NEWSLETTER

European Union Reference Laboratory for *Salmonella*

Vol. 31 No. 2
June 2025

ISSN 2211-6877

Continuation of Newsletter Community Reference Laboratory for *Salmonella*
ISSN 1572-3836

Produced by

European Union Reference Laboratory for *Salmonella*

National Institute of Public Health and the Environment
P.O. Box 1, 3720 BA Bilthoven, The Netherlands

e-mail: EURLSalmonella@rivm.nl

website: www.eurlsalmonella.eu

This activity is co-funded by the European Union. Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union or the granting authority European Health and Digital Executive Agency (HaDEA). Neither the European Union nor the granting authority can be held responsible for them.

EURL *Salmonella*

Co-funded by the European Union

Contents

Editorial Note

Bilthoven, 1 July 2025

Dear colleagues,

Earlier this year, as you know, we had to update the **planning of the EURL-*Salmonella* activities for 2025**. This update was needed because the relocation of our institute to the new building was foreseen for autumn 2025. Recently we have been informed that the relocation is postponed again, but a new date has not yet been determined. Still, we decided to maintain the rescheduled dates of this year's PTs as it may be too confusing to change it again. Meaning that for the **EURL-*Salmonella* PT Primary Production Stage (PPS)** the samples were sent to the NRLs on 2 June 2025 and the deadline for reporting the results is 4 July 2025. For the **EURL-*Salmonella* PT Typing,** the samples will be sent on 11 August 2025 and the deadline for reporting the results is 3 October 2025. The time tables of both PTs have been shared in the previous Newsletter and is again shared in this Newsletter for the PT Typing.

The previous **PT on typing of *Salmonella*** was organised in **November 2024**. The interim summary of the obligatory part on serotyping was sent to the participants in February 2025. Unfortunately, this version contained an editorial error and a corrected version of the interim summary was sent to the participants in April 2025 and is published at the EURL-*Salmonella* website: https://www.eurlsalmonella.eu/en/documenten/interim-summary-report-eurl-salmonella-pt-serotyping-2024version2
The interim summary of the optional part on cluster analysis of this PT was prepared in April/May 2025 and shared with the participants by mid-May 2025. This interim summary report is also available at the EURL-*Salmonella* website: https://www.eurlsalmonella.eu/en/documenten/interim-summary-report-eurl-salmonella-pt-cluster-analysis-2024

In February/March 2025 we organised the **combined Food-Feed PT 2025**. All NRLs-*Salmonella* scored a good performance in this PT and the interim summary was shared with the participants by the end of April 2025 and is also available at the EURL-*Salmonella* website: https://www.eurlsalmonella.eu/en/documenten/interim-summary-report-eurl-salmonella-combined-pt-food-feed-2025

On 20 May 2025 we organised the **30th EURL-*Salmonella* workshop**. This workshop was held online and we were happy to welcome approximately 100 participants. The presentations of the workshop have been published at our website within one week after the workshop and can be found through the following link: https://www.eurlsalmonella.eu/en/workshop-2025

The joint EURLs working group on NGS, of which EURL-*Salmonella* is also part, organised a **joint EURLs training course on NGS** on 17 and 18 June 2025 at the premises of EURL-Coagulase Positive Staphylococci and EURL-*Listeria monocytogenes* (France). This training may have become more important since **EU Regulation 2025/179, related to the generation and sharing of WGS data during foodborne outbreaks,** was published. This new Regulation also demands that the generation of WGS data is performed under EN ISO/IEC 17025 accreditation. Laboratories have until mid-2028 to become accredited. For this purpose, the joint EURLs WG NGS is planning to draft a guidance document for this accreditation. Additionally, also a guidance document for Quality Control

parameters in short-read WGS of foodborne bacteria is being prepared. These guidance documents will be published through the websites of the biological EURLs. Currently available guidance documents produced by the joint EURLs WG NGS, as well as presentations given at the NGS training courses can be found through the following link: https://www.eurlsalmonella.eu/en/methods/ngs

Concerning the **ISO/CEN activities**, I can inform you that the annual meetings of CEN/TC463 and ISO/TC34/SC9, for Microbiology of the food chain, were held in Madrid, Spain from 2 to 6 June 2025. As convenor of WG9 ('Detection of *Salmonella*') and WG10 ('Typing of *Salmonella*'), EURL-*Salmonella* participated in these meetings and presented the progress of these working groups. Information about the activities of these working groups were also shared in the last presentation given at the EURL-*Salmonella* workshop of 20 May 2025: https://www.eurlsalmonella.eu/en/documenten/eurl-salmonella-workshop-2025-presentation-9-by-kirsten-mooijman

ISO and CEN reference methods for *Salmonella* was also the subject for the key note presentation given by EURL-*Salmonella* at the **International Symposium for *Salmonella* and salmonellosis (I3S)** organised from 23 to 25 June 2025 in Saint Malo, France.

Finally, I would like to wish you all a nice, sunny, but not too hot, and relaxing summer break!

Best wishes,
Kirsten Mooijman
Coordinator EURL-*Salmonella*

Contribution of the EURL-*Salmonella*

Timetable EURL-*Salmonella* Proficiency Test Serotyping 2025

Note that this PT Typing 2025 does not contain an optional part on cluster analyses, but only the obligatory part on serotyping of *Salmonella*.

Week	Date	Subject
25	Week of 16 June	Emailing of the link to the registration form for the PT Serotyping. Please **register by 18 July 2025** at the latest.
31	Week of 28 July	Emailing of the protocol 2025.
33	Monday 11 August 2025	Shipment of the parcels to the participants as Biological Substance Category B (UN 3373).
33	Week of 11 August	*Upon receipt*: Starting the identification of the strains, according to the usual practice of the laboratory. Sending the link for the result form on serotyping to the participants.
40	Friday 3 October 2025 at the latest	**Deadline** for completing the electronic submission of serotyping results: **3 October 2025.** After this deadline, the result form will be closed.
	November/December 2025	Evaluation of individual laboratory results and Interim summary report.

If you have questions or remarks about this Proficiency Test, please contact:

Wilma Jacobs
E-mail: EURLSalmonella@rivm.nl
http://www.eurlsalmonella.eu/

From the Literature

Salmonella-related Literature selection from Scopus: April – June 2025

Parzygnat J.L., Crespo R., Fosnaught M., Muyyarrikkandy M., Hull D., Harden L., Thakur S.
Megaplasmid Dissemination in Multidrug-Resistant Salmonella Serotypes from Backyard and Commercial Broiler Production Systems in the Southeastern United States
(2025) Foodborne Pathogens and Disease, 22 (5), pp. 322 - 331
ABSTRACT: Over the past decade, there has been a rise in U.S. backyard poultry ownership, raising concern for residential area antimicrobial-resistant (AMR) Salmonella contamination. This study aims to lay the groundwork to better understand the persistence of AMR Salmonella in residential broiler production systems and make comparisons with commercial systems. Ten backyard and 10 commercial farms were sampled at three time points across bird production. Both fecal (n = 10) and environmental (soil, n = 5, litter/compost, n = 5, feeder, and waterer swabs, n = 6) samples were collected at each visit on days 10, 31, and 52 of production for backyard farms and days 10, 24, and 38 of production for commercial farms. AMR Salmonella was characterized phenotypically by broth microdilution and genotypically by whole-genome sequencing. Overall, Salmonella was more prevalent in commercial farm samples (52.31%) over backyard farms (19.10%). Kentucky (sequence type (ST) 152) was the most common serotype found in both backyard and commercial farms. Multidrug-resistant (MDR, resistance to ≥3 or more antimicrobial classes) isolates were found in both production systems, while ciprofloxacin- and nalidixic acid-resistant and intermediate isolates were more prevalent in commercial (33%) than backyard samples (1%). Plasmids that have been associated with MDR were found in Kentucky and Infantis isolates, particularly IncFIB(K)_1_Kpn3 megaplasmid (Infantis). Our study emphasizes the need to understand the selection pressures in disseminating megaplasmids in MDR Salmonella in distinct broiler production systems. ISSN: 15353141

Bentum K.E., Kuufire E., Nyarku R., Osei V., Adu-Addai B., Frye J.G., Jackson C.R., Samuel T., Abebe W.
Comparative Genomic Profiles of Salmonella Typhimurium and Salmonella Dublin Bovine Isolates from the U.S. Indicate Possible Factors Associated with the Host Adaptation of Salmonella Dublin in the Region
(2025) Microorganisms, 13 (4), art. no. 886
ABSTRACT: Salmonella Dublin (S. Dublin) and Salmonella Typhimurium (S. Typhimurium) are commonly linked to bovine salmonellosis. S. Dublin is, however, considered a bovine-adapted serovar for primarily infecting and thriving in cattle. Using S. Typhimurium (a generalist serovar) as a benchmark, this study investigates genomic factors contributing to S. Dublin's adaptation to cattle hosts in the U.S. A total of 1337 S. Dublin and 787 S. Typhimurium whole-genome sequences from bovine sources were analyzed with CARD (version 4.0.0), ARG-NOTT (version 6), and AMRfinderPlus (version 4.0.3) for antimicrobial resistance (AMR) genes; VFDB and AMRfinderPlus for virulence genes; AMRFinderPlus for stress genes; and Plasmidfinder for plasmids. Existing clonal groups among isolates of the two serovars were also investigated using the Hierarchical Clustering of Core Genome Multi-Locus Sequence Typing (HierCC-cgMLST) model. The results revealed minimal genomic variation among S. Dublin isolates. Comparatively, the IncX1 plasmid was somewhat exclusively identified in S. Dublin isolates and each carried an average of four plasmids (p-value < 0.05). Furthermore, S. Dublin isolates exhibited a higher prevalence of AMR genes against key antimicrobials, including aminoglycosides, beta-lactams, tetracyclines, and sulfonamides, commonly used in U.S. cattle production. Additionally, Type VI secretion system genes tssJKLM and hcp2/tssD2, essential for colonization, were found exclusively in S. Dublin isolates with over 50% of these isolates possessing genes that confer resistance to heavy metal stressors, like mercury. These findings suggest that S. Dublin's adaptation to bovine hosts in the U.S. is supported by a conserved genetic makeup enriched with AMR genes, virulence factors, and stress-related genes, enabling it to colonize and persist in the bovine gut. ISSN: 20762607

Roche S., Renaud D., Gillies M., Nobrega D., Leung D.
Salmonella Dublin in dairy cattle: Review of state of the science

(2025) The Canadian veterinary journal = La revue veterinaire canadienne, 66 (4), pp. 446 - 455
ABSTRACT: Background: Salmonella enterica subsp. enterica serovar Dublin (Salmonella Dublin) is a Gram-negative bacterium of increasing importance to the Canadian cattle sector. Objective animal and procedure: The objective of this narrative literature review was to provide an overview of the epidemiology of Salmonella Dublin in cattle, highlight risk factors associated with infection, discuss diagnostic methods, and review prevention and control strategies, with a specific focus on the Canadian context. Results: Approximately 3 to 30% of dairy farms are positive for Salmonella Dublin, depending on the province. This bacterium can cause high levels of morbidity and mortality and is best controlled by preventing carrier cattle from gaining access to uninfected farms. Conclusion and clinical relevance: Salmonella Dublin is an emerging pathogen and action is necessary to control its spread. ISSN: 00085286

Bolzoni L., Scaltriti E., Bracchi C., Angelone S., Menozzi I., Taddei R., Alba P., Carfora V., Diaconu E.L., Morganti M., Dodi A., Berni M., Manni L., Vinci M., Tambassi M., Mazzera L., Venturelli I., Ambretti S., Battisti A., Pongolini S.
Emergence of Salmonella enterica carrying blaOXA-181 carbapenemase gene, Italy, 2021 to 2024
(2025) Eurosurveillance, 30 (13), art. no. 2500175
ABSTRACT: Between 2021 and 2024, we detected carbapenemase gene blaOXA-181 in 16 of 11,398 Salmonella enterica (SE) isolates: 10 SE 1,4,[5],12:i:-, three Bovismorbificans, two London and one Rissen from pigs, humans, pork meat and wild roe deer. The gene was first detected in pig isolates, later in humans, suggesting zoonotic transmission. Phylogenetic analysis indicated that horizontal transfer, mainly through plasmids, contributed to the spread. These findings highlight a possible emerging public health threat and the importance of One Health surveillance. ISSN: 1025496X

Armstrong C.M., Chen C.-Y., Xie Y., Atencia J., Pierre S., He Y., Lee J., Dykes G.E., Johnson K., Froment B., Martinos S., Capobianco J.
Quantification of Salmonella in Raw Poultry Using Droplet Digital PCR With a Whole Cell, Enrichment-free Approach
(2025) Journal of Food Protection, 88 (5), art. no. 100498
ABSTRACT: Salmonella contamination in poultry remains a persistent public health challenge, despite ongoing regulatory efforts to reduce its presence. Traditional culture-based enrichment methods commonly employed for detecting Salmonella have inherent limitations, such as biases in bacterial growth and inaccurate quantification of initial contamination levels. This study introduces an enrichment-free approach for quantifying Salmonella in raw poultry, utilizing the Pathotrak system for bacterial separation and concentration, followed by Droplet Digital PCR (ddPCR) for absolute quantification. Our findings highlight that whole-cell preparations within ddPCR droplets yield significantly higher detection efficiency compared to extracted DNA, likely due to the reduced loss of genetic material during processing. The method was validated by correlating theoretical inoculation levels with ddPCR measurements, resulting in a strong linear relationship ($R2 = 0.903$) and a slope of 0.99, indicating high accuracy. Residuals from the regression model were normally distributed, confirming its validity. This platform offers a robust, rapid, and precise tool for detecting low levels of Salmonella in poultry products without enrichment, making it a more accurate and efficient approach to bacterial quantification in complex food matrices. ISSN: 0362028X

He Y., Jia Q., Cai K., Xu S., Li H., Xie Q., Qiu Y., Zhang L., Jiao X.
The global, regional, and national burden of Invasive Non-typhoidal Salmonella (iNTS): An analysis from the Global Burden of Disease Study 1990–2021
(2025) PLOS Neglected Tropical Diseases, 2025, art. no. e0012960
ABSTRACT: Objectives Invasive Non-typhoidal Salmonella (iNTS) can cause serious, life-threatening, and invasive infections, posing great challenges to public health. We aimed to systematically review the burden of iNTS disease based on Global Burden of Diseases (GBD) 2021. Methods We extracted data for the incidence, death, and disability-adjusted life-years (DALYs) associated with iNTS from GBD 2021, providing an overview of its epidemiology while examining trends from 1990 to 2021. Additionally, we decomposed changes of iNTS-related burden, and quantified cross-country inequalities. Results GBD 2021 estimated 509976(95%UI,413361 to 606167) incident cases of iNTS worldwide in 2021, with the most cases and highest age-standardized rate (ASR) in Western Sub-Saharan Africa. The low SDI region had the most cases of iNTS in 2021. The incidence and DALYs rates were highest in the Low SDI region. Among all age groups, the incidence, death, and DALYs rate of iNTS were primarily concentrated among the follow-ing age

groups: <1 year, 1-4 years, 5–9 years, 10–14 years, and 15–19 years. The highest rates were observed in the <1-year group. The results of joinpoint regression analysis revealed that the global burden of iNTS increased overall from 1990 to 2005, followed by notable decrease from 2005 to 2021 at varying rates. Decomposition analysis found that population growth (103.93%) and epidemiological change (48.34%) were responsible for motivating the changes in iNTS global burden. Cross-country inequality analysis revealed that the SDI-related inequalities were moderated from 1990 to 2021. Conclusions The global burden of iNTS is still high, and the distribution patterns vary across different countries and territories. The global burden of iNTS was primarily noteworthy among children and adolescents, with the highest burden among infants. The changes in the iNTS burden were primarily driven by population growth and epidemic transition. Despite varying iNTS burdens across different SDI regions, SDI-related inequalities across countries became moderated gradually over time. This study reported the global disease burden and temporal trends of iNTS disease, and underscores the need for age-and region-specific strategies to mitigate the corresponding global burden. ISSN: 19352727

Samper-Cativiela C., Torre-Fuentes L., Diéguez-Roda B., Maex M., Ugarte-Ruiz M., Carrizo P., Hernández M., Höfle Ú., Sáez J.L., de Frutos C., Agüero M., Moreno M.Á., Domínguez L., Herrera-León S., Alvarez J.
Molecular epidemiology of Salmonella Enteritidis in humans and animals in Spain
(2025) Antimicrobial Agents and Chemotherapy, 69 (4)
ABSTRACT: Salmonella Enteritidis, the most prevalent serovar-causing human gastroenteritis, has been traditionally linked to poultry sources. Although antimicrobial resistance (AMR) is not common in this serovar, increasing levels of resistance to fluoroquinolones and ampicillin have been reported in the last few years. Here, 298 isolates retrieved from different sources (human, livestock, wildlife, food, and environment) and years (2002–2021) in Spain were analyzed to evaluate their diversity, the distribution of AMR-conferring genes (ARGs), and mutations and reconstruct the epidemiology of infection due to this serovar. Isolates were clustered in two major clades (I and II), with strains in clade I (including 61.5% of all human isolates) displaying a pan-susceptible phenotype and not carrying AMR determinants. In contrast, clade II included 80.7% of isolates from animal/food/environmental sources, with the majority (69.8%) harboring mutations in the quinolone resistance determinant regions (QRDR). ARGs, although rare, were mostly found in clade II strains that also carried plasmid replicons, among which IncX1 was the most common. Although higher levels of phenotypic resistance were found in animal isolates, extended-spectrum beta-lactamase, plasmid-mediated AmpC, and carbapenemase-encoding genes were only found among human isolates. In summary, the majority of human and animal isolates from Spanish sources in our collection were classified in different phylogenetic branches, suggesting that additional sources are contributing to the occurrence of foodborne infections in Spain. Furthermore, the different distributions of virulence factors and ARGs in isolates from different sources and their association with specific plasmids suggest the presence of different dynamics contributing to the selection of resistant strains. ISSN: 00664804

Rocha A.D.L., Lima L.A., Sales G.F.C., Silva N.J., Gomes M.L.R., Pereira W.E., Givisiez P.E.N., Brown E.W., Allard M.W., Bell R.L., Toro M., Meng J., Oliveira C.J.B.D.
Predictors of Salmonella enterica contamination in agricultural and livestock-impacted natural watersheds
(2025) Environmental Pollution, 371, art. no. 125782
ABSTRACT: Salmonella enterica (S. enterica), a ubiquitous zoonotic foodborne pathogen, remains a worldwide public health hazard and economic burden. In recent years, outbreaks associated with the consumption of plant-based foods probably contaminated by irrigation water highlights the importance of water sources. This study investigated anthropogenic and environmental factors influencing S. enterica occurrence in natural watersheds impacted by agricultural and livestock industries in a 10-month longitudinal study in Paraiba, Brazil. Water samples were obtained from multiple sites within the three major river basins by modified Moore Swabs (MMS) and processed by conventional S. enterica isolation methodologies. Physicochemical parameters, climate, and human activities near the water sources were recorded. A logistic regression model was fitted using Generalized Linear Model (GLM) and further adjusted according to the selected variables using the Least Absolute Shrinkage and Selection Operator (LASSO) method. A non-statistical decision tree model was also fitted using the rpart package in R. Season, rainfall regime, water physicochemical features, and anthropogenic activities were significantly associated with S. enterica contamination. According to the regression tree analysis, rainfall within the sampling month was the strongest predictor of S. enterica

recovery, potentially due to leaching from soil or runoff from adjacent human and animal activities. The complexity of multivariate conditions driving S. enterica contamination in surface waters highlights the need for region-specific investigations. ISSN: 02697491

Zhang R., Yang T., Liu Z., Liao X., Ahn J., Sant'Ana A.S., Feng J., Ding T.
Inducible adhesion and biofilm formation in Salmonella linked to adaptive fatty acid metabolism
(2025) Food Research International, 206, art. no. 116006
ABSTRACT: Salmonella is one of the leading causes of foodborne illness, worldwide. The biofilm formation of this bacterium may be caused by its persistence in the food environment. However, the trigger factors and adaptive metabolism in Salmonella for biofilm formation are not fully known. Here, we observed the distinct biofilm formation of S. typhimurium 2220 in response to the presence of medium-chain fatty acids and found that the level of biofilm formation was positively linked to the chain length of the medium-chain fatty acids. Through dynamics analysis of biofilm formation, we discovered that decanoic acid (10-carbon fatty acid, C10) enhanced the initial attachment of strain 2220 on both biotic and abiotic surfaces, while compromising motility. The attachment was not achieved due to the inhibition of flagella expression but driven by enhanced energy metabolism which was shown as intracellular acidification and elevated ATP level. We found the S. typhimurium 2220 strain could adaptively metabolize fatty acid by enhancing the expression of fadL gene. In summary, Salmonella biofilm formation was inducible by adaptive fatty acid metabolism which resulted in the enhanced attachment. Our results uncovered valuable insights into the physiological alteration of this foodborne pathogen, suggesting the potential biofilm trigger in the food environment. These findings could facilitate the development of a new antibiofilm strategy. ISSN: 09639969

Faliarizao N.T., Fanfan J., Randriamiarintsoa N., Siddiq M., Bergholz T.M., Dolan K.D.
Modeling the combined impact of water activity and temperature on Salmonella Montevideo thermal inactivation on dried chili peppers
(2025) Journal of Food Science, 90 (4), art. no. e70201
ABSTRACT: Salmonella contamination in low-moisture foods remains a continuing food safety and public health problem. The World Health Organization ranked unprocessed red chili peppers as the spice with the highest risk of Salmonella contamination in a risk assessment-based report in 2022. Therefore, appropriate mitigation strategies are required to control Salmonella contamination in dried chilies. The objectives of this research were to investigate thermal inactivation of Salmonella on dried chili peppers at aw 0.33–0.97 and estimate thermal resistance parameters under isothermal and dynamic conditions. The dried chili peppers were inoculated with S. Montevideo and conditioned in a humidity-controlled chamber to achieve the aw of 0.33, 0.50, and 0.97. The samples were placed into 1-mm thick aluminum test cells and heated at 55, 60, 65, and 70°C to estimate the thermal inactivation parameters using the log-linear/modified-Bigelow model. The results showed that the aw played a key role in accurately describing Salmonella lethality on dried chili pepper. At 65°C, a 3-log reduction of S. Montevideo required 100 min at aw = 0.33, compared to only 20 min at aw = 0.50. The modified Bigelow model under dynamic conditions described inactivation significantly better (root mean squared error [RMSE] = 0.646 and corrected Akaike information criterion [AICc] = −120.97) than the modified Bigelow model under isothermal conditions (RMSE = 0.707 and AICc= −76.71). This study provides the food industry with valuable data to optimize thermal processing conditions and improve safety protocols for chili-based products, thereby reducing the risk of Salmonella contamination. ISSN: 00221147

Pharo F., Couto Serrenho R., Greer A.L., Oremush R., Habing G., Gillies M., Keunen A., Renaud D.L.
Exploring the impact and transmission of Salmonella Dublin in crossbred dairy calves
(2025) Journal of Dairy Science, 108 (4), pp. 4225 - 4233
ABSTRACT: Salmonella enterica serotype Dublin (S. Dublin) is an increasing concern within the dairy industry, particularly due to its effect on morbidity and mortality in young dairy calves. The objective of this cohort study was to evaluate the associations between S. Dublin infection and health and growth in young crossbred dairy calves, as well as model the transmission of S. Dublin within this cohort. A total of 160 crossbred male and female dairy calves arrived at a commercial calf raising facility. Research staff observed calves twice daily to evaluate fecal consistency and for signs of respiratory disease, with all individual treatments recorded by facility staff. Blood samples were collected upon arrival (0 d) and departure (77 d) from the facility and submitted to the Animal Health Laboratory at the University of Guelph (Guelph, ON, Canada) for S. Dublin testing using an ELISA.

Fecal samples were collected at arrival, 7 d, 14 d, and 77 d, with bacterial culture conducted to identify the presence of S. Dublin. Calves that died during the study (n = 23) had a postmortem completed by a veterinarian, with samples submitted for bacterial culture. Poisson regression models, Cox proportional hazard models, and a linear regression model were built using Stata 18 to assess the effect of S. Dublin positivity (defined as positive based on fecal culture, serum ELISA, or both at one of the time points) on respiratory disease, diarrhea, and ADG. The effective reproductive number (Re) was estimated to quantify the transmission of S. Dublin within the calves. Salmonella Dublin positivity at arrival, 7 d, 14 d, and 77 d were 5.6%, 11.4%, 1.3%, and 24.4%, respectively. Combining serum ELISA, fecal culture, and postmortem testing, 45.6% of calves tested positive for S. Dublin at least once during the study period. Calves that were positive for S. Dublin had a greater number of observations with respiratory scores of ≥5 and fewer observations with a respiratory score of 0, especially in calves weighing <42.6 kg at arrival. There was no association with growth, or the number of observations of diarrhea. The estimated Re values ranged between 1.32 and 1.79. Salmonella Dublin was associated with increased respiratory disease, though it did not affect growth or incidence of diarrhea. The estimated Re values underscore the epidemic potential of this bacterium, emphasizing the need for further research on effective measures to limit its spread. ISSN: 00220302

Oliveira S.B.S., Oliveira M.M., Lopes L.S., Pia A.K.R., Virgilio-da-Silva J.V., Sant'Ana A.S.
Salmonella enterica Senftenberg (IOC 2319) and Salmonella enterica Typhimurium (ATCC 14028) under low water activity stress: Effects on culturability and cell viability
(2025) International Journal of Food Microbiology, 433, art. no. 111117
ABSTRACT: Salmonella enterica is one of the most important foodborne pathogens for public health worldwide. When Salmonella enterica is exposed to low water activity, changes in cellular behavior may occur. These changes can impact the cells that form a colony on specific nutrient media (culturability) and the metabolically or physiologically active cells (viability) of Salmonella cells, with consequences for the analytical methods and food safety management. Thus, this study studied the impact of continuous and recurrent exposure of S. Senftenberg IOC 2319 and S. Typhimurium ATCC 14028 to water activity (aw) treatments between 0.4 and 0.99 over 24 h and five days. The culturability was determined using the plate count technique, and cell viability was measured by flow cytometry. S. Senftenberg IOC 2319 was shown to be more resistant to aw stress than S. Typhimurium ATCC 14028. A total of 6.9 and 8.5 log CFU/mL reductions were observed for S. Senftenberg IOC 2319 and S. Typhimurium ATCC 14028. Although both bacteria lost culturability on plate counting, the flow cytometry results demonstrated that they remained viable between 7.09 and 9.23 log CFU/mL for S. Senftenberg IOC 2319 and S. Typhimurium ATCC 14028, respectively. This result opens questions about whether they can recover and adapt a food matrix, causing a greater risk to the consumer. In conclusion, low water activity stresses can cause significant changes in Salmonella strains, and the use of Flow cytometry can be a valuable technique to understand the physiological status of microorganisms better and suggest the importance of safer and faster methods for standard microbiological evaluation. ISSN: 01681605

Chaggar H.K., Hudson L.K., Orejuela K., Thomas L., Spann M., Garman K.N., Dunn J.R., Denes T.G.
Salmonella enterica serovar Braenderup shows clade-specific source associations and a high proportion of molecular epidemiological clustering
(2025) Applied and Environmental Microbiology, 91 (4)
ABSTRACT: Salmonella enterica serovar Braenderup (S. enterica ser. Braenderup) is an important clinical serovar in the United States. This serovar was reported by the CDC in 2017 as the fifth most common Salmonella enterica serovar associated with outbreaks in the United States, which have been linked to both fresh produce and food animal products. The goals of this study were to compare the relatedness of human clinical isolates from southeastern USA (Tennessee (n = 106), Kentucky (n = 48), Virginia (n = 252), South Carolina (n = 109), Georgia (n = 159), Alabama (n = 8), Arkansas (n = 26), and Louisiana (n = 91)) and global clinical (n = 5,153) and nonclinical (n = 1,053) isolates obtained from the NCBI. Additionally, we also examined the population structure of S. enterica ser. Braenderup strains (n = 3,131) on EnteroBase and found that all the strains of this serovar are associated with a single cgMLST eBurst group (ceBG 185), confirming that this serovar is monophyletic. We divided the S. enterica ser. Braenderup population into two clades (Clade I and Clade II) and one clade group (Clade Group III). The composition of distinct environmental isolates in the clades differed: Clade I was significantly associated with produce (90.7%; P < 0.0001) and water, soil, and sediment (76.9%; P < 0.0001), and

Clade II was significantly associated with poultry environments (62.8%; P < 0.0001). The clade-specific gene associations (e.g., Clade I-associated competence proteins and cytochrome_c_asm protein and Clade II-associated heme-exporter protein and dimethyl sulfoxide [DMSO] reductase-encoding genes) provide potential insights into possible mechanisms driving environmental adaptation and host–pathogen interaction. Phylogenetic analyses identified 218 molecular epidemiological clusters in the current study, which represented a greater proportion of potentially outbreak-related isolates than previously estimated. ISSN: 00992240

Drauch V., Ghanbari M., Reisinger N., Mohnl M., Hess C., Hess M.
AUTHOR FULL NAMES: Drauch, Victoria (57216868626); Ghanbari, Mahdi (57132281100);
Differential effects of synbiotic delivery route (Feed, water, combined) in broilers challenged with Salmonella Infantis
(2025) Poultry Science, 104 (4), art. no. 104890
ABSTRACT: Salmonella enterica subsp. enterica serovar Infantis (S. Infantis) presents a persistent and multi-drug-resistant threat to poultry production, highlighting the need for effective control strategies. This study evaluated the impact of a S. Infantis infection in broiler chickens across various parameters, including organ colonization, gut microbiota, and immune function. We also assessed the mitigation potential of a synbiotic, multispecies feed additive, administered via three routes applicable for the field: feed only, drinking water only, and a combination of both. Our results demonstrated that the combined administration route yielded notably positive effects on several parameters, followed by the drinking-water only administration. This approach resulted in significant improvements in gut microbiota health, characterized by increased levels of beneficial microbes such as Lactobacillus, Ligilactobacillus, and Butyricicoccus, and a decrease in potentially harmful genera from the Proteobacteria phylum. Reduction of S. Infantis load was observed in caecum, ileum, and spleen over time albeit shedding was not influenced. The drinking water-only administration showed a significant reduction of S. Infantis colonization in the caecum on the last sampling day. Immune response analysis indicated no significant differences in serum antibody levels between control and treatment groups. These findings underscore the impact of both combined and drinking water-only synbiotic, multispecies feed additive administration on the gut microbiota and a possible route for reducing S. Infantis in poultry production. The obtained data provide valuable guidance for optimizing synbiotic use in commercial poultry management, enabling enhanced pathogen control and improved gut health. ISSN: 00325791

Fernandez Moreno T., Kołcz A., Qaheri M., Lewandowski D., Sulik A., Toczyłowski K.
Campylobacter and Salmonella infections in children hospitalized with gastroenteritis in Northeastern Poland, 2020–2023
(2025) European Journal of Pediatrics, 184 (5), art. no. 280
ABSTRACT: This study aimed to investigate the epidemiology, seasonal trends, and clinical characteristics of Campylobacter and Salmonella infections in children hospitalized with acute gastroenteritis (AGE) in Northeastern Poland from 2020 to 2023. The research sought to address the scarcity of localized data on these bacterial pathogens and identify key clinical and demographic markers to improve diagnostic and therapeutic strategies. A retrospective analysis was conducted on medical records of children aged 0–17 years hospitalized at the Bialystok Children's Clinical Hospital. Stool samples were systematically collected and tested for bacterial pathogens following World Health Organization guidelines. Confirmed cases of Campylobacter and Salmonella infections were analyzed for demographic, clinical, and laboratory characteristics. Among 3,392 hospitalized children with acute gastroenteritis, bacterial pathogens were identified in 560 cases, with Campylobacter (33%) and Salmonella (32%) being the most common. A slight male predominance was noted across both pathogens. Salmonella infections were associated with significantly greater clinical severity, characterized by longer duration of diarrhea, higher frequency of vomiting, more persistent fever, greater dehydration, notably elevated inflammatory markers and longer hospital stays compared to Campylobacter. Campylobacter was notably more prevalent among children younger than 2 years. Seasonal peaks for both pathogens consistently occurred during the summer months. Conclusion: Campylobacter and Salmonella are significant contributors to bacterial AGE in children, with distinct clinical and demographic profiles. Public health measures and enhanced diagnostics are critical to reducing the burden of these infections, particularly among younger and vulnerable children. (Table presented.) ISSN: 03406199

Boucher L., Hélie P., Fairbrother J.-H., Chénier S., Morin S., St-Jean G.
Bovine abortions due to the rare Salmonella serovars Kingston and Kedougou

(2025) Journal of Veterinary Diagnostic Investigation, 37 (3), pp. 475 - 478
ABSTRACT: Two aborted bovine fetuses were submitted (6 mo apart) with portions of their chorioallantois for postmortem examination. In both cases, microscopic examination revealed large numbers of gram-negative bacilli in the chorionic vessels and, to a lesser extent, in capillaries and venules of fetal organs of one fetus; the bacteria were not associated with noticeable inflammation or necrosis. Salmonella enterica subsp. enterica serovar Kingston was isolated from the placenta, abomasal contents, lung, and liver in case 1; Salmonella serovar Kedougou was isolated from the abomasal contents, lung, and liver in case 2. Both are rare serovars that have been isolated from various species but are not known to cause clinical disease in cattle, and, to our knowledge, have not been reported as the cause of abortion in dairy cattle. ISSN: 10406387

Gonzalez-Perez A.C., Landgren H., Vainio A., Kitowska W., Pihlajasaari A., Leinonen E., Kuronen H., Lienemann T., Tapanainen H., Kaartinen N.E., Rjabinina J., Sõgel J., Rimhanen-Finne R.
A multi-country outbreak of Salmonella Mbandaka linked to pre-cooked, frozen chicken meat in ready-to-eat products, Finland, 2022 to 2023
(2025) Eurosurveillance, 30 (17), art. no. 2400602
ABSTRACT: In May 2022, the Finnish Institute for Health and Welfare observed an increase in Salmonella Mbandaka cases. Whole genome sequencing (WGS) linked the outbreak strain to a previously reported strain in the United Kingdom. From April 2022 to January 2023, 97 cases were reported across 18 of Finland's 21 hospital districts, with a median age of 27 years (range <1–74 years) and 61% female cases. Based on trawling interviews and national food consumption data, cases were more likely to have eaten at a restaurant or takeaway (odds ratio (OR) = 115; 95% confidence interval (CI): 52–256; p < 0.001) or consumed poultry products (OR = 28; 95% CI: 7–115; p < 0.001). A case–case study linked cases with consumption of ready-to-eat products containing chicken from a specific company (OR = 28; 95% CI: 1.9–1,361; p = 0.004). Traceback investigations identified a pre-cooked, frozen chicken meat product from a country outside the European Union as the likely source. Salmonella Mbandaka was isolated from cases and linked by WGS to this chicken meat product. Our findings highlight the potential health risk of pre-cooked chicken meat containing Salmonella and the value of case–case studies and product images to assist recall during food-borne outbreak investigations. ISSN: 1025496X

Madad A., Vasser M., Viazis S., Neil K.P., Kirchner M., Blessington T., Pightling A., Ingram D.T., Grunenfelder L., Hughes S., Bell R.L., Wang H., Nork B., Fernandez E., Gerrity K., Ladines E., Hise K., Hummadi O., Barnes A., Grant K., Lowe A.-M., Kearney A., Gieraltowski L., Salter M., Bazaco M., Carstens C.K.
An International Outbreak Investigation of Salmonella Enteritidis Infections in the United States and Canada Linked to Peaches – 2020
(2025) Journal of Food Protection, 88 (6), art. no. 100519
ABSTRACT: During August–October 2020, United States federal, state, and Canadian partners investigated an outbreak of Salmonella Enteritidis infections, in the U.S. and Canada, linked to fresh, whole peaches packed and supplied by a grower and packer with multiple orchards (Farm A). In the U.S., a total of 101 ill people and 28 hospitalizations were reported in 17 states, while in Canada, 57 ill people and 12 hospitalizations were reported in two Canadian provinces. The U.S. traceback investigation included 14 points of service (POS), representing 18 illnesses in eight states. Multiple distributors, packinghouses, and orchards supplied bagged and loose peaches during the timeframe of interest to identified POS, with peaches and packinghouses linked to Farm A being the primary source. Orchards of interest were identified for peach fruit, orchard tree leaf, and soil drag swab sample collection using traceback and geospatial analysis. Geospatial analyses showed that several orchards were in proximity to animal operations. While none of the Salmonella isolates recovered matched the outbreak strain, Salmonella Alachua was recovered from peaches and leaf samples, and Salmonella Montevideo was recovered from orchard tree leaves. Whole genome sequencing indicated that these Salmonella isolates were closely related to historical poultry and cattle isolates. Farm A voluntarily recalled loose peaches sold from June 1 to August 3, 2020, and bagged Brand A conventional and organic peaches sold from June 1 to August 19, 2020. Recalled products were likely distributed to at least 14 different countries. Findings suggest that adjacent animal operations may be a potential contributing factor to Salmonella contamination of peaches, with windborne or fugitive dust as a possible route. The findings from this first reported international outbreak of Salmonella linked to peaches grown in the U.S. highlight the importance of grower awareness of adjacent land use. ISSN: 0362028X

Damianos A., Tsitsos A., Economou V., Gioula G., Haidich A.-B.
Systematic review and meta-analysis of the occurrence of ESBL-producing Escherichia coli and Salmonella spp. in foods of animal origin in Europe
(2025) Food Control, 171, art. no. 111127
ABSTRACT: Development of ESBL-resistant bacteria is mainly attributed to cephalosporin use in human and veterinary medicine. Although humans are considered the primary reservoir for ESBL-producing bacteria, the role of alternative reservoirs, like animals, foods, and environment, seem to contribute to their emergence. Transmission of ESBL E. coli and/or Salmonella from foods of animal origin to humans has been proposed, however, limited evidence exists. This study aimed to estimate the pooled prevalence and range of ESBL E. coli and Salmonella spp. in different foods of animal origin in Europe and to identify the main characteristics (ESBL genes, sequence types, multi-drug resistance, phylogroups, and serotypes) of the isolates in each reservoir. A systematic review and a meta-analysis were performed according to PRISMA guidelines. Three bibliographic databases (MEDLINE via PubMed, Scopus, epistemonikos.org), were searched for eligible studies from 2011 to December 2023. A total of 81 studies (n = 81) were included in the systematic review and 63 (n = 63) were eligible for a meta-analysis. The pooled prevalence (95% confidence interval) of ESBL E. coli in Europe was 40% (n = 33, 30–52%) in chicken meat, 5% (n = 19, 3–9%) in pork, 3% (n = 12, 2–5%) in beef, 5% (n = 4, 0–28%) in minced meat, 4% (n = 3, 0–32%) in game meat, 11% (n = 7, 0–40%) in poultry meat, 0% (n = 5, 0–1%) in RTE foods, 2% (n = 7, 0–4%) in seafoods, 2% (n = 6, 0–10%) in milk, 0% (n = 3, 0–2%) in cheese, and 3% (n = 2, 1–6%) in eggs. Six studies on ESBL Salmonella spp. in animal-origin foods were retrieved, with only two of them reporting ESBL Salmonella spp. in poultry meat and pork. Several ESBL genes (n = 29) and sequence types (n = 145) were found in ESBL E. coli of all examined food categories. blaCTX-M-1 was the most prevalent ESBL gene in E. coli, while blaCTX-M-14, blaCTX-M-15, blaSHV-12, and blaTEM-52 were found in most food categories. ST131 has been detected in chicken meat and seafood samples. Chicken meat was identified as a potential reservoir of ESBL E. coli among foods of animal origin. Insufficient data were available for Salmonella spp. preventing drawing any conclusion. ISSN: 09567135

Bermudez-Aguirre D., Carter J., Niemira B.A.
An Investigation About the Historic Global Foodborne Outbreaks of Salmonella spp. in Eggs: From Hatcheries to Tables
(2025) Comprehensive Reviews in Food Science and Food Safety , 24 (3), art. no. e70202
ABSTRACT: Salmonella enterica serovar Enteritidis is the main pathogen of concern in eggs and egg products, although other serotypes have been reported worldwide. Egg processing guidelines and regulations vary widely from country to country; some are ambiguous, incomplete, or obsolete. However, foodborne outbreaks linked to Salmonella spp. and eggs continue to be reported worldwide and are constantly increasing, with many illnesses, deaths, and significant economic impact. This review aims to conduct a comprehensive investigation in egg processing regulations and Salmonella foodborne outbreaks in several countries of six continents in the last 50 years. The manuscript presents and contrasts the lack of surveillance programs, regulations, adequate testing, and traceability in some countries but also the creation of new regulations to reduce the incidence of Salmonella in eggs. One of the newest trends in the egg industry is related to farmers markets and backyard egg producers, which might represent a food safety gap in the production chain if these are not regulated. The review also discusses some interventions and approaches to control the growth and presence of Salmonella in fresh eggs, such as refrigeration. Though regulations in many countries do not require eggs to be under refrigeration and some other countries do not have enough access to them, jeopardizing the food safety of the product. Published 2025. This article is a U.S. Government work and is in the public domain in the USA. Comprehensive Reviews in Food Science and Food Safety published by Wiley Periodicals LLC on behalf of Institute of Food Technologists. ISSN: 15414337

Williams M.S., Ebel E.D., Robertson-Hale K., Shaw S.L., Kissler B.W.
Differences in Salmonella Serotypes in Broiler Chickens Within and Between Slaughter Establishments in the United States
(2025) Journal of Food Protection, 88 (6), art. no. 100506
ABSTRACT: There are more than 2500 serotypes of Salmonella enterica. One interesting feature of this bacterium is that regardless of whether samples are collected from food commodities, a single animal species, humans, or a specific environmental setting, only about 5 serotypes constitute 50% or more of all positive samples. Another interesting feature of Salmonella is that the most common serotypes are not consistent across time or broad geographic region. Examples of this phenomenon are that Salmonella Heidelberg was the third most common serotype found in United States human illness cases in 1996,

but the 53rd most common serotype in 2022. An example of serotype-specific spatial clustering is the occurrence of Salmonella Weltevreden predominantly in continental Southeast Asia. Clustering in space and time presents opportunities to control more pathogenic serotypes. In this study, data from a seven-month survey of broiler chicken carcass production in the United States are used to assess how the occurrence of the dominant serotypes changes as carcasses move through the production process. Samples were collected at rehang and postchill, with the number of positive samples at each location being 2909 and 233, respectively. Different intervention strategies may impact specific serotypes differently. Additional analyses demonstrate how serotypes are clustered (or not) as a function of production volume and corporate ownership. Understanding how the occurrence of serotypes varies across the industry can provide insights into factors that lead to the clustering of specific serotypes and has the potential to help identify intervention strategies that effectively reduce the risk of human salmonellosis.
ISSN: 0362028X

Cason E.E., Reina M., Ayala-Velasteguí D., Shariat N.W.
Sampling method influences Salmonella detection and quantification in pre-harvest commercial broiler production
(2025) Poultry Science, 104 (5), art. no. 104963
ABSTRACT: Effective pre-harvest Salmonella monitoring in broilers relies on accurate, reliable, and reproducible evaluation of pre-harvest Salmonella. In this study, six sampling methods were evaluated and compared to assess Salmonella prevalence and quantification during broiler production across three iterative experiments. In experiment one, bootsocks, electrostatic pad-rollers, feather swabs, cloacal swabs, fecal grabs, and litter grabs were collected from 24 houses across 10 farms (n = 288 samples). In the second experiment, bootsocks, bootsock-rollers, and feather swabs were collected in 16 houses on seven farms (n = 128). Bootsocks and bootsock-rollers were selected as the most reproducible sampling method. In experiment three both methods were performed in triplicate in 20 houses on 10 farms (n = 240). In all experiments, prevalence was determined by qPCR and by culture, then compared by Fisher's Exact test between and McNemar's test within methods. Salmonella was quantified by qPCR and Ct-values were compared using one-sided F-test. In experiment one, prevalence differed between methods by qPCR (p = 0.0150) only and the best performing sampling methods were bootsocks (42/48 culture and 41/48 qPCR positive), feather swabs (42/48 and 36/48), and electrostatic pad-rollers (35/48 and 34/48). In experiment 2, feather swabs differed by qPCR prevalence (p = 0.0004). Bootsocks (30/32 culture and 28/32 qPCR positive) and bootsock-rollers (31/32 and 32/32) performed best. In experiment 3, qPCR prevalence (210/240) was greater than culture (167/240) (p = 0.0021), but no differences were observed between methods or replicates. The average Ct-value for bootsocks and bootsock-rollers were 37.8 and 38.9, respectively and there was no difference in their variance (p = 0.8061). A linear mixed-effect model found that farm contributed 36.34 % of the variance observed while house, house-side, and replicate accounted for 24.69 %, 4.68 % and 3.85 %, respectively. This study shows that sampling methods directly influence both Salmonella detection and load recovery. For surveillance sampling, bootsocks and bootsock-rollers were found to best indicate pre-harvest Salmonella. These two methods were highly reproducible, user friendly, and provide the most reliable Salmonella results indicating the Salmonella prevalence in broiler flocks during production.
ISSN: 00325791

Selim S.
A Comprehensive Review of Antibiotic Susceptibility Patterns in Salmonella enterica Strains Isolated from Food
(2025) Journal of Pure and Applied Microbiology, 19 (2), pp. 818 - 833
ABSTRACT: One of the most important health problems in the world, especially in developing countries, is the spread of multidrug-resistant foodborne pathogens. Such resistant pathogens can spread as an epidemic due to enhanced resistance against therapeutic antibiotics and/or the antibiotics used for growth promotion in livestock. Salmonella enterica strains can cause gastroenteritis leading to more complicated disorders in humans. Contaminated food can quickly spread the pathogen to a larger population, resulting in an epidemic. This review summarizes the antibiotic susceptibility patterns of Salmonella enterica strains isolated from food. ISSN: 09737510

Polat İ., Güngör İ., Şen B.
Prevalence of Salmonella enterica Serotypes Isolated From Broiler Liver and Their Antibiotic Resistance Profiles
(2025) Journal of Food Protection, 88 (7), art. no. 100535

ABSTRACT: Salmonella is an important foodborne pathogen of worldwide significance. The objective of this research was to determine the prevalence of Salmonella in chicken livers in Türkiye. This study obtained 104 packaged chicken liver samples, 13 from each of the 8 brands, from the province of Kırklareli, northwest of Türkiye. The overall prevalence of Salmonella spp. in liver samples was 36.5%. The 38 Salmonella isolates obtained were serotyped by slide agglutination using antisera by the Kauffmann White Le Minor Scheme. Based on standard serotyping results, the dominant serovar was S. Infantis (81.6%), followed by S. Enteritidis (13.1%) and S. Agona (5.3%). Antimicrobial susceptibility testing of 38 Salmonella isolates was performed using disk diffusion method. The Salmonella isolates (n = 38) were resistant to cefepime (60.5%), chloramphenicol (57.9%), trimethoprim-sulfamethoxazole (50.0%), amoxicillin-clavulanic acid (39.5%), azithromycin (28.9%), ofloxacin (26.3%), and cefoxitin (13.2%). Multidrug-resistance (MDR) accounted for 47.4% of Salmonella isolates. MDR was observed in S. Infantis (17/31, 54.8%) and S. Agona (1/2, 50.0%), nevertheless not in S. Enteritidis. ISSN: 0362028X

Bentum K.E., Nyarku R., Kuufire E., Samuel T., Jackson C.R., Abebe W.
Hydrogen Sulfide Negative Salmonella and their Implication for Standard Culture-based Identification
(2025) Journal of Food Protection, 88 (7), art. no. 100549
ABSTRACT: Salmonella typically produces hydrogen sulfide (H2S) gas, which appears as a black precipitate on most selective culture media and serves as a key diagnostic feature in many laboratories. However, the emergence of H2S-negative Salmonella serovars raises concerns about their potential to evade conventional isolation protocols. This review explores the phenotypic variability in H2S production among Salmonella and summarizes recent global reports of H2S-negative serovars. Additionally, it discusses the limitations of current H2S-dependent isolation methods and proposes improved strategies for effectively detecting these atypical strains. We identified several factors, including media composition and incubation duration, that can influence H2S production in Salmonella. By analyzing various methods employed in recent years to isolate H2S-negative strains, we advocate for the early integration of non-H2S-dependent detection techniques to guide isolation workflows and prevent the unintentional exclusion of viable H2S-negative serovars. Specifically, we recommend parallel plating of suspect Salmonella cultures on both H2S-indicating media and non-H2S-based media, such as chromogenic agars, followed by the confirmation of both black and nonblack colonies. In conclusion, this review underscores the continued occurrence of H2S-negative Salmonella serovars and offers practical recommendations to enhance their detection, thereby supporting more comprehensive and accurate pathogen identification. ISSN: 0362028X

Perez K.M., Hernandez S.M., Sieverts O., Norfolk W.A., Francisco R., Shariat N.W., Smith J.C., Locklin J., Sanchez S., Lipp E.K., Yabsley M.J.
Salmonella environmental persistence informs management relevant to avian and public health
(2025) American Journal of Veterinary Research, 86 (6)
ABSTRACT: Salmonellosis is a significant public health threat responsible for millions of human cases annually but is also of significance to domestic and wild animals around the globe. While human infections are often foodborne, an increasing number of cases arise from environmental sources and contact with animals, including wild birds. Understanding the persistence of Salmonella in shared environments is critical for mitigating zoonotic transmission risks and understanding transmission dynamics for pets and free-living wildlife. Two experiments were conducted to investigate Salmonella persistence on surfaces relevant to wild bird-people interactions. One was a controlled experiment to compare the persistence of an avian-derived Salmonella Typhimurium isolate on bird feeders made of different materials. A total of 9 (7%) swabs were culture positive for Salmonella. Although there was no statistical difference in prevalence rates and persistence, Salmonella was primarily reisolated from plastic feeders. The second experiment investigated the prevalence and persistence of Salmonella on picnic tables in a South Florida park that were contaminated with bird feces. Salmonella prevalence on the picnic tables was 27%. When tracking fecal piles over time, 33% to 42% of fecal piles were Salmonella culture positive for 1 to 4 days. A total of 13 to 14 serotypes were detected, of which 5 serovars are in the top 20 for human infections. Our trials indicate that Salmonella can persist on bird feeders and picnic tables and precautionary measures should be adopted to reduce exposure. The com-panion Currents in One Health by Seixas et al, JAVMA, forthcoming 2025, addresses in-depth information about Salmonella epidemiology in free-living birds. ISSN: 00029645

Yates C.R., Weller D.L., Ponder M.A., Liao J., Holloman K., Cheng R.A.
Temporal, Seasonal, and Patient Demographic Trends Among Culture-Confirmed Human Salmonellosis Cases Identify Regional Differences in Salmonella Serotypes Reported in Virginia, USA From 2012 through 2022
(2025) Journal of Food Protection, 88 (7), art. no. 100548
ABSTRACT: The U.S. federal government established a national goal of reducing the salmonellosis incidence to ≤11.5 cases/100,000 persons by 2030. To assess progress toward this goal in Virginia, we used data from culture-confirmed salmonellosis cases reported to the Virginia Department of Health during 2012–2022 (N = 11,411). A Bayesian negative binomial splines model was implemented to estimate changes in incidence/100,000 persons during 2012–2022 statewide and for specific localities (for example: county or independent city). Incidence varied substantially by locality and over time. Output from modeled incidence suggests limited progress toward federal salmonellosis reduction goals in Virginia. During 2012–2022, statewide modeled incidence ranged between 11.6 (in 2022) and 12.9 (in 2018). From 2018 to 2022, there was a consistent decrease in the modeled incidence of culture-confirmed salmonellosis in Virginia. In contrast to FoodNet trends, the inclusion of culture-independent diagnostic tests in the case definition did not significantly reduce the number of culture-confirmed cases, suggesting a high rate of reflex culturing among patients in Virginia. Among 187 Salmonella serotypes reported, 64.2% of culture-confirmed infections were attributed to six serotypes: Typhimurium (including the monophasic variant, I 4,[5],12:i:-; 20.3%), Enteritidis (18.0%), Newport (10.7%), Javiana (7.7%), Bareilly (3.9%), and Braenderup (3.6%). Trends in salmonellosis attributable to specific serotypes varied substantially; modeled incidence of infections caused by some serotypes decreased substantially (e.g., S. Typhimurium/I 4,[5],12:i:-) and others increased (e.g., S. Braenderup). This may indicate that serotype-specific trends may be masking changes in salmonellosis epidemiology and contributing to the apparent overall stability in salmonellosis incidence in Virginia; efforts to meet federal goals may need to be tailored to reduce the incidence of specific serotypes that are increasing in incidence. ISSN: 0362028X

Barmettler K., Kelbert L., Horlbog J.A., Cernela N., Biggel M., Stephan R.
Salmonella in Swiss and Imported Retail Chicken Meat – A Cross-Sectional Study
(2025) Journal of Food Protection, 88 (7), art. no. 100532
ABSTRACT: Non-typhoidal Salmonella enterica (NTS) are significant foodborne pathogens responsible for many cases of enterocolitis worldwide, with the increasing threat of antimicrobial resistance (AMR) posing a growing public health concern. Salmonella Infantis has emerged as a predominant multidrug-resistant (MDR) serotype, particularly in poultry. This study investigated the Salmonella prevalence in 200 chicken meat samples from Swiss retail stores. Six (3%) samples tested positive; all were imported, and the isolates were all identified as S. Infantis. Whole genome sequencing confirmed the presence of the pESI (plasmid of emerging S. Infantis) megaplasmid, which is associated with enhanced persistence, biofilm formation, and multidrug resistance. Statistical analysis revealed a significant correlation between Salmonella prevalence and imported, unlabeled products. These findings highlight the effectiveness of Swiss control measures in the poultry production but underscore the importance of maintaining consumer awareness to mitigate Salmonella transmission and MDR risks. ISSN: 0362028X

Malkiely Y., Endeshaw G., Maler I., Elnekave E.
Non-typhoidal Salmonella contamination of food sources from animal origin in Israel between 2007 and 2021
(2025) Preventive Veterinary Medicine, 239, art. no. 106508
ABSTRACT: Non-typhoidal Salmonella (NTS) are one of the main causes of food poisoning, a major global threat for human health. Consumption of contaminated food products of animal origin contributes to majority of the NTS illness outbreaks. Poultry, an important protein source, is considered the main animal source for NTS. However, contamination with different serotypes of NTS may be attributed to various animal hosts. We aimed to determine the prevalence, trends, and potential risk factors for NTS contamination of food sources in Israel. A dataset including 192,340 test results for the detection of NTS contamination in food products in Israel between 2007 and 2021 was analyzed. Food samples were collected as part of routine testing and targeted programs for NTS detection from different facilities, such as food factories and slaughterhouses. The collected food samples included: non-thermally treated (raw) and mainly thermally treated ready-to-eat (RTE) products. Data were summarized and associations between NTS detection and different covariates were estimated using either: (i) Poisson regression model; or (ii) $\chi 2$-tests. The odds ratio (OR) or prevalence ratio and 95 % confidence intervals (CI95 %)

were calculated. The number of food products tested for NTS identification and further serotype classification has declined in recent years. However, the percentage of NTS positive results increased over time, reaching 18.11 % positive samples by 2021. The risk for NTS contamination was significantly higher in raw vs. RTE products: OR (CI95 %) = 290.60 (239.39–352.76), $p < 0.001$. The percentage of samples found positive for NTS in RTE products varied between sources, yet remained below 0.49 % for each source. However, in raw products, the NTS prevalence ranged between 1.05 % and 35.03 %, with food products from the chicken source significantly more positively associated with NTS contamination in comparison beef, fish, pig and turkey sources. Imported food, and slaughterhouses had a significantly higher prevalence of NTS contamination compare to factories food hygiene testing. With certain facilities, within each category, demonstrating significantly higher contamination compared to others. Moreover, the ten most common serotypes reported in human infections throughout this period were mostly found in chicken and turkey sources. The identification of certain sources and facilities/importers/slaughterhouses which may pose higher risk for NTS contamination was possible despite the declining resources invested in sampling and classification of NTS isolates in recent years. Therefore, our study further emphasizes the potential and importance of establishing a real-time surveillance for better tracing of NTS contaminations in food sources to protect public health. ISSN: 01675877