., Schulze-Dieckhoff, B.G. and Steinhoff-Wagner, J. (2022) A risk-oriented evaluation of biofilm and other influencing factors on biological quality of drinking water for dairy cows. *J. Anim. Sci.*, 100(5): skac112.
98. Constable, P.D., Hinchcliff, K.W., Done, S.H. and Grünberg, W. (2017) 3 - Biosecurity and infection control. In: *Veterinary Medicine*. 11th ed. W.B. Saunders, Philadelphia, PA, p36–42.
99. Adebawale, O.O., Adeyemo, F.A., Bankole, N., Olasoju, M., Adesokan, H.K., Fasanmi, O., Adeyemo, O., Awoyomi, O., Kehinde, O. and Fasina, F.O. (2020) Farmers' perceptions and drivers of antimicrobial use and abuse in commercial pig production, Ogun State, Nigeria. *Int. J. Environ. Res. Public Health*, 17(10): 3579.
100. Mallioris, P., Dohmen, W., Luikenm R.E.C., Wagenaar, J.A. and Stegeman, A., Mughini-Gras, L. (2022) Factors associated with antimicrobial use in pig and veal calf farms in the Netherlands: A multi-method longitudinal data analysis. *Prev. Vet. Med.*, 199: 105563.
101. Taylor, N.M., Wales, A.D., Ridley, A.M. and Davies, R.H. (2016) Farm level risk factors for fluoroquinolone resistance in *E. coli* and thermophilic *Campylobacter* spp. on poultry farms. *Avian Pathol.*, 45(5): 559–568.
102. Mallioris, P., Teunis, G., Lagerweij, G., Joosten, P., Dewulf, J., Wagenaar, J.A., Stegeman, A., Mughini-Gras, L. and EFFORT consortium (2022) Biosecurity and antimicrobial use in broiler farms across nine European countries: Toward identifying farm-specific options for reducing antimicrobial usage. *Epidemiol. Infect.*, 151: e13.
103. van Asseldonk, M., de Lauwere, C., Bonestroo, J., Bondt, N. and Bergevoet, R. (2020) Antibiotics use versus profitability on sow farms in the Netherlands. *Prev. Vet. Med.*, 178: 104981.
104. Takeuti, K.L., Malgarin, C.M., Amaral, A.F. and Barcellos, D.E.S.N.D. (2016) Frequency of methicillin-resistant *Staphylococcus aureus* (MRSA) in fattening pigs in the state of Rio Grande do Sul, Brazil. *Acta Sci. Vet.*, 44(1): 4.
105. Holstege, M.M.C., de Bont-Smolenaars, A.J.G., Santman-Berends, I.M.G.A., van der Linde-Witteveen, G.M., van Schaik, G., Velthuis, A.G.J. and Lam, T.J.G.M. (2018) Factors associated with high antimicrobial use in young calves on Dutch dairy farms: A case-control study. *J. Dairy Sci.*, 101(10): 9259–9265.
106. Schmithausen, R.M., Kellner, S.R., Schulze-Geisthoevel, S.V., Hack, S., Engelhart, S., Bodenstein, I., Al-Sabti, N., Reif, M., Fimmers, R., Körber-Irrgang, B., Harlizius, J., Hoerauf, A., Exner, M., Bierbaum, G., Petersen, B. and Bekeredjian-Ding, I. (2015) Eradication of methicillin-resistant *Staphylococcus aureus* and of *Enterobacteriaceae* expressing extended-spectrum beta-lactamases on a model pig farm. *Appl. Environ. Microbiol.*, 81(21): 7633–7643.
107. Miao, L., Li, H., Ding, W., Lu, S., Pan, S., Guo, X., Zhou, X. and Wang, D. (2022) Research priorities on one health: A bibliometric analysis. *Front. Public Health*, 10: 889854.
108. O' Cathain, A., Croot, L., Duncan, E., Rousseau, N., Sworn, K., Turner, K.M., Yardley, L. and Hoddinott, P. (2019) Guidance on how to develop complex interventions to improve health and healthcare. *BMJ Open*, 9(8): e029954.
109. Horvat, A., Luning, P.A., DiGennaro, C., Rommens, E., van Daalen, E., Koene, M. and Jalali, M.S. (2022) The impacts of biosecurity measures on *Campylobacter* contamination in broiler houses and slaughterhouses in the Netherlands: A simulation modelling approach. *Food Control*, 141: 109151.
110. Gelli, A., Headey, D., Becquey, E., Ganaba, R., Huybregts, L., Pedehombga, A., Santacroce, M. and Verhoef, H. (2019) Poultry husbandry, water, sanitation, and hygiene practices, and child anthropometry in rural Burkina Faso. *Matern. Child. Nutr.*, 15(4): e12818.
111. Ngure, F., Gelli, A., Becquey, E., Ganaba, R., Headey, D., Huybregts, L., Pedehombga, A., Sanou, A., Traore, A., Zongo, F. and Zongrone, A. (2019) Exposure to livestock feces and water quality, sanitation, and hygiene (WASH) conditions among caregivers and young children: Formative research in rural Burkina Faso. *Am. J. Trop. Med. Hyg.*, 100(4): 998–1004.
112. Whitley, L., Hutchings, P., Cooper, S., Parker, A., Kebede, A., Joseph, S., Butterworth, J., Van Koppen, B. and Mulejaa, A. (2019) A framework for targeting water, sanitation and hygiene interventions in pastoralist populations in the Afar region of Ethiopia. *Int. J. Hyg. Environ. Health*, 222(8): 1133–1144.
113. Hamilton, K.A., Ahmed, W., Rauh, E., Rock, C., McLain, J. and Muenich, R.L. (2020) Comparing microbial risks from multiple sustainable waste streams applied for agricultural use: Biosolids, manure, and diverted urine. *Curr. Opin. Environ. Sci. Health*, 14: 37–50.
114. Macedo, G., Olesen, A.K., Maccario, L., Hernandez Leal, L., Maas, P.V.D., Heederik, D., Mevius, D., Sørensen, S.J. and Schmitt, H. (2022) Horizontal gene transfer of an IncPl plasmid to soil bacterial community introduced by *Escherichia coli* through manure amendment in soil microcosms. *Environ. Sci. Technol.*, 56(16): 11398–11408.
115. Penakalapati, G., Swarthout, J., Delahoy, M.J., McAliley, L., Wodnik, B., Levy, K. and Freeman, M.C. (2017) Exposure to animal feces and human health: A systematic review and proposed research priorities. *Environ. Sci. Technol.*, 51(20):

- 11537–11552.
116. Sano, D., Haas, C. and Rose, J. (2019) A QMRA framework for sanitation treatment decisions. In: *Water and Sanitation for the 21st Century: Health and Microbiological Aspects of Excreta and Wastewater Management (Global Water Pathogen Project)*. Michigan State University, E. Lansing, MI.
117. Xin, H., Gao, M., Wang, X., Qiu, T., Guo, Y. and Zhang, L. (2022) Animal farms are hot spots for airborne antimicrobial resistance. *Sci. Total Environ.*, 851(Pt 1): 158050.
118. Lupolt, S.N., Agnew, J., Burke, T.A., Kennedy, R.D. and Nachman, K.E. (2022) Key considerations for assessing soil ingestion exposures among agricultural workers. *J. Expo. Sci. Environ. Epidemiol.*, 32(3): 481–492.
119. Butte, G., Niwagaba, C. and Nordin, A. (2021) Assessing the microbial risk of faecal sludge use in Ugandan agriculture by comparing field and theoretical model output. *Water Res.*, 197: 117068.
120. Byrne, D.M., Hamilton, K.A., Houser, S.A., Mubasira, M., Katende, D., Lohman, H.A.C., Trimmer, J.T., Banadda, N., Zerai, A. and Guest, J.S. (2021) Navigating data uncertainty and modeling assumptions in quantitative microbial risk assessment in an informal settlement in Kampala, Uganda. *Environ. Sci. Technol.*, 55(8): 5463–5474.
121. Li, J., Xie, S., Ahmed, S., Wang, F., Gu, Y., Zhang, C., Chai, X., Wu, Y., Cai, J. and Cheng, G. (2017) Antimicrobial activity and resistance: Influencing factors. *Front. Pharmacol.*, 8: 364.
122. Wolfe, M., Kaur, M., Yates, T., Woodin, M. and Lantagne, D. (2018) A systematic review and meta-analysis of the association between water, sanitation, and hygiene exposures and cholera in case-control studies. *Am. J. Trop. Med. Hyg.*, 99(2): 534–545.
