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RESEARCH ARTICLE

EPIDEMIOLOGY, DIVERSITY AND RESISTANCE TO ANTIBIOTICS IN *SALMONELLA* STRAINS ISOLATED FROM HUMAN IN TWO CITIES OF NIGER REPUBLIC

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ABSTRACT

In sub-Saharan Africa, *Salmonella* cause of acute gastroenteritis and invasive disease. The aim of this study was to assessthe diversity the distribution and antibiogram profile of *Salmonella* isolates in two cities of Niger. *Salmonella* strains isolated from patients duringthe period 2015-2016 were biotyped using Api20E and serotyped withspecific antisera. All strains were subjected to a set of 18 antibiotics to study their antibiogram, using the Baeur–Kirby disk diffusion method.Biochemical analysis revealed ten (10) phenotypic clusters. Serotyping resulted intoseventeen (17) different serotypes with Paratyphi A as the most prevalent (14.75%) of all *Salmonella* strains followed by Paratyphi B (11.48%), Typhimurim (9.84%), Typhi (6.56%), Paratyphi C (3.28%), Poona (3.28%).The proportion of Paratyphi A in infants (< 5 years old) represented 50%.Overall, high resistance to ampicillin (49.06%), amoxicillin (47.06%), trimethoprime-sulfamethoxazol (45.60%); chloramphenicol (35.30%);colistin (20.75%) and amoxicillin + clavulanic acid (20.60%) was observed.This study showed the diversity of *Salmonella* biotypes, serotypes and antimicrobialssusceptibility.The level of the antimicrobial resistance in *Salmonella* in Niger is quite high. Therefore, there is an urgent need to establish a close monitoringof resistance in *Salmonella* in Niger to assist in recommendations on the use of antimicrobials in both human and animals.

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INTRODUCTION

Salmonellosis is a bacterial infection of both humans and animals caused by various strains of *Salmonella* species. The genus *Salmonella* contains 2579 different antigenic types (Patrick *et al.,* 2007). According to the most recent estimation of the World Health Organization approximately 21 million cases and 222 000 typhoid-related deaths occur annually worldwide (WHO 2007-2015; Trong *et al.,* 2015). Salmonellosis includes two types of infections: typhoid and paratyphoid fevers. Non-typhoidal *Salmonella* (NTS) species are important food borne pathogens with acute gastroenteritis being the most common clinical manifestation (Khawla *et al.,* 2017). It has been recently estimated that the relative proportion of bacteremia due to invasive *Salmonella* infections in Sub-Saharan Africa has increased dramatically (Crump 2014). Particularly as other major causes of bacteremia such as *Streptococcus pneumoniae* and *Haemophilus influenzaetype b* are decreasing with the implementation of targeted control through immunization programs (Lozano *et al.,* 2010;Murray *et al.,*2010). *Salmonella* epidemics fromhuman have been well described in Niger among children from 0 to 59 months in the region of Maradi (Typhimurimum) (Langendorf *et al.,* 2015) and more recently in Burkina faso (Paratyphi B) (Somda *et al.,* 2017). A total of 6.396 cases of gastroenteritis were reported in 2012by the Surveillance and Response to Epidemics Directorate (DSRE), Ministry of Public Healthin Niger. The specific mortality rate due to diarrheal diseases in 2012 is 5.14%.Furthermore, Harouna *et al.,* (2000), showed that 73% of peritonitis per perforation is atyphoid intestinal perforation. It is therefore important to understand the diversity of *Salmonella* species in the country, and their reaction to common antibiotics in order to implement efficient control and treatment strategies. This studywas carried out in only two cities of Niger, i.e Niamey and Maradi, where a microbiology laboratorywas available. The aims of this study was toassess theepidemiology, the phenotype and the antimicrobial susceptibility of strains of *Salmonella* isolated from patient suffering from Salmonellosis.

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MATERIALS AND METHODS

Sampling procedure

Human *Salmonella* strains were collected from three laboratories using general microbiology tools. The laboratories used were those of Hôpital National de Niamey (HNN) and Tsoho Labo (TsL) in the city of Niamey and the Hôpital Régional de Maradi (HRM) in the region of Maradi. The variables selected and used for the study were the patient age and sex, the date of the arrival of the sample, the type of sampling, the macroscopic appearance of stools and the culture results.

A total of 69 isolates of *Salmonella* from patients with stools cultures, blood cultures, puncture fluids and pus were collected during the period2015-2016.Within these 69 isolates, 56.52% (39/69) were from HNN; 33.33% (23/69)were from TSL and10.14% (7/69) were from HRM. All samples were processed at the Laboratoire Gestion et Valorisation de la Biodiversité au Sahel (GeVaBioS) of Faculty of Sciences and Technics of Université Abdou Moumouni (UAM) in Niamey for pathogens isolation and stored for further analysis at -30°C.

Microbiological analyses

Firsty, the *Salmonella* samples were placed on Mueller Hinton Agar and incubated at 37°C for 18–24h. The colonies were subjected to biochemical reactions using Enteric API 20E according to manufactures' instructions for further confirmation. The biochemical profiles obtained were transformed into a numerical profile i.e. a number which enables the easy transcription of all the results obtained for an organism and compared with the profiles listed in the Index. The corresponding 6 reactions are coded in the same manner, which gave a 9 figure numerical. In addition, serotyping was done by slide agglutination using *Salmonella* antisera (Bio-Rad. France) according to the Kauffmann-White classification scheme (Popoff 2004).

Finally, all isolates were tested for susceptibility to 18 different antimicrobial agents using the disk diffusion method on Mueller Hinton II agar (Bio-Rad France) following the European Committee on Antimicrobial Susceptibility Instructions (EUCAST) guidelines (EUCAST, 2013). The antimicrobial disks used were ampicillin: AMP (10µg); amoxicillin: AML(25µg); amoxicillin + clavulanic acid: AMC (20/10µg);ceftazidim: CAZ (30µg); céfotaxim: CTX :(30µg); ceftriaxon: CRO(30µg); céfépim: FEP : (30µg); chloramphenicol:C(30 µg); gentamicin: GM:(10µg); aztreonam: AZT(30µg); amikacin: AK(30µg); Trimethoprim-sulfamethoxazole : SXT(1.25/23.75µg); nalidixic acid: NA(30µg);colistin: COL(10µg) ; ciprofloxacin: CIP(5µg);imipenem: IPM(10µg).Inhibition diameters of the antibiotics were interpreted according to the EUCAST (EUCAST. 2013).

Data Analysis

XL-Stat 2010software was used to determinate the prevalence and to determine p-value of the various parameters (age, sex, type of sampling and serotypes). PCORD was used forCluster analysisand the relationships between isolated *Salmonella* strains. Minitab 16 was used to drawthebox plots.

RESULTS

Epidemiology

Figure 1 shows the monthly distribution of *Salmonella* isolates over the sampling period. The peak of *Salmonella* infections was found in Augusts (22.03%) which coincided with rainy season and February (15.25%) which coincided with cool season and no record was reported in Apriland June which coincided with hot and dry season in Niger. Regarding sex desegregated data, this study showed high prevalence of *Salmonella* from males 52.17 %(36/69) as compare tofemales28.99 % (20/69) while 18.84 %(13/69) of the samples were not labelled. The age segregated data revealed that 30.43% (21/69) of *Salmonella* were isolated from patients between 0-5years; 11.59 % (8/69) of patients from 6 to15 years; 10.14 % (7/69) of patients from16 to 25 years; 8.70 %(6/69) of patients from26 to35 years similar to the group from36 to 60years, while30.43 % (21/69) were not labelled (Table 1). The majority of strains 72.46% (50/69) were isolated from stools and 18. 84 % (13/69) are Unknown. The nature of the samples for the remaining8.70% (8/69) is shown in table 2. Table 2. Nature of *Salmonella* isolates from humans, by source of isolation

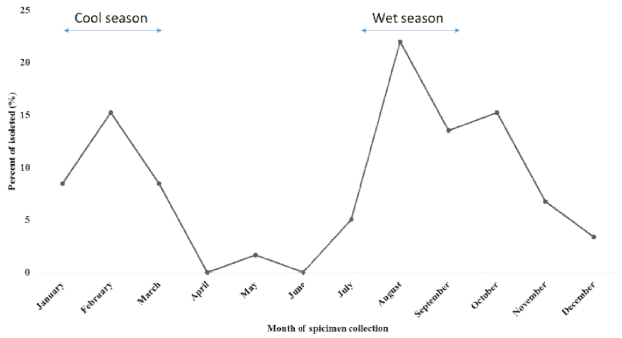


Figure 1. Percentage of reported *Salmonella* isolates by month of specimen collection in Niger during the period 2015-2016

Biochemical characterization

The characterization were performed on 61 isolated isolates out of from the total of 69 isolated, as the other 8 isolates didn't grow. The samples were identified as belonging to the genus *Salmonella* spp based on biochemical properties. Biochemical phenotyping data was used to analyze the diversity of the samples using Agglomerative Hierarchical Clustering (AHC) at a similarity level of 87.5%.All strains were grouped in ten phenotypic clusters (Figure X). The most frequently encountered biochemical phenotype (Cluster 1) showing the reading code for the determination of the genus: 6704752 represented 36.07% (22/61) of the isolated. It differs from Cluster 2accounting for 29.51% (18/61) by the ability of isolates to ferment inositol (INO+) showing the reading code for the determination of the genus: 6704552.Cluster 3 accounted for 13.11% (8/61) of the isolates and differed from those of other two clusters in their inability to ferment melibiose (MEL-) and showed the reading code for the determination of the genus: 6704712. Cluster 4 accounting for 6.56% (4/61) of the isolates differed from Cluster 3 in their inability to ferment inositol (INO-) and showed the reading code for the determination of the genus: 6704512. Cluster 5 and Cluster 10 accounting together for 8.20% (5/61) differs from the other cluster by the absence of the enzyme Arginine DiHydrolase (ADH).Cluster 6,7,8,9 contained only one isolates each.

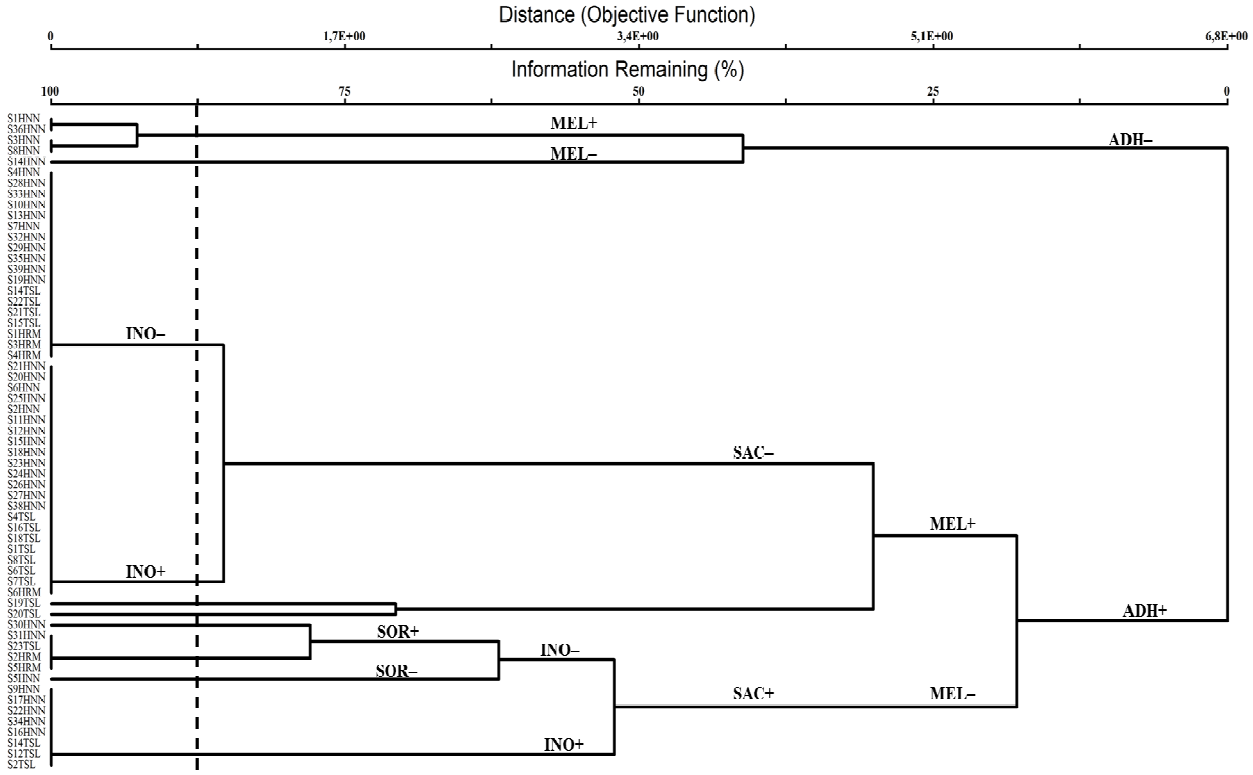
Table 1. *Salmonella* distribution by laboratory age and sex

		Age (years)						
Sex		0-5	6-15	16-25	26-35	36-60	Unknown	Total
Males	HNN	7	7	2	2	1	4	23
	TsL	1	1	1	2	-	3	8
	HMR	4	-	-	-	-	1	5
Sub-total		12	8	3	4	1	8	36 (52.17%)
Females	HNN	7	-	1	1	4	-	13
	TsL	-	-	3	1	1	-	5
	HMR	2	-	-	-	-	-	2
Sub-total		9	-	4	2	5	-	20(28.99%)
Unknown	HNN	-	-	-	-	-	3	3
	TsL	-	-	-	-	-	10	10
Sub-total		-	-	-	-	-	13	13(18.84%)
Total		21(30.43%)	8(11.60%)	7(10,14%)	6(8.7%)	6(8.7%)	21(30.43%)	69(100%)

-: means 0 case reported ; HNN : Hôpital National de Niamey, TsL: Tsoho Labo ; HRM : Hôpital Régional de Maradi,

Table 2.Nature of *Salmonella* isolates from humans, by source of isolation

Samples	Nature of samples	Frequence	Percentage (%)
Stools	Pasty	26	37,68
	Watery	10	14,49
	Loose	6	8,70
	Mucous	4	5,80
	Hard	2	2,90
	Semi-liquid	2	2,90
Sub-total		*50*	*72,46*
Remains isolats	Blood culture	4	5,80
	Puncture fluids	1	1,45
	Pus	1	1,45
Sub-total		*6*	*8,70*
Unknown		13	18,84
Total		69	100



Cluster 1: S21HNN, S20HNN, S6HNN, S25HNN, S2HNN, S11HNN, S12HNN, S15HNN, S18HNN, S23HNN, S24HNN, S26HNN, S27HNN,S38HNN, S4TSL, S16TSL, S18TSL, S1TSL, S8TSL, S6TSL, S7TSL, S6HRM. Cluster 2:S4HNN, S28HNN, S33HNN, S10HNN, S13HNN, S7HNN, S32HNN, S29HNN, S35HNN, S39HNN, S19HNN, S14TSL, S22TSL, S21TSL, S15TSL, S1HRM, S3HRM, S4HRM.Cluster 3: S9HN, S17HN, S22HN, S34HN, S16HN, S14TSL, S12TSL, S2TSL. Cluster 4:S30HNN, S31HNN, S23TSL, S2HRM, S5HRM.Cluster 5:S1HNN, S36HNN, S3HNN, S8HNN. Cluster 6: S19TSL. Cluster 7: S20TSL. Cluster 8: S5HNN.Cluster 9: S30HNN. Cluster 10: S14HNN.

Figure 2. Clustering dendrogram showing relationships between Salmonella strains isolated from human based on biochemical characteristics similarity profiles

Serotype determination

The serotype characterization was performed on 61 isolated, the same that were used for biochemical characterization. In total, 17 different serotypes were identified. Serotype Paratyphi A: 14.75% was the most prevalent of all *Salmonella* strains followed by Paratyphi B:11.48%, Typhimurim:9.84%, Typhi: 6.56%, Paratyphi C:3.28%,Poona: 3.28%. (Table 3) Table 3: Distribution of *Salmonella* Poly groups, Serogroups and Serotypes in Humans by laboratory

serotype Paratyphi A. Serotype Paratyphi B was detected primarily amongst all age groups (0 to 60 years old).

Sensitivity to antibiotics

The commonlyhigher resistance encountered were resistance to the family of penicillinA [ampicillin (49.06%), amoxicillin (47.06%), amoxicillin + clavulanic acid (20.60%)]; trimethoprim-sulfamethoxazol (45.60%); phenicol (chloramphenicol: (35.30%)) and Polymyxin (colistin (20.75%)) (Figure X).

Table 3. Distribution of *Salmonella* Poly groups, Serogroups and Serotypes in Humans by laboratory

			HNN	TSL	HRM	Total
Poly Group	Serogroups	Serotypes	Nber (%)	Nber (%)	Nber (%)	Nber (%)
OMA	Serogroup A	Paratyphi A	6(9.84)	3(4.92)	*(*)	9(14.75)
	Serogroup B	Paratyphi B	5(8.20)	2(3.28)	*(*)	7(11.48)
		Typhimurim	1(1.64)	4(6.56)	1(1.64)	6(9.84)
		Bredeney	1(1.64)	*(*)	*(*)	1(1.64)
		Chester	1(1.64)	*(*)	*(*)	1(1.64)
		Derby	*(*)	*(*)	1(1.64)	1(1.64)
		Haifa	1(1.64)	*(*)	*(*)	*(*)
		Stanley	1(1.64)	*(*)	*(*)	1(1.64)
		4.5/i÷ (monophasic)	1(1.64)	*(*)	*(*)	1(1.64)
		S.spp	4(6.56)	2(3.28)	*(*)	6(9.84)
	Serogroup D1	Typhi	2(3.28)	*(*)	2(3.28)	4(6.56)
	Serogroup E1	Muenster	1(1.64)	*(*)	*(*)	1(1.64)
	Serogroup E4	Senftenberg	1(1.64)	*(*)	*(*)	1(1.64)
		Vilvoorde	*(*)	1(1.64)	*(*)	1(1.64)
	Serogroup G	Bron	1(1.64)	*(*)	*(*)	1(1.64)
		Poona	2(3.28)	*(*)	*(*)	2(3.28)
OMB	Serogroup C	Paratyphi C	*(*)	1(1.64)	1(1.64)	2(3.28)
	Serogroup F	Marseille	1(1.64)	*(*)	*(*)	1(1.64)
OMC	ND	*S*.spp	*(*)	4(6.56)	1(1.64)	5(8.20)
OMA/OMB/OMC/OMD −			7(11.48)	3(4.92)	1(1.64)	11(18.03)
Total			36(59.02)	19(31.15)	6(9.84)	61(100)

− = negative,*(*) : 0(0)= 0 number and 0 percentage , ND:not determined, *S*.spp:*Salmonella*spp

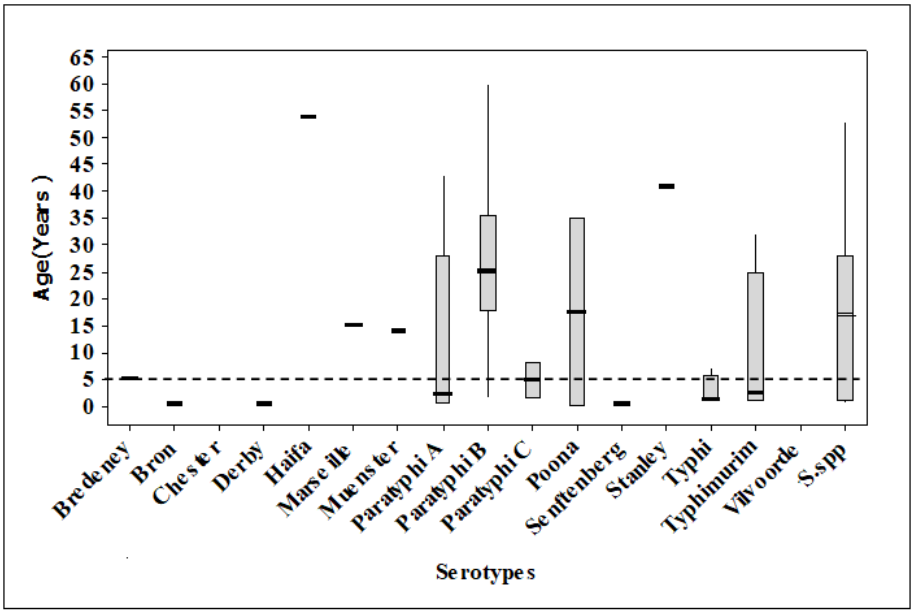


Figure 2. Age distribution for the prevailing serotypes.Box plots representing age according to serotype. Box plots provide distribution quartiles of 25%, 50%, 75% and 100%; Box length indicates interquartile ranges. Thick horizontal lines: median values; whiskers: range of values within 1.5 interquartile range

Serotype distribution in age groups

The distribution of serotypes was influenced by age (Figure 2). Those infected with serotype Paratyphi A were in majority under 5 years old. Serotypes Paratyphi C, Typhi and Typhimurium were encountered in the same age groups as

Lower frequency of resistance was observed in cephalosporins [ceftazidime (11.76%), cefotaxime (8.82%), Ceftriaxone (8.82%),cefepime (7.54%)]; Aminoside (Gentamicin: (8.82%)) and Quinolones [Nalidixique acid (8.82%),Ofloxacin (7.46%); Ciprofloxacin (5.88%)]. We observed 14.92% isolates with reduced sensitivity to amikacin.

Table 4. Frequency of antimicrobial resistance in *Salmonella*isolates from Human in 2015-2016

Antibiotics	Serotypes																	
	Paratyphi A n=9	Paratyphi B n=7	Typhimurim n=6	Typhi n=4	Senftenberg n=1	Marseille n=1	Derby n=1	Haifa n=1	4.5/i:- (monophasic) n=1	Poona n=2	Chester n=1	Stanley n=1	Bredeney n=1	Bron n=1	Muenster n=1	Paratyphi C n=2	Vilvoorde n=1	S.spp n=22
	Nber (%)	Nber (%)	Nber (%)	Nber (%)	Nber (%)	Nber (%)	Nber (%)	Nber (%)	Nber (%)	Nber (%)	Nber (%)	Nber (%)	Nber (%)	Nber (%)	Nber (%)	Nber (%)	Nber (%)	Nber (%)
AMP	3(33.33)	7(100)	3(50)	3(75)	1(100)	1(100)	1(100)	1(100)	*(*)	*(*)	1(100)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	6(27.27)
AML	5(55.56)	7(100)	4(66.67)	4(100)	1(100)	1(100)	1(100)	1(100)	1(100)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	8(36.36)
AMC	1(11.11)	2(28.57)	3(50)	4(100)	1(100)	*(*)	1(100)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	2(9.09)
CAZ	2(22.22)	*(*)	*(*)	*(*)	1(100)	1(100)	*(*)	*(*)	*(*)	1(50)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	3(13.64)
CTX	2(22.22)	*(*)	1(16.67)	*(*)	1(100)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	2(9.09)
CRO	3(33.33)	*(*)	*(*)	*(*)	1(100)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	2(9.09)
CFM	4(44.44)	*(*)	1(16.67)	*(*)	1(100)	1(100)	*(*)	*(*)	*(*)	1(50)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	3(13.64)
FEP	2(22.22)	*(*)	*(*)	*(*)	1(100)	1(100)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)
C	3(33.33)	7(100)	4(66.67)	2(50)	1(100)	*(*)	1(100)	1(100)	1(100)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	5(22.73)
GEN	2(22.22)	1(14.29)	*(*)	*(*)	1(100)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	2(9.09)
AK	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)
SXT	7(77.78)	6(85.71)	3(50)	4(100)	1(100)	*(*)	1(100)	1(100)	1(100)	1(50)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	7(31.82)
CST	1(11.11)	1(14.29)	1(16.67)	1(25)	*(*)	*(*)	*(*)	1(100)	*(*)	*(*)	*(*)	1(100)	*(*)	*(*)	*(*)	*(*)	*(*)	5(22.73)
NA	2(22.22)	1(14.29)	*(*)	*(*)	1(100)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	2(9.09)
PEF	2(22.22)	1(14.29)	1(16.67)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	1(4.55)
CIP	1(11.11)	*(*)	*(*)	*(*)	1(100)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	2(9.09)
AZT	3(33.33)	*(*)	*(*)	*(*)	1(100)	1(100)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	3(13.64)
IMP	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)	*(*)

AMP:ampicillin; AML:amoxicillin; AMC:amoxicillin + clavulanic acid; CAZ:ceftazidim; CTX: céfotaxim;CRO: ceftriaxon; FEP : céfépim; C: chloramphenicol; GM: gentamicin; AZT:aztreonam; AK :amikacin; SXT :Trimethoprim-sulfamethoxazole ;NA:nalidixic acid; COL:colistin; CIP :ciprofloxacin; IPM:imipenem. *(*) : 0(0)= 0 number and 0 percentage

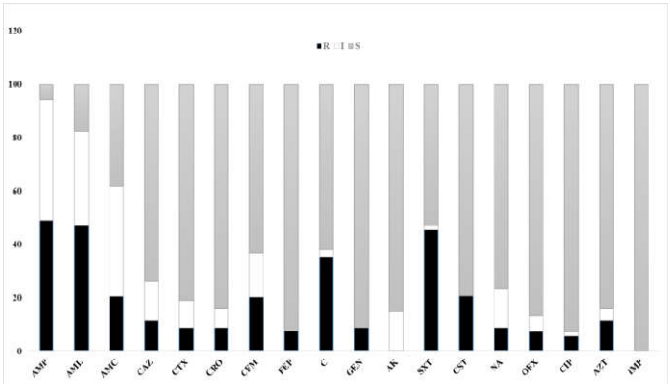
All the *Salmonella* isolates were susceptible to imipenem. (Figure 3) Among the different serotypes tested, high resistance was observed within Paratyphi Ato ampicillin (33.33%), amoxicillin (55.56%), and trimethoprim-sulfamethoxazol (77.78%). High resistance was alsorecordedwithin Paratyphi B with 100% for both ampicillinand amoxicillin and 85.71% for trimethoprim-sulfamethoxazol

DISCUSSION

In Niger, for the period 2015-2016, two peaks of *Salmonella* infections were recorded. One from August to November and between January to March. The first peak corresponds to the period of rainfall and the second peak corresponds to the cool period. Both periods correspond to the availability of many fresh produce from agriculture. These results were similar to those of Guiraud *et al.,* (2017) who found two peaks, one in September and the other in February in Burkina Faso. (Another study in Ghana found two samilar seasonality peaks (Labi *et al.,* 2014). This finding was confirmed by a study on the dynamics of *Salmonella* in market garden products where the prevalence is very high, whatever the season in Niger (Alio *et al.,* 2017b).

Contaminated irrigation and processed water were indentified as possible sources of *Salmonella* contamination in several fresh agricultural produce (Greene, *et al.,* 2008). Water is more likely to be polluted in the wet season because the rains may wash debris and littered garbage into wells and streams used as domestic sources of water(Verena *et al.,* 2002). During the sampling period, only 69 isolates of *Salmonella* from the different patient's samples were analyzed. Male were observed to have a higher infection rate than female (Table 1). This was similar to the findings of Langendorf *et al.,* 2015; Anchau *et al.,* 2016; and Somda *et al.,* 2017,who reported higher infection rate in male than in female.

The differences in the isolation rate of *Salmonella* between the two genders could be due to differences in level of hygiene, awareness occupation and behavioral factorssuch as more outdoor activities for males. The patients in the age group 0-5 years were found to have the highest *Salmonella* infection 30.43 %. This also agrees with earlier findings from two studies in Nigeria which reported higher infection rate in children (Abdullahi *et al.,* 2012; Anchau *et al.,* 2016). However our results are not in agreement with the findings of a study carried out in Burkina Faso, where reports indicated higher infection rate in young peoples between 12 and 23 years (Somda *et al.,* 2017).



S: Sensitive, I: Intermediate, R: Resistance. AMP: ampicillin; AML: amoxicillin; AMC: amoxicillin + clavulanic acid; CAZ: ceftazidim; CTX: céfotaxim; CRO: ceftriaxon; FEP: céfépim; C: chloramphenicol; GM: gentamicin; AZT: aztreonam; AK: amikacin; SXT :Trimethoprim-sulfamethoxazole ; NA: nalidixic acid; COL: colistin; CIP :ciprofloxacin; IPM: imipenem.

Figure 3. Antibiotic sensitivity profile of *Salmonella* isolates from Human 2015-2016

This could be linked to the under developed immune system of children which makes them more prone to *Salmonella* infection as few cells are required to initiate infection (Unhanand 1993). The low infective dose of *Salmonella* needed to initiate infection makes exposed children easily infected (Gendrel, 1998). The classification of isolates according to their rate of biochemical activity generated ten clusters (figure 2).They differ from each other by argi nine decarboxylation (ADH).Further study indicated that arginine decarboxylation showed the diversity by isolates and the vast majority of isolates showed the reduced susceptibility to antimicrobials tests (Lee *et al.*, 2003). In addition to arginine decarboxylation, the degradation of sugar Melibiose (MEL) also discriminated between the isolates. All the strains belonging to the four classes Cluster 1,Cluster 2, Cluster 6 and Cluster 7 were able to degrade the inositol sugar (INO +).A study reported that the *Salmonella* inositol polyphosphatase delivered to the host cell mediates actin cytoskeleton rearrangements and bacterial entry (Guy*et al.,*2001).

The biochemical profiles recorded with *Salmonella* of human origin concerning the metabolism of sugars inositol and sucrose are probably related indirectly to the invasive mechanism of *Salmonella*e (Eckmann *et al.,* 1997). The distribution of serotypes of *Salmonella* from isolates comprised the Paratyphi A: 14.75% followed by Paratyphi B: 11.48%, Typhimurim: 9.84%, Typhi: 6.56%, Paratyphi C: 3.28%, Poona 3.28%.This finding were not in agreement with those reported in Burkina Faso where Paratyphi B: 34% had higher frequency followed by Typhi: 21%, Paratyphi C: 14%, Paratyphi A: 10% (Somda *et al*., 2017). Similarly, these resultsdo not confirm those reported by Alio *et al*., (2017a) who recorded in a meta analyses,in West Africa the predominance of Typhimurium 20,91% followed by Enteritidis 16,59% and Corvallis 11,06%. Serotype distribution in this study presents a predominance of Paratyphi A in children under 5 years of age the same that Paratyphi C, Typhi, Typhimurium. The results of the study indicated that the collected strains were resistant to ampicillin, amoxicillin, amoxicillin + clavulanic acid, trimethoprim-sulfamethoxazol, phenicol and to a greater extent colistin as compared to other classes of antibiotics tested. In this study an high rates of resistance have been described in Paratyphi A, Paratyphi B and Senftenberg.

These classes of antibiotics are widely used in African countries because they are quite affordable and available in non-conventional structures and promoting a strong selection pressure at hospital community(Timbiné 2013). The beta-lactams are widely used in therapeutic environment in Africa especially to self-medication in non-conventional structures and usually used by non-professionals which increased the resistant rates reaching 100%.

Conclusion

Accurate serotype determination of *Salmonella* involved is a perquisite tovaccine introduction and epidemiological surveillance. Our study could serve as an updated national baseline serotype distribution of *Salmonella* in Niger. Over the study period (2015–2016),Paratyphi A was the most commonly identified serotype, possibly due to the unsystematic and extensive use of antimicrobials in animal and human. Overall, the level of antimicrobial resistance of *Salmonella* in Niger is very high. There is therefore an urgent need to reinforce the surveillance system of *Salmonella* antimicrobial resistance in Niger and update the recommendations on the use of antimicrobials in both human and animals.

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