Salmonellosis is a leading cause of foodborne illnesses in humans with cattle being one of the reservoirs for *Salmonella*. We estimated a pooled prevalence of *Salmonella* in apparently healthy cattle and examined serotype diversity through systematic review and meta-analysis of studies published between 2000 and 2017. Peer reviewed publications reporting the prevalence of *Salmonella* in cattle were searched through five electronic databases (PubMed, Google scholar, Agricola, Scopus, CAB direct) and through manual search. We obtained 71 publications with 75 datasets consisting a total of 52,766 animals examined and 5,010 *Salmonella* positive cattle from 29 countries in six continents (except from Antarctica). Pooled prevalence of *Salmonella* in cattle was 9% (95% confidence interval: 7–11%). Significantly high heterogeneity ($I^2 = 98.7\%$, $P < 0.01$) was observed among all studies as well as within continents. Prevalence varied from 2% (Europe) to 16% (North America). Overall, 143 different serotypes were reported with the most diverse serotypes being reported from Africa (76 different serotypes) followed by North America (49 serotypes). The 10 most frequently reported serotypes (Montevideo, Typhimurium, Kentucky, Meleagridis, Anatum, Cerro, Mbandaka, Muenster, Newport, and Senftenberg) accounted for 65% of the isolates for which specific serotype information was reported. *Salmonella* Montevideo and S. Dublin are the most frequently reported serotypes in North America and Europe, respectively, while S. Typhimurium was the most frequent in Africa, Asia and Australasia. Our results indicated variability both in the prevalence and serotype diversity of *Salmonella* in cattle across continents. Although all *Salmonella* serotypes are potentially pathogenic to humans, five (Montevideo, Typhimurium, Anatum, Mbandaka, and Newport) of the top 10 serotypes identified in this study are among the serotypes most commonly associated with clinical illnesses in humans.

**Keywords:** *Salmonella*, cattle, prevalence, serotypes, systematic review, meta-analysis
BACKGROUND

Foodborne illnesses pose public health and economic burdens both in developed and developing countries (1, 2). Annually, foodborne illnesses are responsible for an estimated 600 million cases, 420,000 deaths, and 33 million disability adjusted life years lost worldwide. Salmonella is a major cause of foodborne illnesses in humans (3–5). Salmonella are Gram-negative, non-spore forming, mostly motile, facultative anaerobic bacilli within the family Enterobacteriaceae. The species Salmonella enterica consists of six subspecies and more than 2,579 serovars (6, 7). Based on the clinical profiles of infections caused in humans S. enterica can be divided into typhoidal—which are human specific—and non-typhoidal Salmonella (NTS)—having a broad host range (6). The NTS serotypes are leading causes of bacterial diarrhea and invasive bacterial infections in young children, the elderly and the immune-compromised individuals throughout the world. Salmonella Typhimurium and S. Enteritidis together account for approximately 50% of all isolates globally reported from human clinical cases (8–10). The global incidence of diarrheal disease due to the NTS accounts for about 94 million enteric infections each year, of which 80.3 million cases are considered foodborne and resulting in 155,000 human deaths annually (11). Human salmonellosis is also recognized as an important socioeconomic disease posing considerable economic burden in the world (12, 13).

Salmonella colonizes mainly the intestinal tracts of humans and animals including cattle. Foods of animal origin are important sources of Salmonella infections in humans (13–18). Humans acquire the infection mainly through consumption of contaminated products including beef and beef products (19), by direct contact with infected animals or their environment (20) and by direct human-to-human transmission (21). Carcass contamination with Salmonella during slaughter, particularly under unsatisfactory hygienic operations, poses a significant public health risk (22–25). The transfer of NTS to food processing plants and equipment used for food preparation also plays an important role, ultimately leading to the risk of salmonellosis after the consumption of contaminated foods (21). Knowledge about the overall occurrence of Salmonella and the diversity of serotypes in cattle provides important information for decision making and to promote reliable efforts toward prevention and control of foodborne salmonellosis associated with cattle. Therefore, the objectives of this study were to determine the prevalence of Salmonella in apparently healthy cattle, and to assess the diversity of Salmonella serotypes associated with cattle production systems through a systematic review and meta-analysis of peer-reviewed publications between 2000 and 2017.

METHODS

Systematic Review of the Literature

Preferred reporting items for systematic reviews and meta-analysis protocols (PRISMA-P) 2015 checklist was followed for the systematic review and meta-analysis of studies reporting Salmonella serotypes and prevalence in cattle (26). Five electronic databases were searched: PubMed (http://www.ncbi.nlm.nih.gov/pubmed), Google scholars (https://scholar.google.com/), Agricola (http://agricola.nal.usda.gov/), Scopus (http://www.scopus.com/), and CAB direct (http://www.cabdirect.org/). Additional publications were obtained by the manual scanning of the reference list from the retrieved publications. Salmonella, cattle, and prevalence were the main key words used for the search. The search was conducted with alternative terms for each key term using the general protocol [Salmonella AND (cattle OR bovine OR heifer OR bull OR bullock OR ruminant OR steer OR cow OR cull OR calf OR calves OR yearling OR beef OR dairy OR feedlot) AND (prevalence OR isolation OR identification OR “antimicrobial resistance” OR “antimicrobial susceptibility”)] that was modified and tailored to search strategies of each database when needed.

Relevance Screening

The retrieved articles were imported to Refworks to manage and exclude duplicated studies (27). The duplicated records were excluded manually after making the bibliography list and prior to the eligibility assessment. The eligibility criteria were: (i) articles published in English between January 1, 2000 (since full articles could not be available online, publications prior to 2000 were not considered) and January 4, 2017 (the last date of literature search); (ii) reported on apparently healthy cattle (no statement is given about the inclusion of sick/diseased animals) from different production categories (dairy, beef, mixed) and sample sources (slaughter plant/abattoir/slaughter house, dairy farm, beef farm, ranch, feedlot, grazing point, market place, mixed cattle farm); (iii) samples collected from the intestinal content (feces from the rectum and other intestinal contents); (iv) prevalence report from any part of the world; and (v) cross-sectional study in which animal level prevalence was reported or could be calculated from the information provided in the publication during data extraction. The exclusion criteria were: (i) irrelevant records to the objective of the review; (ii) articles on sick or diseased cattle; (iii) non-cross-sectional study design; (iv) report on inappropriate samples such as ground or pen fecal or pooled fecal samples from which animal level prevalence was unknown, lymph nodes, rumen contents or other body parts of cattle; (v) when only citations or abstracts were available.

Data Extraction

A peer-reviewed publication that describes prevalence of Salmonella in cattle was considered as a study unit. Cattle were considered positive for Salmonella when samples from the intestinal contents were tested and confirmed positive. When different prevalence reports in the content from various sites of intestinal tract were observed in a single study, we considered this one with the highest proportion for better precision to minimize under estimation. From each eligible publication, we extracted the following information: author, year of publication, year of study, study location (country and continent), detection method, production type (beef, dairy, and mixed), sampling location (abattoir, farm, market, ranch, grazing points, feedlot), age (calves and adults), amount of tested samples, sample size, number of Salmonella positive samples and serotypes identified, and number within each serotype. The extracted information was
entered to a Microsoft excel spread sheet for quality assessment and data preparation for analysis.

**Data Analysis**

Frequency distributions were used to describe the characteristics of the eligible publications and the diversity and proportion of *Salmonella* serotypes. Meta-analysis was conducted using the metaprop-one package (28), a Stata based program specifically designed for binominal data, that allows the computation of studies with 0 or 100% prevalence. Analysis was done in STATA version 14 (29). The prevalence of *Salmonella* in cattle was defined as the proportion of *Salmonella* positives based on the intestinal content samples. The pooled prevalence of *Salmonella* was computed by meta-analysis from the prevalence values of the individual publications by accounting for potential heterogeneity between studies and weighted on sample size (30). A logistic-normal random-effects model was used to model the within-study variability. The 95% confidence intervals (CIs) for the proportion of cattle *Salmonella* positive for the separate publications and their pooled prevalence was computed with the exact binomial method with the Freeman-Tukey double arcsine transformation which gives the CIs within admissible values. Further analysis of sub-groups of the overall estimate was performed according to age, production type, detection method, and continent categories. Heterogeneity of the effect sizes among the publications was assessed by Cochrane Q test and inverse variance index ($I^2$) test and quantified as recommended by Higgins and Thompson (31). A $P < 0.01$ was set as an indication of a statistically significant heterogeneity. The basic results from the meta-analysis were visually presented using forest plots. Frequency distributions were used to describe the characteristics of the eligible studies and the diversity and proportion of *Salmonella* serotypes.

**RESULTS**

**Systematic Review of the Literature**

A flow chart showing the systematic literature search procedure is shown in Figure 1. A total of 2,655 records were retrieved from the five search engines (PubMed, Google scholar, Agricola, Scopus, and CAB direct) and by manual search. After de-duplicating the references, 1,753 publications were retained for further screening. After relevance screening of the titles and abstracts, 1,573 publications were retained for further screening. After relevance screening of the titles and abstracts, 1,625 articles were excluded resulting in 128 potentially eligible full articles. Further in-depth eligibility assessment of the full articles resulted in 71 eligible publications for data extraction and analysis. The references of all the eligible articles are listed in Supplementary Table 1.

**Data Extraction and Meta-Analysis**

Data were extracted from the 71 peer-reviewed publications comprising 75 data sets. Two separate datasets were extracted from three publications (32–34) based on age and from one study (35) based on sampling points. Therefore, 75 data sets
The pooled prevalence of *Salmonella* is higher in the adult cattle [9% (95% CI: 7–12%)] than in the calves [6% (95% CI: 2–11%)], in beef cattle [14% (95% CI: 7–23%)] than in other production types, and in North America [16% (95% CI:12–20%)] than in other continents. Studies within each category of the strata defined by detection method and continent, showed significantly high degrees of heterogeneities (P < 0.01). However, no significant heterogeneity was observed between the age groups, among production types and when comparing only between immunomagnetic separation (IMS) and non-IMS detection methods (P > 0.01).

**Diversity of Serotypes**

Serotype information was not reported for 1,926 *Salmonella* positive cattle from a total of 16,175 cattle examined in 27 publications representing 29 data sets. In the remaining 44 publications representing 46 datasets for which serotype information was available, 3,191 *Salmonella* isolates were reported from 3,084 *Salmonella* positive cattle from a total of 36,591 cattle examined. Among the 3,191 isolates with serotyping information, specific serotypes were reported in 91.6% (2,923/3,191) of the isolates while 2.8% of the isolates were untypable, and the remaining 5.6% were reported as “other serotypes” where the list of which was not stated in the publication.

Overall, 143 different serotypes were reported among the 2,923 *Salmonella* isolates listed in the data sets included in the meta-analysis. The most frequently (with ≥1%) reported serotypes are shown in Table 3 and the list of serotypes (<1%) categorized as “others” in the latter table is presented in the Supplementary Table 2. The 10 most frequently reported cattle associated serotypes across all studies were S. Montevideo, Typhimurium, Kentucky, Meleagridis, Anatum, Cerro, Mbandaka, Muenster, Newport, and Senftenberg. These 10 most frequently isolated serotypes comprised 69.5% (2,032/2,923) of total isolates for which specific serotypes were reported. There were variations in the frequency and diversity of *Salmonella* serotypes in the six continents for which publications were retrieved (Table 4). S. Montevideo was the most frequent reported serotype from North America, while this serotype did not belong to the five most frequently reported serotypes in most other continents. *Salmonella* Typhimurium was the most frequently reported serotype in Africa, Asia, and Australasia, while S. Dublin was the most frequently reported serotype in Europe. The most diverse serotypes were reported from Africa (76 different serotypes) followed by North America (49 different serotypes), Australasia (39 serotypes), Asia (23 serotypes), Europe (12 serotypes), and South America (2 serotypes).

**DISCUSSION**

To the best of our knowledge, this is the first estimate of the overall *Salmonella* prevalence and the diversity of serotypes in apparently healthy cattle. We used a systematic method to...
FIGURE 2 | Forest plot showing estimated individual and overall Salmonella prevalence in apparently healthy cattle (ES, effect size; CI, confidence interval; $I^2$, Inverse variance index).
identify articles reporting the prevalence of *Salmonella* and the serotypes in such cattle, followed by a quantitative meta-analysis to estimate the overall prevalence of *Salmonella* at the global level.

*Salmonella* colonizes the gastrointestinal tract of food animals (7) and is shed via feces (36–39). Cattle are asymptomatic carriers or reservoirs for *Salmonella* and may function as a source of foodborne infection (8, 23, 24). A number of serotypes frequently isolated from humans have been isolated from sick or asymptomatic cattle and some human cases have also been linked to direct exposure to cattle (20). Knowing the prevalence and diversity of *Salmonella* serotypes in cattle can provide important information necessary to develop preventive measures and strategies at different stages of the food chain such as application hazard analysis and critical control point (HACCP) programs in beef and milk production industries to ensure food safety (40).

There was high heterogeneity in the estimated *Salmonella* prevalence among the studies included in the analysis. The *Salmonella* prevalence can vary depending on the detection method used, the amount of sample processed, production type, and geographical variation in the distribution of the *Salmonella* (32, 41). The overall pooled prevalence of 9% is higher compared to other reported national level prevalence values ranging from 0.2 to 7.1% (42–46). This is not surprising since our meta-analysis provides a precise estimate (with narrow confidence interval) as it includes a higher amount of samples and total number of positive cattle for *Salmonella* by pooling 75 datasets from 71 publications.

The prevalence was higher in the adult cattle [9% (95%CI: 7–12%)] than in the young age group [6%(95%CI: 2–11%)]. Although the effect of age needs further investigation, this variation can presumably be in part due to variation in the number of studies included in the meta-analysis in each age group. In the young age group there were 12 publications representing only 14.2% (n = 7,477) of total cattle examined compared to 63 publications in the adult cattle with 86% of the total cattle examined. Over 70% of the publications were conducted at processing plants and in culled dairy cows destined for slaughter perhaps because of the higher public health significance at the final stage of production chain that is close to consumers (47). Even though *Salmonella* colonizes the intestinal tracts of cattle, there is no difference in the colonization and shedding of *Salmonella* between healthy calves and adult cattle (7). However, a higher prevalence of *Salmonella* shedding animals occurs when asymptomatic chronically infected carrier cattle are present on the farm and stay on the farm for long periods (45), which may contribute to transmission and persistence of *Salmonella* on the farm.

Although not statistically significant, the prevalence was higher in beef cattle compared to dairy cattle. This apparent difference can be attributed to how the animals were sampled. In most of the studies culled dairy cows were sampled at farms before shipment as opposed to beef cattle which

### TABLE 2 | Pooled prevalence of *Salmonella* in apparently healthy cattle determined by meta-analysis of 75 datasets studies by age, production type, detection method, and continent.

| Subgroups | No. of publications | No. of datasets | No. of animals tested | No. of animals positive | Pooled prevalence (95% confidence interval) | Heterogeneity test |
|-----------|---------------------|----------------|----------------------|------------------------|---------------------------------------------|-------------------|
| **AGE**   |                     |                |                      |                        |                                             |                   |
| Adult     | 62                  | 63             | 45,289               | 4,624                  | 9 (7-12)                                   | 98.7              | <0.01  |
| Calves    | 12                  | 12             | 7,477                | 386                    | 6 (2-11)                                   | 97.4              | <0.01  |
| **PRODUCTION TYPE** |     |                |                      |                        |                                             |                   |
| Beef      | 17                  | 18             | 5,085                | 366                    | 14 (7-23)                                  | 98.3              | <0.01  |
| Dairy     | 26                  | 28             | 30,970               | 3,746                  | 10 (7-13)                                  | 98.7              | <0.01  |
| Mixed     | 13                  | 14             | 10,154               | 588                    | 5 (2-9)                                    | 98.0              | <0.01  |
| Not specified | 15              | 15             | 6,557                | 310                    | 5 (2-11)                                   | 97.9              | <0.01  |
| **DETECTION METHOD** |     |                |                      |                        |                                             |                   |
| Non-IMS   | 64                  | 68             | 50,311               | 4,696                  | 8 (6-11)                                   | 98.7              | <0.01  |
| PCR       | 1                   | 1              | 50                   | 25                     | 50 (37-63)                                 | -                 | -      |
| IMS       | 6                   | 6              | 2,405                | 289                    | 10 (5-16)                                  | 92.1              | <0.01  |
| **CONTINENT** |     |                |                      |                        |                                             |                   |
| Africa    | 16                  | 16             | 3,153                | 314                    | 9 (3-16)                                   | 98.2              | <0.01  |
| Asia      | 14                  | 15             | 3,116                | 202                    | 4 (1-8)                                    | 94.9              | <0.01  |
| Australasia | 6               | 6              | 6,370                | 287                    | 4 (1-11)                                   | 98.8              | <0.01  |
| Europe    | 8                   | 9              | 6,470                | 88                     | 2 (0-3)                                    | 92.0              | <0.01  |
| North America | 26             | 28             | 33,577               | 4,108                  | 16 (12-20)                                 | 99.0              | <0.01  |
| South America | 1              | 1              | 80                   | 11                     | 14 (8-23)                                  | -                 | -      |
| **Total** | 71                  | 75             | 52,766               | 5,010                  | 9 (7-11)                                   | 98.7              | <0.01  |

*Inverse variance index that describes the percentage of variation across studies attributed to heterogeneity rather than chance.
were commonly sampled at the processing plants. Temporary restriction or complete feed withdrawal (48) and exposure to stress such as transport (42, 49, 50) can result in increased fecal shedding of *Salmonella* in feedlot cattle prior to slaughter.

Variations in prevalence that ranged from 2% (Europe) to 16% (North America) in various continents of the world could partly be attributed to the differences in the number of publications and the number of cattle samples included in the analysis. For North America, 26 publications (28 data sets) were retrieved consisting of 33,577 cattle samples, being the majority of the articles. In contrast, the very low prevalence estimate (2%) observed in Europe, was estimated only from 8 publications (9 data sets) in which 6,470 cattle sampled. The prevalence in South America was 14%, however this does not represent the pooled estimate as only one article was included in the analysis. The differences might also be associated with differences in the monitoring and surveillance mechanisms among the continents (51).

Difference in the prevalence was also observed among categories of detection methods. In the majority (91%) of the studies, *Salmonella* was detected using traditional culturing methods which are in general considered less sensitive methods. Limited number of studies used immunomagnetic separation beads or PCR. Moreover, variation in the sensitivity of culture detection methods can influence the prevalence and consequently the observed heterogeneity (52).

In this systematic review, S. Montevideo and S. Typhimurium were the two most frequent and dominant serotypes reported where S. Montevideo was majorly reported from North America. *Salmonella* Typhimurium is one of the major serotypes that accounted for human clinical cases globally (10). Human infections and outbreaks due to S. Montevideo is also increasing around the globe (53) and reported in the USA, Europe, Australia, and Asia (54–56). There were differences in the most commonly reported serotypes and their proportions among different continents. *Salmonella* Typhimurium which is historically associated with cattle ranked number one in Africa, Asia, and Australasia. In North America and Europe, however, S. Montevideo and S. Dublin ranked number one, respectively. The implication of the shift in serotype with respect to public health requires further study. Interestingly, among the top 10 *Salmonella* serotypes identified in this study, S. Montevideo, S. Typhimurium, S. Anatum, S. Mbandaka, and S. Newport are among the World Health Organization’s top 20 serotypes associated with human salmonellosis across the world (52). Spatial and temporal effects on the distribution and diversity of *Salmonella* have been reported (57, 58), which may explain the observed differences in the serotype diversity among the studies reporting *Salmonella*. Some of the serotypes reported in the present review were identified as the dominant serotypes elsewhere in cattle at varying proportions. For instance, in the USA, S. Newport (48.7%) and S. Typhimurium (7.1%) (59); in Ethiopia, S. Typhimurium (17.4%), S. Newport (13%) and S. Anatum (5.8%) (42), and in Europe, S. Typhimurium (38.6%) were reported to be the most frequent and dominant serotypes (60). On the contrary, none of these serotypes were reported from the national survey of *Salmonella* serotypes in cattle carried out in Japan (41).

All non-typhoidal *Salmonella* serotypes except a few serotypes which are host-specific, can potentially cause disease in humans and reside in one or more animal species (61). *Salmonella* serotypes were reported to be linked to several outbreaks following the consumption of contaminated beef, milk, and
products thereof (62). S. Enteritidis and S. Typhimurium are the two most important serotypes transmitted from animals to humans in most parts of the world (51, 60, 63, 64). In the USA, 29 cases of diarrheal illness caused by S. Typhimurium were associated with the consumption of raw milk or raw-milk products from dairy cattle (65). During the period 1973–2011, of the 1,965 Salmonella outbreaks where a food vehicle was implicated, 96 were attributed to beef, accounting for 3,684 illnesses in USA. S. Newport and S. Typhimurium accounted for 18 and 17% of illnesses, and 29 and 18% of hospitalizations, respectively (19). The multidrug-resistant S. Typhimurium DT104 has also been associated with outbreaks related to beef contamination and resulted in hospitalization rates twice as that of other foodborne salmonellosis cases (65). From a total of 1,168 foodborne outbreaks of human salmonellosis in 2013 reported by the European member states, 1.6% of the cases were attributed to beef and beef products (60). This systematic review showed that S. Typhimurium was the most frequently reported serotype from cattle in Africa, Asia, and Australasia. Cattle could also contribute to the invasive non-typhoidal Salmonella disease in people who have contact with cattle feces. This is particularly important in regions like Africa where invasive non-typhoidal Salmonella infections are endemic as reviewed by Marks et al. (66). All the above evidence supports the importance of cattle and cattle associated serotypes for human salmonellosis.

Besides the datasets from the publications included in this review and meta-analysis, other relevant information was available in new articles that were published in the years 2017 and 2018 while the manuscript was under preparation by the authors. During this period, 6 full articles and three published abstracts representing 11 datasets were retrieved using the search engines. The studies were reported from Africa (67–74) except one study which was from South America (75). Among the total of 5,868 cattle examined, 9.2% (554/6,018), which is nearly equal to the pooled prevalence estimate, were reported to be positive for Salmonella species with different serotypes. The global level pooled prevalence of Salmonella in cattle was higher (9%) as compared to the pooled prevalence estimates of E. coli O157 (5.68%), which is also excreted by cattle showing the relative public health importance of Salmonella (76).

**CONCLUSIONS**

This study based on systematic reviews and meta-analysis provides an overall prevalence of Salmonella and serotype diversity in apparently healthy cattle at a global level. The results indicated variations in the level of Salmonella carriage...
in cattle across the world, and the presence of a diverse number of *Salmonella* serotypes. The estimated *Salmonella* prevalence was higher in North America. The predominant detection method is traditional culturing. Because of the possibility of *Salmonella* contamination of carcasses during slaughtering and milk during milking, cattle can be a potential source of *Salmonella* and can lead to public health risk and economic loss if the necessary hygienic measures are not properly followed.

**AUTHOR CONTRIBUTIONS**

FG, GA, RA, LD, and LDZ designed the study and identified the search engines and key words for literature search. FG, GA, RA, LD, and LDZ identified the sources. FG, GA, LD, RA, LDZ, and SG revised the manuscript. FG wrote the manuscript. GA, RA, LD, LDZ, and SG revised the manuscript.

**REFERENCES**

1. Glavin MO. A single microbial sea: food safety as a global concern. *SAIS Rev.* (2003) 23:203–20. doi: 10.1353/sais.2003.0012
2. Kirk MD, Pires SM, Black RE, Caipo M, Crump JA, Devleeschauwer B, et al. World Health Organization estimates of the global and regional disease burden of 22 foodborne bacterial, protozool, and viral diseases, 2010: a data synthesis. *PLoS Med.* (2015) 12:e1001940. doi: 10.1371/journal.pmed.1001940
3. D’Aoust JY. *Salmonella*. In: Lund BM, Baire-Parker AC, Gould GW, editors. *The Microbiology Safety and Quality of Food*. Gaithersburg, MD: Aspen Publishers (1999). p. 1233–99.
4. Schlundt J, Toyofuku H, Jansen J, Herbst SA. Emerging food-borne zoonoses. *Rev Sci Tech.* (2004) 23:513–34. doi: 10.20506/rst.23.2.1506
5. Rosel K, Delia G. Can Participation Improve Food Safety?. *Food Safety and Informal Markets: Animal Products In Sub-Saharan Africa*. (2014). Available online at: https://cgspace.cgiar.org/handle/10568/42438
6. Tindall BJ, Grimont PA, Garrity GM, Euzéby JP. Nomenclature and taxonomy of the genus *Salmonella*. *Int J Syst Evol Microbiol.* (2005) 55:521–4. doi: 10.1099/ijs.0.65580-0
7. Andino A. *Salmonella enterica*: survival, colonization, and virulence differences among serovars. *Sci World J.* (2015) 2015:520179. doi: 10.1155/2015/520179
8. Feasey NA, Dougan G, Kingsley RA, Heyderman RS, Gordon MA. Invasive non-typhoidal *Salmonella* disease: an emerging and neglected tropical disease in Africa. *Lancet.* (2012) 379:2489–9. doi: 10.1016/S0140-6736(11)61752-2
9. de Freitas Neto OC, Penha Filho RA, Barrow P, Berchieri Jr A. Sources of human non-typhoid salmonellosis: a review. *Rev Bras Ciência Avícola.* (2010) 12:01–11. doi: 10.1590/S1516-635X2010000100001
10. Tennant SM, MacLennan CA, Simon R, Martin LB, Khan MJ. Non-typhoidal *Salmonella* disease: current status of vaccine research and development. *Vaccine.* (2016) 34:2907–10. doi: 10.1016/j.vaccine.2016.03.072
11. Majowicz SE, Musto J, Scallan E, Angulo FJ, Kirk M, O’Brien SJ, et al. The global burden of non-typhoidal *Salmonella* gastroenteritis. *Clin Infect Dis.* (2010) 50:882–9. doi: 10.1086/650733
12. Ao TT, Feasey NA, Gordon MA, Keddy KH, Angulo FJ, Crump JA. Global burden of invasive non-typhoidal *Salmonella* disease, 2010. *Emerg Infect Dis.* (2015) 21:941–9. doi: 10.3201/eid2106.140999
13. Tauxe RV, Doyle MP, Kuchenmüller T, Schlundt J, Stein CE. Evolving public health approaches to the global challenge of foodborne infections. *Int J Food Microbiol.* (2010) 139:S16–28. doi: 10.1016/j.ijfoodmicro.2009.10.014
14. Buncic S, Sofos J. Interventions to control *Salmonella* contamination during poultry, cattle and pig slaughter. *Food Res Int.* (2012) 45:641–55. doi: 10.1016/j.foodres.2011.10.018
15. EFSA. Analysis of the baseline survey on the prevalence of *Salmonella* in holdings with breeding pigs, in the EU, 2008, part A: *Salmonella* prevalence estimates. *EFSA J.* (2009) 7:1377. doi: 10.2903/j.efsa.2009.1377
16. Ejeta G, Molla B, Alemayehu D, Muckel CA. *Salmonella* serotypes isolated from minced meat beef, mutton and pork in Addis Ababa, Ethiopia. *Rev Med Vet.* (2004) 155:547–51. Available online at: https://www.revmedvet.com/2004/RMV155_547_551.pdf
17. Pires SM, Evers EG, van Pelt W, Ayers T, Scallan E, Angulo FJ, et al. Attributing the human disease burden of foodborne infections to specific sources. *Foodborne Pathog Dis.* (2009) 6:617–24. doi: 10.1089/fpd.2008.0208
18. Scallan E, Hoekstra RM, Angulo FJ, Tauxe RV, Widdowson MA, Roy SL, et al. Foodborne illness acquired in the United States—major pathogens. *Emerg Infect Dis.* (2011) 17:7–15. doi: 10.3201/eid1701.P11101
19. Laufer AS, Grass J, Holt K, Whichard JM, Griffin PM, Gould LH. Outbreaks of *Salmonella* infections attributed to beef–United States, 1973–2011. *Epidemiol Infect.* (2015) 143:2003–13. doi: 10.1017/S0950268814003112
20. Hoelzer K, Switt AI, Wiedmann M. Animal contact as a source of human non-typhoidal salmonellosis. *Vet Res.* (2011) 42:43. doi: 10.1186/1297-9716-42-43
21. Pui CF, Wong WC, Chai LC, Tunung R, Jeyaleathum P, Hidayah N, et al. *Salmonella*: a foodborne pathogen. *Int Food Res J.* (2011) 18:465–73. Available online at: http://www.ifrj.upm.edu.my/18%20(02)%202011/(1)%20FRJ-2010-306.pdf
22. Abdunaser D, Almabrouk F, Ashraf W, Yves M, Olivier C, Moez S. Quantitative risk assessment of human salmonellosis linked to the consumption of ground beef. *Iraqi J Vet Sci.* (2009) 23:263–73. Available online at: https://pastel.archives-ouvertes.fr/pastel/00003795/document
23. Agga GE, Arthur TM, Schmidt JW, Wang R, Brichta-Harhay DM. Diagnostic accuracy of rectal microbial mucosal swab of feedlot cattle for detection and enumeration of *Salmonella enterica*. *J Food Prot.* (2016) 79:531–7. doi: 10.4315/0362-028X.JFP-15-409
24. Cheney WE, Agga GE, Nguyen SV, Arthur TM, Bosilevac JM, Dreyling E, et al. Rapid detection and classification of *Salmonella enterica* shedding in feedlot cattle utilizing the roka biosciences atlas salmonella detection assay for the analysis of rectal mucosal swabs. *J Food Prot.* (2017) 80:1760–7. doi: 10.4315/0362-028X.JFP-17-124
25. Mannion C, Fanning J, McLernon J, Lendrum L, Gutierrez M, Duggan S, et al. The role of transport, lairage and slaughter processes in the dissemination of *Salmonella* spp. in pigs in Ireland. *Food Res Int.* (2012) 45:871–9. doi: 10.1016/j.foodres.2011.02.001
26. Moher D, Shamseer L, Clarke M, Ghersi D, Liberati A, Petticrew M, et al. Preferred reporting items for systematic review and meta-analysis protocols (PRISMA-P) 2015 statement. *Syst Rev.* (2015) 4:1. doi: 10.1186/s40643-014-0012-1
27. ProQuest. RefWorks. (2016). Available online at: https://www.refworks.com/
39. Narváez-Bravo C, Rodas-González A, Fuenmayor Y, Flores-Rondón C, Al Mawly J, Grinberg A, Prattley D, Moffat J, French N. Prevalence of endemic Salmonella in beef cattle from transport to slaughter. J Food Prot. (2002) 65:1687–93. doi: 10.3109/0362-028X.65.11.1687
40. Corrier DE, Purdy CW, DeLoach JR. Effects of marketing stress on fecal excretion of Salmonella spp. in feedlots. Avian Dis. Vet Res. (1990) 35:866–9.
41. Millermann Y, Goubert S, Remy D, Colman C. Evaluation of IS200-PCR and comparison with other molecular markers to trace Salmonella enterica subsp. enterica serotype Typhimurium bovine isolates from farm to meat. J Clin Microbiol. (2000) 38:2204–9.
42. Tadesse G, Tessema TS. A meta-analysis of the prevalence of Salmonella enteropathogens of calves in New Zealand dairy farms. N Z Vet J. (2015) 63:280–3. doi: 10.1080/0362-028X.65.2.50.280
43. Dargatz DA, Fedorka-Cray PJ, Lidgard J, Gould LH, et al. Introduction to United States Department of Agriculture VetNet: status of Salmonella and Campylobacter databases from 2004 through 2005. Foodborne Pathog Dis. (2007) 4:241–8. doi: 10.1089/fpd.2006.0067
44. EFSA. The European Union summary report on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in 2013. EFSA J. (2015) 13:3991. doi: 10.2903/j.efsa.2015.3991
45. Eng SK, Puspaprajah P, AbMutalib NS, Ser HL, Chan KG, Lee LH. Salmonella: a review on pathogenesis, epidemiology and antibiotic resistance. Front Life Sci. (2015) 8:284–93. doi: 10.1007/s11555-015-1052-1
46. Greig JD, Ravel A. Analysis of foodborne outbreak data reported internationally for source attribution. Int J Food Microbiol. (2009) 130:77–87. doi: 10.1016/j.ijfoodmicro.2008.12.031
47. Youssef AE, Carlstrom C. Salmonella. In: Youssef AE, Carlstrom C, editors. Food Microbiology: A Laboratory Manual. John Wiley and Sons Inc (2003). p. 165–205.
48. Marks F, von Kallekrehn V, Aaby P, Adu-Sarkodie Y, El Tayeb MA, Ali M, et al. Incidence of invasive Salmonella disease in sub-Saharan Africa: a multicentre population-based surveillance study. Lancet Global Health. (2017) 5:10–23. doi: 10.1016/S2214-109X(17)30022-0
49. Aziz SA, Abdel-Latef GK, Shany SA, Rowby, SR. Molecular detection of Integron and antimicrobial resistance genes in multidrug resistant Salmonella isolated from poultry, calves and human in Beni-Suef
governorate, Egypt. Beni-Suef University. J Basic App Sci. (2018)7: 535–42. 
doi: 10.1016/j.bjbas.2018.06.005
68. Ball TA, Fedorka-Cray PJ, Horovitz J, Thakur S. Molecular characterizat 
on of Salmonella spp. from cattle and chicken farms in Uganda. Online J Public 
Health Inform. (2018) 10:e148. doi: 10.5210/ojphi.v10i1.8934
69. Çetin E, Serbecioglu T, Temelli S, Eyigor A. Non-typhoid Salmonella carriage, 
serovar profile and antimicrobial resistance phenotypes in slaughter cattle. J 
Food Safety. (2018) e12603. doi: 10.1111/jfs.12603
70. Fashae K, Leekitcharoenphon P, Hendriksen RS. Phenotypic and genotypic 
comparison of salmonellae from diarrhoeic and healthy humans and 
cattle, Nigeria. Zoonoses Public Health. (2018) 65:185–95. doi: 10.1111/zph. 
12427
71. Ketema L, Ketema Z, Kiflu B, Alemayehu H, Terefe Y, Ibrahim M, et al. 
Prevalence and antimicrobial susceptibility profile of Salmonella serovars 
isolated from slaughtered cattle in Addis Ababa, Ethiopia. BioMed Res Int. 
(2018)2018:9794869. doi: 10.1155/2018/9794869
72. Kore K, Asrade B, Demissie K, Aragaw K. Characterization of Salmonella 
isolated from apparently healthy slaughtered cattle and retail beef in 
Hawassa, southern Ethiopia. Prev Vet Med. (2017) 147:11–6. 
doi: 10.1016/j.prevetmed.2017.08.018
73. Nouichi S, Ouatouat R, Can HY, Mezali L, Belkader C, Ouar-Korichi 
M, et al. Prevalence and antimicrobial resistance of Salmonella isolated from 
bovine and ovine samples in slaughterhouses of Algiers, Algeria. J 
Hellenic Vet Med Soc. (2018) 69:863–72. doi: 10.12681/jhvm. 
16441
74. Takele S, Woldemichael K, Gashaw M, Tassew H, Yohannes M, Abdissa 
A. Prevalence and drug susceptibility pattern of Salmonella isolates from 
apparently healthy slaughter cattle and personnel working at the Jimma 
municipal abattoir, south-West Ethiopia. Trop Dis Travel Med Vaccines. 
(2018) 4:13. doi: 10.1186/s40794-018-0072-6
75. Fuenmayor Y, Rodas-González A, Carruyo G, Hoet AE, Wittum T, Narváez-
Bravo C. Salmonella prevalence and antimicrobial drug resistance in dual-
purpose cattle operations in the eastern region of Zulia State, Venezuela. 
Foodborne Pathog Dis. (2018). 16:205–13. doi: 10.1089/fpd.2018.2515
76. Islam MZ, Musekiwa A, Islam K, Ahmed S, Chowdhury S, Ahad 
A, et al. Regional variation in the prevalence of E. coli O157 in 
cattle: a meta-analysis and meta-regression. PLoS ONE. (2014) 9:e93299. 
doi: 10.1371/journal.pone.0093299

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