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TACKLING BACTERIA RESISTANCE IN FARMS: FOCUS ON FLUOROQUINOLONES, BETA-LACTAMS AND CYCLINS IN POULTRY FARMS OF THE BAMBOUTOS DIVISION, WEST-CAMEROON

Léticia Saurelle Mbognou[1,2], Blandine Pulcherie Tamatcho Kweyang[3], Anselme Michel Yawat Djogang[1,4*], O'Neal Dorsel Youté[1,2], Serge Honoré Tchoukoua[1,2] and Pierre René Fotsing Kwetche[1,2,4]

[1]School of Biomedical Sciences, Higher Institute of Health Sciences, Université des Montagnes; Bangangté, Cameroon.
[2]Laboratory of Microbiology, Université des Montagnes Teaching Hospital; Bangangté, Cameroon.
[3]Laboratory of Microbiology, University of Yaoundé I, Yaoundé.
[4]School of Pharmacy, Higher Institute of Health Sciences, Université des Montagnes; Bangangté, Cameroon Cameroon.

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***Corresponding Author: Anselme Michel Yawat Djogang**
School of Biomedical Sciences, Higher Institute of Health Sciences, Université des Montagnes; Bangangté, Cameroon.

ABSTRACT

As one of the biggest known global health challenges of the 21st century, antimicrobial resistance (AMR), influences human and animal welfare more rapidly beyond anticipation and affects the dynamics of biotic and abiotic systems. Identifying and prioritizing needs and actions in farming systems, healthcare and other sectors where engines of selection and dissemination of resistant traits occur appears primordial to address the threat. The present transversal descriptive survey was conducted in four poultry farms in the Bamboutos Division (West-Cameroon) on common farming practices and bacterial susceptibility/resistance trends to antibiotics. Information on farm' management were collected with a questionnaire prior to biological specimens that were subjected to laboratory screening according to standard guidelines in the "Université des Montagnes" Teaching Hospital Laboratory of Microbiology. Primarily, the survey focused on fluoroquinolones, beta-lactam and cyclins in the target farms. All farmers recognized the importance of antibacterial drugs in preventing and controlling infectious diseases in animal husbandry and acknowledged that their inappropriate use could negatively affect their effectiveness. Data analysis from the 471 isolates recovered revealed highest isolation rates of Gram-positive bacteria, overwhelmed by coagulase-negative *Staphylococcus* (59.3%), while in Gram-negative bacteria (40.7%), *Proteus* predominated. Resistance rates were largely above 50% for most drugs tested. Overall, the high rates observed with resistance against fluoroquinolones, beta-lactams and cyclins represent reliable motives for incentive policies aiming at addressing antibacterial resistance in Cameroon. Mapping resources, potential threats and prioritizing actions appear primordial to bring the threat under control, built on assets like the human resources that could undergo easy training based on their academic background.

KEYWORDS*: Bacteria, Resistance, Susceptibility, Antibiotic, Poultry, Bamboutos Division, West-Cameroon.*

INTRODUCTION

For influential regulatory, sanitary, economic and political organizations across the globe, antimicrobial resistance (AMR) represents one of the biggest Global Health threats of the 21st century. All subscribe to the new paradigm that AMR should not be addressed with reference to healthcare facilities and related immediate outcomes along anymore; but as consequence of multiple and interconnected natural and anthropic factors (Resende *et al.*, 2020). In fact, most ecological systems host drivers of selection for resistance traits which propagate almost stochastically throughout in-contact microbial populations including common etiologies of infectious diseases (IDs) in animals, humans and plants (Hernando-Amado *et al.*, 2019; Resende, 2020). Otherwise, human health that has long been the key motivation for research initiatives in controlling IDs in general and AMR especially relies on interconnected sets of dynamic considerations encompassing biotic and abiotic regulators and should be regarded as much as possible holistically. AMR has reached ecological importance which goes beyond the risks associated with therapeutic failures in human health, due to the facilitated dissemination of resistance genetic traits in diverse microbial populations (Martínez and Baquero, 2014; Baquero *et al.*, 2021).

The microbial populations of humans, animals, plants, water and soils are, for instance, intersected entities through which bacterial genes do flow more or less easily with reference to their phylogenetic proximity (Martínez and Baquero, 2014; Baquero *et al.*, 2021). With the genetic homogenization oriented by the struggle for higher productivity, homogenization and dissemination of genetic traits amplify, justifying this holistic approach in addressing AMR. This view is advocated by the above (but not limited to) global health regulatory bodies under the "One health concept" which considers human, animal and environmental health as intimately dependent on one another. Though the exhaustive list of interacting components that maintain sustainably the threat caused by AMR is yet to be designed, known major segments include animal husbandry (Yawat Djogang *et al.*, 2018; Fotsing Kwetché *et al.*, 2021; Ngandjui Yonga *et al.*, 2021; Hanna *et al.*, 2023), crop production, industries (Resende *et al.*, 2020; Van den Meersche *et al.*; 2021; Hanna *et al.*, 2023) and other biocides that alter environmental microbial flora dynamics (Maillard, 20217). The selection and dissemination amplitudes in these sectors strongly associate human activity and welfare, with the therapeutic failure orchestrated in healthcare as the most obvious in-result.

IDs caused by bacteria are among the most prominent based on their diversity, their severity and their rates at the global scale, aggravated by resistance to antibacterial arsenals that are generally scarce in resource-limited contexts. Penicillin in the 1940s was very effective in fighting against staphylococcal infections. By the 1945s, bacterial resistance to penicillin was reported, alleged to be related to inappropriate use of this antibacterial agent in humans. Similar trends developed with other antibiotic thereafter, as their use extended to animal husbandry and crop production (Aubry-Damon *et al*., 2005; Davies and Davies, 2010). Animal farms represent conducive environment for selection of antibiotic-resistant bacteria especially in contexts of poor sanitation (Levy *et al.*, 1976; Endtz *et al.*, 1991, Levy; 1998; Sanders, 2005; Yawat Djogang *et al.*, 2018; Fotsing Kwetché *et al.*, 2021; Ngandjui Yonga *et al.*, 2021; Simo Louokdom *et al.*, 2018) favoured by the sub-lethal doses used for growth promotion, IDs prophylaxis (Levy *et al.*, 1976; Simo Louokdom *et al.*, 2018).

At varied levels and amplitudes, drug-resistant bacteria stochastically pass from farms into human communities. No matter what, these amplitudes of selection and spread correlate with to the use of selective engines and sustained effective pathways for dissemination of genetic determinants (Martínez and Baquero, 2014; Baquero *et al.*, 2021). Acknowledging that humans can control (at least partially) most these factors, actions on the issue could mitigate the threat. Otherwise, clear understanding of the role of biocides in farms would guide assessing the extent of resistance spread, which could in turn be used as reliable stools for policy advocacy aiming at controlling AMR (Courvalin, 2008; Magill *et al.*, 2015). A few studies in that vein have be conducted in West-Cameroon (Simo Louokdom *et al.*, 2016; Simo Louokdom *et al.*, 2018; Yawat Djogang *et al.*, 2018) but additional piece of information are required for effective actions. It is in the framework aiming at addressing antibacterial resistance that the present investigation on the use of antibacterial and the outcome for resistance to fluoroquinolones, beta-lactams and cyclins was conducted in a few poultry farms of the Bamboutos Division, West-Cameroon. The high rates and enabling factors discussed represent reliable motives for incentive policies that could contain antibacterial resistance emergence and spread in Cameroon. Thorough mapping of local resources, potential threats and prioritizing interventions would appear primordial for their sustainable management based on shared assets.

MATERIAL AND METHODS

Study design

The present cross-sectional descriptive study was conducted from August through October 2019. To be undertaken, an ethical clearance from the "Université des Montagnes" Board of Ethics (reference N° 2019/120/UdM/PR/CIE) and a research authorization from the "Université des Montagnes" Teaching Hospital (reference N° 2019/208/CUM/ADM) were obtained. The West region of Cameroon is the most important basin for poultry activity in Cameroon. Also regarded as one of the most densely populated area in Cameroon, its populations firmly attach to wide ranges of agro-pastoral activities. Sampling was performed in the town of Mbouda and the surrounding neighbourhoods. Inhabitants in this area share socio-economic and cultural determinants like beliefs and other sets of inter-community social values. Specimen screening was thereafter, conducted in the Laboratory of Microbiology at the "Université des Montagnes" Teaching Hospital.

Field data collection, specimen collection and bacteria isolation

Prior to biological specimens, several pieces of information on farm management were recorded on survey sheets after the farmers' informed consent. Thereafter, specimen collection conducted according to standard procedures in four poultry farms were immediately conveyed to the Laboratory for microbiological screening. These specimens included chicken excreta (manure), food in feeders, stored feed, animal drinking water, water from supply tank and cloacal swabs.

Cultures and isolations were achieved according to the fundamentals principles provided by standard guidelines (Denis *et al.*, 2011). Isolation was performed on

Liofilchem® agar namely Mannitol salt, McConkey, Hektoen, Mannitol Mobility, DNase, Mueller Hinton with 5% sheep blood. The same reference repository (Denis *et al*., 2011) was used for morphological, biochemical and enzymatic profile of isolates.

Bacterial Susceptibility profile

For susceptibility/resistance profiles screening, bacteria isolates underwent disk diffusion (Kirby-Bauer) tests with 19 conventional antibacterial agents selected from drug families that are most commonly used in both human medicine and animal husbandry. All tests were performed with a 24-h bacterial fresh pure population grown nutrient agar. For the purpose, a suspension adjusted at 0.5 turbidity of the McFarland standard was prepared in 0.9% physiological saline then, readjusted to the final opacity recommended for susceptibility tests by agar diffusion technique on Mueller Hinton medium. All test procedures and interpretations were performed according to the standard guidelines provided by the "Comité de l'Antibiogramme de la Société Française de Microbiologie" (CA-SFM, May 2019). The antibacterial agents tested included: Amoxicillin (25 µg), Amoxicillin/clavulanic acid (20/10 µg), Aztreonam (30 µg), Cefotaxime (5 µg), Cefoxitine (30 µg), Ceftazidime (30 µg), Ceftriaxone (30 µg), Ciprofloxacin (5 µg), Clindamycin (2 µg), Erythromycin (15 µg), Gentamicin (10 µg), Imipenem (10 µg), Levofloxacin (5 µg), Nitrofurantoin (300 µg), Norfloxacin (10 µg), Oxacillin (1 µg), Penicillin (10 U), Tetracycline (30 µg), and Trimethoprim/Sulfamethoxazole (1.25/23.75 µg). Reference bacterial strains used in quality control for identification and susceptibility tests were *Staphylococcus aureus* QC1625, *Escherichia coli* ATCC 25922 and *Enterococcus faecalis* ATCC 29212.

Data processing and expected outcomes

Expected pieces of information included bacterial isolation rates and distributions, antibiotic susceptible/resistant isolates profiles. These variables were recorded and analyzed with statistical tools provided by Microsoft Excel 2013 software

RESULTS

Farmers' knowledge and practice

An insight through survey sheet data indicated that all participants were male. From this 25% and 75% had attended primary and secondary education, respectively. Farmers mainly used well water, chlorinated water and large varieties of antiseptics solutions for routine disinfection at the entry of the breeding areas. For infectious disease prevention, they also adopted routine cleaning and prophylaxis with antimicrobials (antibiotics 80% and antiseptics 20%). A decontamination solution was available at all farm entry. The use of antiseptics was 75% of the times done by direct on-farm spraying, 25% as cleaning solutions. All farms used antibiotics by direct administration to animals through drinking water. The antiseptics used included primarily alcohol, chlorinated water, Cresil and Tripuricides. The antibiotics in the routine were Flumequine, Furaltadone and Oxytetracycline (systematically used by all farmers as first choice); Norfloxacine, Amoxicillin and Norfloxon (systematically used by all farmers as second choice); Norfloxan, Tylodox (Tylosine + Doxycycline) and Ciprofloxacin (used in case of outbreak).

On the role of antimicrobial agents in farms, all farms personnel acknowledged its benefits in animal protection against outbreaks but also recognized that treatment failure with antibacterial agents might be due to their inappropriate use. They were also aware of the danger that the poor use of antibacterial agents might represent for the farm animals and human communities that depend on the farms' products and services. It was also observed that in all farms, customers were allowed entry in the premises during sales to choose the animals they would buy.

Identified bacterial contaminants in farms

Overall, 100 specimens of chicken excreta (manure), chicken feed, stored feed, animal drinking water, water from supply tank and cloacal swabs were collected from the four target farms. In the majority of these specimens, bacterial growth was recorded. Further related pieces of information were re-organized as displayed in table 1, 2 and 3 for specimen and bacterial isolates per farm, respectively. Table 1 shows that the highest bacterial population was globally recorded in manure. This was followed by drinking water, food in feeders and cloacal swabs.

Table 2 observation indicates manure as the category for which bacterial polymorphism was the highest in all the farms. In addition, most common organisms belonged to the Gram-positive group (59.3%) encompassing of coagulase-negative *Staphylococcus* (30.6%), *Staphyloccocus aureus* (17.2%) and by *Bacillus* (11.5%). In the Gram-negative, members of the *Enterobacteriaceae* overwhelmed the isolation rates (40.7%). These Gram-negative rods were predominantly represented in decreasing order by *Proteus* (12.7%), *Klebsiella* (5.7%) and *Morganella* (5.1%).

Table 1: Overall distribution of bacterial isolates per specimen type on the farms.

Location	**Bacterial isolates per specimen type [n (%)]**						**Total**
	Food in feeders*	**Stored feeds***	**Drinking water***	**Cloacal swabs***	**Excreta****	**Water from supply tank***	
Farm 1	24 (20)	15 (12)	24 (20)	18 (15)	36 (29)	6 (5)	123
Farm 2	18 (13)	15 (11)	33 (23)	21 (15)	51 (36)	3 (2)	141
Farm 3	21 (19)	6 (6)	21 (19)	18 (17)	36 (33)	6 (6)	108

Farm 4	21 (21)	9 (9)	18 (18)	24 (24)	27 (27)	0 (0)	99
Total	84	45	96	81	150	15	471

* Four specimens per farm for these products, ** Five specimens per farm for these products

Table 2: Bacterial type per location and specimen (part 1/2).

Farms	**Bacterial isolate**	**Specimen types**						**Total**
		Food in feeders	**Stored feeds**	**Drinking water**	**Cloacal swabs**	**Excreta**	**Water from supply tank**	
Farm 1	*Klebsiella* spp.	0	0	3	6	0	0	9
	Morganella spp.	0	0	0	0	6	3	9
	Proteus spp.	3	6	3	0	0	0	12
	Providencia spp.	3	0	0	0	6	0	9
	Yersinia spp.	0	0	3	0	0	3	6
	S. aureus	3	9	6	6	6	0	30
	CNS	12	0	9	6	9	0	36
	GPR	3	0	0	0	9	0	12
Farm 2	*E. coli*	0	0	0	0	3	0	3
	Enterobacter spp.	3	0	0	0	0	3	6
	Klebsiella spp.	0	0	6	0	0	0	6
	Morganella spp.	0	0	0	0	3	0	3
	Proteus spp.	0	6	0	3	3	0	12
	Providencia spp.	0	0	6	0	3	0	9
	P. aeruginosa	0	0	0	6	9	0	15
	Yersinia spp.	0	0	3	0	0	0	3
	S. aureus	12	6	9	3	0	0	30
	CNS	3	3	9	9	15	0	39
	GPR	0	0	0	0	15	0	15

CNS: Coagulase-negative *Staphylococcus*, GPR: Gram-positive rods

Table 3: Bacterial type per location and specimen (part 2/2).

Farms	**Bacterial isolate**	**Specimen types**						**Total**
		Food in feeders	**Stored feeds**	**Drinking water**	**Cloacal swabs**	**Excreta**	**Water from supply tank**	
Farm 3	*Enterobacter* spp.	0	0	0	6	0	0	6
	Klebsiella spp.	0	0	0	3	3	0	6
	Morganella spp.	0	0	0	0	6	0	6
	Proteus spp.	0	3	6	0	3	6	18
	Providencia spp.	3	0	0	0	0	0	3
	P. aeruginosa	0	0	3	0	0	0	3
	Yersinia spp.	0	0	3	0	0	0	3
	S. aureus	3	0	3	0	6	0	12
	CNS	9	3	6	9	9	0	36
	GPR	6	0	0	0	9	0	15
Farm 4	*E. coli*	0	0	0	0	3	0	3
	Klebsiella spp.	0	0	3	3	0	0	6
	Morganella spp.	6	0	0	0	0	0	6
	Proteus spp.	0	0	3	6	9	0	18
	Salmonella spp.	0	0	3	3	0	0	6
	Yersinia spp.	0	0	3	3	0	0	6
	S. aureus	0	0	3	6	0	0	9
	CNS	12	6	3	3	9	0	33
	GPR	3	3	0	0	6	0	12

CNS: Coagulase-negative *Staphylococcus*, GPR: Gram-positive rods

Susceptibility/resistance profile of bacterial isolates from farms

The isolates recovered from farms expressed high rates of resistance to sulfonamides (73%), beta-lactam (72%), cyclins (69%), macrolides (63%) and fluoroquinolones (52%). Tables 4 to 6 provide additional details on the susceptibility/resistance profile of the isolates from these farms. A global view indicates that amongst Gram-negative rods, the resistance rates were above 54%. Highest values were recorded with beta-lactams (Aztreonam: 73%, Amoxicillin: 69%, Ceftriaxone: 62%, Amoxicillin/Clavulanic acid: 58%, Ceftazidime: 56%, Cefoxitin: 55%), cyclines (Tetracycline: 69%), sulphonamides (Trimethoprim/Sulfamethoxazole: 76%) and macrolides (Erythromycin: 62%). Further details reveal that among Gram-positive cocci, the resistance rates were also invariably high, exemplified with beta-lactams (Oxacillin: 81%, Ceftriaxone: 79% and Ceftazidime: 75%), sulphonamides (Co-trimoxazole: 59%), macrolides (Erythromycin: 64% and Clindamycin: 52%) and fluoroquinolones (Levofloxacin: 57%). In Gram-positive rods resistance were also invariably very high. Related summarized trends were beta-lactams (Oxacillin 100%, Penicillin G: 75%, Ceftazidime: 73%, Amoxicillin/Clavulanic acid: 59%), sulphonamides (Co-trimoxazole: 84%), and macrolides (Clindamycin: 70%). Further, Imipenem, Gentamicin and Levofloxacin were the most effective drugs.

Table 4: Antibiotic susceptibility profile of isolates from farms (part 1/3).

Antibiotics	Phenotypes	Farm 1			Farm 2			Farm 3			Farm 4		
		Isolates (%)			Isolates (%)			Isolates (%)			Isolates (%)		
		GNR	GPR	GPC	GNR	GPR	GPC	GNR	GPR	GPC	GNR	GPR	GPC
Levofloxacin	**I**	2	2	1	5	2	2	10	0	1	1	7	9
	R	24	17	49	40	47	44	29	33	77	44	33	57
	S	74	81	50	55	51	54	61	67	22	55	60	34
Norfloxacin	**I**	7	11	4	15	8	10	16	6	1	8	5	2
	R	33	8	42	60	47	26	40	33	37	56	25	48
	S	60	81	54	25	45	64	44	61	62	36	70	50
Ciprofloxacin	**I**	15	-	-	3	-	-	0	-	-	12	-	-
	R	24	-	-	37	-	-	42	-	-	29	-	-
	S	61	-	-	60	-	-	58	-	-	69	-	-
Tetracycline	**I**	5	-	-	4	-	-	2	-	-	3	-	-
	R	90	-	-	46	-	-	58	-	-	83	-	-
	S	5	-	-	50	-	-	40	-	-	14	-	-
Amoxicillin	**I**	6	6	0	5	3	2	5	3	4	6	1	1
	R	64	25	32	70	20	28	80	67	46	64	50	29
	S	24	69	68	25	77	80	15	30	50	30	49	70
Amoxicillin – Clavulanic acid	**I**	4	10	2	7	5	2	3	10	6	0	1	7
	R	56	67	38	61	80	42	69	40	44	44	50	48
	S	40	23	60	30	15	56	28	50	50	56	49	45
Cefoxitin	**I**	2	-	-	17	-	-	5	-	-	10	-	-
	R	62	-	-	63	-	-	40	-	-	53	-	-
	S	36	-	-	20	-	-	55	-	-	37	-	-

GNR: Gram-negative rods; GPR: Gram-positive rods; GPC: Gram-positive Cocci; - : Not tested.

Table 5: Antibiotic susceptibility profile of isolates from farms (part 2/3).

Antibiotics	Phenotypes	Farm 1			Farm 2			Farm 3			Farm 4		
		Isolates (%)			Isolates (%)			Isolates (%)			Isolates (%)		
		GNR	GPR	GPC	GNR	GPR	GPC	GNR	GPR	GPC	GNR	GPR	GPC
Ceftriaxon	**I**	9	4	0	0	3	9	2	5	2	6	3	3
	R	71	67	80	53	87	81	58	80	88	64	92	67
	S	20	29	20	47	10	10	40	15	10	30	5	30
Ceftazidim	**I**	3	5	1	1	2	2	5	7	2	1	11	9
	R	67	50	79	49	93	68	58	73	73	49	75	81
	S	30	45	20	50	5	30	38	20	25	50	14	10
Aztreonam	**I**	2	-	-	9	-	-	3	-	-	2	-	-
	R	78	-	-	61	-	-	73	-	-	78	-	-
	S	20	-	-	30	-	-	24	-	-	20	-	-
Imipenem	**I**	0	0	0	0	0	0	0	0	0	0	0	0
	R	9	25	17	16	40	15	7	47	13	11	42	24
	S	91	75	83	84	60	85	93	53	87	89	58	76
Oxacillin	**I**	-	0	2	-	0	6	-	0	5	-	0	2

	R	-	100	89	-	100	74	-	100	83	-	100	79
	S	-	0	9	-	0	20	-	0	12	-	0	19
Penicillin G	**I**	-	1	6	-	2	4	-	11	2	-	2	5
	R	-	67	24	-	87	36	-	87	58	-	58	50
	S	-	32	70	-	11	60	-	2	40	-	40	45

GNR: Gram-negative rods; GPR: Gram-positive rods; GPC: Gram-positive Cocci; - : Not tested.

Table 6: Antibiotic susceptibility profile of isolates from farms (part 3/3).

Antibiotics	**Phenotypes**	**Farm 1**			**Farm 2**			**Farm 3**			**Farm 4**		
		Isolates (%)			**Isolates (%)**			**Isolates (%)**			**Isolates (%)**		
		GNR	**GPR**	**GPC**	**GNR**	**GPR**	**GPC**	**GNR**	**GPR**	**GPC**	**GNR**	**GPR**	**GPC**
Trimethoprim – Sulfamethoxazole	**I**	0	0	0	5	0	0	0	0	0	0	0	0
	R	67	67	65	65	100	46	84	93	63	87	75	60
	S	33	33	35	30	0	54	16	7	37	13	25	40
Gentamicin	**I**	6	4	0	0	0	10	9	3	20	11	0	10
	R	36	8	14	44	53	20	62	67	23	44	17	19
	S	58	88	86	56	47	70	29	30	57	45	83	71
Erythromycin	**I**	6	6	1	8	2	3	5	5	3	3	4	10
	R	51	75	89	63	27	57	53	40	58	82	42	52
	S	43	19	10	29	71	40	42	55	39	15	54	38
Clindamycin	**I**	-	2	6	-	1	3	-	1	10	-	2	3
	R	-	58	44	-	60	42	-	93	65	-	67	57
	S	-	40	50	-	39	57	-	6	25	-	31	40
Nitrofurantoin	**I**	4	-	-	2	-	-	5	-	-	3	-	-
	R	36	-	-	44	-	-	33	-	-	36	-	-
	S	60	-	-	54	-	-	62	-	-	61	-	-

GNR: Gram-negative rods; GPR: Gram-positive rods; GPC: Gram-positive Cocci; - : Not tested.

DISCUSSION

The present work on use of antimicrobial agents and bacterial susceptibility/resistance trends to fluoroquinolones, beta-lactams and cyclins in four poultry of the Bamboutos Division disclosed sets of tools that could be used to contain AMR.

From interviews on the farms, it was observed that antibacterial from the fluoroquinolone, beta-lactams and cyclin subsets were most commonly used for infection prevention and disease control. Previous authors also reported similar trends, with the dominant role of fluoroquinolones (Fotsing Kwetché *et al.*, 2021; Ngandjui Yonga *et al.*, 2021). Quinolones in general are bactericidal agents that act on and impair the functions of the bacterial genome. Unlike beta-lactams which are also bactericidal (but act on the cell wall synthesis) residues of fluoroquinolones strongly resist biological degradation (Berendonk *et al.*, 2015) and could play important role in the resistance traits' selection and dissemination throughout diverse ecological systems. Antibiotics like chloramphenicol, tetracyclines, penicillins, cephalosporins, quinolones, sulfonamides and macrolides were banned in animal husbandry in Brazil (Resende *et al.*, 2020) with regards to their side effect in promoting genetic modification in microbial world. Or, most of these are found to be common in the area were the present investigation was conducted, and in Cameroon in general (Simo-Louokdom *et al.*, 2018; Yawat Djogang *et al.*, 2018; Fotsing Kwetché *et al.*, 2021; Ngandjui Yonga *et al.*, 2021). The increased use of fluoroquinolones in this context is most likely due the product availability and affordability, consistent with findings from current reports (Yawat Djogang *et al.*, 2018; Fotsing Kwetché *et al.*, 2021; Ngandjui Yonga *et al.*, 2021).

As bactericidal antibiotics in addition, empirical use that generally provides immediate and good therapeutic effects motivates the use of quinolones, regardless of the effect of residues that could have long-term impacts on resistance selection affecting global modification of systems' microbial diversity (Resende *et al.*, 2020). Concerning beta-lactams, findings from data analysis could be justified by the fact that it represents one of the most diverse groups of antibiotics. With quinolones, beta-lactams are also most common in human medicine, although that trend of drug administration in farm animals globally overwhelms the ones recorded in human care (CDC, 2019; Kusi *et al.*, 2022).

Moreover, beta-lactams are characterized by specific assets like low toxicity, availability and affordability (Pandey and Cascella, 2022). Like beta-lactams and quinolones, cyclins are broad-spectrum antibiotics that effectively act on against Gram-positive and Gram-negative bacteria. In some countries, it was observed that agents from the cyclins family were the most widely used in animal husbandry (Sambyal and Baxi, 1980; Gaastra *et al.*, 1996; Noukela Noumi *et al.*, 2017). Data from the present study reported similar trends, consistent with previous ones, more likely in connection with their broad spectrum of action, which promotes empirical use. Unlike quinolones and beta-lactams, however, antibiotics from cyclins subset are not as common in human medicine. In contexts with low drug regulation like the one in which the present investigation was conducted, and in line with their immediate benefit, one could anticipate the choice for fluoroquinolones, beta-lactams and cyclins, for their broad spectrum and their availability and affordability combine. These three characteristics are most likely at the origin of their excessive use.

Used for several purposes, antibiotics primarily exert selection pressure on endogenous bacterial flora and eventually (if ever) on pathogens (van den Bogaard and Stobberingh, 2000). Otherwise, non-pathogens are naturally most likely involved in selection and dissemination of resistant traits than pathogens, with reference to their numbers in all natural environments. According to Baquero *et al*. (2021) collateral expansion has strongly influenced the spread of antibiotic resistance within beta-lactams. Further details indicated that the route for drug administration identified was typically oral (100%). Oral drug administration was identified as major route by Simo-Louokdom *et al.* (2018) and Yawat Djomgang *et al*. (2018) in previous surveys conducted in West-Cameroon. The potential for proper education was good in these communities of breeders where the majority has attended secondary education. The education potential was observed in previous survey within West Cameroon (Yawat Djogang *et al*., 2018; Fotsing Kwetché *et al*., 2021; Ngandjui Yonga *et al*., 2021). Policies regarding AMR control could sustainably built on assets like this one.

In connection with the isolation rates, data analysis revealed a high polymorphism of bacterial populations, primarily in animal excreta. Bacterial loads would also have similar trends, though they were not investigated in the present study. Both variables would then combine to reflect the intestinal microbiome and its putative potential in selecting and disseminating resistant traits across phylogenetic groups and environments. Ingested antibacterial agents through animal drinking water directly act on the polymorphism intestinal bacteria, in agreement with the putative predominant role of the intestinal microbial resistance growth discussed above.

Frequent isolation of bacteria from stored animal feed, instant food in feeders and drinking water would also reflect cross-contamination, most likely from poultry faeces (Fotsing Kwetché *et al*., 2021). This cross-contamination is otherwise, revealed by the lower polymorphism recorded in water from supply tank and stored feed, compared to drinking water and instant food in feeders. This finding stress the important role the biosafety and biosecurity have in farming as observed by other investigators (Hernando-Amado *et al*., 2019; Kusi *et al*., 2022). Moreover, and beyond the role of antibiotic residues, lower dosage of antibiotics in drinking water represents powerful engines for resistance selection; acknowledging that drug potentials reduce with time in water. Then, hosts of factors could justify the invariably high resistance rates observed in all bacteria types and for all antibiotics tested.

Bacteria frequently isolated among Gram-positive included coagulase-negative *Staphylococcus* (47.8%), *Staphylococcus aureus* (17.2%) and *Bacillus* (13.9%) while in Gram-negative, *Proteus* overwhelmed the isolation rates. The distribution of isolates belonging to the *Enterobacteriaceae* family is certainly related to the same or related environmental parameters for which Gram-positive bacteria are adapted, in addition with the chemical organization of bacterial cell envelopes as observed by Simo-Louokdom *et al*. (2018). Most of these bacteria are environmental hosts that can, according to above development, play significant roles in genetic traits' selection as ubiquitous dominant organisms (Casagrande Proietti *et al*., 2007). This dominance could further be justified by low sanitation standards, and affinity with molecular oxygen (facultative anaerobes), some of which can develop additional attributes like capsules or resistance spores. Other investigators reported isolation of *Salmonella* (Bonhomme, 2003; Tchapdie Ngassam *et al*., 2017) as recorded in the present work. Beyond the resistance threat posed by endogenous and environmental hosts which could evolve as opportunistic pathogens, inherent pathogenicity is an additional health threat (Sambyal and Baxi, 1980, Gaastra *et al*., 1996; Bonhomme, 2003) in *Salmonella*. Like most Gram-negative rod and *Staphyloccoci*, *Bacillus* are ubiquitous host of diverse environments. In connection with their life style, *Bacillus* were suggested as tools for resistance control in animal farms.

On-farm susceptibility test results revealed high levels of resistance to large numbers of antibiotics. Similar trends were observed from previous surveys in West (Yawat Djogang *et al*., 2018; Simo Louokdom *et al*., 2018), South (Fotsing Kwetché *et al*., 2021) and Littoral (Ngandjui Yonga *et al.,* 2021) Cameroon. These resistances represent serious threat to farming activity sustainability and indirectly threatens human welfare (Adil *et al*., 2011) as it undermines effectiveness of therapeutics with antibiotics. The resistance rates observed to sulfonamides, macrolides, amynoglycosides or to some specific drugs like Imipenem could be due to co- and/or cross-resistance, since they were not as common as fluoroquinolones, beta-lactams and cyclins in animal husbandry (Marcusson *et al*., 2009; Cantón and Ruiz-Garbajosa, 2011).

Overall and beyond the farms where the activity is seriously threatened with drug-resistant aetiologies of IDs, the related economic burdens in the breeding activity, which is likely high, is yet to be clearly addresses (kusi *et al*., 2022). The multiple-level threat (husbandry activity, human health burden, economic loses and sustainability) could effectively serve in drawing awareness on the rational use of antibiotics and other resistance-selection engines in animal husbandry. The role of improved sanitation and incentive policies appears primordial in addressing this threat, which is likely to affect other world biological systems through biotic and abiotic entities (Hernando-Amado *et al*., 2014; Berendonk *et al*., 2015; CDC, 2019). With the degenerate and universal feature of the genetic code, anticipating that the relentless changes in microbial genome might cause modifications of global ecosystems beyond current believe is reasonably feasible. Globally, mapping resources, potential threats and prioritizing actions are primordial for sustainable management.

CONCLUSION

Findings from the present survey indicated invariably high resistance rates regardless of the bacterial types, with cross-adulteration favoured by poor sanitation in polymorphic microbial ecosystems. Data analysis specified that with the existing predisposed human potential incentive policies, improved sanitation and drug regulation might mitigate resistance to antimicrobial agents and primary outcomes. Mapping resources, potential threats and prioritizing actions appeared primordial for sustainable farming.

Conflict of interest

The authors declare that this work is devoid of any conflict of interest

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Authors' contributions

All the authors made substantial contributions to the design of the work, and to the acquisition, analysis and interpretation of the data. They also drafted the manuscript, revised it and approved the version for publication.

Data availability

All the data of this work are present in this paper.

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