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Review Article
Avian Salmonellosis and Colibacillosis: Risk Factors, Antibiotic Resistance, Public Health Impact and Biological Control

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Abstract

Salmonella spp. and *Escherichia coli* are the two leading causes of foodborne bacterial zoonosis in the world. Respectively responsible for avian pullorosis/typhosis and colibacillosis in poultry, these pathogens represent major constraints for the poultry industry (layers, broilers) in the world because of the mortality and economic losses generated. The isolation of multidrug resistant *Salmonella* and *E. coli* strains in poultry farms in several parts of the world reflects the global aspect of the problem. Antibiotics are essential in the treatment and control of these two bacterial diseases. Resistance results in the progressive ineffectiveness of several families of antibiotics, which constitutes a threat to animal health, food safety and public health. This article reviews the various studies conducted on avian salmonellosis and colibacillosis. The antibiotic molecules to which *Salmonella* spp. and *Escherichia coli* strains are resistant are discussed. The virulence and resistance genes associated with the different serotypes are reported. Finally, the risk factors, the impact on public health and some pyhtotherapeutic solutions are described. A better knowledge of this information will allow the poultry industry to make further progress in the elimination of salmonellosis and avian colibacillosis, the reduction of antibiotic use and the potential public health risks.

Key words: Salmonellosis, colibacillosis, antibiotics, public health, aviculture

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INTRODUCTION

Poultry farming is one of the most important sources of animal protein and income in the world in general and particularly in Africa[1]. It is a sub-sector that contributes considerably to the economy of several African countries and thus play key role in fighting against hunger and poverty. Despite of its importance, this sub-sector is facing major disease challenges that hinder the agricultural and socio-economic development of many countries. Among these, salmonellosis and colibacillosis are the main bacterial diseases caused by *Salmonella* spp. and *Escherichia coli* respectively and are considered as one of the main causes of morbidity and mortality either as a primary or secondary pathogen[2]. In West Africa, salmonellosis alone causes significant economic losses with mortalities of up to 90%[3]. Antibiotic therapy with synthetic molecules is one of the ways to control these diseases. These molecules are used either for curative or preventive purposes, or as growth promoters in feed[4]. Their use in poultry farming has undoubtedly improved the productivity[5]. However, the frequent and uncontrolled use of these molecules has progressively contributed to the emergence of resistant bacteria, in this case *Salmonella* and *Escherichia coli* strains that are multi-resistant to different families of antibiotics[6]. According to Chang *et al.*[7]; Economou and Gousia[8], the use of antibiotics in veterinary medicine and farm animals is of constant concern because of the possible transmission of resistant bacteria to human through food consumption and environment. New effective and accessible treatment methods must therefore be envisaged to reduce the speed at which this microbial resistance develops. Medicinal plants, through their pharmacological effects, are an option to be considered. Used for thousands of years, they represent a significant source of new drugs. The abundance of research work in this area confirms the renewed interest in their use in the treatment of animals[9]. In Benin, the poultry sub-sector is booming but bacterial resistance related to *Salmonella* and *Escherichia coli* is one of the major challenges for it. The objective of this article is to: (1) Synthesize recent information on the different serotypes isolated and their associated virulence genes, (2) Determine the bacterial resistance to antibiotics and and their impact on public health (3) Review some phytosanitary treatments performed against these bacteria in several regions of the world.

Avian salmonellosis and colibacillosis

Avian salmonellosis: Avian salmonellosis is one of the most common bacterial infections of poultry. It is caused by the multiplication in the body of germs of the *Salmonella* genus, a facultative intracellular pathogenic bacterium causing local or systemic infections and belonging to the *Enterobacteriaceae* family[10]. The genus *Salmonella* currently includes 2659 serovars belonging to two species: *Salmonella enterica* which has 6 subspecies (enterica, salamae, arizonae, diarizonae, houtenae, indica) and *Salmonella bongori*. Of these many serovars, only 10% have been isolated from poultry and over 50% from humans[2]. In poultry farming, there are two types of infection due to *Salmonella* Pullorum and *Salmonella* Gallinarum are the etiological agents of pullorosis and avian typhosis, respectively, which cause huge economic losses to the poultry industry. Besides the serovar Gallinarum/Pullorum recognized as specific to poultry, there are other serovars (*Salmonella enteritidis*, *S.* Typhimurium, *S.* Hadar, *S.* Heidelberg, *S.* Saintpaul and *S.* Infantis) less or non-specific, also responsible for the development of poultry infections and moreover, involved mainly in the public health problem via the consumption of food of animal origin[11]. Two types of transmission are possible in poultry farms: vertical and horizontal transmission. Vertical transmission can be transovarial (direct contamination of the egg during its formation from the infected ovary or oviduct)[12]. Horizontal transmission, on the other hand, occurs orally, through contact with virulent materials (feces), the environment as well as water and food. It can infect chicks, pullets as well as adult hens. Thus, several *Salmonella* serotypes have been isolated from poultry farms, their environments, poultry carcasses and also table eggs[13,14]. Apart from the different *Salmonella* serotypes isolated till date, different virulence genes associated with them have also been determined by PCR technique from DNA and also plasmid analysis. Table I summarizes the recently identified *Salmonella* serovars and their associated virulence genes.

Avian colibacillosis: Avian colibacillosis is one of the commonly reported bacterial diseases in poultry farming. It is caused by *Escherichia coli*, a non-sporulating, facultative anaerobic gram-negative bacterium[51]. *E. coli* infections represent one of the important causes of economic losses in poultry farming and are often considered secondary pathogens[2,52]. Because *Escherichia coli* are commensal hosts in the poultry digestive tract, most strains are not pathogenic. However, a group of these (10-15%) are associated with colibacillosis syndrome and are referred to as "Avian Pathogenic *E. coli*" or APEC belonging to specific serotypes[53]. In chickens, the respiratory tract is the primary route of entry for avian pathogenic *E. coli* followed by ingestion of contaminated feed and the intestines are their most important reservoir. Pathogenic strains can also contaminate eggs via

Table 1: *Salmonella* serovars and virulences genes associated

Serovars	Sources	Virulence genes	Country	References
S. Enteritidis, *S.* Typhimurium, *S.* Kentucky, *S.* Agona, *S.* Virchow, *S.* Anatum, *S.* Derby, *S.* Hato, *S.* Chester, *S.* Jedburgh, *S.* Schwarzengrund, *S.* Tennessee, *S.* Albany, *S.* Duesseldorf, *S.* Poona, *S.* Eastbourne, *S.* Gaminara, *S.* Drac, *S.* Alexanderplatz, *S.* Brancaster, *S.* Bredeney, *S.* Amoutive, *S.* Telelkebir, *S.* Liverpool, *S.* Muester, *S.* Monschaui	Chicken droppings	-	Burkina Faso	[15]
S. Anatum, *S.* Brandenburg, *S.* Choleraesuis, *S.* Derby, *S.* Enteritidis, *S. gallinarum* var. Gallinarum/Pullorum, *S.* Minnesota, *S.* Ohio, *S.* Rissen, *S.* Senftenberg, *S.* Agona, *S.* Livingstone, *S.* Mbandaka	Poultry and its food derivatives	-	Belgium	[16]
S. Enteritidis and *S.* Typhimurium	Eggs of laying hens	-	France	[17]
S. Typhimurium	Chickens	-	India	[18]
S. Gallinarum	Droppings from laying hens	-	Mali	[3]
S. Derby, *S.* Typhimurium, *S.* Brancaster, *S.* Hato, *S.* Kentucky, *S.* Ouakam, *S.* Cannstatt, *S.* Essen	Eggs and droppings of laying hens	-	Burkina Faso	[13]
S. Infantis, *S.* Typhimurium, *S.* Senftenberg, *S.* Agona, *S.* Mbandaka, *S.* Tennessee, *S.* Worthington, *S.* Sofia	Chickens for meat	-	Brazil	[19]
S. Derby, *S.* Hato, *S.* Chester, *S.* Agona, *S.* Suberu, *S.* Essen, *S.* Hessarek, *S.* Kissangani	Broiler gizzard, liver and spleen	-	Niger	[20]
S. Sofia, *S.* Abortusovis, *S.* Adelaide, *S.* Typhimurium	Broiler meat	-	Australia	[21]
S. Enterica, *S.* Agama, *S.* Typhimurium, *S.* Albany, *S.* Colindale, *S.* Istanbul, *S.* Larochelle, *S.* Nigeria, *S.* Orion	Liver, spleen, heart, ovary, cecum, chicken environment	-	Nigeria	[22]
S. Heidelberg	Broiler carcasses	*lpf*A, *csg*A, *inv*A, *siv*H, *msg*A, *tol*C	Brazil	[23]
S. Aberdeen, *S.* Schwarzengrund, *S.* Kentucky	Broiler carcasses	-	Brazil	[24]
S. Bolton, *S.* Newport, *S.* Typhimurium, *S.* Hadar, *S.* Heidelberg	Chicken droppings and chicken environment		Uganda	[25]
S. Infantis, *S.* Abony, *S.* Agona, *S.* Schwarzengrund, *S.* Anatum, *S.* enterica O: 4, 5; *S. enterica* O: 6, 7.	Chicken carcass	-	Brazil	[26]
S. Enteritidis, *S.* Typhimurium	Liver and intestine of broilers	*inv*A, *fli*C, *sdf*I, *sdf*II, *sdf*III, *sef*A	Egypt	[11]
S. Derby, *S.* Jerusalem, *S.* Bovismorbificans, *S.* Enteritidis,	Laying hen environment	-	China	[27]
S. Infantis, *S.* Paratyphi A, *S.* Limete, *S.* Mbandaka, *S.* Anatum, *S.* Idikan, *S.* Derby, *S.* Choleraesuis, *S.* Gallinarum, *S.* Virchow, *S.* Enteritidis	Modern chicken environment	-	Chad	[16]
S. Larochelle, *S.* Muester, *S.* Enterica, *S.* Typhimurium	Droppings, cloacal swabs, food scraps	*fim*A, *sef*C	Nigeria	[28]
S. Kentucky, *S.* Poona, *S.* Elisabethville	Droppings, food and water residue, litter	-	Nigeria	[29]
S. Enteritidis, *S.* Infantis, *S.* Typhimurium, *S.* Mbandaka, *S.* Orion, *S.* Shwarzengrund, *S.* Cubana, *S.* Montevideo, *S.* Senftenberg, *S.* Grumpensis, *S.* Tennessee	Poultry	-	Brazil	[30]
S. Corvallis, *S.* Brancaster, *S.* Albany	Carcass and environment of chickens	-	Malaysia	[31]
S. Typhimurium	Chicken eggs	-	India	[32]
S. Hadar, *S.* Typhimurium, *S.* Enteritidis, *S.* Derby, *S.* Muester, *S.* Heidelberg, *S.* Chester, *S.* Kentucky, *S.* Drac, *S.* Oakland	Poultry	-	Niger	[33]
S. Kentucky, *S.* Muester, *S.* Enteritidis, *S.* Virchow, *S.* Rubislaw, *S.* Cairina, *S.* Haifa, *S.* Nima, *S.* Poona, *S.* Derby, *S.* Bochum, *S.* Stanleyville, *S.* Duisburg, *S.* Typhimurium, *S.* Ituri, *S.* Oskarshamn	Droppings, carcass and leftover drinking water and food	-	Ghana	[34]
S. Cardoner, *S.* Sambre, *S.* Schwarzengrund.	Cloacal and rectal swabs	-	South Africa	[35]
S. Infantis, *S.* Enteritidis, *S.* Corvallis	Caeca of broilers		Ecuador	[36]
S. Kentucky, *S.* Enteritidis	Poultry meat	-	Morocco	[37]
S. Paratyphi B, *S.* Hvittingfoss, *S.* Muester	Broiler carcasses	*inv*A	Colombia	[38]
S. Thompson, *S.* Enteritidis, *S.* Typhimuruim, *S.* Newport, *S.* Hadar	Gizzard, liver, heart and meat of chickens	-	Iran	[39]
S. Typhimurium, *S.* Apeyeme, *S.* Kentucky, *S.* Daula, *S.* Newport, *S.* Tamale, *S.* Molade, *S.* Colindale, *S.* Lexington, *S.* Bargny, *S.* Enteritidis, *S.* Papuana, *S.* Labadi, *S.* Santiago, *S.* Magherafelt, *S.* Rechovot, *S.* Takoradi, *S.* Angers, *S.* Shubra, *S.* Inganda, *S.* Infantis, *S.* Larochelle, *S.* Virchow, *S.* Vejle, *S.* Shangani, *S.* Jedburgh, *S.* Alfort, *S.* Wingrov	Chickens, ducks, turkeys, quails	-	Egypt	[40]

Table 1: Continue

Serovars	Sources	Virulence genes	Country	References
S. Enteritidis, *S.* Havana, *S.* Typhimurium	Eggs, poultry houses, meat, leftover feed and water	-	South Africa	[41]
S. Typhimurium, *S.* Enteritidis, *S.* Newport	Broiler carcass and environment	*inv*A, *spv*C	South Africa	[42]
S. Hadar, *S.* Blockley, *S.* Irumu, *S.* Anatum	Chicken carcasses	-	South Africa	[43]
S. Enteritidis, *S.* Typhimurium, *S.* Infantis, *S.* Kentucky, *S.* Tsevie, *S.* Chiredzi, *S.* Heidelberg	Spleens, livers, cloacal swabs, gall bladders, egg yolk	-	Egypt	[43]
S. Enteritidis, *S.* Typhimurium, *S.* Virchow, *S.* Gallinarum, *S.* Reading, S. Altona	Droppings and swabbing of caeca	-	India	[44]
S. Typhimurium, *S.* Enteritidis, *S.* Typhi	Chicken droppings, leftover feed and chicken environment	*sdf*I, *via*B	India	[45]
S. Kentucky, *S.* Parkroyal, *S.* Agona, *S.* Saintpaul, *S.* Typhimurium, *S.* Enteritidis, *S.* Heidelberg, *S.* Newport, S. Ruzizi	Broiler turkey droppings	*inv*A	Morocco	[46]
S. Enteritidis	Peritoneal sampling in chickens	-	South Africa	[47]
S. Corvallis, *S.* Rissen, *S.* Hadar, *S.* Enteritidis, *S.* Stanley, S. Weltevreden	Chicken carcass and environment	-	Thailand	[48]
S. Enteritidis, *S.* Typhimurium, *S.* Agona, *S.* Infantis, *S.* Brandenburg, *S.* Saintpaul, *S.* Enterica, *S.* Sandiego	Chicken feed	*spv*C, *inv*A, *sef*A, *pef*A	Brazil	[49]
S. Gallinarum, *S.* Typhimurium, *S.* Typhi, *S.* Pullorum, *S.* Enteritidis, *S.* Paratyphi A	Droppings, leftover feed, eggs	-	Nigeria	[50]

surface fecal matter and cause significant mortality in young chicks[54]. Numerous pathological syndromes such as yolk sac infections, omphalitis, enteritis, head swelling, respiratory tract infection and septicemia are observed in chicks[55,56]. In the subacute form, predominant lesions such as pericarditis, aerosacculitis and perihepatitis are observed[55]. More than 1,000 serotypes of *E. coli* have been isolated but very few are implicated in avian disease[57]. Early studies showed that serotypes O_{35}, O_{78}, O_1 and O_2 were frequently isolated from poultry farms followed by serotypes O_8, O_{15}, O_{18}, O_{19} O_{84}, O_{88}, O_{109}, O_{115} and O_{116}[58,59]. Most of these serotypes are associated with colibacillosis. In recent studies, the presence of serotypes O_2, O_8, O_{132}, O_{25}, O_{24}, O_{20}, O_{19}, O_{18}, O_{116}, O_{115}, O_{78}, O_{86} and O_{81} has been confirmed[55,60]. The factors driving the virulence of APEC strains are numerous and diverse with their associated genes. These are essentially the fimbriae or a fimbrial adhesins; type 1 fimbriae and type P fimbriae (*firm*A, *firm*F, *fim*H, *fim*C (type 1 fimbriae), *pap*A, *pap*C, *pap*EF, *pap*GI, *pap*GII, *pap*GIII, feIA (P fimbriae), toxins (*hly*F, *hly*A, *hly*E, *cdt*B, *cdt*S, *vat*, *sat*, *stx2f*, *ast*A, *pic*, *EAST-1*, *esp*C, *ace*4/35), iron acquisition mechanism (*iut*A, *iuc*C, *iuc*D, *aer*J, *iuc*A, *iuc*B, *iro*BCDEN, *fyu*A, *sit*ABCD, *mnt*H, *feo*B, *irp*2, *ire*A, *eit*ABCD, *fep*C, *chu*A, *bfr*), serum resistance (*iss*, *tra*T, *omp*T, *kps*MT(K1), *kps*MT(II), *kps*MT(III), *neu*C, *neu*S, *neu*D, *kff*C-K5, *bet*A) and invasins (*ibe*A, *ibe*B, tia, *gim*B)[57,61-63]. PCR is one of the most widely used techniques in detecting these virulence factors and associated genes involved in avian colibacillosis[60,64].

Risk factors: The risk of salmonellosis and colibacillosis is high due to the increased infectious pressure in the environment[2]. Fecal contamination of soil is largely responsible for the persistence of *Escherichia coli* and *Salmonella* spp. in the chicken environment[65]. For example, it has been shown that dust present in farms could contain up to 10^5-10^6 *E. coli* per gram of fecal matter[57]. The presence of rodents, parasitic insects, coprophages, necrophages are also a risk factor for contamination, as these species are potential reservoirs for *E. coli* [53]. The presence of other animals on farms as well as poor management of droppings are also risk factors[66].

Salmonella are enteropathogens that can be isolated from a variety of natural environments such as freshwater, marine water and soil. *Salmonella* and *E. coli* can survive for more than 6 months in feces or bedding, drinking water and food[67]. They can also survive for more than a month in dormancy in an insect, so total elimination is difficult when the barn has previously housed affected birds[68]. The use of untreated water, contaminated feed, movement from one building to another by the farmer without disinfecting, uncontrolled presence of visitors inside the farms are many factors related to the environment[69,70]. Clinical manifestations of colibacillosis and salmonellosis also vary with the age of the animal. Respiratory colibacillosis is the most frequently observed infection with a peak incidence in birds at 4-9 weeks of age[71]. In poultry farming, studies have shown that the subjects most affected by salmonellosis are the young including day-old chicks. Indeed, the maximum number of cases was recorded between 7^e and 9^e days old while the highest mortality rate was recorded in chicks aged 1-2 weeks[2,72]. Other risk factors still lose and relate to the duration of exposure of animals, virulence of germs, breed and immune status of chickens[73].

Antibiotic resistance

Concept of bacterial resistance to antibiotics: Bacterial resistance to antibiotics is the ability of bacteria to tolerate a higher concentration of antibiotic than that which inhibits the development of the majority of strains of the same species or individuals of the same culture[74]. Indeed, the bactericidal and/or bacteriostatic action of antibiotics is the result of their interactions with the different biological targets present in bacteria. Thus, some groups of antibiotics inhibit the synthesis of the bacterial wall, or cytoplasmic membrane, others inhibit the synthesis of protein or DNA of the bacteria[75]. However, any mechanism modifying one of these actions can lead to a selection of resistant bacteria[76]. Two types of resistance are then distinguished: intrinsic and acquired resistance. Intrinsic resistance or natural resistance concerns all members of a group of bacteria towards an antibiotic molecule or antimicrobial class. In contrast, acquired resistance takes into account a characteristic specific to a few strains of bacteria of a particular genus or species, causing resistance to emerge and spread among populations of normally susceptible germs[5]. This resistance results either from transfer of a resistance gene by chromosomal mutation or by integration of that gene into a plasmid, transposon, or integron[77]. Resistance by chromosomal mutation concerns approximately 10-20% of clinically isolated cases, while resistance by acquisition of resistance genes concerns almost all antibiotics and represents the majority of clinically isolated cases[78]. Resistance gene acquisition is observed in all bacteria, both Gram-negative and Gram-positive. However, bacterial resistance to antibiotics can result from three main mechanisms:

- **The decrease in the permeability of bacteria to antibiotics:** this concerns Gram-negative bacteria to a much greater extent due to the composition of their wall, which gives them permeability barriers to hydrophilic and hydrophobic antibiotics[79]. Thus, hydrophilic antibiotics (β-lactam or fluoroquinolone) enter the bacteria through the porins and hydrophobic antibiotics simply diffuse through the phospholipid layer[80]. The decrease in permeability of these bacteria is therefore the consequence of a mutation in the genes that code for the porins thus affecting their structures or decreasing their expressions. This mechanism leads to quantitative or qualitative modifications of the porins inducing an acquired resistance often crossed to several antibiotics[80]. This is the case in enterobacteria such as *Escherichia coli* where the reduction in the expression of *Omp*F and *Omp*C porins leads to a reduction in sensitivity to quinolones, beta-lactams, tetracyclines, sulfonamides, trimethoprim and chloramphenicol[81,82]. This is also the case in *Pseudomonas aeruginosa* where the loss of the OprD porin leads to a decrease in permeability to beta-lactams[83].
- **The synthesis of enzymes that inactivate antibiotics:** this results from the production of certain enzymes by bacteria. These enzymes inactivate the action of antibiotics by modifying or hydrolyzing them, which prevents them from attaching to their target and causes a loss of their activity[84]. This is the main mechanism of bacterial resistance to beta-lactams, aminoglycosides, phenicolates, tetracyclines and MLS groups (macrolides, lincosamides, streptogramins) and fluroquinolones[5,85]. This type of resistance has been described for example in *Achromobacter xylosoxidans*[86] and in *Acinetobacter baumannii*[87].
- **Modification of the target of the antibiotic:** this is a resistance mechanism described for practically all antibiotics. It results either from the acquisition of genetic material encoding a specific enzyme that modifies the target of the antibiotic or from a mutation in the nucleotide sequence of the target[88].

It is important to remember that several factors are at the origin of the emergence of several strains of resistant bacteria in both human and veterinary medicine. Indeed, any antibiotic therapy leads to a selection of resistant bacteria and the more antibiotics are used, the higher the risk of appearance of multi-resistant bacteria[89]. The increasing number of bacteria resistant to antibiotics is therefore the consequence of changes in the frequency and distribution of resistance genes in these bacteria[90,91]. Antibiotic residues in the environment as a result of antibiotic use in agriculture are a factor in the emergence of multidrug resistant bacteria through the possibilities of transfer of resistance genes between bacteria[92]. In veterinary medicine, the use of the same antibiotics in an uncontrolled manner and as growth promoters by some farmers are factors that have promoted the emergence of multidrug-resistant bacteria in many countries[16]. The presence of antibiotic residues in food of animal origin also represents a significant factor in bacterial resistance because bacteria isolated from animals and humans share the same resistance mechanisms[93,94]. Studies have shown to this effect, a correlation between on the one hand, the type and frequency of distribution of antibiotic resistance genes in the human microbiome and on the other hand, the use of antibiotics in medicine and agriculture in some countries[95].

Antibiotic resistance of *Salmonella* and *Escherichia coli* strains: In the modern broiler and layer farming system, antibiotics and antibiotic-based products are commonly used for therapeutic, prophylactic and growth promotion purposes[96]. Several antibiotics from different families are therefore used in poultry farming to control bacterial infections such as salmonellosis and colibacillosis. These include antibiotics of the tetracycline class, sulfonamides, penicillins, quinolones, aminoglycosides, polymyxins and macrolides[97,98]. The frequent use of these different classes of antibiotics has allowed over the years the emergence of multidrug resistant strains of *Salmonella* and *Escherichia coli*[3,11,13]. Thus, many authors through their work have demonstrated that several strains of *Salmonella* isolated from chicken farms have developed resistance to tetracyclines, sulfonamides, quinolones and polymyxins[16,99,100]. Furthermore, studies conducted on antibiotic resistance of pathogenic *Escherichia coli* strains in poultry farming (APEC) revealed that they have developed resistance to tetracyclines, trimethoprim-sulfonamide combination, penicillins, cephalosporins, quinolones, polypeptides and phenicols[57,101]. Apart from these resistance profiles, several resistance genes are also associated and identified in several studies. Table 2, provides some recent information on the antibiotic resistance profile of *Salmonella* and *E. coli* strains and associated resistance genes.

Impact on public health: The transmission of multidrug-resistant bacteria from animals to humans from animal-derived foods and the spread of resistance genes continue to be a real threat[122,123]. Among all the emerging challenges in the poultry industry, antimicrobial resistance and public health issues require heightened vigilance and attention for food safety from farm to table. Antimicrobial resistance is a significant threat to human health[124] as it is responsible for approximately 700,000 human deaths each year worldwide[125]. This could significantly increase in the near future if nothing is done to effectively control these microbial agents.

Avian colibacillosis and salmonellosis are considered the most important bacterial diseases affecting the poultry industry worldwide, which are commonly transmitted to humans[2]. Thus, the control of the presence of multidrug-resistant *Salmonella* and *E. coli* is important because these zoonotic agents can cause foodborne disease and have a negative impact on public health[122]. Indeed, it has been reported that resistant strains of *E. coli* from the gut easily contaminate poultry carcasses at slaughter[126,127]. The same is true for eggs, which are contaminated during egg laying[55]. Thus, resistant fecal *E. coli* from poultry can infect humans both directly (direct human-animal contact) or via the food chain[128,129]. Humans with colibacillosis typically manifest respiratory and blood disorders[130], diarrhea, which may be complicated by other syndromes depending on the *E. coli* serotype. These complications can include fever, dysentery, shock and purpura[128]. *Escherichia coli* also causes urinary tract infections (UTIs); approximately 80% of UTIs in humans[131], abdominal sepsis and meningitis.

Salmonellosis due to *Salmonella* spp. is the second most frequently reported bacterial zoonosis in many European countries[132]. The food chain plays an important role in the transmission of *Salmonella* spp. to humans[66]. To this end, Dookeran *et al.*[133] reported that poultry meat, eggs and poultry meat products can be contaminated at different stages of the food chain including during production, processing, distribution, retail, handling and cooking.

Chicken meat and eggs are the main sources of *Salmonella*[134]; with outbreaks of salmonellosis in humans often associated with consumption of this meat and eggs[135], Thus, it has been reported that in Canada, one of the most common sources of foodborne salmonellosis is improperly prepared poultry meat[136].

Laying hens are the primary transmission hosts for *Salmonella* to humans; accounting for 42% of all cases in many European countries[137]. Some strains such as *Salmonella* Typhimurium and *Salmonella* Heidelberg are capable of being transmitted to eggs from infected laying hens by vertical transmission[13]. They have been identified in egg-related outbreaks[138].

Salmonellosis is therefore a common risk associated with poultry consumption[139]. It represents an important public health problem globally, causing substantial morbidity and thus a significant economic impact[140]. It is the leading cause of hospitalizations and deaths due to foodborne illness in the United States[141]. CDC[142] estimates *Salmonella enterica* cause approximately 1.35 million infections (212,500 infections due to antimicrobial-resistant isolates), 26,500 hospitalizations and 420 deaths in the United States each year. In developing countries, primarily those in sub-Saharan Africa and Southeast Asia; countries in which animal husbandry, slaughter and general hygiene conditions are less stringent, the incidence of this disease is thought to be higher.

Salmonellosis infection in humans cause enteric fever, gastroenteritis[143] and even potentially fatal consequences[144], vomiting[145] and sometimes even death[146].

The widely distributed serotypes Typhimurium, Heidelberg and Enteritidis are the focus of public health concern. Enteritidis and Heidelberg are the most

Table 2: Drug-resistant pattern and associated resistance genes of *Salmonella* spp. and *E. coli* strains isolated from poultry

Bacteria	Sources	Profiles	Genes	Country	References
Salmonella	Laying hens	AK, GEN, SPM, FEP, FOX, CHL, TET, SXT, AMC	*bla*CTX-M-65, *tet*A, *Sul*1	Ecuador	102
	Laying hens	EHC, AMC, TET, TTC	-	Burkina-Faso	13
	Local chickens	SPM, TET, AMC, CMX	bla_{TEM}, bla_{CTX-M}	Kenya	103
	Laying hens	STM, TET, GEN, CT, DXC, FMQ, KMC, EHC	-	Mali	3
	Laying hens	CIP, TMP, TET, CHL, NMC	-	Ethiopia	104
	Broilers	CIP, CHL, SFM, SCC	-	Brazil	99
	Laying hens	CIP, TET, SSS, CHL, NDA, AMP, CEF, SPM, AMC, GEN, ENR	*tet*A, *cat*, bla_{TEM}, *sul*1, *qnr*A, *aad*A	South Africa	105
	Broilers	AMP, AMC, CAZ, CTX, FOX, CIP, NDA, SFM, TET	bla_{CMY-2}, *sul*2, *tet*A	Brazil	106
	Broilers	CIP, AMP, CHL, LVX, NDA, TET, SPM, SXT	*bla*TEM-57, *aad*A1, *aad*A2, *cml*A1, *sul*3, *tet*A, *dfr*A, *sul*2, *flo*R, *aph*(30)-*la*	Egypt	107
	Broiler turkeys	TET, CIP, SPM, NDA, AMP, TMP, SXT, GEN, KMC, AMC	-	Morocco	65
	Broilers	AMP, EHC, TET, SXT, CIP, GEN, FC	-	Chad	108
	Broilers	AMC, TET, NDA, SFM,	$blaStrA_{TEM,}$, *sul*2, *Tet*A, *gyr*A	Cambodia	109
	Broilers	AMP, TET, CHL, SXT, SFM	*cat*1, *sul*1, *sul*3, bla_{TEM}, *tet*C, *tet*A, *aad*A1, *aad*A2, *str*A, *flo*R	Egypt	11
	Broilers	CT, AMC, KMC, SXT, TMC, AKC	-	Chad	16
	Laying hens	NDA, CIP, AMC, TET, SSS, SPM, CEF	-	Morocco	100
	Local chickens	AMP, TET, CIP, SFM, TMP, AMP, NDA	-	Ghana	34
	Laying hens	SPM, TET, EHC	-	Mauritius	110
	Broilers	MPA, CRO	*bla*CTX-M-2, *bla*CTX-M-1, $bla_{TEM, blaSHV}$	Brazil	111
	Broilers, laying hens	SSS, NDA, AMP, SPM, GEN, CIP	*sul*1, *sul*2, bla_{TEM-1}, bla_{SHV}	Egypt	112
	Broilers, ducks	SXT, TET, CHL, CIP, AMC, NDA, GEN, EHC	*aac*(3)-Id, *aad*A7	Egypt	113
E. coli	Laying hens	AMP, TET, GEN, SPM, FIS, AMC, FOX, CFU, CRO	*aac*3-VI, *aac*3, *aph*(3)IA, *aad*A, $bla_{TEM,}$tetA, *dfr*17,sull, *qacEΔ1*, *int*1,*pco*A, *pco*D, *pco*E, *ars*C, *sil*P, *ise*C12	USA	60
	Broilers	CIP, ENR, OTT, SSS	*bla*CTX-M, bla_{TEM}	Russia	114
	Broilers	AMP, AMC, TET, CT, DXC, SMC, FFC, CTX, CIP	-	Egypt	57
	Broilers	TET, NDA, SXT, CHL	*bla*CTX-M, *sul*1, *tet*A, *tet*B	South Africa	115
	Broilers	TET, CHL, NDA, DOX AMP, GEN, AMK, SXT, CTX, CRO, SPM	bla_{TEM}, *blaaph*A3$_{CTX-M}$, *aad*C2, *tet*A, *tet*B, *tet*C, *sul*1, *sul*2	China	116
	Broilers	NDA, AMC, AMP, TCC, PPA, SXT	-	Algeria	117
	Laying hens	CRX, TMC, MMC, CFN, SPM, AMC	*str*A, *str*B, bla_{CMY-2}, $bla_{CTXM-19}$, bla_{TEM-1} *B*,*fos*A, *mph*A, *flo*R, *sul*2, *tet*A, *tet*B	China	118
	Broiler turkeys	EHC, AMC, TET, OTT, LCC, SCC, SXT	$bla_{CTX-M-2}$, $bla_{CTX-M-8,}$ $bla_{CTX-M-8/25}$, bla_{TEM}, bla_{SHV}, *bla*CMY-2	Brazil	119
	Broilers	TET, SSX, AMC, SXT, SPM, CFU, FOX, CIP	*gyr*B, *par*C, bla_{CTX-M}, bla_{OXA-1}, bla_{TEM}, bla_{SHV}, *tet*A, *dhrf*VII	Senegal	120
	Broilers	CT	*mcr*-1	South Africa	121

AMC: Amoxicillin+clavuanic acid, AMK: Amikacin, AMP: Ampicillin, CAZ: Ceftazidime, CEF: Cefepime, CFN: Cefazolin, UFC: Ceftiofur, CHL: Chloramphenicol, CIP: Ciprofloxacin, CMX: Co-trimoxazole, CRO: Ceftriaxone, CRX: Cefuroxin, CT: Colistin, CTX: Cefotaxime, DXC: Doxycycline, EHC: Erytromicin, ENR: Enrofloxacin, FC: Fusidic acid, FEP: Cefepin, FFC: Florfenicol, FIS: Sulfisoxazole, FMQ: Flumequine, FOX: Cefoxitin, GEN: Gentamycin, KMC: Kanamycin, LCC: Lincomycin, LVX: Levofloxacin, MMC: Medemycin, NDA: Nalidixic acid, NMC: Neomycin, OTT: Oxytetracycline, PNC: Penicillin, PPA: Pepidimic acid, SCC: Spectinomycin;, SFM: Sulfamethoxazole, Spiramycin, SMC: SPM: Streptomycin, SSS: Sulfonamides, SXT: Trimethoprim/Sulfamethoxazole, TCC: Ticarcillin+clavuanic acid, TET: Tetracycline, TMC: Tobramycin, TMP: Trimethoprime

commonly reported serotypes of *S. enterica* associated with human infections[147]. However, *S.* Enteritidis has always been considered the primary infectious serotype, with an apparent specific capacity for transovarial infection and internal egg contamination[148]. *Salmonella* Typhimurium, *S.* Enteritidis and many other serotypes have also been implicated in food borne outbreaks. Other serotypes with a low frequency of presentation such as *S.* Mbandaka, *S.* Urbana, *S.* Agona, *S.* Muenchen, *S.* Braenderup and *S.* Senftenberg have been identified as a cause of food borne illness and associated with different animal products[149,150]. These serotypes are mainly observed in the poultry house environment, where they are isolated from chicken meat samples, dust, litter, chicken feces and boot swabs[151].

Escherichia coli of serotype O_2: K_1 and O_{78} isolates isolated from human urinary tract infections and septicemic chickens

are phenotypically very similar, indicating that chickens could be a source of human septicemic infections[131,152]. However, a few studies have suggested that these avian isolates possess very few attributes required to cause disease in humans. Conversely, human isolates can be pathogenic to day-old chicks after subcutaneous inoculation as serotypes O_1, O_2, O_{18} and O_{78}. In humans, *E. coli* O_{157}: H_7 is an important enterohemorrhagic pathogen producing Shiga toxin and chicken can be easily infected experimentally and naturally in different geographical settings[153].

Biological control: Antibiotics and antibiotic resistance appeared at the same time and evolved simultaneously. Indeed, research has led to the hypothesis that the mode and rate of bacterial evolution have been transformed by the use of antibiotics with an increase in horizontal transfers of genetic material, genetic recombination at chromosomal sites[91].

It is therefore important to find alternative solutions to reduce the pressure of antibiotic therapy. To this end, plants in general and medicinal plants in particular, have always been used by populations for the treatment of several diseases, whether viral, bacterial or parasitic. They therefore offer the possibility of identifying phytochemicals that can be used as potential antimicrobial agents but also the possibility for small farms and certain populations to make effective treatments without resorting to commercial antibiotics. This last aspect is all the more important in developing countries.

Table 3: Some plant extracts effective against *Salmonella* and *E. coli*

Therapeutic indications	Drug substances	Minimum Inhibitory Concentration (MIC)	Minimum bactericidal Concentration (MBC)	Country	References
Salmonellosis	Essential oil of *Ocimum gratissimum*	0.20-0.53 mg mL^{-1}	0.26-1.05 mg mL^{-1}	Benin	[155]
	Essential oil of *Syzygium aromaticum*	0.63-1.26 mg mL^{-1}	1.26-2.51 mg mL^{-1}		
	Hexane extract of *Cynara scolymus* leaves	6.25 mg mL^{-1}	25 mg mL^{-1}	Tunisia	[156]
	Ethylacetate extract of *Cynara scolymus* leaves	25 mg mL^{-1}	6.25 mg mL^{-1}		
	Aqueous extract of the leaves of *Cynara scolymus*	25 mg mL^{-1}	6.25 mg mL^{-1}		
	Ethanolic extract of *Cynara scolymus* leaves	25 mg mL^{-1}	100 mg mL^{-1}		
	Aqueous extract of *Mallotus oppositifolius*	6.25-25 mg mL^{-1}	25 to 50 mg mL^{-1}	Ivory Coast	[157]
	Ethanolic extract of *Mallotus oppositifolius*	6.25-50 mg mL^{-1}	25 to 50 mg mL^{-1}		
	Essential oil of *Satureja hortensis*	0.31-0.62 µL mL^{-1}	0.625 µL mL^{-1}	Iran	[158]
	Ethanolic extract of *Cussonia arborea* roots	50 mg mL^{-1}	200 mg mL^{-1}	Cameroon	[159]
	Hydroethanol extract of *Cussonia arborea* roots	100 mg mL^{-1}	200 mg mL^{-1}		
	Aqueous extract of *Cyperus alternifolus*	12.5 µg mL^{-1}	25 µg mL^{-1}	Democratic	[160]
	Aqueous extract of *Echinocloa pyramidalis*	12.5 µg mL^{-1}	25 µg mL^{-1}		
	Aqueous extract of *Eriosema verdikii*	3.1 µg mL^{-1}	6.3 µg mL^{-1}		
	Aqueous extract of *Imperata cylindrica*	3.1 µg mL^{-1}	6.3 pg mL^{-1}		
	Aqueous extract of *Typha augustifolia*	6.3 µg mL^{-1}	12.5 µg mL^{-1}		
	Aqueous extract of *Zingiber officinale*	3.1 µg mL^{-1}	6.3 µg mL^{-1}		
	Methanolic extract of *Cyperus alternifolus*	3.1 µg mL^{-1}	6.3 µg mL^{-1}		
	Methanolic extract of *Echinocloa pyramidalis*	3.1 µg mL^{-1}	6.3 µg mL^{-1}		
	Methanolic extract of *Eriosema verdikii*	3.1 µg mL^{-1}	6.3 µg mL^{-1}		
	Methanolic extract of *Imperata cylindrica*	1.7 µg mL^{-1}	3.1 µg mL^{-1}		
	Methanolic extract *Typha augustifolia*	3.1 µg mL^{-1}	6.3 µg mL^{-1}		
	Methanolic extract of *Zingiber officinale*	3.1 µg mL^{-1}	6.3 µg mL^{-1}		
	Ethanolic extract of *Coctus afer*	0.07 mg mL^{-1}	0.15 mg mL^{-1}	Cameroon	[161]
	Ethanolic extract of *Coctus afer*+*Annickia chlorantha*	0.15 mg mL^{-1}	0.15 mg mL^{-1}		
	Ethanolic extract of *Aloe vera* gel	50 mg mL^{-1}	-	Ghana	[162]
	Essential oil of *Aellanthus pubescens*	0.41-0.83 mg mL^{-1}	-	Benin	[163]
	Essential oil of *Pulicaria gnaphalodes*	125 mg mL^{-1}	-	Iran	[164]
	Essential oil of *Ducrosia anethifolia*	62.5 mg mL^{-1}.	-		
	Essential oil of *Carum copticum*	1.95 mg mL^{-1}	3.91 mg mL^{-1}		
	Essential oil of *Foeniculum vulgare* Mill	62.5 mg mL^{-1}	250 mg mL^{-1}		
	Essential oil of *Majorana hortensis* Moench	3.91 mg mL^{-1}	7.8125 mg mL^{-1}		
	Essential oil of *Ossimum gratissimum*	0.5-1 mg mL^{-1}	0.5-1 mg mL^{-1}	Cuba	[165]
	Essential oil of *Lippia graveolens*	0.5 mg mL^{-1}	0.5-1 mg mL^{-1}		
	Essential oil of *Thymus vulgaris*	0.5-1 mg mL^{-1}	0.5-1 mg mL^{-1}		
	Hydroethanol extract *of Euphorbia hirta*	1.25 mg mL^{-1}	2.5 mg mL^{-1}	Benin	[166]
	Hydroethanol extract of *Phyllanthus amarus*	0.625 mg mL^{-1}	1.2 mg mL^{-1}		
	Essential oil of *Ocimum gratissimum*	0,008-0,016 mg mL^{-1}	0,016-0,036 mg mL^{-1}	Benin	[167]
	Essential oil of *Ocimum basilicum*	0,018-0,036 mg mL^{-1}	0,072-0,144 mg mL^{-1}		
	Chloroformic extract of *Zingiber chrysanthum.*	20 µL	-	India	[168]

Table 3: Continue

Therapeutic indications	Drug substances	Minimum Inhibitory Concentration (MIC)	Minimum bactericidal Concentration (MBC)	Country	References
Colibacillosis	Aqueous extract of the fruits of *Rubus* sp.	20 µL	-		
	Hexane extract of *Pistacia integerrima* galls	20 µL	-		
	Chloroformic extract of *Calotropis procera* leaves	20 µL	-		
	Chloroformic extract of *Grewia disperma* leaves	20 µL	-		
	Chloroformic extract of *Plantago lanceolata* seeds	20 µL	-		
	Essential oil from whole plant of *Aeollanthus pubescens*	0.44 mg mL^{-1}	0.87 mg mL^{-1}	Benin	[169]
	Essential oil of *Satureja hortensis*	0.07-0.15 µL mL^{-1}	0.15 µL mL^{-1}	Iran	[158]
	Ethanolic extract of *Ocimum gratissimum*	40 g L^{-1} (oral)	-	Nigeria	[170]
	Aqueous extract of garlic bulbs (*Allium sativum* L)	10 mg mL^{-1}	-	Egypt	[171]
	Aqueous extract of ginger powder (*Zingiber officinale*)	20 mg mL^{-1}	-		
	Ethanolic extract of *Aloe vera* gel	100 mg mL^{-1}	-	Ghana	[162]
	Ethanolic and methanolic extracts of the leaves of *Artemisia nilagirica*	20 µL	-	India	[168]
				India	[168]
	Hexane, chloroformic and ethanolic extracts of *Zingiber chrysanthum* flowers.	20 µL		-	
	Chloroformic, ethanolic and methanolic extracts of *Zingiber chrysanthum* rhizomes	20 µL	-		
	Ethanolic and aqueous extracts of *Rubus sp*	20 µL	-		
	Hexane and chloroform extracts of *Allium sp.* rhizomes	20 µL	-		
	Hexane extract of *Pistacia integerrima* galls	20 µL	-		
	Chloroformic extract of *Calotropis procera* leaves	20 µL	-		
	Hexane, chloroformic, ethanolic and methanolic extracts of the aerial part of *Solanum* sp.	20 µL	-		
	Hexane and chloroform extracts of *Podocarpus* sp. leaves	20 µL	-		
	Chloroformic extract of the fruits of *Solanum viarum*	20 µL	-		
	Chloroformic and methanolic extracts of *Grewia disperma* leaves	20 µL	-		
	Hexane extracts of *Verbascum thapsu* leaves	20 µL	-		
	Hexane and chloroform extracts of *Valerian jatamansi* leaves	20 µL	-		
	Chloroform extract of *Plantago lanceolata* seeds	20 µL	-		
	Essential oil of *Pulicaria gnaphalodes*	125 mg mL^{-1}	250 mg mL^{-1}	Iran	[164]
	Essential oil of *Ducrosia anethifolia*	7.8125 mg mL^{-1}	15.625 mg mL^{-1}		
	Essential oil of *Carum copticum* Benth	0.98 mg mL^{-1}	1.95 mg mL^{-1}		
	Essential oil of *Foeniculum vulgare* Mill	3.91 mg mL^{-1}	15.625 mg mL^{-1}		
	Essential oil of *Majorana hortensis* Minch	3.91 mg mL^{-1}	7.8125 mg mL^{-1}		
	Hydroethanol extract of *Euphorbia hirta*	1.25 mg mL^{-1}	2.5 mg mL^{-1}	Benin	[166]
	Hydroethanol extract of *Phyllanthus amarus*	0.625 mg mL^{-1}	1.2 mg mL^{-1}		
	Aqueous extract of *Thonningia sanguinea*	500 mg (oral)	-	Ivory coast	[172]

The scientific exploration of medicinal plants for target molecules is a serious research opportunity[154]. Several plants in various forms (extract, essential oil, powder,...) have been tested by many authors in different parts of the world on *Salmonella* spp. and *E. coli* strains. Table 3 reviews some phytotherapeutic options to control or eliminate these bacteria.

CONCLUSION

Antibiotics have been the first therapeutic solution against bacterial infections since their discovery. But excessive use has led to the rapid emergence and development of drug resistance that is increasing at an alarming rate concerning public health. Phytogenic extracts are considered as an alternative therapy to reduce the use of antibacterial as medicinal plants have always been used for the treatment of several cost inflicting diseases. Many plants have been tested so far and found effective in controlling the *Salmonella* spp. and *E. coli* strains of zoonotic importance that are most often encountered in poultry farms. Slaughter of infected birds and processing of contaminated meat can lead to widespread cross-contamination of poultry carcasses. Therefore, on-farm control of resistant bacteriais important to reduce the risk of

contaminated poultry meat reaching the final consumer. Phytotherapy offers avenues to explore for the development of new active molecules against this global issue.

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