total prevalence of 4.29% in Benue State. At the LGA level, Gboko and Katsina-Ala LGAs recorded the highest number of positive cases out of 70 sub samples. Here, there were four (4) cases each representing 22.2% of the positive cases and prevalence of 5.71%. Oju and Kwande LGAs had 3 (16.7%) cases each and prevalence of 4.29%. Makurdi and Otukpo recorded the least number of cases (2 cases each representing 11.1% of the positive cases) and prevalence of 2.89%. In the study area, prevalence of Salmonella infection did not depend on locations of sampling since no significant association was established between the two variables ($\chi 2 = 1.89$, $P > 0.05$).

Table : Prevalence of Salmonella Infections in ifferent ocations of Benue State

General Hospital	Sample size	No and Percentage of positive sample	Prevalence (%)
Gboko	70	4 (22.2%)	5.71
Makurdi	70	2 (11.1%)	2.86
Oju	70	3(16.7%)	4.29
Adikpo	70	3(16.7%)	4.29
Katsina-Ala	70	4(22.2%)	5.71
Otukpo	70	2 (11.1%)	2.86
Total	420	18	4.29

$\chi 2$ (5)(location and prevalence) = 1.89, P= 0.863($P > 0.05$)

As given in table 4, occurrence of Salmonella infection was caused by two species: S.enterica and S.bongori. The latter had 5.6% occurrence with prevalence of 0.24% while the former was the dominant type with 94.4% occurrence and prevalence of 4.05%. Hence, occurrence of Salmonella infection was significantly tied to species type ($\chi 2 = 78.85$, $P < 0.05$)

Prevalence of Salmonella Infections based on Species Type in Benue State.

Salmonella species	Frequency and Percentage Occurrence	Prevalence (%)
S.enterica	17 (94.4%)	4.05
S.bongori	1 (5.6%)	0.24
Total	18	4.29

There were 4 distinct serovars of S.enterica and one from S.bongori, totaling eight different groups of Salmonella pathogens (table 5). S.entericaTyphimurium was the highest with 6 cases (33.33%) and prevalence of 1.43% followed by S.enterica Enteritidis with 4 cases (22.22%) and prevalence of 0.95%. Other serovars had <0.5% prevalence. S.entericaTyphi and S.enterica Heidelberg had 2 cases each while the remaining four (S.enterica Agona, S.enterica Paratyphi B, S.enterica Huaian and S.bongori) had a lone case each. Significant association was established between occurrence of Salmonella infection and causative serovars ($\chi 2 = 57.93$, $P < 0.05$).

Table 5: Prevalence of Salmonella Infections

Salmonella serovars	Frequency and Percentage Occurrence	Prevalence %
S.enterica Agona	1 (5.56%)	0.24
S.enterica Paratyphi B	1 (5.56%)	0.24
S.enterica Heidelberg	2 (11.1%)	0.48
S.enterica Typhi	2 (11.1%)	0.48
S.enterica Typhimurium	6 (33.33%)	1.43
S.enterica Enteritidis	4 (22.22%)	0.95

S.enterica Huaian	1 (5.56%)	0.24
S.bongori	1 (5.56%)	0.24
Total	18 (100%)	4.29

Based on serovars relationships among 18 Salmonella strains identified using plasmid gene sequencing data. Dendrogram formed 2 main clusters (numbered 36 and 81) and 2 divergent strains. The first sub cluster of main cluster (numbered 57) comprised four strains isolated from different locations: S.entericaHeidelberg-MG663473.1 sourced from Gboko, S.entericaTyphimurium-JQ228518.1 sourced from Katsina-Ala, S.enterica Typhimurium-CP014981.1 sourced from Makurdi and S.enterica Typhimurium-CP023166.1 sourced from Kwande. Male and female patients were equally represented. All age groups were equally represented (18, 35, 45 and 50 years old patients respectively). However, 75% of strains in this group was of the Typhimurium serovars. In this group, S.entericaTyphimurium-CP023166.1 sourced from Kwande was a unique strain that showed wider genetic variability but closely related to the check strain (S.bongori strain KU060291.1). The second sub cluster of a main (numbered 98) also consisted of 3 strains all of different serovars of S.enterica and one strain of another species. They are: S.entericaParatyphi B-JQ694526.1; S.enterica Heidelberg-CP019176.1; S.enterica Typhimurium-CP024619.1 and S.bongori-FR877557.1. The latter belongs to the same group with Paratyphi serovar and even closely related with Paratyphi B strain MF772492.1 used as a check.

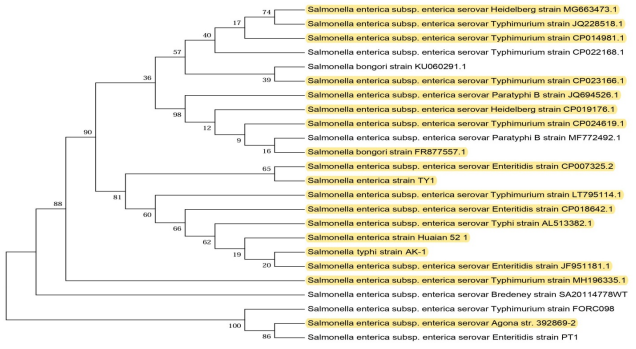

Figure 1: Phylogenetic Construction of Salmonella strains from Plasmid Gene Sequencing.

The second main cluster (numbered 81) comprised 8 strains belonging to 4 Enteritidis, 2 Typhi, 1 Huaian and 1 Typhimurium cutting across all locations except Gboko. Within this group, 4 strains showed wider relationships with other members and they were all of different serovars while Typhimurium strains were either closely clustered to themselves or to the Typhi strain regardless of the sex status of the infected patients. From the dendrogram, S.entericaTyphimurium-MH196335.1 was a divergent strain identified It diverged from the source of the main clusters (88) bearing no close relationship with any existing check strain. It was isolated from a 20 year old female patient in Adikpo General Hospital. The most unique of all the 18 strains identified was the S. enterica serovar Agona strain 392869-2 isolated from a 50 year old male patient in Gboko General Hospital. It bore a close relationship with a known check Enteritidis strain. The bands made up of 23,130 base pair (Figure 2).

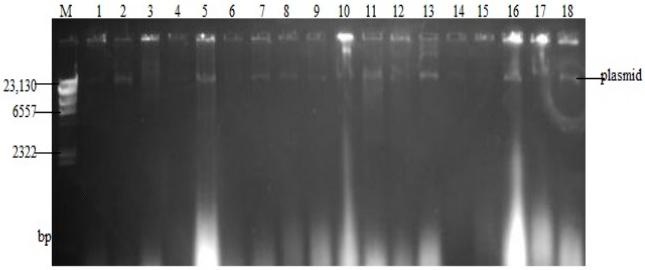

Figure 2: Amplified gel image of Plasmids from Salmonella strains (23,130bp)

- 1=S.entericaAgona-392869-2
- 2=S.entericaParatyphi B-JQ694526.1
- 3=S.entericaHeidelberg-MG663473.1
- 4=S.entericaHeidelberg-CP019176.1
- 5=S.entericaTyphi-AK-1
- 6=S.entericaTyphimurium-CP014981.1
- 7=S.entericaEnteritidis-CP007325.2
- 8=S.entericaTyphi-AL513382.1
- 9=S.entericaTyphimurium-CP024619.1
- 10=S.entericaTyphimurium-MH196335.1
- 11=S.entericaTyphimurium-CP023166.1
- 12=S.entericaEnteritidis-JF951181.1
- 13=S.entericaHuaian-H52.1
- 14=S.bongori-FR877557.1
- 15=S.entericaTyphimurium-LT795114.1
- 16= S.entericaTyphimurium-JQ228518.1
- 17=S.entericaEnteritidis-TY1
- 18= S.entericaEnteritidis-CP018642.1

DISCUSSION

Salmonella species, isolated from patients in selected health facilities of Benue State, have been successfully characterized using both conventional and molecular approaches. Prevalence and serovar distribution in relation to demographic parameters have been determined. Coventionally, both cultural and biochemical methods of characterization yielded accurate preliminary identification at the generic level within the limit of their diagnostic resolutions. For instance, all the 18 Salmonella positive cases were congruent in both cultural and biochemical methods. They were also confirmed true in the molecular analysis. However, the molecular approach was more specific as sequencing data led to precise Salmonella identification at the

sub species level including serovars and strains consummating in the determination of phylogenetic relationship among them. Similar view was previously upheld among epidemiologists (39). Information obtained from plasmid profiling has given insight into the antibiotic susceptibility or resistance pattern of the serovars and the nature of the genes carried on such plasmids.

Based on the result, thetotal prevalence of Salmonella cases in Benue State was 4.29%. This is lower than the 5% permissible limits of the WHO (40). Previous studies on Salmonella had higher seroprevalence rates than what was found in this study. For instance, 42.4% Salmonella incidence was reported among University of Ilorin Students (7). Also, 40% prevalence was reported in Biu Bornu State (41). Adeshina et al. (18) found 9.3% prevalence among Federal College of Education students and 16.5% prevalence among Ahmadu Bello University students in Zaria.

Salmonella infection is highly prevalent in tropical regions and in populations that lack access to safe water and adequate sanitation (42, 22). These are the prevailing factors in the six studied locations. Thus, it is expected that prevalence rate is higher than the present finding possibly because the subjects were hospital patients attending the selected health care facilities. Other infected persons in each locality who did not attend hospitals within the time frame of this study might not have been captured. It is possible that those uncaptured infected persons decided to use alternative methods of treatments such as herbal therapy. This view aligns with the findings of Kosek et al. (43) where 70% of infected persons in rural communities preferred herbal method treating typhoid fever as a more potent remedy than the orthodox medicine. Thus, studies that focus on achieving total seroprevalence rate must capture not only hospital patients but also populations of those not attending hospitals in the rural areas or students' populations.

In spite of this, Gboko and Katsina-Ala recorded the highest number of positive cases and prevalence of 5.71% higher than the WHO permissible limits. However, all the six LGAs have equal chances of Salmonella infection unlike in most studies in Nigeria where the infection is location dependent (42, 44). Thus, predisposing factors highlighted are equally present in the six locations of the study area. For instance, all locations are facing the challenges of unsafe drinkable water, poor food handling among farmers or vendors and poor sanitary conditions. Poultry and other poultry products thought to be the foremost means of transmission of Salmonella (45, 46) are commonly seen. All locations have similar market structures where fruits and vegetables are sold in the open.

Two Salmonella species (S.enterica and S.bongori) are present in all samples but the dominant one is S.enterica accounting for 94% of cases. This result is consistent with previous findings globally (47, 48). According to Brenner et al. (4), S. enterica subsp. enterica is the subspecies of most concern because the strains within these serogroups areknown to cause 99 % of Salmonella infections in humans.

Accordimg to Raufu et al. (11), most enteric infections in humans are caused by more than one serovars of a given species, which may vary from country to country and over time. In the present work, seven distinct serovars of S. enterica together with a lone case of S, bongori have emerged. It suggests a huge diversity in the genomics and physiological adaptation of the microbe in the host. This has a huge implication in disease treatment and control because wider genetic make-up may widen the chances of multi drug resistance (MDR) and ability to develop different mechanisms for virulence. This view aligns with previous reports on salmonellosis as a bacterial infection caused by more than one Salmonella species with many subspecies and serotypes (8, 11). S. enterica, for example, is a pathogen that is currently divided into 2,587 serovars (2).

It is also likely that every serovar is pathologically distinct since there are evidences on the capability of every serovar to acclimate itself to the environment inside its host in a unique way (50). These adaptations are ascribed to copious virulence factors and other microbial physiognomies of a precise serovar which makes it survive in the host. This may account for why Salmonella originates a wide array of human diseases which include enteric fever, gastroenteritis and bacteremia. Similar observation was made in the work of Monteville and Mathew (51). It should be borne in mind that Salmonella may cause further intestinal infection like meningitis, osteomyelitis, pneumonia, colecystitis, peritonitis, pericarditis, vasculitis, pyelonephritis, endocarditis and chronic conditions like aseptic arthritis and Reiter's syndrome (52).

Apart from the epidemiological implication of diverse serotypes, the cost implications in the identity of broad spectrum of all the serovars affecting a given population is huge. This can only be consummated at the molecular level as consummated in this work thus changing the routine conventional method of diagnosis in public health, thus making treatment difficult. Serovar identification is an integral part of disease control because it determines the correct choice of antibiotics (6, 53). In this work, Salmonella infection depends on the type of serovar and it should be handled differently as such. Here, the predominant serovars are S. Typhimuriumand S. Enteritidis accounting for approximately 33% and 22% of the serovars respectively. S. Typhiand S. Heidelberg accounted for 11% each while S. Agona, S. Paratyphi B, S. Huaian and S.bongori accounted for approximately 6% each.

Though there might be slight variation in the composition of serovar types when compared with many studies, there is a unifying point of agreement, all reporting the predominance of S. Typhimurium and/or S. Enteritidis. From previous studies, the commonly reported serovars in some African countries include S. Enteritidis, S. Typhimurium, S. Concord and S. Isangi (54,55.). In the work of Fashae et al. (16) carried out in Ibadan South West Nigeria, S. Typhimurium and S. Enteritidis were the most predominant serovars among others such as S. Apapa, S. Dublin, S. Infantis, S. Jukestown, S. Monaschaui and S. Oritamerin. In Lagos, Akinyemi et al. (17) reported only S. Enteritidis from stools of children under five years. In Abuja, North Central Nigeria, three serovars: S. Zanziba, S. Brancaster and S. Enteritidis were recovered from children with acute gastroenteritis but the latter was the most dominant (56). Other

studies have also claimed that the major pathogenic serovars of Salmonella enterica that infect humans from a variety of different food products include the Enteritidis and Typhimurium serovars (57, 58 and 59).

Nevertheless, prevalence rate of each serovar is less than 5%. This result deviate from previous findings in Nigeria reporting higher prevalence rates based on serovar types. Some workers reported 45.0% prevalence of S.Typhi among other bacterial isolates in Northern parts of Nigeria (11). Also, Anejo-Okpobi et al. (37) published 27% for S. Paratyphi A, 25 % for S. Paratyphi B, 13.7% for S. Paratyphi C and 20% for S. Typhi among human subjects in Jos Plateau State, Nigeria. Umeh and Agbulu (20) reported 57.6% for S.Typhi, 26.3% for S. Paratyphi and 15% for the mixture of both serovars in Okpokwu Local Government Area of Benue State.

The total prevalence of Salmonella cases in Benue State was 18 (4.29%). Gboko and Katsina-Ala recorded the highest prevalence of 5.71% but all the six LGAs have equal chances of Salmonella infection. Two Salmonella species (S. enterica and S. bongori) and eight genetically diverse serovars were present in all samples but the dominant species one was S.enterica accounting for 94% of cases while the dominant serovars were S. Typhimurium and S. Enteritidis accounting for approximately 33% and 22% respectively. The use of Gene sequencing should be encouraged on all Salmonella isolates in future studies for precise strain identification.

REFERENCES

1. Feasey, Dougan, Kingsley, Hederman, R.S, Gordon et al.(2012) Invasive non-typhoidal Salmonella disease An emerging and neglected tropical disease in Africa Lancet (379)2489-2499.
2. Grimont, Weill, F.X. (2007) Antigenic Formulae of the Salmonella Serovars Edition World Health Organization Collaborating Centre Reference and Research on Salmonella Institut Pasteur, Paris, France.
3. Uzzau, Brown, Wallis, Rubino, Leori, Bernard, Casadesus, Olsen et al. (2000) Host adapted serotypes of Salmonella enterica Epidemiology of Infectious Diseases (2) 229-255.
4. Anyanwu A. L, Fasina, F. O, Ajayi, O. T, Rapu I, Fasina et al.(2010) Antibiotic Resistant Salmonella and Escherichia coli Isolated from Day-Old Chicks, Vom, Nigeria African Journal of Clinical and Experimental Microbiology (1) 129136.
5. Dong P, Zhu L, Mao Y, Liang R, Niu L, Zhang Y et al.(2014) Prevalence and profile of Salmonella from samples along the production line in Chinese beef processing plants Food Control 38 54–60.
6. World Health Organisation (2018) Typhoid Facts Sheet.
7. Udeze, A.O, Abdulrahman, F, Okonkolo (2010) Seroprevalence of Salmonella typhi and Salmonella paratyphi among the first year students of University of Ilorin Ilorin Nigeria Middle-EastJournal of Scientific Research (3) 257-262.
8. Lar, M, Omojevwe, Onah (2006) Mixed infections of Schistosoma and Salmonella in the Federal Capital Territory m Abuja Journal of Natural Sciences (10) 1119-1104.
9. Ohad, G, Erin, Guntram (2014) Same species different diseases how and why typhoidal and non typhoidal Salmonella enterica serovars differ PMC Frontier in Microbiology 5 391
10. Crump, J.A., Luby, Mintz (2004) The global burden of typhoid fever Bulletin of World Health Organisation 82 346-353.
11. Raufu, I, Bortolaia, V, Svendsen, C.A, Ameh, J.A, Ambali, A.G, Aarestrup et al.(2013) The first attempt of an active integrated laboratory-based Salmonella surveillance programme in the North-Eastern region of Nigeria Journal of Applied Microbiology 115 1059-1067.
12. Abdullahi, M, Olonitola, S. o, Umoh, V. J, Inabo, I. H et al. (2014) Antibacterial Resistance Profile and PCR Detection of Antibiotic Resistance Genes in Salmonella serovars Isolated from Blood Samples of Hospitalized Subjects in Kano NorthWest Nigeria British Microbiology Research Journal 3 245-256.
13. Kingsley, R.A, Msefula, C.L, Thomson, N.R, Kariuki, Holt, K.E et al. (2009) Epidemic multiple drug resistant Salmonella Typhimurium causing invasive disease in sub-Saharan Africa have a distinct genotype Genome Research 19 2279–2287.
14. Agada, G. O. A, Abdullahi, I. O, Aminu, M, Odugbo, M, Chollom, S. C, Kumbish, P. R, Okwori, A. E. J et al.(2014) Prevalence and Antibiotic Resistance Profile of Salmonella Isolates from Commercial Poultry and Poultry Farm-handlers in Jos Plateau State Nigeria British Microbiology Research Journal 4 462-479.
15. Anyanwu A. L, Fasina, F. O, Ajayi, O. T, Rapu I,Fasina, M. M et al. (2010) Antibiotic Resistant Salmonella Escherichia coli Isolated from Day-Old Chicks Vom Nigeria African Journal of Clinical and Experimental Microbiology 1 129136.
16. Fashae, K., Ogunsola, F, Aarestrup, F.M, Hendriksen, R.S et al. (2010) Antimicrobial susceptibility and serovars of Salmonella from chickens and humans in Ibadan Nigeria.Journal of Infectious Disease in Developing Countries 8 484-494.
17. Akinyemi, K.O, Phillip, W, Beyer, w, Bohm, R et al.(2007) In-vitro antimicrobial susceptibility Patterns of Salmonella enterica serovars and emergence of Salmonella phage type DT071 in a suspected community-associated outbreak in Lagos Nigeria Journal of Infection in Developing Countries 1 48-54.
18. Adeshina, G, Osuagwu, N, Okeke, C, Ehinmidu, J, Bolaji, et al. (2009) Prevalence and Susceptibility of Salmonella Typhi and Salmonella Paratyphi in Zaria Nigeria International Journal of Health Research 4 353-369.
19. Abdullahi, M, Olonitola, S. O, Umoh, V. J, Inabo, I. H et al. (2014) Antibacterial Resistance Profile and PCR Detection of Antibiotic Resistance Genes in Salmonella serovars Isolated from Blood Samples of Hospitalized Subjects in Kano, NorthWest, Nigeria. British Microbiology Research Journal, 3 245-256.
20. Umeh, E, Agbulu, C (2009) Distribution pattern of salmonella typhoidal serotypes in Benue State The International Journal of epidemiology 1 1-7.
21. Njunda, A.L, Oyerinde, J.P (1996) Salmonella typhi infection in Schistosoma infected mice. West Africa Journal of Medicine 1 2430.
22. Centre for Disease Control (CDC) (2008) U.S. Department of Health & Human Services.
23. Scherer, C. A, Miller, S. I. (2001) Molecular pathogenesis of Salmonellae In Principles of Bacterial Pathogenesis Principles of Bacterial Pathogenesis Groisman E. A. Academic Press United States of America 265-316.

24. Talabi, H. A (1994) Medical aspects of typhoid fever in Nigeria Nigerian Postgraduate Medical Journal 1 51-56.

25. Akinyemi, K. O, Smith, S. I, Oyefolu, A. O, Coker, A. O et al.(2005) Multidrug resistance in

26. Salmonella enterica serovar Typhi isolated from patients with typhoid fever complications in Lagos Nigeria Public Health 119 321-327.

27. Food and Agricultural Organization (FAO) (2015) FAOSTAT.

28. Amenu, D. (2014) Antimicrobial Resistance for Enteric Pathogens isolated from acute gastroenteritis patients and Antibiotic Resistance Review of Science Technology 16 709-715.

29. Fagbamila, I, Kabir, J, Abdu, P , Omeiza, G, Ankeli, P. et al. (2010) Antimicrobial screening of commercial eggs and determination of Tetracycline residue using two microbiological methods International Journal of Poultry Science 9 959-962.

30. Ao, T.T, Feasey, N.A , Gordon, M.A , Keddy, K.H , Angulo, F.J. Crump, J.A et al. (2010) Global burden of invasive nontyphoidal Salmonella disease. Emerging Trend in Infectious Disease.

31. Mamman, P.H , Kazeem, H.M, Raji, M.A, Nok, A.J. Kwaga J K P et al. (2014) Isolation and characterization of Salmonella Gallinarum from outbreaks of fowl typhoid in Kaduna State, Nigeria International Journal of Public Health and Epidemiology 3 082-088.

32. Barbiour, E.K , Ayyash, DB, Alturkistni, W, Alyahiby, A, Yaghmoor, S, Iyer, A et al.(2015) Impact of sporadic reporting of poultry Salmonella serovars from selected developing countries Journal of Infectious Diseases 9 1-7.

33. Muhammad, M, Muhammad, L U, Ambali, A.G., Mani, A.U, Azard, Barco et al. (2010) Prevalence of Salmonella associated with chick mortality at hatching and their susceptibility to antimicrobial agents Veterinary Microbiology 140 131-135.

34. Orji, M.C, Onuigbo, H, Mbata, T.I (2005) Serological survey of mycoplasmosis and pullorum disease in Plateau State of Nigeria InternationalJournal of Infectious Diseases 2 86-89.

35. Cheesebrough (2002) District Laboratory Practice in Tropical Countries Tropical Health Technology Publishers Great Britain 40-56.

36. Winn, W, Allen, S, Janda, W, Koneman, E, Procop, G , Schreckenberger et al. (2005) Koneman's Color Atlas and Textbook of Diagnostic Microbiology. 6th Edition. New York, USA: Lippincott Wilkins 165- 171.

37. Jinu, M , Agarwal, R.K , Sailo, B, Wani, M.A , Kumar, A , Dhama, Singh et al.(2014) Comparison of PCR and conventional cultural method for detection of Salmonella from poultryblood and faeces Asian Journal of Animal VeterinaryAdvances 9 690-701.

38. Anejo-Okpobi, J.A, Isa, S.E, Audu O, Fagbamila, I.O, Iornenge, J.C, Smith et al. (2016) Isolation and polymerase chain reaction detection of virulence invA gene in Salmonella spp from poultry farms in Jos NigeriaJournal of Medical Microbiology in the Tropics 18 98-102.

39. Hoffmann, M, Muruvanda, T, Allard, M. W, Korlach, J, Roberts, R. J, Timme et al.(2013) Complete genome sequence of a multidrug-resistant Salmonella enterica Serovar Typhimurium var 5- strain isolated from chicken breast Genome Announcement 1 01068–13.

40. Arlet, G, Barrett, T.J, Butaye, P, Cloeckaert, A, Mulvey, M.R, a White, D.G et al.(2006)Salmonella resistant to extended-spectrum cephalosporins: prevalence and epidemiology Microbial infection 7 1945-54.

41. World Health Organisation (2017)Typhoid Facts Sheet.

42. Jacob, N.J, Cohen, M.B (2016) Update on Diarrhoea. Paediatrics in Review 37 8 313-322.

43. Abioye, J.O.K , Bulus, Adogo (2017) Prevalence of Salmonella Typhi infectin in Karu LGA of Nasarawa State Nigeria Journal of Advances in Microbiology 2 1-8.

44. Kosek, M., Bern, Guerrant (2003) The global burden of diarrhoeal disease, as estimated from studies published between 1992 and 2000 Bulletin of World Health.

45. Igwe, N.N, Agbo, E.A (2014) Incidence of co-infection of enteric Salmonella and Schistosoma in Kachia LGA of Kaduna State Nigeria International Journal of Tropical Medicine and Public Health 1 12-17.

46. EFSA (2013) Scientific Report of EFSA and ECDC The European Union summary report on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in 2011 EFSA Journal 11 3129.

47. Kaniz, F, Mahfuzur, R, Suvomoy, D, Mehadi, H.M et al. (2014) Comparative analysis of multi- drug resistance pattern of Salmonella spp. isolated from chicken faeces and poultry meat in Dhaka city of Banghladash Journal of Pharmacy and Biological Sciences 9 147-149.

48. Amber, H, Trevor, T,Hye, J.S, Florian (2006) Interaction between Salmonella and Schistosomiasis A Review PLoS Pathogens 12 1005928.

49. Hsiao, A, Toy, T, Seo, H.J, Marks, F et al.(2016) Interaction between Salmonella and Schistosomiasis A review PLos Pathology 2 1005928.

50. Brenner, F. W, Villar, R.G, Angulo, F. J, Tauxe, R.V, Swaminathan, B et al.(2000) Salmonella nomenclature Journal of Clinical Microbiolology 38 2465-2467.

51. Thiennimitr, P, Winter, S. E, Winter, M. G, Xavier, M. N, Tolstikov V,Huseby, D. L et al.(2011) Intestinal inflammation allows Salmonella to use ethanolamine to compete with the microbiota Proceding of National Academy of Science 108 17480–17485.

52. Monteville, T, Matthews, K (2008) Salmonella species In Food Microbiology ASM Press 97-112.

53. Andino, A,Hanning, I (2015) Salmonella enterica Survival colonization and virulence differences among serovars Science World Journal 52 1 7-9.

54. Asrat, D (2008). Shigella and Salmonella serogroups and antibiotic susceptibility patterns in Ethiopia East Mediterranean Health Journal 14 760-767.

55. Ajiboye, R. M, Solberg, O. D , Lee, B. M, Raphael, E , Debroy, C, Riley, L. W et al. (2009) Global spread of mobile antimicrobial drug resistance determinants in human and animal Escherichia coli and Salmonella strains causing community-acquired infections Clinical Infectious Diseases 49 365–371.

56. Hyeon, J.Y, Chon, J.W, Hwang, I.G, Kwak, H.S, Kim, M.S, Kim, S.K, Choi, I.S, Song, C.S, Park, C, Seo, K.H et al. (2011) Prevalence antibiotic resistance and molecular characterization of Salmonella serovars in retail meat products. Journal of Food Protocol 74 161–166.

57. Jones, F.T (2011) A review of practical Salmonella control measures in animal feed Journal of Applied Poultry Resources 20 102-113.

58. Kramarenko T, Nurmoja I, Karssin A, Meremae K, Horman A, Roasto M et al. (2014) The prevalence and serovar diversity of Salmonella in various food products in Estonia. Food Control 42 43–47.

59. Yang, X., Huang, J, Wu, Q, Zhang, J, Liu, S, Guo, W et al.(2016) Prevalence, antimicrobial resistance and genetic diversity of Salmonella isolated from retail ready-to-eat foods in China. Food Control 60 50–56.

60. Ed-dra A, Filali F. R, Karraouan B, El-Allaoui, A, Aboulkacem A, Bouchrif, B et al.(2017) Prevalence molecular and antimicrobial resistance of Salmonella isolated from sausages in Meknes Morocco Microbial Pathogens 105 340–345.