Clinical Microbiology: Open Access

Dougnon, et al., Clin Microbiol 2016, 5:3
DOI:10.4172/2327-5073.1000251

Review Article Open Access

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

Tamègnon Victorien Dougnon[1,2*], **Honoré Sourou Bankolé**[1], **Roch Christian Johnson**[2], **Gildas Houmanou**[1], **Muriel de Souza**[1], **Lamine Baba-Moussa**[3] **and Michel Boko**[2]

[1]*Laboratoire de Recherche en Biologie Appliquée (LARBA), Ecole Polytechnique d'Abomey-Calavi (EPAC), University of Abomey-Calavi, Benin*

[2]*Laboratoire d'Hygiène, Assainissement, Toxicologie et de Santé Environnementale, ex-Laboratoire de Toxicologie et de Santé Environnementale (HeCOTHES), Centre Interfacultaire de Formation et de Recherche en Environnement pour le Développement Durable (CIFRED), University of Abomey-Calavi, Benin*

[3]*Laboratoire de Biologie et de Typage Moléculaire en Microbiologie, Faculté des Sciences et Techniques, University of Abomey-Calavi, Benin*

[*]**Corresponding author:** Tamègnon Victorien Dougnon, Laboratoire de Recherche en Biologie Appliquée (LARBA), Ecole Polytechnique d'Abomey-Calavi (EPAC), University of Abomey-Calavi, Benin, E-Mail: victorien88@hotmail.com

Received date: May 03, 2016; **Accepted date:** June 25, 2016; **Published date:** June 30, 2016

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. 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.*

Citation: Dougnon TV, Bankolé HS, Johnson RC, Houmanou G, Souza MD, Baba-Moussa L, Boko M (2016) Review on the Problematic of Salmonellosis and Interests of Traditional Herbs in the Treatment. Clin Microbiol 5: 251. doi:10.4172/2327-5073.1000251

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 endemio-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. 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 leukoytes 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-1β, 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].

Antibiotiques 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, fluoroquinones, 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 β-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 canthioïdes, 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 salmonelloses. 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 salmonelloses 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 leukoytes to the intestinal lumen. Plasmids often carry genes associated with virulence or antibiotic resistance. Antimicrobia 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.

References

1. Onyango DM, Wandili S, Kakai R, Waindi EN (2009) Isolation of Salmonella and Shigella from fish harvested from the Winam Gulf of Lake Victoria, Kenya. J Infect Dev Ctries 3: 99-104.
2. Acha PN and Szyfres B (2003) Zoonoses and Communicable Diseases Common to Man And Animals Scientific And Technical Publication No. 580 3 Third Edition. Vol.1. Bacterioses and Mycoses. Pan American Health Organisation pp: 233-244 .
3. Gurakan GC, Aksoy C, Ogel ZB, Oren NG (2008) Differentiation of Salmonella typhimurium From Salmonella enteritidis And Other Salmonella Serotypes Using Random Amplified Polymorphic DNA Analysis. Poult Sci 87: 1068-1074
4. Su LH, Chiu CH, Chu C, Ou JT (2004) Antimicrobial Resistance in Nontyphoid Salmonella Serotypes: A Global Challenge. Clin Infect Dis 39: 546-551.
5. Parry CM, Threlfall EJ (2008) Antimicrobial resistance in typhoidal and nontyphoidal salmonellae. Curr Opin Infect Dis 21: 531-538.
6. Andino A, Hanning I (2015) Salmonella Enterica: Survival, Colonization, and Virulence Differences Among Serovars. E Scientific World Journal, Article ID 520179, 16 Pages.
7. Grimont PA, Weill FX (2007) Antigen Formulas of the Salmonella Serovars. WHO Collaborating Centre for Reference and Research on Salmonella. Institut Pasteur, 28 Rue Du Dr. Roux, 75724 Paris Cedex 15, France pp: 166.
8. Soumet C, Ermel G, Rose N, Rose V, Drouin G, et al. (1999) Evaluation Of Multiplex PCR Assay For Simultaneous Identification of Salmonella Spp. Salmonella enteritidis And Salmonella typhimurium From Environmental Swabs Of Poultry Houses. Letters In Applied Microbiology 28: 113-117.
9. Herikstad H, Motarjemi Y, Tauxe RV (2002) Salmonella surveillance: a global survey of public health serotyping. Epidemiol Infect 129: 1-8.
10. Raufu IA, Lawan FA, Bello HS, Musa AS, Ameh JA et al. (2014). Occurrence And Antimicrobial Susceptibility Profiles of Salmonella

Serovars From Fish In Maiduguri, Sub-Saharah, Nigeria. Egyptian Journal of Aquatic Research 40: 59-63.

11. Romich JA (2008). Understanding Zoonotic Diseases. Thomson Delmar. Learning, a Part of The Thomson Corporation, Canada.
12. Amini K, Salehi TZ, Nikbakht G, Ranjbar R, Amini J, et al. (2010). Molecular Detection Of Inva And Spv Virulence Genes in Salmonella enteritidis Isolated From Human And Animals In Iran. African Journal of Microbiology Research 4: 2202-2210.
13. Hassanein R, Ali SFH, El-Malek AMA, Moemen AM, Elsayh KI (2011). Detection and Identification Of Salmonella Species In Minced Beef And Chicken Meats By Using Multiplex PCR In Assiut City. Journal Of Veterinary World 4: 5-11.
14. Kosek M, Bern C, Guerrant RL (2003) The global burden of diarrhoeal disease, as estimated from studies published between 1992 and 2000. Bull World Health Organ 81: 197-204.
15. Scallan E, Majowicz SE, Hall G, Banerjee A, Bowman CL, et al. (2005) Prevalence of diarrhoea in the community in Australia, Canada, Ireland, and the United States. Int J Epidemiol 34: 454-460.
16. Dovonou AC, Adoukonou TA, Sanni A, Gandaho P (2011) Aspects Epidémiologique, Clinique, Thérapeutique et Evolutif Des Salmonelloses Majeures dans Ie Service de Médecine Interne du CHDU/Borgou Au Nord Du Bénin. Medecine D'afrique Noire 58: 527-532.
17. Majowicz SE, Musto J, Scallan E, Angulo FJ, Kirk M, et al. (2010) The Global Burden of Nontyphoidal Salmonella Gastroenteritis. Clin Infect Dis 50:882–889.
18. Olgunoglu I (2012) Salmonella in Fish And Fishery Products, Salmonella – A Dangerous Foodborne Pathogen, Dr. Barakat S M Mahmoud (Ed.), Intech, China
19. García-del Portillo F (2001) Salmonella intracellular proliferation: where, when and how? Microbes Infect 3: 1305-1311.
20. Dougan G, John V, Palmer S, Mastroeni P (2011) Immunity to salmonellosis. Immunol Rev 240: 196-210.
21. MacLennan CA, Gondwe EN, Msefula CL, Kingsley RA, Thomson NR, et al. (2008) The neglected role of antibody in protection against bacteremia caused by nontyphoidal strains of Salmonella in African children. J Clin Invest 118: 1553-1562.
22. Tennant SM, Hartland EL, Phumoonna T, Lyras D, Rood JI, et al. (2008) Influence of gastric acid on susceptibility to infection with ingested bacterial pathogens. Infect Immun 76: 639-645.
23. O'Ryan ML, Nataro JP, Cleary TG (2011) Microorganisms Responsible For Neonatal Diarrhea. In: Remington JS, Klein JO, Wilson CB, Nizet V, Maldonado Y (Eds). Remington: Infectious Diseases of The Fetus And Newborn, 7th Edn. Elsevier, Philadelphia, P. 359–418
24. Moir S, Fauci AS (2010) Immunology. Salmonella susceptibility. Science 328: 439-440.
25. Abruzzi A, Fried B (2011) Coinfection of Schistosoma (Trematoda) with bacteria, protozoa and helminths. Adv Parasitol 77: 1-85.
26. Santos RL, Zhang S, Tsolis RM, Umler AJ, Adams LG (2002) Morphologic and Molecular Characterization Of Salmonella typhimurium Infection In Neonatal Calves. Vet Pathol 39: 200-215.
27. Mezal EH, Sabol A, Khan MA, Ali N, Stefanova R, Khan AA (2014) Isolation and Molecular Characterization Of Salmonella enterica Serovar Enteritidis From Poultry House And Clinical Samples During 2010. Food Microbiol 38: 67-74.
28. Parkhill J, Dougan G, James KD, Thomson NR, Pickard D, et al (2001) The Complete Genome Sequence of A Multiple Drug Resistant Salmonella enterica Serovar Typhi CT18 Provides Insight Into The Evolution Of Host Restriction And Antibiotic Resistance. Nature 413: 848-53.
29. McClelland M, Sanderson KE, Clifton SW, Latreille P, Porwollik S, et al. (2004) Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of Salmonella enterica that cause typhoid. Nat Genet 36: 1268-1274.
30. Anjum MF, Marooney C, Fookes M, Baker S, Dougan G, et al. (2005) Identification of core and variable components of the Salmonella enterica subspecies I genome by microarray. Infect Immun 73: 7894-7905.
31. Baker S, Dougan G (2007) The genome of Salmonella enterica serovar Typhi. Clin Infect Dis 45 Suppl 1: S29-33.
32. Collard JM, Place S, Denis O, Rodriguez-Villalobos H, Vrints M, et al. (2007) Travel-Acquired Salmonellosis Due To Salmonella Kentucky Resistant To Ciprofloxacin, Ceftriaxone and Cotrimoxazole and Associated With Treatment Failure. J Antimicrob Chemother 60: 190-192.
33. OIE Terrestrial Manual (2012) Laboratory Methodologies For Bacterial Antimicrobial Susceptibility Testing Guideline 2.1
34. Angulo FJ, Johnson KR, Tauxe RV, Cohen ML (2000) Origins and Consequences Of Antimicrobial-Resistant Nontyphoidal Salmonella: Implications For The Use Of Fluoroquinolones In Food Animals. Microbiological Drug Resistance 6: 77-83
35. Threlfall EJ, Ward LR, Frost JA, Willshaw GA (2000) The emergence and spread of antibiotic resistance in food-borne bacteria. Int J Food Microbiol 62: 1-5.
36. Okeke IN, Klugman KP, Bhutta ZA, Duse AG, Jenkins P, et al. (2005) Antimicrobial resistance in developing countries. Part II: strategies for containment. Lancet Infect Dis 5: 568-580.
37. Swartz MN (2002) Human diseases caused by foodborne pathogens of animal origin. Clin Infect Dis 34 Suppl 3: S111-122.
38. Hur J, Jawale C, Lee JH (2012) Antimicrobial Resistance of Salmonella Isolated From food Animals: A Review. Food Research International 45: 819-830.
39. Rajashekara G, Haverly E, Halvorson DA, Ferris KE, Lauer DC, et al. (2000) Multidrug-resistant Salmonella typhimurium DT104 in poultry. J Food Prot 63: 155-161.
40. Davis MA, Hancock DD, Besser TE (2002) Multiresistant Clones Of Salmonella enterica: The Importance of Dissemination. J Lab Clin Med 140: 135–141.
41. Alcaine SD, Warnick LD, Wiedmann M (2007) Antimicrobial resistance in nontyphoidal Salmonella. J Food Prot 70: 780-790.
42. Mather AE, Reid SW, Maskell DJ, Parkhill J, Fookes MC, et al. (2013) Distinguishable Epidemics Of Multidrug-Resistant Salmonella typhimurium DT104 In Different Hosts. Science 341: 1514–1517.
43. Acheson D, Hohmann EL (2001) Nontyphoidal Salmonellosis. Clinical Infectious Diseases 32: 263-269.
44. Varma JK, Molbak K, Barrett TJ, Beebe JL, Jones TF et al. (2005) Antimicrobial–Resistant Nontyphoidal Salmonella is Associated With Excess Bloodstream Infections And Hospitalizations. J Infect Dis 191: 554–561.
45. Alain KY, Pascal ADC, Boniface Y, Paul TF, Alain AG, et al. (2015) Chemical Characterization and Biological Activities of Extracts from Two Plants (Cissus Quadrangularis and Acacia Polyacantha) used In Veterinary Medicine in Benin. Journal of Pharmacognosy and Phytochemistry 3: 91-96.
46. Dassou GH, Adomou AC, Yédomonhan H, Ogni AC, Tossou GM. et al. (2015) Flore Médicinale Utilisée Dans Le Traitement Des Maladies Et Symptômes Animaux Au Bénin. Journal of Animal &Plant Sciences 26: 4036-4057.
47. Tchibozo AD, De Souza C, Anani KT, Koumaglo K, Toukourou F, et al. (2001) Evaluation Des Activites Cytotoxique, Antivirale, Antibacterienne Et Antifongique De Six Plantes Medicinales Pharm. Mée/.Trad. AF Jool, Vou L, pp: 93-L05.
48. Omogbai BA, Eneh TO (2011) ANTIBACTERIAL ACTIVITY OF DACRYODES EDULIS SEED EXTRACTS ON FOOD-BORNE PATHOGENS. Journal of Pure And Applied Sciences 4: 17-21.
49. Bolou GEK, Bagré I, Ouattara K, Djaman AJ (2011) Evaluation of The Antibacterial Activity Of 14 Medicinal Plants in Côte d'Ivoire. Tropical Journal Of Pharmaceutical Research 10: 335-340.