

## Review on the Problematic of Salmonellosis and Interests of Traditional Herbs in the Treatment

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### Abstract

**Objective:** *Salmonellae* are facultative anaerobic Gram-negative rod-shaped bacteria generally 2-5 microns long by 0.5-1.5 microns wide and motile by peritrichous flagella. *Salmonella* spp are among the group of bacteria in the family Enterobacteriaceae commonly known as enteric bacteria that live in gastrointestinal tracts of warm-blooded animals. Worldwide surveillance data has demonstrated an overall increase in antibiotic resistance among non-typhoid *Salmonella*, although significant geographical and serotype variability exist. The use of medicinal plants in the treatment of salmonellosis has become more than compulsory nowadays especially with the new trend of antibiotic resistance and the effectiveness of the properties of these plants. The current study aimed to assess the importance of salmonellosis in Benin and the potentialities of treatment by medicinal plants.

**Materials and Methods:** A systematic online search was performed whereby key-words such as "*Salmonellae*", "Salmonellosis Benin", "non-typhoidal salmonellosis", "Medicinal plants Benin" and "traditional plants Benin" were entered in PubMed database, Google Scholar and [www.google.bj](http://www.google.bj). Obtained articles were included based on the reliability of their source, the study area (basically Benin and Africa) and the topic.

**Results:** Host factors predisposing to severe non-typhoidal *Salmonellae* infection include reduced gastric acidity, impaired cell mediated and humoral immunity, and impaired phagocytic function. Antimicrobial resistance in *Salmonella* can be associated with horizontal transfer of antibiotic resistant genes and with increased treatment failure and risk of invasive disease. Several scientists around the world have researched this matter and confirmed the antimicrobial properties of plants on bacterial infections mainly salmonellosis

**Conclusion:** The use of medicinal plants in the treatment of salmonellosis has become more than compulsory nowadays especially with the new trend of antibiotic resistance and the effectiveness of the properties of these plants.

**Keywords:** *Salmonella* spp; Epidemiological factors; Treatment; Medicinal plants

### Introduction

*Salmonella* infection represents a considerable burden in both developing and developed countries. The disease is normally transmitted by fecal-oral route through eating contaminated food with fecal materials [1]. *Salmonella* infections are the second leading cause of bacterial food-borne illness in the world. Specific *Salmonella* spp which are responsible for typhoid in humans are *Salmonella typhi* and *Salmonella paratyphi* A and B [2,3]. Similarly, sources of *Salmonella* spp in fish and aquatic environment are attributed to human activities [4]. Worldwide surveillance data has demonstrated an overall increase in antibiotic resistance among non-typhoid *Salmonella*, although significant geographical and serotype variability exist [5,6]. This increased resistance to antibiotics requires the research of alternative methods like natural products from the treatment of salmonellosis.

The use of medicinal plants in the treatment of salmonellosis has become more than compulsory nowadays especially with the new trend of antibiotic resistance and the effectiveness of the properties of these plants. Thus, the current study aimed to assess the importance of salmonellosis in Benin and the potentialities of treatment by medicinal plants.

### Background on *Salmonella* spp and salmonellosis

*Salmonellae* are facultative anaerobic Gram-negative rod-shaped bacteria generally 2–5 microns long by 0.5–1.5 microns wide and motile by peritrichous flagella [7].

*Salmonella* spp are among the group of bacteria in the family Enterobacteriaceae commonly known as enteric bacteria that live in gastrointestinal tracts of warm-blooded animals [3]. The genus *Salmonella* comprises about 2,579 serovars [8]. The serovars which are most frequently isolated in food borne illnesses in humans are *Salmonella enteritidis* and *Salmonella typhimurium* [9-11]. Globally, *S.*

*enteritidis* is the most prevalent species [12,13] and is followed by *S. typhimurium*. Another species, *S. weltevreden*, is confined to Asia [2]. These *Salmonella* spp are responsible for salmonellosis which is a worldwide health problem in humans and animals.

*Salmonella* infection represents a considerable burden in both developing and developed countries. The disease is normally transmitted by fecal-oral route through eating contaminated food with fecal materials [1]. *Salmonella* infections are the second leading cause of bacterial food-borne illness in the world. Approximately 95% of cases of human salmonellosis are associated with consumption of contaminated foods such as meat, poultry, eggs, milk, seafood and fresh produce [2,11]. *Salmonella* species are a leading bacterial cause of acute gastroenteritis. Although the global human health impact of *Salmonella* infections has not been estimated, gastroenteritis is a major cause of morbidity and mortality, worldwide, both in children under 5 years old and in the general population [14,15]. Salmonellosis constitutes an endemo-epidemic disease in Benin. For instance, in the Departmental hospital of Borgou, about 5.4% of all hospitalized cases are due to salmonellosis [16].

A recent study estimated that 93.8 million cases of gastroenteritis due to *Salmonella* species occur globally each year, with 155,000 deaths and out of these, 80.3 million cases are foodborne [17].

*Salmonella* spp are also responsible for typhoid in human in which an estimated 12-33 million cases of typhoid fever occurs globally each year and mortality rate of 10% to 30% reported in Asia and Africa respectively each year [3]. Specific *Salmonella* spp which are responsible for typhoid in humans are *Salmonella typhi* and *Salmonella paratyphi* A and B [2,3]. Similarly, sources of *Salmonella* spp in fish and aquatic environment are attributed to human activities [4]. Water bodies carry animals, plants and human wastes from point and non-point sources and channel to the lake via rivers. This creates a favorable environment for bacterial growth [18].

## Methodology

A systematic online search was performed where by key-words such as “*Salmonellae*”, “Salmonellosis Benin”, “non-typhoidal salmonellosis”, “Medicinal plants Benin” and “traditional plants Benin” were entered in PubMed database, Google Scholar and [www.google.bj](http://www.google.bj). Obtained articles were included based on the reliability of their source, the study area (basically Benin and Africa) and the topic.

## Results

### Virulences and molecular characteristics of *Salmonella* spp

*Salmonellae* are facultative intracellular pathogens that can survive within host macrophages [19]. Unlike typhoidal *Salmonella*, which have the ability to evade the immune system, non-typhoidal *Salmonellae* tend to induce a localized inflammatory response in immunocompetent individuals, provoking a large influx of polymorphonuclear leukocytes to the intestinal lumen [20]. They can also colonize small and large intestinal mucosa thus facilitating prolonged periods of shedding [20].

Host factors predisposing to severe non-typhoidal *Salmonellae* infection include reduced gastric acidity, impaired cell mediated and humoral immunity, and impaired phagocytic function [20,21]. *Salmonellae* are unable to survive at a gastric pH less than 2.5 [22]. This is especially relevant to neonates where the combination of

relative achlorhydria and frequent milk feeds may contribute to their increased risk of non-typhoidal *Salmonellae* bacteremia [23].

T-cell immunity is important in controlling *Salmonella* as evidenced by increased susceptibility to invasive Non-typhoidal *Salmonella* in HIV-infection and with corticosteroid use [24]. Children with congenital defects in humoral immunity including X-linked agammaglobulinaemia and common variable immunodeficiency are also reported to have increased risk of persistent diarrhea and invasive disease [20]. Impaired phagocytic function seen in chronic granulomatous disease, haemoglobinopathies and malaria similarly increase the risk of invasive Non-typhoidal *Salmonellae* infection [20]. In addition, co-infection with *Schistosoma* has been reported to cause prolonged and severe illness due to altered macrophage function and replication and survival of *Salmonella* within the parasite [25]. Furthermore, in cattle, the infection with *S. typhimurium* results in an acute neutrophilic inflammatory response that is associated with the upregulation of CXC chemokines, IL-1 $\beta$ , IL-1Ra, and IL-4 [26].

Genome sizes of *Salmonellae* vary among serovars with ranges from 4460 to 4857 kb [7,27]. Characterized *Salmonella enteritidis* from poultry and reported that isolates were positive for various virulence genes mostly found in *S. enterica* such as *spvB*, *spiA*, *pagC*, *msgA*, *invA*, *sipB*, *prgH*, *spaN*, *orgA*, *tolC*, *iroN*, *sitC*, *IpfC*, *sifA*, *sopB*, and *pefA*. They carried a typical 58 kb plasmid, type Inc/FIIA. Some clinical isolates carried small plasmids with 3.8, 6, 7.6 and 11.5 kb whereas others carried plasmids, with sizes 36 and 38 kb, types IncL/M and IncN, and 81 kb plasmid, type IncI. A comparison of the genomes of several sequenced enteric bacteria including *Salmonellae* highlights some important common traits. All have a single chromosome, normally 4.3–5.0 Mb in size [28,29].

Different strains also harbor extra chromosomal DNA in the form of plasmids. Plasmids often carry genes associated with virulence or antibiotic resistance and can be considered to be a rapidly evolving gene pool. Comparison of the chromosomes of *Salmonellae* identifies a common set of so called “core genes” that are, in general, shared among enteric species [30]. These core genes can be regarded as genes that perform “household” functions associated with the common shared lifestyle of intestinal colonization and transmission (environmental survival). Such core genes play a role in central metabolism or polysaccharide biosynthesis or encode common structural proteins. The genomes of *Salmonella* spp. as for many other enteric bacteria are under intensive selective pressure because of factors that include competition within the normal flora, coping with fluctuating nutrient sources in the host and the environment, and pressure from the host immune system [31].

### Antibiotics resistance pattern of *Salmonella* spp.

The emergence of antibiotic resistant bacteria is a serious global problem which has been classified by World Health Organisation (WHO) as an important aspect in public health [32]. Furthermore, the World Organisation for Animal Health (OIE) and the Food and Agriculture Organisation (FAO) recognise the spread of multiple antimicrobial resistant pathogenic bacteria as a growing threat to human and animal health globally [33]. The spread of antimicrobial resistance in non-typhoid *Salmonella* spp isolates in humans is attributed to the use of antimicrobial agents in food animal production [34,35]. The antibiotic resistant bacteria can be transmitted to human through water and food when they are contaminated with these bacteria and cause major threat to public health [36]. Resistant *Salmonella* strains are commonly found in food animal sources [37,5].

Mismanagement of antimicrobial agents for treatment in humans and animals and the use of growth promoters in livestock have promoted antimicrobial resistance in *Salmonellae* [5,38].

The occurrence of *Salmonella* serovars resistant to quinolones, fluoroquinolones, and third generation cephalosporins which are medically significant treatments has increased [39,40].

The serovars with greater resistance to antimicrobials are *Typhimurium* specific to ampicillin, chloramphenicol, streptomycin, sulfamethoxazole/sulfisoxazole, and tetracycline, as well as *Enteritidis* with resistance to nalidixic acid. Although *S. Enteritidis* is highly prevalent in human infections; it has lower antimicrobial resistance compared to other serovars. Antimicrobial resistance in *Salmonella* can be associated with horizontal transfer of antibiotic resistant genes characteristically found on mobile genetic elements among *Salmonella* strains and other *Enterobacteria* or by clonal spread of antimicrobial drug resistant serovars that are particularly effective in worldwide dissemination [41,42]. *Salmonella* Newport has been identified to harbor plasmids encoding ACSSuT and produces  $\beta$ -lactamase, which inactivates cephalosporins, providing resistance to ampicillin and chloramphenicol (AmpC) [43]. Antibiotic-resistant non-typhoid *Salmonella* are associated with increased treatment failure and risk of invasive disease [44]. Worldwide surveillance data has demonstrated an overall increase in antibiotic resistance among non-typhoid *Salmonella*, although significant geographical and serotype variability exist [5,6]. This increased resistance to antibiotics requires the research of alternative methods like natural products from the treatment of salmonellosis.

### Use of medicinal plants in the treatment of salmonellosis

With respect to the emergence of multi-drug resistant *Salmonellae*, alternative therapeutic methods like the use of natural products are ancient and effective methods. Several scientists around the world have researched this matter and came up with interesting results demonstrated the antimicrobial activity of *Cissus quadrangularis* and *Acacia polyacantha* in the treatment of salmonellosis in poultry and cattle gastrointestinal diseases from Benin [45]. Such results were actually attributed to the presence of several secondary metabolites such as saponins, catechic tannins, mucilages, and flavonoids, anthocyanins, reducing compounds, sterols and terpenes in these plants. Moreover, [46] concluded from an investigation among Beninese farmers that over 241 plant species are used in the treatment of 45 animal diseases and symptoms. They also pointed out that decoction and maceration were the most commonly used modes of preparation.

Furthermore, a previous study conducted by revealed that leaves of plants such as *Rytigynia canthioides*, *Securinega virosa*, *Dialium guineense*, *Pavetta corymbosa*, *Sansevieria liberica* and *Uvaria chamae*, have *in-vitro* antimicrobial effect on a number of bacteria and fungi including *Salmonella typhimurium* [47]. Various other authors have confirmed the antimicrobial properties of plants on bacterial infections mainly salmonellosis. The antibacterial effect of aqueous and ethanolic seed extracts of *Dacryodes edulis* was studied against bacterial species including *Salmonella typhi* [48]. Furthermore, *Terminalia glaucescens*, *Bersama abyssinica* ssp. paullinioides and *Abrus precatoriu* showed the most promising broad spectrum antibacterial properties inhibiting *Salmonella typhi* in the study of [49]. The use of medicinal plants in the treatment of salmonellosis has become more than compulsory nowadays especially with the new trend of antibiotic resistance and the effectiveness of the properties of these plants. There is therefore a need

to explore the vegetation of each country in order to come up with the most valuable medicinal plant species that can effectively replace chemical drugs.

### Conclusion

Out of this study it has been noticed that *Salmonella* species are a leading bacterial cause of acute gastroenteritis. Several situations give them Non-typhoidal *Salmonellae* virulence. He induces a localised inflammatory response in immunocompetent individuals, provoking a large influx of polymorphonuclear leukocytes to the intestinal lumen. Plasmids often carry genes associated with virulence or antibiotic resistance. Antimicrobial host factors predisposing to severe non-typhoidal *Salmonellae* infection include reduced gastric acidity. Resistance in *Salmonella* can be associated with horizontal transfer of antibiotic resistant genes, antibiotic-resistant non-typhoid *Salmonella* are also associated with increased treatment failure and risk of invasive disease

Various other authors have confirmed the antimicrobial properties of plants on bacterial infections mainly salmonellosis. There is therefore a need to explore the vegetation of each country in order to come up with the most valuable medicinal plant species that can effectively replace chemical drugs.

### Conflict of Interest

The authors declare that there is no conflict of interest regarding the publication of this article.

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