Genomic diversity and antimicrobial resistance among non-typhoidal *Salmonella* associated with human disease in The Gambia

Authors:

Saffiatou Darboe[1], Richard S. Bradbury[2], Jody Phelan[3], Abdoulie Kanteh[1], Abdul-Khalie Muhammad[1], Archibald Worwui[1], Shangxin Yang[4], Davis Nwakanma[1], Blanca Perez-Sepulveda[5], Samuel Kariuki[6], Brenda Kwambana-Adams[1,7]* and Martin Antonio[1]*

***These authors contributed equally to this article**

Author affiliations

1. Medical Research Council Unit, The Gambia at London School of Hygiene and Tropical Medicine
2. Federation University, Melbourne, Australia
3. London School of Hygiene and Tropical Medicine, London, United Kingdom
4. University of California, Los Angeles, California, USA
5. University of Liverpool, United Kingdom
6. Kenyan Medical Research Institute, Nairobi, Kenya
7. University College London, London, United Kingdom

Corresponding author:

Saffiatou Darboe, Laboratory Services, Medical Research Council Unit The Gambia at London School of Hygiene and Tropical Medicine, P.O Box 273 Banjul, The Gambia; email: Saffiatou.Darboe@lshtm.ac.uk

Article summary line:

This study revealed high serovar diversity in non-typhoidal *Salmonella* serovars in The Gambia with *Salmonella* Typhimurim ST19 and *Salmonella* Enteritidis ST11 the most prevalent serovars causing bacteraemia. Serovars responsible for gastroenteritidiss were much more diverse. Importantly, high genetic diversity was noted for *Salmonella* Enteritidis with the presence of the virulent multidrug resistant *S.* Enteritidis West African clade present.

Running title:

Genetic diversity and antibiogram of non-typhoidal *Salmonella* in The Gambia

Key words:

Non-typhoidal *Salmonella* (NTS), invasive NTS (iNTS), *Salmonella* Typhimurium, *Salmonella* Enteritidis, The Gambia.

Abstract:

Non-typhoidal *Salmonella* associated with multidrug resistance cause invasive disease in sub-Saharan African. Specific lineages of serovars *S.* Typhimurium and *S.* Enteritidis are implicated. We characterised the genomic diversity of 100 clinical Non-typhoidal *Salmonella* collected from 93 patients in 2001 from the eastern and 2006 to 2018 in the western regions of The Gambia respectively. Phenotypic susceptibility applied Kirby Baur disk diffusion and whole genome sequencing utilized Illumina platforms. The predominant serovars were *S.* Typhimurium ST19 (31/100) and *S.* Enteritidis ST11 (18/100) restricted to invasive disease with the notable absence of *S.* Typhimurium ST313. Phylogenetic analysis performed in the context of 495 African strains from the European Nucleotide Archive confirmed the presence of the *S.* Enteritidis virulent epidemic invasive multidrug resistant West African clade. Multidrug resistance including chloramphenicol and azithromycin has emerged among the West African *S.* Enteritidis clade 7/9 (78%) with potential for spread, thus having important implications for patient management warranting systematic surveillance and epidemiologic investigations to inform control.

Data summary:

Sequences are deposited in the NCBI sequence reads archive (SRA) under BioProject ID:PRJEB38968. The genomic assemblies are available for download from the European Nucleotide Archive (ENA) **:** http://www.ebi.ac.uk/ena/data/view/. Accession numbers SAMEA6991082 to SAME6991180

Introduction:

Non-typhoidal *Salmonella* (NTS) serovars are a common cause of foodborne gastroenteritis but can also cause severe disseminated infections dependent on the pathogen's virulence and the host's immune status [1,2]. Globally, there are over 2,800 serovars, some of which are adapted to non-human hosts [3]. The global annual estimate of *Salmonella* gastroenteritis is 93.8 million illnesses with 155,000 deaths [4]. The highest mortality occurs in Africa which accounts for 4,100 deaths annually with an incidence of 320/100,000 population [4]. Most cases of *Salmonella* gastroenteritis in immunocompetent hosts are self-limiting and do not require antimicrobial therapy; however, infections in infants, the elderly and immunocompromised patients do require antimicrobial treatments such as ciprofloxacin, 3rd generation cephalosporins or azithromycin [5].

The clinical characteristics of non-typhoidal salmonellosis emerging in Africa represent a changing disease pattern, from gastroenteritis to invasive disease with a case fatality ratio of 20-25% [1,6–8]. Although NTS in diarrhoea is less well characterised in Africa, it may be predisposition to invasive disease. Invasive NTS (iNTS) disease, mainly bacteraemia. iNTS is globally estimated at 3.4 million illnesses annually, disproportionately affecting those in sub-Saharan Africa (sSA), with over 50% associated with HIV infection, malnutrition, recent malaria and children between 6 months to 3 years of age [6,8,9]. iNTS disease has a markedly different presentation, closer to enteric fever in its clinical form than typical NTS disease [8]. The predominant serovars responsible for invasive disease in sSA are specialised lineages of *Salmonella enterica* serovars Enteritidis and Typhimurium that are distinct from those circulating in other parts of the world [1,10]. Whole genome sequencing (WGS) has provided new insights into the host adapted signatures associated with pathogenicity and metabolism of these *S.* Typhimurium lineages and *S.* Enteritidis clades characterised by genomic degradation and accessory genome [1,11].

The closely related *S.* Typhimurium ST313 lineages I and II evolved independently around 52 and 35 years ago respectively with the acquisition of the chloramphenicol acetyltranferase (*cat)* resistance gene [7]. Both lineages have been shown to carry a *S.* Typhimurium virulence plasmid, commonly known as pSLT, which also encodes genes conferring resistance to common antimicrobials including tetracycline, sulfamethoxazole-trimethoprim and chloramphenicol [7,11]. In addition, two related, but phylogenetically different epidemic clades of *S.* Enteritidis ST11, the West African clade and the Central/Eastern African clade, characterised by the presence of chloramphenicol acetyl resistance genes *catA1* and *catA2*, respectively, plus the incomplete set of *tra* genes, emerged between 1933 and 1945 [1]. The utility of second-line antimicrobials such as fluoroquinolones, azithromycin and extended spectrum cephalosporins is limited in treating these emerging MDR strains [12].

In The Gambia, iNTS remains a leading cause of invasive diseases, [13] unlike *S.* Typhi which causes typhoid fever in many low and middle income countries (LMIC). We previously described regional serovar variation and emerging MDR in The Gambia [14,15]: *S.* Typhimurium was found to be more prevalent in the western region, while *S.* Enteritidis, including MDR strains, were found to be more prevalent in the eastern region. In this context, we performed whole-genome analysis of clinical NTS isolates to determine prevalent genotypes and antimicrobial resistance genes. The resulting analysis can be used to help guide clinical management and control of NTS diseases in The Gambia.

Methods and Materials:

Study setting and population

The study was conducted at the Medical Research Council Unit The Gambia at the London School of Hygiene and Tropical Medicine (MRCG @ LSHTM) using clinical NTS isolates from the eastern (Upper River Region) and western (West Coast Region and Greater Banjul Area) regions of The Gambia (Figure 1). The eastern region, located on the far east side of the river Gambia, is the commercial centre and a busy economic hub, with an estimated population of 200,000 people. It is an important transit point for merchandise and people going into eastern Senegal, Mali and Guinea Conakry. The western region is densely populated, with a population of over 1 million people including the capital city, Banjul (Figure 1) [16]. Malaria declined in recent years but remains endemic with peak transmission occurring from July to November [17]. Malnutrition remains a problem with the prevalence of underweight, stunting and wasting among children under 5 years old estimated at 16.4%, 25.0% and 4.3% respectively [18]; HIV prevalence among adults aged 15 – 49 years is estimated at 2.1% [19].

Sample collection, microbiological procedures and antimicrobial susceptibility testing

The study evaluated 100 clinical NTS from 93 patients admitted to hospital with suspected sepsis, gastroenteritis or other focal infections in the eastern and western regions of The Gambia (Table 1). Seven patients had multiple samples collected during the same infection episode (Table 2). Three patients had concurrent bacteraemia and gastroenteritis, two had bacteraemia with meningitis whilst two had bacteraemia with two sampling episodes. All NTS from the eastern region (20) were isolated in 2001 from 18 patients, and those from the western region (80) were isolated between 2006 to 2018 from 75 patients (Table 1). All isolates were stored in 15% (v/v) glycerol broth at -70^{o}C. The isolates were grown on MacConkey agar overnight at 37^{o}C in the Clinical Microbiology Laboratory. The laboratory is accredited to

Good Clinical Laboratory Practice (GCLP; 2010) and ISO15189 (2015) as previously described [14]. Antimicrobial susceptibility for amoxicillin-clavulanate, ampicillin, cefotaxime, cefoxitin, ceftazidime, ceftriaxone, cefuroxime, chloramphenicol, ciprofloxacin, gentamicin, nalidixic acid, sulfamethoxazole-trimethoprim and tetracycline, were tested on Mueller-Hinton agar (MHA) using the Kirby-Bauer disk diffusion method. Interpretation was done according to the 2017 Clinical Laboratory Standard Institute (CLSI) guidelines [20]. Antimicrobial agents were from BD Oxoid (Basingstoke, United Kingdom) and *Escherichia coli* (ATCC 25922) was used for quality control.

DNA extraction and whole genome sequencing

Genomic DNA was extracted and sequenced in two locations; the MRCG (n=33), and sample processing (n=67) at the University of Liverpool (UK) with DNA sequencing at the Earlham Institute (UK). The extraction protocol for the MRCG used the QIAamp DNA Mini kit (Qiagen, Germany) to extract the DNA from 1mL of an overnight culture grown in triple soya broth (TSB) from BD Oxoid (Basingstoke, United Kingdom) at 37^{o}C, according to manufacturer's instructions, and quantified using a Qubit fluorometer (ThermoFisher, Qubit dsDNA HS Assay). Libraries were prepared using the Nextera XT kit using the Illumina MiSeq system. The DNA extraction and sequencing of samples processed at the University of Liverpool were carried out using an optimised method for large-scale sequencing [21], including the bespoke LITE (Low Input, Transposase Enabled) pipeline for library construction, and Illumina HiSeq sequencing technology. Both sites used the 2x150 bp read protocol.

Genome assembly and *in silico* analysis

The quality of the raw reads was assessed using FASTQC [22] where on average, all reads had a quality Phred score (Qscore) above 30. Paired-end reads were trimmed using Trimommatic

[23] and assembled into contigs using SPades, with default settings [24]. *In silico* serotyping of the core genome MLST (cgMLST) and serovar was predicted using the *Salmonella in Silico* Typing resource (SISTR) platform [25]. eBurst Groups (eBGs) were assigned using the Enterobase platform which is based on the allelic identity that accounts for homologous recombination, defined by Achtman as closely related natural genetic clusters/populations of two or more sequence types connected by pair-wise identity or single locus variants [26].

Phylogenetic analysis

Assembled contigs were annotated using Prokka (v1.14.6). The pan-genome was determined using Roary (v3.13.0) [27], taking the GFF files from Prokka as input with default settings. The pan-genome was aligned using Mafft (v7.464) to generate a high-quality sequence alignment. The alignment was used to create a maximum likelihood phylogeny using IQ-TREE (v1.6.12). The phylogenetic tree was visualised and annotated using the interactive Tree Of Life (iTOL). ITOL annotations input files for the tree were generated using custom python scripts (https://github.com/jodyphelan/itol-config-generators). Antimicrobial resistance (AMR), plasmids and virulence genes were detected by ResFinder [28], PlasmidFinder [29] and virulence factor gene database (VFDB) with a minimum coverage and nucleotide identity of 90% as the cut-off. Publicly available data was downloaded from the European Nucleotide Archive (ENA) to compare the strains from this study against other African strains. All sequence reads from the African samples belonging to the taxid 149539 (NCBI:txid149539) were downloaded and assembled/annotated using the same methods as detailed above. The pangenome phylogeny was constructed using the same methods as outlined above.

Statistical analysis:

The independent variables were serovars and the dependent variable was disease category. The relationships between the serovar and disease were analysed using logistic regression with

176 measures of association expressed in odds ratios. No power calculations were performed and
177 an alpha value of 0.1 was considered statistically significant. All statistical analyses were
178 performed in Stata, Version 13.1 (StataCorp. 2013. Stata Statistical Software: Release 13.
179 College Station, TX: StataCorp LP.)

180 **Ethical Review and Approval**

181 The study received ethical approval from the Joint MRC/Gambia Government Ethics
182 Committee (SCC1498).

Results:

Isolate source, associated disease syndrome and regional serovars differences

One hundred isolates recovered from clinical samples from eastern (n=20) and western (n=80) regions of The Gambia were analyzed (Table 1). Isolates were recovered from patients of all ages, with a median age range of 5-14 years. Isolates from the eastern region were predominantly from invasive disease (17 blood and 2 CSF) with only 1 gastroenteritis (stool) source cases. Isolates from the western region were associated with invasive disease (48 blood and 1 CSF), gastroenteritis (25 stool), and other focal non-invasive infections (5 abscesses/pus and 1 urine) (Table 3). Overall, high serovar diversity was noted. *Salmonella* serovars other than *S.* Enteritidis, *S.* Typhimurium and *S.* Virchow were primarily responsible for gastroenteritis (17/26; 65.4%), whilst *S.* Typhimurium was the leading cause of invasive disease (Table 4). *S.* Typhimurium and *S.* Enteritidis were 5 times and twice as likely to cause invasive disease than gastroenteritis respectively.

Sequence types and eBurst groups

All *S.* Typhimurium were in eBG1 and assigned to a single sequence type, ST19 with one or two allelic variants (Table 5). All *S.* Enteritidis belonged to eBG4 assigned to ST11 and ST1925, including two isolates having single locus allelic variants. *S.* Virchow was in eBG9 and assigned to three different STs as follows: ST181, ST755 and ST841. The four *S.* Hull isolates belonged to eBG330 and assigned ST1996 with single locus variant. *S.* Stanleyville eBG79 (ST339), *S.* Poona eBG46 (ST308) and *S.* Give eBG67 all belonged to ST516.

AMR genes, AMR phenotypes, plasmid replicons and virulence genes

Antimicrobial resistance genes belonging to eight classes of antimicrobials were detected, plus a biocide tolerance genetic determinant. Interestingly, genes *aac(6')-Iaa_1* and *mdf(A)_1* encoding an aminoglycoside modifying enzyme and a multidrug transporter, respectively, were present in all strains, but did not have any detectable phenotypic effects on our isolates (Figure

208 2). Other AMR genes were harboured by 16/100 (16.0%) isolates and confer resistance to
209 aminoglycosides (*aph*_3_Ib and *aph*_6_Id; n=12), tetracyclines (*tet*_A and *tet*_B; n=4),
210 trimethoprim (*dfr*A14, *dfr*A7 and *dfr*A8; n=8), sulfamethoxazole (*sul2* and *sul1*; n=7),
211 ampicillin (*blaTEM*-1B; n=8), fosfomycin (*fos*A7_1; n=8), azithromycin (*mph*_A; n=3) and
212 chloramphenicol (*cat*A1_1; n=2) (Figure 2). Possession of three or more AMR genes was
213 found in 9/100 (9.0%) isolates, 7/9 (77.8%) of which were found in *S*. Enteritidis.

214 Phenotypic resistance was observed for tetracycline, ampicillin, sulfamethoxazole-
215 trimethoprim and chloramphenicol in 9/100 (9%) isolates, correlating with the presence of
216 resistance genes, except for streptomycin, fosfomycin and azthromycin that were not
217 phenotypically tested (Figure 2). The odds of resistance to ampicillin, sulfamethoxazole-
218 trimethoprim and tetracycline were 51, 20 and 25 times more likely for *S*. Enteritidis than all
219 other serovars combined (Table 6). No resistance to gentamicin was observed phenotypically
220 despite the presence of two aminoglycoside resistance genes (*aph_3_Ib* and *aph_6_Id)*, which
221 only confer resistance to streptomycin.

222 Nineteen different plasmid replicons were detected in 66/100 (66%) isolates; 7 isolates
223 harboured one plasmid replicon, 39 harboured two, 16 harboured three and 4 harboured four
224 plasmid replicons (Supplementary table 2). The most common plasmid types were *IncFII*
225 (n=55) and *IncFIB* (n=50), harboured by all *S*. Typhimurium and all but the two
226 chloramphenicol-resistant *S.* Enteritidis (Table 7). The *IncN_1* plasmid was associated with
227 MDR including azithromycin resistance and was only found in *S*. Enteritidis from the eastern
228 region (Figure 4a). The *Inc* plasmid is reported to be associated with beta-lactam, streptomycin
229 and sulphonamide resistance. Interestingly, the *IncI*1_Alpha was harboured by the two
230 chloramphenicol MDR *S.* Enteritidis strains from the western region and the susceptible strains
231 from the eastern region (Figure 4b). Notably, no plasmid replicons were detected in *S.*
232 Bradford, *S.* Hull, *S.* Stanleyville, *S.* Rubislaw, *S.* Vinohrady and 1,4,12,27:g,m:1,2 serovars.

A total of 115 virulence genes were found with notable absence of *entA, entB, entE, faeC, faeD, faeE, fepC, fepG* in all Gambian NTS serovars (Figure 3). We also identified virulence genes encoding toxins, fimbriae and flagella facilitate invasion, adhesion, type III secretion and survival within host, among other functions increasing bacterial virulence (Figure 3). The highest average number of virulence genes was seen for *S.* Typhimurium (mean: 111/115; 96.52%) with the notable absence of the *cdtB, ssPH1* and *shdA* genes. In contrast, the number of virulence genes *S. Enteritidis* isolates was smaller (mean: 105/115, 91%), with most isolates missing the *cdtB, gogB, grvA, shdA, sinH, slrP, sseK2* and *ssPH1* genes.

Phylogenetic analysis

The SNP analysis showed the isolates are clustered into respective serovars and geographic location (Figure 3). *S.* Typhimurium ST19 demonstrasted clonality whilst *S.* Enteritidis was much diverse (Supplemetary figures 1 and 2). To put our data within the wider regional context, we compared our *S.* Enteritidis strains to 495 available African *S.* Enteritidis genomes from the European Nucleotide Archive (ENA). Our analysis revealed considerable genetic diversity which fell into three clades: the North American poultry-associated clade [30] and the global epidemic clade known to cause human gastroenteritidis in addition to the West African clade known to cause invasive diseases carrying the *cat*A1 gene [1] (Figure 4a). All *S.* Enteritidis strains from the eastern region (n=9) and 3 from the western region fell within the West African clade, clustering closely with *S.* Enteritidis strains from Ghana, Guinea and Mali. Among these, 7/12 (58.3%) were MDR (5 from the eastern region and two from the western region) and the remaining were pan susceptible strains (4 from the eastern region plus one western region). Among all strains within the West African clade from the subregion in the study, azithromycin resistance *mph*_A_2 gene was only harboured by strains from the eastern region (Figure 4b). Strains belonging to the North American clade were isolated from blood (n=1) and stool (n=2), whilst those within the global epidemic strains were isolated from blood (n=2) and urine (n=1).

Discussion:

We used phylogenetic analysis to confirm the circulation of a diverse range of NTS serovars including, the epidemic *S.* Enteritidis West African clade mainly in the eastern region of The Gambia, as far back as 2001. This clade is associated with high mortality, harbouring MDR and exhibit genome degradation facilitating an invasive lifestyle, warranting further epidemiological investigations and surveillance as it has important implication in treatment [1,31]. Interestingly, not all *S.* Enteritidis in this study within the clade harboured resistance genes. The *S.* Enteritidis exhibited diversity with other global lineages present. Remarkably, this study found a closely related clonal lineage of *S.* Typhimurium ST19 causing invasive NTS disease as opposed ST313 virulent lineage, which was reported to be circulating in other parts of sSA [7,32]. A possible explanation is that the sequence type ST313 is mainly associated with HIV infection which has a low prevalence in The Gambia [19]. Nevertheless, Panzenhagen *et al.,* reported *S.* Typhimurium ST19-lineage that has evolved in Brazil similar to ST313 restricted to invasive diseases [33]. This unique pathogenesis warrants further comparative genomic and epidemiological investigations into the *S.* Typhimurium ST19-lineage [13].

Two-thirds of serovars responsible for gastroenteritidis in this setting were serovars other than *S.* Typhimurium and *S.* Enteritidis as opposed to other parts of the world where these two serovars account for the highest burden [34]. The great diversity in serovars causing gastroenteritis as opposed to iNTS may suggest that NTS gastroenteritis may not be a predisposition to iNTS in The Gambia. In addition, NTS was not a major cause of gastroenteritis in this setting [35]. Although a huge gap exist regarding transmission dynamics of NTS in sSA [36], more insight is needed in understanding the relationship between NTS gastroenteritis and iNTS disease. In addition, the past two decades has revealed geographical serovar diversity between the two regions, indicating a possible regional specific

283 epidemiological pattern of NTS in The Gambia. However, the time difference in the sampling
284 between the two regions may confound the difference in location and warrant further
285 investigation. Nonetheless, previous phenotypic studies have highlighted these serovar
286 differences [14,15].The changing disease pattern of NTS in sSA, associated with specific
287 lineages of *S*. Typhimurium and *S*. Enteritidis remain a major concern and warrant surveillance
288 [1,9,10,37]. Although a recent decline has been reported for iNTS, it remains a leading cause
289 of bacteraemia in The Gambia [38,39]. Three cases of *Salmonella* bacterial meningitis were
290 included in this study, all of which were found in paediatric patients under 10 years old.
291 Although rare, NTS meningitis has been reported elsewhere in Africa, and is often associated
292 with high case fatality [40,41]. Therefore, NTS needs to be considered in the differential
293 diagnosis of bacterial meningitis following post-vaccine declines in the prevalence of Hib,
294 *Neisseria meningitidis* and pneumococcal meningitis [38,42].

295 Antimicrobial resistance was found to be correlated with serovar, plasmid replicon and
296 geographical location. MDR was confined within *S.* Enteritidis noted for first-line antibiotics
297 such as ampicillin, sulfamethoxazole-trimethoprim, tetracycline and chloramphenicol.
298 Although no fluroquinolone or cephalosporin resistance was identified, implying these drugs
299 might still be effective in The Gambia, the emergence of azithromycin resistance gene *mph*_A
300 requires further monitoring as a recommended drug of choice for iNTS [43]. Nevertheless, the
301 aminoglycoside resistance gene *aac(6')-Iaa* and a multi-drug transporter gene *mdf(A)* were
302 present in all serovars including pan-susceptible isolates. This highlights the potential of using
303 genomic-based AMR prediction to monitor AMR determinants for emerging resistance. Our
304 study did not phenotypically test streptomycin susceptibility which lacks clinical breakpoints
305 and it is not used in the treatment of infections. In addition, the streptomycin resistance genes
306 were frequently found to lack expression [44]. While the development of AMR has been mainly
307 attributed to antibiotic misuse in humans and animals, evidence has shown that environmental

308 factors such as poor sanitation, hygiene and access to clean water may be equally responsible
309 for driving resistance in LMIC [45,46].

310 Although the differences in sampling timepoint was a major limitation in the study, the
311 diversity of AMR between serovars and geographic regions highlights the need for real-time
312 surveillance as well as region-appropriate interventions to effectively combat AMR.
313 Geographic differences seen in AMR may suggest differences in selective pressure and
314 ecological factors thus suggesting need for location specific control measures. The study by
315 Carroll *et al.* underscored distinct factors such as use of antimicrobials in food producing
316 animals as contributing to emergence and dispersal of AMR in humans [47]. Our findings are
317 consistent with other studies that show NTS serovar differences in geographical locations
318 within the same country [47,48]. A correlation between phenotypic and genotypic resistance
319 was also observed (Figure 2). The *IncN* type plasmid was strongly associated with resistance
320 and was found only in MDR *S.* Enteritidis, thus requiring closer surveillance. This plasmid is
321 associated with dissemination of antimicrobial resistance with high potential of spread [49].

322 We found many virulence genes, however, the identification of virulence factors coding for
323 specific phenotypic traits can be challenging, due to differences in specific traits among
324 serovars [50]. Notwithstanding, the pathogenic success of NTS serovars is directly linked to
325 their plethora of virulence factors aided by host susceptibility, serovar fitness, infectious dose
326 and antimicrobial resistance (AMR) [51]. Further studies are needed to understand the clinical
327 implications of these virulence genes.

328 There are several limitations in this study. First, the isolates were collected at different time
329 points, with a lag of up to 18 years between the two different regions, which may lead to
330 missing temporal differences. However, the higher AMR prevalence of *S.* Enteritidis in the
331 eastern region as early as 2001 compared to the more recent western region proves the point
332 that AMR emerged a lot earlier and more prevalent in the eastern region. Second, relatively

few isolates were analysed from only two regions due to limited microbiology capacity and therefore our results may not reflect the entirety of strains and lineages of the NTS in The Gambia.

In conclusion, this study has revealed great serovar diversity in serovars responsible for gastroenteritis and iNTS and provides evidence for the emergence of MDR *S.* Enteritidis epidemic West African clade in The Gambia. These findings have important implications for antimicrobial prescription policies and regional surveillance of NTS disease. We have demonstrated that a robust genomic epidemiological surveillance of NTS by WGS can be instrumental in generating the critical knowledge and timely information for better disease management and prevention.

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Author notes: Supporting data and protocols are provided as supplementary material and available.

Conflict of interest:

We declare no conflict of interest

358 **Author contributions:**

359 Conceptualiztion: SD, RSB, MA and BKA.

360 Laboratory analysis and sequencing of isolates in MRCG: SD

361 Data transfer of sequence reads into analysis pipeline AW, AK and JP

362 Processing and sequencing of isolates in the UK, including data transfer. BPS

363 Data curation: SD, AW, AK

364 Formal analysis: SD and AKM

365 Writing original draft: SD

366 Review and editing: SD, RSB, SY, DN, BPS, BKA, MA

367 Review of final draft: all authors

368 Supervision: SK, BKA and MA

369 Project Administration: SD

370

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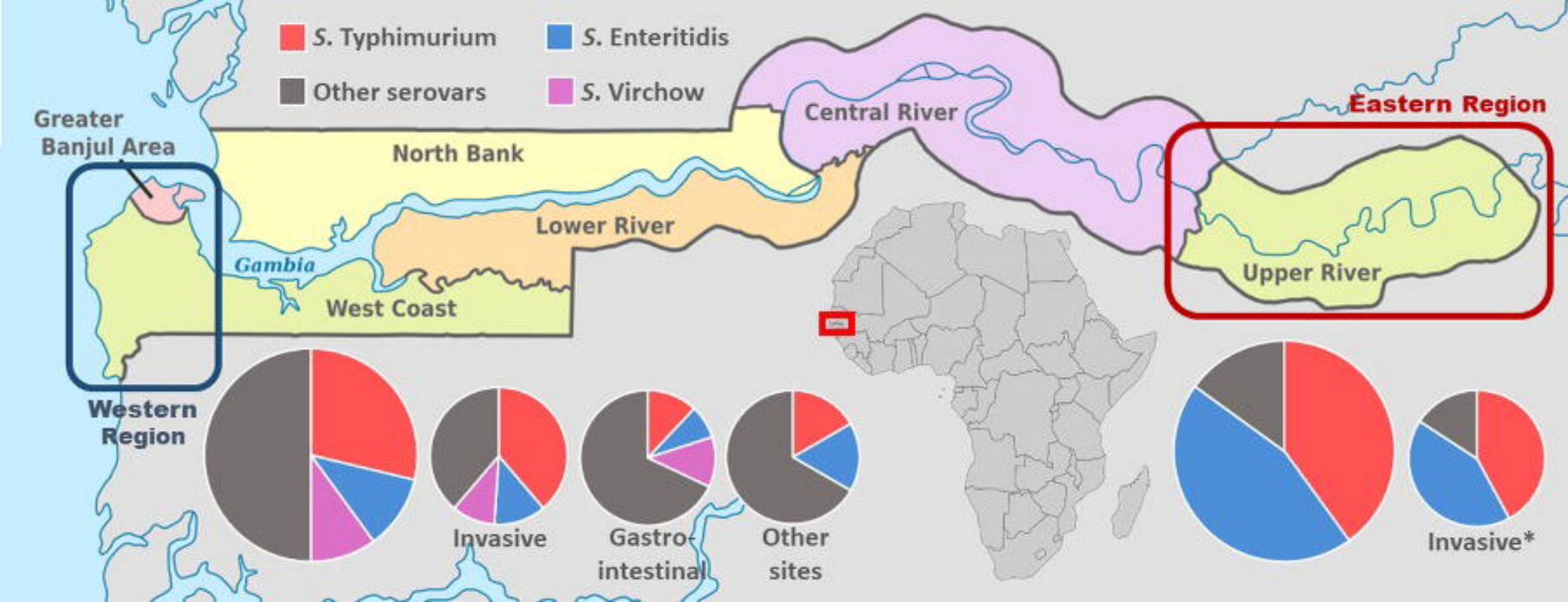
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S. Enteritidis
Other serovars
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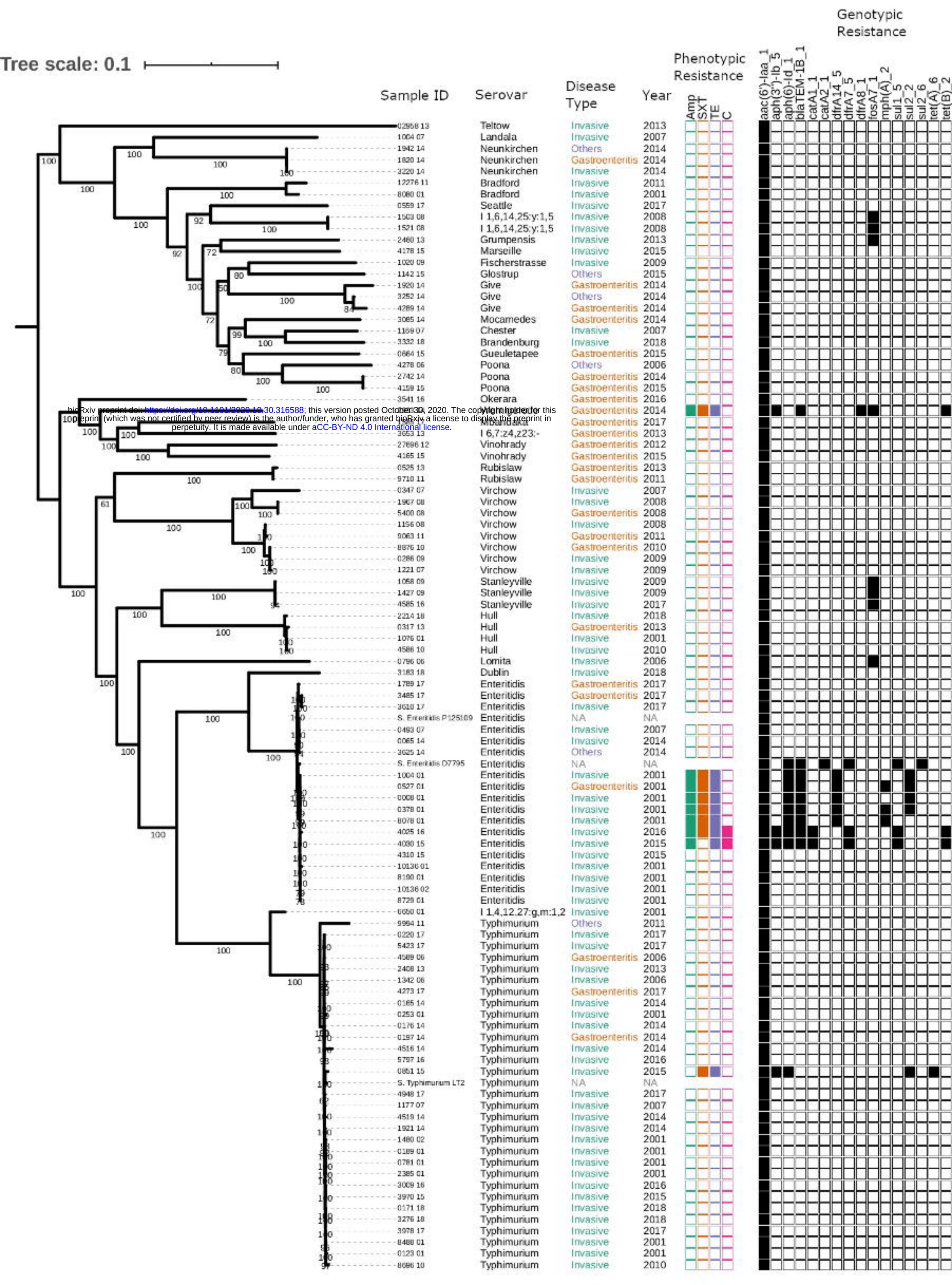
Central River
Eastern Region
Lower River
Gambia
West Coast
Upper River
Western Region
Invasive
Gastro-intestinal
Other sites
Invasive*



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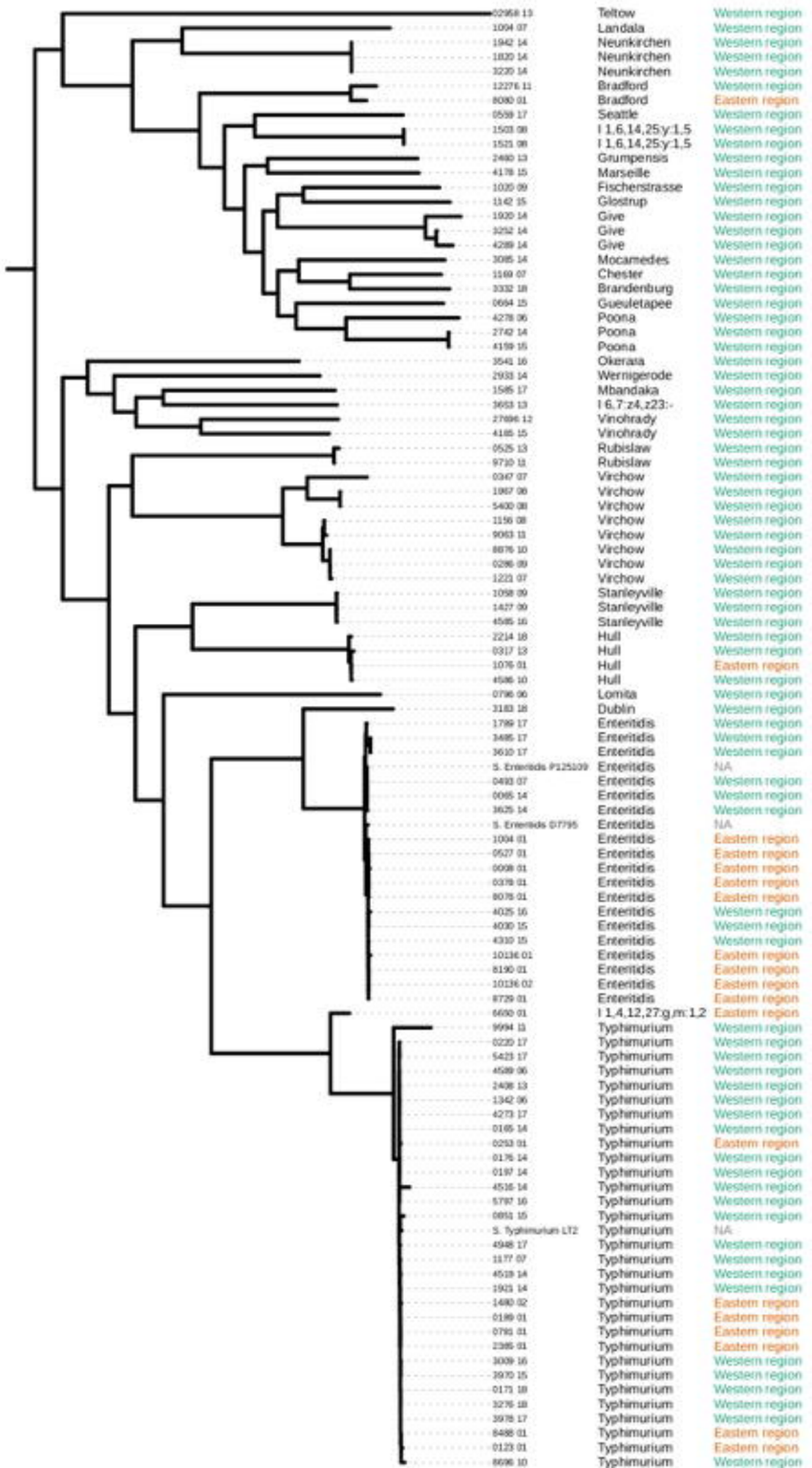

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1942 14	Neunkirchen	Western region
1820 14	Neunkirchen	Western region
3220 14	Neunkirchen	Western region
12276 11	Bradford	Western region
8080 01	Bradford	Eastern region
0559 17	Seattle	Western region
1503 08	I 1,6,14,25:y:1,5	Western region
1521 08	I 1,6,14,25:y:1,5	Western region
2480 13	Grumpensis	Western region
4178 15	Marseille	Western region
1020 09	Fischerstrasse	Western region
1142 15	Glostrup	Western region
1920 14	Give	Western region
3252 14	Give	Western region
4289 14	Give	Western region
3085 14	Mocamedes	Western region
1169 07	Chester	Western region
3332 18	Brandenburg	Western region
0664 15	Gueuletapee	Western region
4278 06	Poona	Western region
2742 14	Poona	Western region
4159 15	Poona	Western region
3541 16	Okerara	Western region
2933 14	Wernigerode	Western region
1585 17	Mbandaka	Western region
3653 13	I 6,7:z4,z23:-	Western region
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0525 13	Rubislaw	Western region
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0347 07	Virchow	Western region
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5400 08	Virchow	Western region
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2214 18	Hull	Western region
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0796 06	Lomita	Western region
3183 18	Dublin	Western region
1789 17	Enteritidis	Western region
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S. Enteritidis P125109	Enteritidis	NA
0493 07	Enteritidis	Western region
0065 14	Enteritidis	Western region
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S. Enteritidis D7795	Enteritidis	NA
1004 01	Enteritidis	Eastern region
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0378 01	Enteritidis	Eastern region
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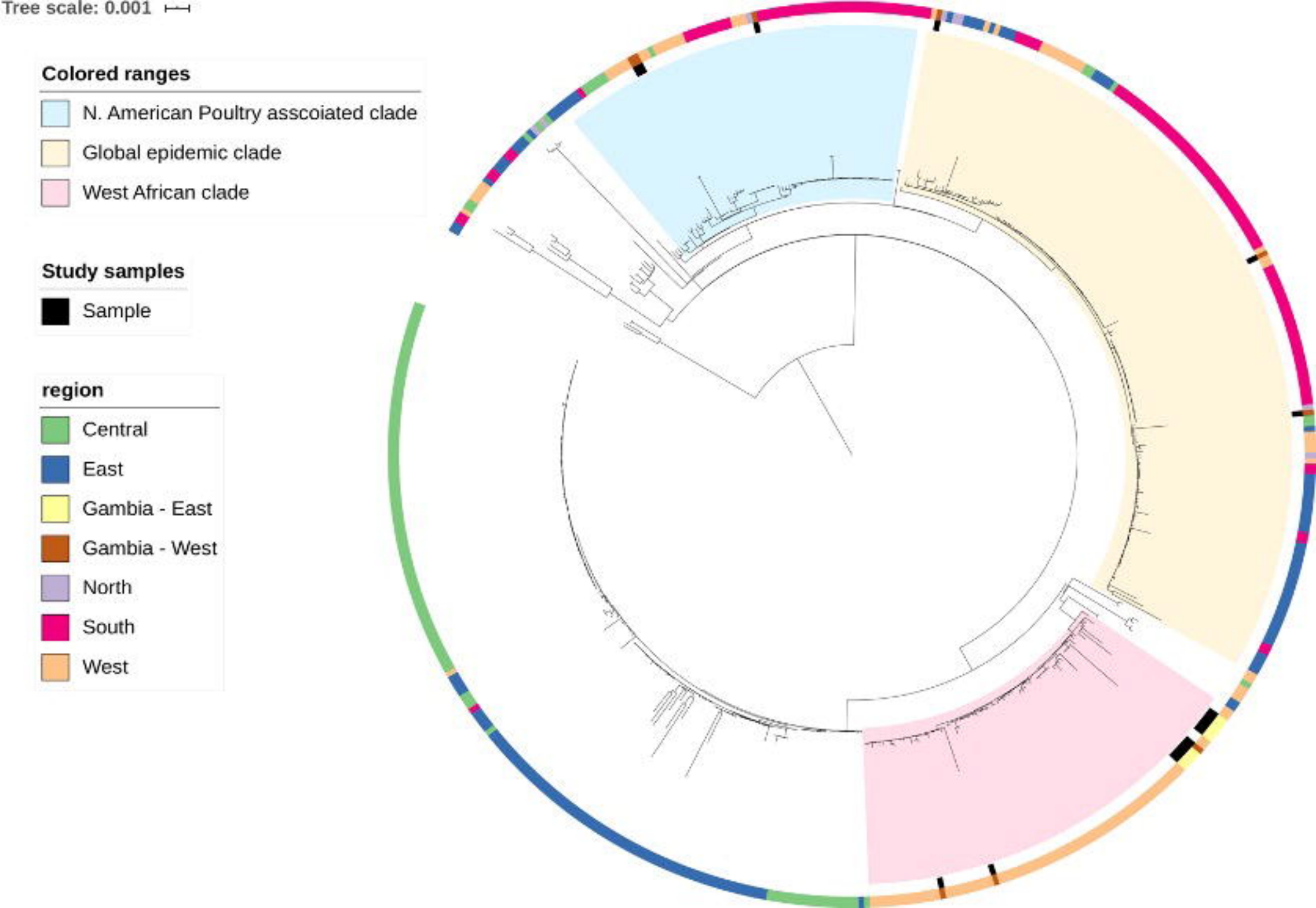
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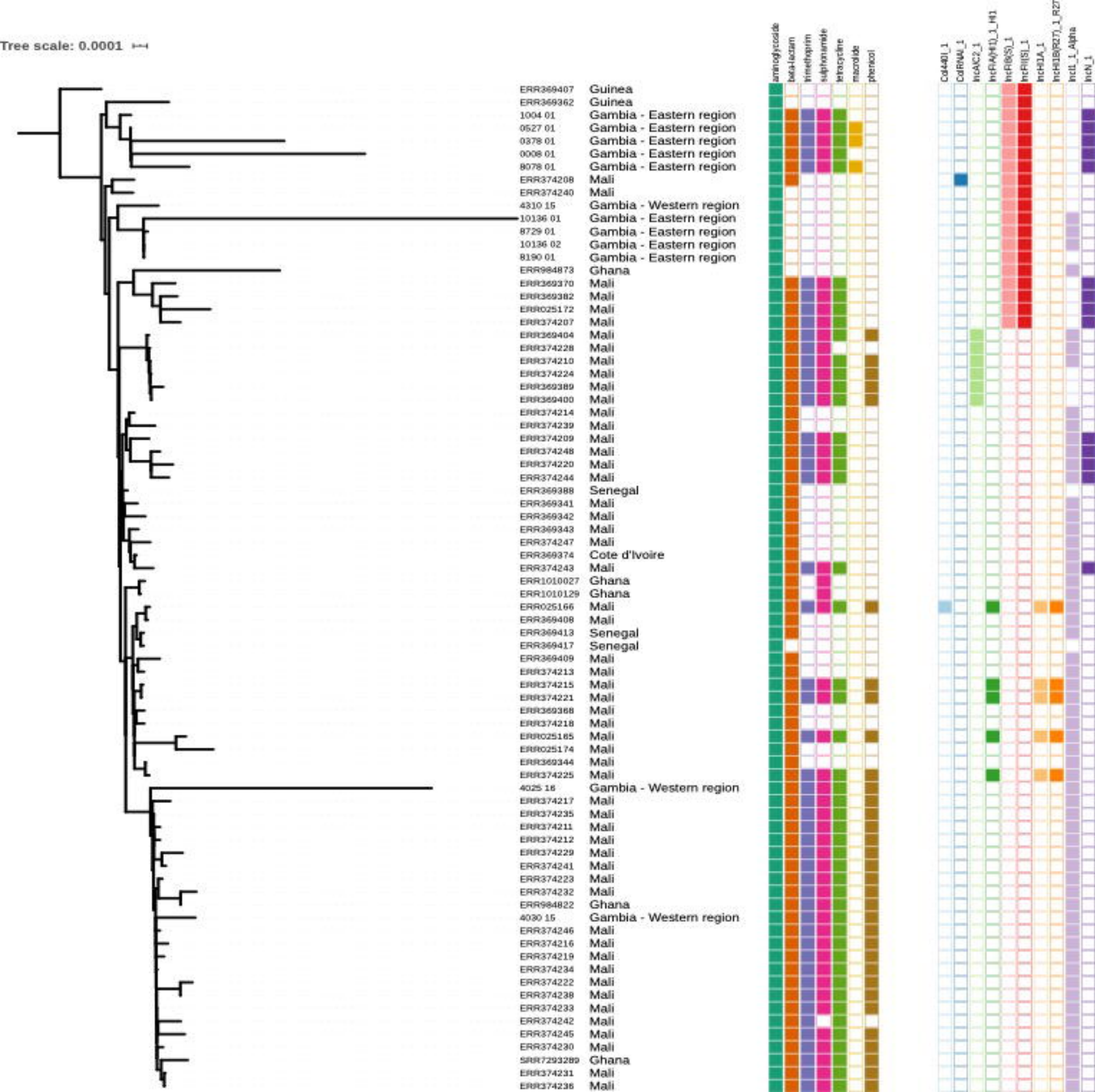
Global epidemic clade
West African clade
Study samples
Sample
region
Central
East
Gambia - East
Gambia - West
North
South
West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0008 01 Gambia - Eastern region
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ERR374208 Mali
ERR374240 Mali
4310 15 Gambia - Western region
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8729 01 Gambia - Eastern region
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beta-lactam
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tetracycline
macrolide
phenicol
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ColRNAI_1
IncAC2_1
IncFIA(HI1)_1_HI1
IncFII(S)_1
IncFII[S]_1
IncHI1A_1
IncHI1B(R27)_1_R27
IncIL_1_Alpha
IncN_1

Table 1. Baseline characteristics of Gambian non-typhoidal *Salmonella* disease patients from whom isolates were cultured for use in this study

		N (%)	*eastern region*	*western region*
Age range	0-4 years	42 (45.2)	4 (25.0)	38 (50.7)
	5-14 years	21 (22.6)	12 (65.0)	9 (12.0)
	≥15 years	26 (27.9)	2 (10.0)	24 (32.0)
	Unknown	4 (4.3)	0	4 (5.3)
Gender	Male	51(54.3)	10 (55.6)	41 (54.7)
	Female	38(41.5)	7 (38.9)	31 (41.3)
	Unknown	4 (4.2)	1 (5.5)	3 (4.0)
Source	Invasive disease	68 (68.0)	19 (95.0)	49 (61.2)
	Gastroenteritis	26 (26.0)	1 (5.0)	25 (31.3)
	Other	6 (6)	0	6 (7.5)
Serovars	*S*. Enteritidis	18 (18.0)	9 (45.0)	9 (11.2)
	S. Typhimurium	31 (31.0)	8 (40.0)	23 (28.8)
	S. Virchow	8 (8.0)	0	8 (10.0)
	Other serovars*	43 (43.0)	3 (15.0)	40 (50.0)

*Shown in figure supplementary table

Table 2. Patients with multisite NTS simultaneous infections

Patient	Sex	Age range (yrs)	Infection source	Serovar	Region	Date isolated
1	Male	0-4	Bacteraemia	*S.* Enteritidis	western	19/9/2017
			Gastroenteritis	*S.* Enteritidis		14/9/2017
2	Female	35-39	Bacteraemia	*S.* Typhimurium	western	1/1/2014
			Gastroenteritis	*S.* Typhimurium		1/1/2014
3	Male	0-4	Bacteraemia	*S.* Virchow	western	1/3/2009
			Meningitis	*S.* Virchow		1/3/2009
4	Male	30-34	Bacteraemia	*S.* Typhimurium	western	1/11/2006
			Gastroenteritis	*S.* Typhimurium		1/11/2006
5	Female	0-4	Bacteraemia	1,6,14,25:y:1,5	western	1/10/2008
			Bacteraemia	1,6,14,25:y:1,5		1/10/2008
6	Male	5-9	Bacteraemia	*S.* Enteritidis	eastern	1/10/2001
			Bacteraemia	*S.* Enteritidis		1/10/2001
7	Male	0-4	Bacteraemia	*S.* Typhimurium	eastern	1/12/2001
			Meningitis	*S.* Typhimurium		1/12/2001

Table 3. Gambian non-typhoidal *Salmonella* serovar distribution by infection in this study

	eastern region (2001) n=20					**western region (2006-2018) n=80**				
	Infection source									
	Total	**Invasive disease**		**Gastroenteritis**	**Other**	**Total**	**Invasive disease**		**Gastroenteritis**	**Other***
		19		**1**	**0**		**49**		**25**	**6**
		Bacteraemia	**Meningitis**				**Bacteraemia**	**Meningitis**		
		17	**2**				**48**	**1**		
S. Enteritidis	**9**	8 (47.1)	0	1	0	**9**	6 (12.5)	0	2 (8.0)	1 (16.6)
S. Typhimurium	**8**	6 (35.3))	2	0	0	**23**	19 (39.6)	0	3 (12.0)	1 (16.6)
S. Virchow	**0**	0	0	0	0	**8**	4 (8.3)	1	3 (12.0)	0
Other serovars	**3**	3 (17.6)	0	0	0	**40**	19 (39.6)	0	17 (68.0)	4 (66.8)

*Other = Abscess/pus and urine isolates

Table 4. Gambian non-typhoidal *Salmonella* serovar distribution and disease prevalence

Serovar	Total	Invasive N (%)	Gastroenteritis N (%)	Others N (%)	Odds of Invasive vs Gastroenteritis	95% CI	p value
	100	**68**	**26**	**6**			
S. Typhimurium	31	27 (39.7)	3 (11.5)	1 (16.7)	5.05	1.38; 18.48	**0.014**
S. Enteritidis	18	14 (20.6)	3 (11.5)	1 (16.7)	1.99	.52; 7.58	0.315
S. Virchow	8	5 (7.4)	3 (11.5)	0 (0)	0.61	0.13, 2.75	0.519
Other serovars	43	22 (32.4)	17 (65.4)	4 (66.7)	0.25	0.10; 0.66	0.005

Table 5. eBurst groups of the major Gambian NTS serovars responsible for clinical disease

Serovars	Sequence type	eBG	Number
S. Enteritidis	11	4	15
	1925	4	1
	11	4	2*
S. Typhimurium	19	1	29
	19	1	2*
S. Virchow	181	9	2
	755	9	1
	841	9	4
	841	9	1*

*One or two allelic variants of ST.

Table 6. Odds of *S.* Enteritidis resistance against other NTS serovars causing disease in The Gambia

Antimicrobials	*S.* Enteritidis n=18	Other serovars n=72	Odds of *S.* Enteritidis vs all serovars	95% CI	P-value
Ampicillin	7	1	51.5	5.78; 459.60	<0.001
sulfamethoxazole-trimethoprim	6	2	20.0	3.61; 110.74	0.001
Tetracycline	7	2	25.5	4.68; 138.39	<0.001
Chloramphenicol	2	0	1	NA	NA

Table 7. Summary of plasmid replicons and serovar in The Gambian non-typhoidal *Salmonella* isolates

Plasmid Type	**Total**	***S.* Enteritidis n=18**	***S.* Typhimurium n=31**	***S.* Virchow n=8**	**Other serovars n=43**
IncFII_S__1	55	16	31	0	8
IncFIB_S__1	50	16	31	0	3
IncI1_1_Alpha	6	5	0	0	1
IncN_1	5	5	0	0	0
IncX1_1	4	0	2	0	2
IncFIB_pKPHS1__1_pKPHS1	4	0	0	0	4
IncFII_SARC14__1_SARC14	3	0	0	0	3
IncFII_p14__1_p14	3	0	0	0	3
IncL/M_pOXA-48__1_pOXA-48	3	0	1	0	2
pSL483_1	3	0	3	0	0
ColRNAI_1	2	0	1	0	1
Col_MG828__1	2	0	1	1	0
IncFIB_pB171__1_pB171	2	0	0	0	2
IncI2_1_Delta	2	0	1	0	1
IncX1_4	1	1	0	0	0
IncX3_1	1	1	0	0	0
repUS21__rep_pWBG764	1	0	0	0	1
IncFII_pRSB107__1_pRSB107	1	0	0	0	1
pENTAS02_1	1	0	0	0	1