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ANTIBIOTIC SUSCEPTIBILITY/RESISTANCE PROFILE OF BACTERIA FROM FARM WASTES: FINDINGS IN EXCRETA FROM FOUR POULTRIES OF WEST CAMEROON

Josué Simo Louokdom [1,2,3], Pierre René Fotsing Kwetché*[1,2,4], Anselme Michel Yawat Djogang[1,2], Sandrine Gamwo Dongmo[1,2], William Lelorel Nankam Nguekap[2,4], Serge Honoré Tchoukoua[1,2], Jonas Kouamouo[1,2], Omer Njajou Tchikamgoua[5], Jules Roger Kuiaté[3], Jean Michel Tekam[1,2]

[1]School of Pharmacy, Higher Institute of Health Sciences, Université des Montagnes; Bangangté, Cameroon.
[2]Laboratory of Microbiology, Université des Montagnes Teaching Hospital; Bangangté, Cameroon
[3]Faculty of Science, University of Dschang; Dschang, Cameroon.
[4]School of Medical biology, Higher Institute of Health Sciences, Université des Montagnes; Bangangté, Cameroon.
[5]One Health Workforce Africa, University of Minnesota; USA.

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Corresponding Author: Pierre René Fotsing Kwetché
School of Pharmacy, Higher Institute of Health Sciences, Université des Montagnes; Bangangté, Cameroon.

ABSTRACT

The present investigation was undertaken to address the trend of bacterial resistance to antibacterial agents in poultry and related consequences. Precisely, it was initiated to gather necessary information on bacterial communities in farms, the types of antimicrobial agents used and the susceptibility/resistance profile of bacteria to common antibiotics. Chicken excreta collected from four farms in Bafoussam and Bandjoun (two neighborhoods in the West Region of Cameroon) underwent microbiological analysis and susceptibility testing according to standard protocols by the CAS-SFM (2017). The overall picture from data analysis indicated that most common bacteria isolates belonged to three major groups: *Enterobacteriaeae, Bacillus and Staphylococcus*, members of which are potent etiologies of zoonotic infections and powerful engines for resistance traits selection and dissemination. Resistance to antibiotics like Oxacillin, Tetracycline, Co-trimoxazole and Ceftriaxone were common and invariably high, regardless of the bacteria group targeted. In further details, resistance rates were higher than 60% for 34% and 25% of the antibiotics used in Gram-negative rods from Bafoussam 1 and Bafoussam 2, respectively. In Bandjoun 1, resistance rates higher than 60% were obtained in 34%, 32% and 46% of the antibiotics used for Gram-negative rods, Gram-positive rods and Gram-positive cocci, respectively. The respective rates were 48%, 41% and 60% in Bandjoun 2. Overall, antimicrobial agents frequently used were more affected by resistance while the farmers recognized the threat resistance might pose in their activity. Though yet to be addressed, both the isolation and resistance rates could help anticipate that the economic burden of farm-related infections might by very high. Biological alternatives to antimicrobials for growth promotion and fighting against pathogens in farms was, therefore, thought to be primordial, feasible, then strongly advocated.

KEYWORDS: Bacteria, resistance/susceptibility, profile, poultry, West-Cameroon.

INTRODUCTION

Discovery and introduction of Penicillin in human medicine (1928-1939s) was a unique experience in controlling infectious diseases throughout the history of humanity. This contribution was particularly obvious during the Second World War (1939-1945) when in injured war victims its use reduced the numbers of related deaths. This successful management experience led to a surge in the search for other antibiotics, while bacterial tolerance to Penicillin emerged in strains of the genus *Staphylococci* (Barber, 1961) and reduced the successful caretaking rates.[1] This tolerance expressed by the strains rapidly spread with its sustained use (and that of other drugs which were developed subsequently) such a way that resistance to antibiotics became a major public health concern in the 1980s with the discovery of extended spectrum betalactamases in members of the *Enterobacteriaceae* family.[2,3] Nowadays, bacterial infections are difficult to control because they are costly and diversified, in connection with the bacterial species and strains in cause, exacerbated by the high flexibility of the bacterial genome and the use of several engines for resistantce selection and dissemination of resistant strains to common available and affordable drugs, facilitated by stochastic changes that occur in bacteria within mixed populations of interacting entities composed of the living and inanimate components of ecosystems.[4]

This phenomenon of bacterial adaptation to antibiotics is recognized as global concern.[5,6] Although known as a natural phenomenon at the origin, evidences prove that it becomes exacerbated by human activities related to appropriate and/or inappropriate use of resistance phenotype-selectiing agents in human medicine, animal husbandry, agriculture and industries.[2,5] At different levels and depending on several parameters, selection and dissemination of resistance phenotypes is challenging and concerns all types of antibacterial agents used in the management of infections in humans or animals.[7] Common ecosystems for humans and animals are in fact privileged environments for selection and dissemination of fitness-promoting traits including virulence and resistance among bacteria, aided by mobile genetic elements that may carry unpredictable combinations of genes that could encode and spread resistance amongst close and phylogenetically distant species.[8,9] Engines enabling exacerbation of this phenomenon are numerous in fact. Though poorly investigated so far, growth supplements and prophylactic treatments in animal husbandry appear as some of the biggest contributors which act through the use of subtherapeutic doses in overcrowded farms.[2,10] Bacterial resistance to antibiotics is a real threat to modern medicine because it progresses faster than the development of new antibacterial agents, and that exposure of human or animal populations to resistant bacteria may indirectly affect other populations.[2,10] It is likely that the impact in animal breeding would be greater than that actually attributed to poor use of drugs in human medicine.[3,11]

However, studies to address the real impact of farms in the selection of resistance observed in human medicine are fewer and limited to high-income countries. Or, in resource-limited areas where the low purchasing power contrasts with the rates of infectious diseases, they are necessary.[5] They would make it possible to evaluate the extent of the phenomenon in order to raise awareness and enforce mitigation strategies through development of policies that would help controlling the flow of the threat and the related consequences like longer hospitalization, higher morbidity and mortality rates, and higher economic burden.[3,12]

It is in this frame that the present work was initiated to appreciate the extend of antibiotic resistance that develops in poultry, in connection with antimicrobial agents used. More specifically, this piece of work will provide information about bacterial communities in a few farms, the types of antimicrobial agents used and the trends of bacterial susceptibility/resistance profile to common antibacterial agents. In the short run the findings thereof will help to understand the risk involved with the use of antimicrobials and provide projection to optimize farm production outputs without (or with reduced) antimicrobial use by farmers in their activity. In the intermediate and long run, they will serve as tools for monitoring the evolution of these phenomena and as key to designing mitigation policies with the farmers as major actors.

MATERIAL AND METHODS

Ethical consideration, study site and population

The go-ahead was obtained from the Head of the Université des Montagnes' Teaching Hospital under reference number: Ref: 2017/0104/CUM/ADM for specimen analysis in its Laboratory of Microbiology. The West region of Cameroon is known as the most important basin for poultry in Central Africa and regarded by some as the country's reserve. This study was carried out in Bafoussam and Bandjoun, respectively urban and rural areas which have similar climatic and socio-economic determinants like believes, trade and agropastoral activities.

Field data collection, stool sample collection and bacteria isolation

This was a descriptive experimental study. From December 27, 2017 to March 15, 2018, this study was conducted in Bandjoun and Bafoussam where sample collection was conducted. Specimens type was chicken excreta collected in four poultry farms. Through questionnaires, pieces of information about farm management were recorded after the consent obtained from farmers. The samples of excreta were thereafter collected according to standard procedures in small, clean, sterile plastic bags, then conveyed without delay to the Laboratory of Microbiology of the Université des Montagnes' Teaching Hospital for processing. All cultures, isolations and identifications were conducted according to standard guidelines.[13] In short for the different targeted bacterial species, colony isolation was performed on Mannitol salt agar, McConkey agar, Hektoen agar, chocolate agar, Mueller Hinton with 5% sheep blood. All identifications were performed according to standard morphological and biochemical procedures as recommended by the same reference repository.

Antimicrobial Susceptibility testing

Susceptibility tests were carried out by disk diffusion (Kirby-Bauer) with 22 conventional antibacterial agents that are commonly used in Cameroon. In short, this was conducted on 24 h bacterial pure culture obtained by streaking bacterial isolates on fresh nutrient agar and allowing for an overnight incubation at 37 °C. From the resulting bacterial population, a suspension to the density of a McFarland 0.5 turbidity standard prepared in 0.9% saline was adjusted to the final opacity recommended for susceptibility tests by agar diffusion technique on Mueller Hinton agar. All test procedures and interpretations were done according to the standard guidelines recommended by the Comité de l'Antibiogramme de la Société Française de Microbiologie. [14] The antibiotic disks tested included: Penicillin (10 µg), Imipeneme (10 µg), Cefotaxime (5 µg), Amoxicillin/clavulanic acid (20/10 µg), Amoxicillin (30 µg), Ceftazidime (30 µg), Ceftriaxone (30 µg), Nitrofurantoin (300 µg), Cefoxitin (30 µg), Cefuroxime (30 µg), Gentamicin (120 µg), Vancomycin (30 µg), Ciprofloxacin (30 µg), Nalidixic acid (30 µg), Trimethoprim/sulfamethoxazole (1.25/23.75 µg), Oxacillin (1 µg), Erythromycin (15 µg), Norfloxacin (30 µg), Levofloxacin (30 µg), Tetracycline (30 µg), Aztreonam (30 µg) and Clindamycin (2 µg). For identification and susceptibility tests, *Staphylococcus aureus* QC1625, *Escherichia coli* ATCC 25922 and *E. faecalis* ATCC 29212 were the reference bacterial strain used for quality control.

RESULTS

From January 3 to April 7 2018, 80 specimens of chicken feces were collected from 4 farms. Four related survey sheets were parallelly filled by the farmers.

Based on pieces of information from the survey sheets, it was observed that responders consisted of 75% male and 25% female. With regard to the educational background, 75% have completed university studies and 25% secondary classes.

All farmers used water, cresyl bleach and other antiseptics solutions for disinfection. To prevent disease outbreak in the farm, they adopted routine cleaning and antimicrobials (antibiotics 80%; antiseptic 20%). The use of these antimicrobials was at 50% done by direct on-farm spraying, 50% as cleaning solutions and 100% on all farms by direct administration to animals. Namely, antibiotics used consisted of Flumequine, Furaltadone and Oxytetracycline (systematically used by all farmers); Norfloxant, Enrofloxacin, Ciprofloxacin and Norfloxon (used as the second line). These drugs were used at varied doses and frequencies, depending on the targeted goals (prevention or infection management). 90% alcohol was the only antiseptic used in farms for outbreak prevention. A decontamination solution was always available at the farm entries.

Selection of ready-to-sell animals was made in all the farms by the clients that were otherwise allowed to get into the farm to select the animals they would pay for. The main sources of water used in all farms were either the wells or pipes, and the animal populations found between 50 and 1,500 for 50% and above 1,500 animals for 50% of farms.

On the relevance of antimicrobial agents in farms, 75% farm staff acknowledged the benefit provided in animal protection against outbreaks, recognized that resistance development may be caused by poor drug use and, were aware of the threat it might represent for the farm animals and human communities that depended on the products and services from the farms (average surface area: 7x16 m^2).

Distribution of samples

During this study, 294 isolates were recovered from 80 stool specimens. Susceptibility/resistance profile according to bacterial types and isolation sites per major bacteria group was displayed as shown in Table I and Table II for Bafoussam and Bandjoun, respectively.

Table I: Susceptibility/resistance profile of isolates from Bafoussam.

Antibiotic/phenotype		Location and bacteria category					
		BAFOUSSAM 1			BAFOUSSAM 2		
Antibiotic	Phenotype (%)	Gram-negative rod n= 98	Gram-positive rod n= 12	Gram-positive cocci n= 40	Gram-negative rod n= 68	Gram-positive rod n= 24	Gram-positive cocci n= 52
Vancomycin	I	NA	20	47	NA	41	60
	R	NA	40	32	NA	17	24
	S	NA	40	21	NA	42	16
Gentamicin	I	22	17	10	3	17	8
	R	18	0	35	15	17	8
	S	60	83	55	82	66	85
Ciprofloxacin	I	2,	0	10	15	0	0
	R	41	50	70	44	58	65
	S	57	50	20	41	42	35
Trimethoprim/sulfamethoxazole	I	0	0	0	0	0	6
	R	71	25	82	45	50	65
	S	29	75	18	55	50	29
Nalidixic acid	I	10	17	0	6	8	4
	R	45	50	65	50	50	69
	S	45	33	35	44	42	27
Norfloxacin	I	6	0	0	0	0	0
	R	31	50	79	50	42	62
	S	63	50	21	50	58	38
Erythromycin	I	11	0	33	12	0	0
	R	78	100	0	38	67	33

	S	11	0	67	50	33	67
Clindamycin	I	14	0	33	0	22	25
	R	57	50	44	0	22	17
	S	29	50	23	100	56	58
Nitrofurantoin	R	19	0	0	41	0	13
	S	80	100	100	59	100	87
Levofloxacin	R	65	**72**	67	73	75	70
	S	**35**	**28**	33	27	25	30
Amoxicilline/Clavulanic acid	I	0	17	5	0	0	0
	R	57	0	5	15	0	0
	S	43	83	90	85	100	100
Imipeneme	R	0	0	0	0	0	0
	S	100	100	100	100	100	100
Oxacillin	R	100	100	100	100	83	96
	S	0	0	0	0	17	4
Penicillin	R	100	75	83	NT	67	48
	S	0	25	17	NT	33	52
Cefoxitin	I	4	0	0	8	0	0
	R	33	0	6	18	8	4
	S	63	100	94	74	92	96
Aztreonam	I	19	0	0	0	0	33
	R	38	0	100	100	4	0
	S	43	100	0	0	98	67
Cefuroxime	I	0	10	0	6	75	0
	R	87	56	0	58	0	0
	S	14	34	100	36	25	100
Ceftriaxone	I	33	0	6	6	8	0
	R	45	100	72	82	92	100
	S	22	0	22	12	0	0
Amoxicillin	I	0	0	0	0	0	17
	R	84	50	0	32	48	17
	S	16	50	100	68	52	66
Ceftazidime	I	23	25	11	20	0	37
	R	17	75	68	20	100	63
	S	60	0	21	60	0	0
Tetracycline	I	2	17	13	8	0	4
	R	52	67	73	71	73	81
	S	46	16	13	21	27	15
Cefotaxime	I	0	0	0	6	10	10
	R	0	0	33	6	10	0
	S	100	100	67	88	80	90

NA: not applicable

Overall, resistance rates were higher than 60% for 34 % and 25% of the antibiotics used in Gram-negative rods from Bafoussam 1 and Bafoussam 2, respectively. In Gram-positive rods, similar rates were recorded in both settings (32%), while those observed in Gram-positive cocci isolated from the respective farms were slightly different (50% and 41%). Resistance to Tetracycline and Oxacillin appeared invariably high for the three categories and in both farms (the lowest resistance rate to Tetracycline > 50%). The reverse trend was recorded with Gentamicin, Nitrofurantoin and, to a lesser extend amoxicillin and Amoxicillin/clavulanic acid for which susceptibility was relatively higher. In addition, resistance to fluoroquinolones varied with types of drugs. Resistance to 3rd generation cephalosporins was highest with Ceftriaxone, while Oxacillin appeared among the least effective drug used.

Likewise, analysis conducted on data from Bandjoun highlighted other salient facts from which some of the most significant in the study's scope were summarized and presented in Table II.

Table II: Susceptibility/resistance profile of isolates from Bandjoun.

Antibiotic/phenotype		Location and bacteria category					
		BANDJOUN 1			BANDJOUN 2		
Antibiotic	**Phenotype (%)**	**Gram-negative rods n= 134**	**Gram-positive rods n= 16**	**Gram-positive cocci n= 72**	**Gram-negative rods n= 4**	**Gram-positive rod n= 8**	**Gram-positive cocci n= 14**
Vancomycin	I	NA	25	31	NA	25	42
	R	NA	25	22	NA	50	29
	S	NA	50	47	NA	25	29
Gentamicin	I	8	25	19	0	0	0
	R	25	50	31	0	0	29
	S	67	25	50	100	100	71
Ciprofloxacin	I	5	0	3	0	0	0
	R	32	38	76	100	50	86
	S	63	62	21	0	50	14
Trimethoprim/sulfamethoxazole	I	0	0	3	0	0	0
	R	60	75	89	100	50	100
	S	40	25	8	0	50	0
Nalidixic Acid	I	2	13	9	0	0	0
	R	58	62	74	100	25	100
	S	40	25	17	0	75	0
Norfloxacin	I	16	0	4	0	0	0
	R	35	50	81	100	75	86
	S	49	50	15	0	25	14
Erythromycin	I	2	0	0	0	33	60
	R	77	0	100	100	0	0
	S	21	100	0	0	67	40
Clindamycin	R	NA	71	52	NA	50	71
	S	NA	29	48	NA	50	29
Nitrofurantoin	R	68	0	67	0	2	60
	S	32	100	33	100	98	40
Levofloxacin	I	7	50	20	9	52	16
	R	47	25	47	45	24	47
	S	46	25	33	46	24	37
Amoxicilline/ clavulanic acid	R	45	13	17	0	75	16
	S	55	85	83	100	25	85
Imipeneme	I	3	0	0	5	2	0
	R	54	14	36	52	12	34
	S	43	86	64	43	86	66
Oxacillin	I	0	0	6	40	0	0
	R	67	100	85	0	100	100
	S	33	0	9	60	0	0
Penicillin	R	**17**	86	35	0	100	43
	S	**83**	14	65	0	0	57
Cefoxitin	I	10	0	0	0	0	0
	R	23	0	17	0	0	14
	S	67	100	83	100	100	86
Aztreonam	R	0	100	83	2	80	90
	S	100	0	17	98	20	10
Cefuroxime	I	0	50	40	0	75	33
	R	67	0	30	100	0	0
	S	33	50	30	0	25	67
Ceftriaxone	I	17	13	0	0	0	0
	R	45	87	81	100	100	100
	S	38	0	19	0	0	0
Amoxicillin	R	75	0	75	100	0	0
	S	25	100	25	0	100	100
Ceftazidime	I	1	25	6	0	50	0
	R	48	63	81	100	50	100
	S	51	12	13	0	0	0
Tetracycline	R	80	85	100	100	100	100
	S	20	15	0	0	0	0
Cefotaxime	I	0	0	0	3	5	7
	R	10	0	30	6	10	0
	S	90	100	70	91	85	93

NA: not applicable

In Bandjoun 1, resistance rates higher than 60% were obtained with 34%, 32% and 46% of the antibiotics used for Gram-negative rods, Gram-positive rods and Gram-positive cocci, respectively. Likewise, the respective rates were 48%, 41% and 60% in Bandjoun 2; but, here the isolation rates were very low. Across farms, the most reduced susceptibility rates were recorded for antibiotics like Tetracycline, Oxacillin, Co-trimoxazole, Nalidixic acid and Ceftriaxone. Higher effectiveness was obtained with Cefotaxime, Cefoxitin and Gentamicin.

The overall picture from both locations (Bafoussam and Bandjoun) indicated that resistance to antibiotics like Oxacillin, Tetracycline, Co-trimoxazole and Ceftriaxone were common and invariably high, regardless of the bacteria groups targeted.

DISCUSSION

Overall, data analysis from the present survey indicated that resistance rates to commonly used drugs were high, consistent with the putative mixed microbial populations' dynamic that provides conditions for interactions like those enabling gene transfer for the fitness and survival expected to develop with resistome in complex ecosystems like farms. These interactions may be beneficial, neutral or antagonistic, with regards to the community types diversity in farms with low sanitation. Otherwise, most of these events occur in unhygienic farms and highlight the need to mitigate the microbial loads in order to mitigate in turn, the inherent genetic related traits dissemination.[15,16] Susceptibility/resistance profiles in both locations were quite similar; with higher effectiveness observed with Gentamicin, unlike fluoroquinolones and other large spectrum antibiotics for which the rates of resistance were very high. In previous surveys conducted in health facilities, fluoroquinolones, Gentamicin and Nitrofurantoin were shown to have higher effectiveness.[3,17,18] These latter developments might raise questions about why resistance to Gentamicin does not evolve as rapidly as that to other antibiotics in the presence of selective agents. Though resisting comprehensive answer, pointing out the influence of the spectrum of activity might be reasonable. In fact, the spectrum of Gentamicin is more linked to aerobic bacteria contrary to that of other drugs which typically extend to aerobic, anaerobic and micro-aerophilic species, potentiating thereby the selection process.[12] Otherwise, the number of bacteria cells affected by Gentamicin in a given ecosystem is lower than that exposed to antibiotics which act on all of these major bacterial categories.

Basically, more than 50% resistance rate for an antibiotic is obviously likely to cause drastic reduction of the likelihood with which this drug is expected to help in the control of infections caused by the wild bacterial type. Very few cases in the current survey are below the 50%, representing therefore a serious health threat to the farm animals first and indirectly to the exposed human populations. When in a location it is observed that for large numbers of antibiotics this resistance rates are considerably high; it implies that no matter what, control of a potential infection in farm animal is less likely. Or, the bacteria diversity recorded in the present study readily predisposed to high risks for ranges of bacterial infections. This assumption firmly holds with the high rates of Gram-negative isolates belonging to the *Enterobacteriaceae* family, naturally known to play significant role in genes dissemination in the bacterial world.[12,19] Bacteria from this large group express ranges of resistance phenotypes including inducible cephalosporinases and extended spectrum beta-lactamases that can easily be disseminated through complex mobile genetic elements like plasmids, integrons and trasnposons.[11,20] They therefore represent resistance gene reservoirs for polymorphic microbial populations in which a comprehensive understanding of types and amplitude of interactions should be addressed on holistic basis .[15,21] The origins are virtually difficult to identify clearly, but several steps in connection with resistance evolution seem to be related, as shown in the present study, to the use of antimicrobials in farms for prophylaxis, outbreak management and growth promotion; though none of these practices is clearly demonstrated to improve the production output in the farm.[22–26] This view is in line with the frequency of resistant Gram-negative rods, known as etiologies of infections in poultry.[27]

In fact, the reduced effectiveness of antibiotics rather promotes the growth of resistant strains in the vicious cycle that enhances the microbial fitness which opposes in turn, effectiveness of therapeutic attempts in both farm animals and exposed human communities; given that the ready-to-sell animals were selected by the clients that were allowed free contacts with all the animals in the farms. Otherwise, it could hardly be taken for granted instant and reliable management of bacterial infections caused by common resistant strains, including those in cause in pneumonia, foodborne illnesses, and other human healthcare-associated infections. As more strains of bacteria become resistant to larger numbers of antibiotics, the impact could reasonably be anticipated in human medicine with increased rates of drug-resistant bacterial infections.

Resistance to Nitrofurantoin reflected the intense use of nitrofurans in the farms as indicated by the data recorded. Otherwise, high resistance rates to nitrofurantoin, alongside with that to others like quinolones (Nalidixic acid, fluoroquinolones) and Tetracycline are consistent with the selection due to inappropriate use of these or related drugs (oxytetracycline, for instance) hypothesis. In previous surveys, Nitrofurantoin was amongst the most effective drugs in hospitals while high resistance rates were recorded with other drugs known to be used in the specimen collection site and assumed to have played substantial role in direct selection, co-selection or cross-selection.[17,18] While this drug wasn't heavily affected was then thought to be related to its limited use, in connection with unavailability, once against consistent with above developments. In the present survey, the overwhelmingly high resistance trend is most likely associated with the use of closely related drugs. Both findings might imply that unlike cross-selection, the co-selection process' amplitude might be limited against nitrofurans. The lowest isolation rates recorded in Bandjoun 2 was due to the fact that antimicrobials were spread on the farm the day earlier.

Bacillus spp. was amount the common isolates. Strains from this genus produce hydrogen cyanide (HCN) that inhibits the growth of pathogens (bacteria and fungi) and promotes successful competition with pathogens for nutrients and ecological niches.[28–32] They are then known to have adapted to ranges of environments thanks to the high flexibility of their genome, like *Enterobacteriaceae.* Accordingly, members of both groups are ubiquitous like *Staphylococci*. The genotypic diversity of *Bacillus* is known to have evolved by gain of function selection through horizontal gene transfer from other bacteria and loss of unneeded ancestral functions.[33,34] Unlike *Enterobacteriaceae* and *Staphylococci*, however, *Bacillus* are also endospore-forming, therefore more resistant to environmental stresses. Former authors suggested that bacteria from this group could appropriately serve as useful indicators for monitoring resistance in stewardship programs in line with their ubiquitous features, genome flexibility and homology with other bacterial populations.[3,12,17,18,32] Still others reported that *Bacillus* could be used as growth promoters in farm animals, probably in connection with its ability to synthesize and secrete lactocepin that selectively degrade inflammatory cytokines and prevent barrier dysfunction; in addition to the successful competition ability against pathogens.[35] In this, they enhance the supply in essential nutrients as previously observed with plants.[36,37] Many others investigators are conducting researches in that direction.[38,39] One would wonder whether they could effectively be used in animal husbandry instead of antibiotics. Though likely and desirable, further sustained studies are necessary to address conclusively this very important concern.

The high resistance rates to large numbers of antibacterial agents recorded in the present study predicts the economic impact, first in the farm, then in the human communities. In fact, high resistance in farm would imply poor response in case of outbreaks and the subsequent financial losses due to high morbidity and mortality and/or the use of more costly drugs for infection control in farm animals and in humans. In such cases, transfer of resistant bacteria to human is facilitated, primarily through close contact with animals as observed in this study, wastes used as fertilizers or accidental channeling into streams.[40] The obvious results anticipatable would be the facilitated communication of the traits to the endogenous, environmental and pathogenic flora, that will be (at least partly) in cause in treatment failure in case of infection, and will cause in turn longer hospitalization and use of more costly antibiotics for case management in the vicious cycle that encourages poor hygienic practices and rampant poverty. Typically, the amplitude of the threat would vary with time and space depending on the living standards (and related factors) of the general populations known to modulate drug use and hygienic practices in turn.[27] In other words, poor practices as observed in all farms targeted by the present investigation would promote resistance growth and generate additional financial burden.

Future fields of research should focus on other alternatives to growth supplementation than antimicrobials. With available financial means, this solution is feasible if minimal policies are enforced with committed human resources (most of which have good educational background) in the ongoing and future works on identification of biological alternatives for growth supplementation and for the struggle against pathogens and infections in farms.[37,39]

CONCLUSION

Data analysis indicated that resistance trends were invariable high in all the farms investigated; most likely in connection with the varieties of drugs used by farmers for different purposes. Bacterial types known to be potent vectors of gene transfer and etiologies of infectious diseases in animals and humans (*Enterobacteriaceae*, *Bacillus* and *Staphylococci*) were also frequently recovered. Though yet to be addressed, both the isolation and resistance rates could help anticipate that the economic burden of farm-related infections might be very high. Biological alternatives to antimicrobials for growth promotion and fighting against pathogens in farms was, therefore, thought to be primordial, feasible, then strongly advocated.

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Additional notice: The authors declare that this work is devoid of any conflict of interest.

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