

NEWSLETTER

European Union Reference Laboratory for *Salmonella*

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Contents

EDITORIAL NOTE	4
CONTRIBUTION OF THE EURL-SALMONELLA	6
EURL- <i>SALMONELLA</i> ACTIVITIES FORESEEN IN 2026	6
TIMETABLE EURL- <i>SALMONELLA</i> PROFICIENCY TEST FOOD 2026 DETECTION OF <i>SALMONELLA</i> IN A FOOD MATRIX	7
FROM THE LITERATURE	8

Editorial Note

Bilthoven, 3 April 2026

Dear colleagues,

Last year, I bothered you in several Newsletters about the fact that our institute (RIVM) at some point will move to a new building in Utrecht, but that the planning was delayed several times. Currently there is still no new planning, but there are some rumors that the relocation may start later this year. However, like indicated in the previous Newsletter, as long as we do not know the exact dates for the relocation, we stick to the 'normal' **planning for our EURL-*Salmonella* activities for this year** (see the overview of this planning on page 6 of this Newsletter).

Despite the fact that we try to stick to the normal planning, we still had to slightly amend the planning of the **Proficiency Test (PT) on detection of *Salmonella* in a food matrix**, the first PT this year. This amendment was, however, not due to the relocation plans, but due to a technical problem with the sample bags. Thanks to the efforts of our great EURL team, we were able to resolve the problems relatively quickly and have prepared a full new set of samples. The samples will be sent to the NRLs-*Salmonella* on 7 April 2026, which is only 3 weeks later than the originally planned date. The updated version of the timetable of this PT is included in this Newsletter on page 7.

The planning of the **EURL-*Salmonella* workshop** remains unchanged. As announced, this workshop is organised as a hybrid meeting on 12 and 13 May 2026 in Zaandam, the Netherlands. The registration has gone well, with the majority (40) of the total number of registered participants (75) participating onsite in Zaandam. Our secretariat has booked the flights for the ones participating physically for our budget and details have been sent to the participants. The draft programme of the workshop is ready and will be shared with all participants, together with additional details about the workshop, very soon. We look forward to meet you all in May!

Like in previous years, the **inter EURLs Working Group NGS** will organise a **joint training course on NGS** this year. This training is organised at the premises of the EURL-AMR in Denmark in June 2026. In fall last year, the inter EURLs WG sent two surveys to the NRLs of all 8 EURL/NRL networks to collect views and needs on the use of NGS and on the training needs. It took some time and discussion within the WG to translate the information of the surveys into a set-up of the NGS training for this year. This is also the reason why details have not yet been shared with the NRLs. For now, I can inform you that it is planned to organise an online training for the 'theoretical' part in May, so that there will be more time for the hands-on training in June. It is planned to share more details with all NRLs of the 8 EURL/NRL networks very soon.

The inter EURLs Working group on NGS has also been working very hard on drafting **Guidelines for the validation of Whole Genome Sequencing for accreditation**. I am happy to inform you that the first version of this document has been finalised and was recently added to the list of Guidance documents NGS at our website, see: <https://www.eurilsalmonella.eu/en/methods/ngs/guidance-documents>

In the first quarter of 2026, the following EURL-*Salmonella* reports were published:

Pol-Hofstad, I.E., Jacobs-Reitsma, W.F. and Mooijman, K.A., 2026. EURL-*Salmonella* Combined Proficiency Test – Interlaboratory Study for Primary Production Stage and Food, 2024. Detection of *Salmonella* in fabric swabs. RIVM report 2025-0036. National Institute for Public Health and the Environment, Bilthoven, the Netherlands.

<https://www.rivm.nl/bibliotheek/rapporten/2025-0036.pdf>

Diddens, R.E. and Mooijman, K.A., 2026. EURL-*Salmonella* Proficiency Test Primary Production Stage 2025; Detection of *Salmonella* in chicken faeces samples. RIVM Report 2025-0151. National Institute for Public Health and the Environment, Bilthoven, the Netherlands.

<https://www.rivm.nl/bibliotheek/rapporten/2025-0151.pdf>

Best wishes,
Kirsten Mooijman
Coordinator EURL-*Salmonella*

Contribution of the EURL-*Salmonella*

EURL- *Salmonella* activities foreseen in 2026

Date(s)	Activity
7 April – 6 May 2026	EURL- <i>Salmonella</i> Proficiency Test Food 2026; Detection of <i>Salmonella</i> in a food matrix.
12 & 13 May 2026	Hybrid EURL- <i>Salmonella</i> workshop, Zaandam, the Netherlands
June 2026	Joint Training Course of the inter EURLs Working Group on NGS in Denmark.
September – October 2026	EURL- <i>Salmonella</i> Proficiency Test Primary Production Stage (PPS).
November 2026 – January 2027	EURL- <i>Salmonella</i> Proficiency Test Typing; Serotyping and (optional) WGS Cluster analysis.

Timetable EURL-*Salmonella* Proficiency Test Food 2026
Detection of *Salmonella* in a food matrix
Version 2

Week	Date	Subject
5	Friday 30 January 2026 at the latest	Please register by 30 January 2026 at the latest.
10	Week of 2 March 2026	E-mailing the link for the result form to the participants. E-mailing the protocol and instructions for the result form to the NRLs.
		Preparation of media by the NRLs.
12	Tuesday 7 April 2026	Shipment of the parcels with PT samples to the participants as Biological Substance Category B (UN3373).
12-13	Immediate after receipt of the parcel and at the latest on 13 April 2026	Start performance of the Proficiency Test.
16	Wednesday 6 May 2026 at the latest	Deadline for completing the result form: 6 May 2026 (23:59h CET) After this deadline the result form will be closed.
	June/July 2026	Interim summary report

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

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RIVM / Z&O (internal Pb 63) EURL- *Salmonella*

P.O. Box 1, 3720 BA Bilthoven, the Netherlands

<https://www.eurlsalmonella.eu/>

From the Literature

Salmonella-related Literature selection from Scopus: January - March 2026

Dayan O., Kroupitski Y., Sayas T., Saldinger S.S., Kleiman M.

Tomato leaf microstructure affects the adhesion and localization of Salmonella enterica as shown using biomimetics

(2026) *Food Microbiology*, 133, art. no. 104893

ABSTRACT: Non-typhoidal *Salmonella enterica* serovars are a major cause of diarrheal diseases worldwide and represent a significant health concern. Several *Salmonella* outbreaks worldwide originated from bacteria residing on plants, specifically on leaves. Understanding the adhesion and survival of *Salmonella* upon the leaf surface is, hence, of great importance. Among other factors involved in the localization and adhesion of *Salmonella* to the leaf surface, the surface microstructure did not receive significant attention. Here, we study the localization and adhesion of *Salmonella* to the surface of tomato leaves, with emphasis on the role of the leaf surface microstructure. To do so, we use biomimetics, a field in chemistry and material sciences aimed at mimicking biological systems. We formed synthetic replication of the leaf surface microstructure, to isolate the microstructure property from all other leaf properties. We found that the distribution of *Salmonella* upon the leaf surface is not random and there is a clear localization preference to the intercellular spaces and the trichomes. We found that this localization repeats in the synthetic system, suggesting this phenomenon is due to the microstructural features of the leaf. The localization of *Salmonella* on the trichome is independent of flagella, curli or cellulose, and does not require bacterial viability. However, the overall adhesion of *Salmonella* to both natural and synthetic leaf surfaces decreased in the cellulose mutant. This result emphasizes the strength of the model synthetic system we developed. A better understanding of *Salmonella* interaction with leaf surfaces could yield new directions for prevention methods. The findings in this research could assist in the development of such directions. ISSN: 07400020

Patil K., Adhikari M., Acuff J.C.

Environmental factors and inoculation methods impact transfer of Salmonella Tennessee on surfaces to nonfat dried milk

(2026) *Food Microbiology*, 133, art. no. 104901

ABSTRACT: Cross-contamination during low-moisture food (LMF) processing poses a serious food safety risk, especially when pathogens like *Salmonella* persist on surfaces such as equipment and tools. Environmental factors, particularly relative humidity (RH), may significantly influence this risk. This study evaluated the persistent bacterial populations (PBP) of *Salmonella Tennessee* on stainless steel surfaces and its transfer to nonfat dry milk (NFDM) under varying RH conditions. Stainless steel coupons were inoculated with either high (7–8 log CFU/cm²) or low (3–4 log CFU/cm²) concentrations of *Salmonella Tennessee* using two contamination methods: (1) a premixed slurry of NFDM and inoculum, or (2) NFDM pressed onto the inoculum. Coupons were then stored at 25 °C and either 30 % or 70 % RH. Cross-contamination was simulated on day 3 or 7 by placing each coupon into a tube with 10 g of non-inoculated NFDM and vortexing for 2 min. Bacteria recovered from both the coupon and NFDM, and percent transfer (PT) was calculated and log transformed. ANOVA and Tukey's HSD revealed that PT decreased with higher initial inoculum and varied significantly by RH, matrix, and contamination method ($P < 0.05$). The highest levels of *Salmonella* transferred to the NFDM was 5.3 log CFU/g in the high inoculum group and 3.5 log CFU/g in the low inoculum group, both using the slurry method at 30 % RH after 7 days. These findings highlight how RH, contamination method, and bacterial load influence cross-contamination in LMF systems, suggesting the need for tailored hygiene interventions in food processing environments. ISSN: 07400020

Adegboye O.A., Amarasena T., Khan M.A., Ajulo H., Pak A., Taniar D., Emeto T.I.

Too Hot, Too Wet: Bayesian Spatial Modeling of Climate-Driven Salmonella Risk in New South Wales, Australia, 1991–2022

(2026) *GeoHealth*, 10 (1), art. no. e2025GH001617

ABSTRACT: *Salmonella* infections contribute significantly to gastrointestinal-related hospitalisations in Australia and remain a major global public health concern. Although seasonal patterns in *Salmonella* incidence have been documented globally, there is limited

evidence on the influence of climatic factors, particularly rainfall, humidity, flooding, and temperature, in the Australian context. This study investigated the relationship between climatic extremes and *Salmonella* infections across Local Health Districts (LHDs) in New South Wales (NSW), Australia, using a Spatial Bayesian Distributed Lag Non-Linear Model. Spatial modeling revealed a marked geographical heterogeneity in the risk of *Salmonella* related to climate in NSW. High ambient temperatures consistently increased risk, with 99th-percentile contrasts typically yielding relative risks (RR) of 2.4–4.8 across LHDs. Monthly rainfall showed the opposite direction statewide: very dry months were associated with a higher risk, whereas very wet months were generally protective (RR (Formula presented.) 1). In contrast, discrete flooding events were strongly and positively associated with risk (99th-percentile flood index RR (Formula presented.) 18–23.5), with the greatest effects in some LHDs of the metropolitan/coastal region. Humidity displayed modest but consistent positive associations (99th-percentile RR (Formula presented.) 1.1–1.5). Temperature and humidity exhibited J-shaped exposure-response relationships, where the lowest risk occurred at moderate values. This contrasts with rainfall, which demonstrated an inverse (protective) association, and flooding, which showed a monotonic increase in risk with intensity. These results have important public-health implications under a warming, flood-prone climate. ISSN: 24711403

Lee S., Kong F., Chen J.

Heat Tolerance of Wildtype Salmonella Tennessee and Its Knock-Off Mutants in Peanut Butter and Peanut Spread

(2026) *Microbiology Research*, 17 (1), art. no. 13

ABSTRACT: *Salmonella enterica* from low-moisture food has been found to have a higher thermal tolerance than from high-moisture food. However, the molecular mechanism underlying the association of thermal tolerance of this pathogen with low-moisture foods, such as peanut butter and peanut spread, has not been fully elucidated. We previously found that mutants of *S. Tennessee* with a defective gene encoding a cell membrane lipoprotein (*Lpa*) or cell division protein (*ZapC*) formed significantly ($p \leq 0.05$) less biofilm than the wildtype strain. To assess the possible role of these genes in the thermal tolerance of *S. Tennessee*, this study compared the surviving populations of the wildtype *S. Tennessee* and its mutants defective in *Lpa* or *ZapC* in different types of peanut products (regular, reduced-fat, and natural) at 74 °C for 0, 2.5, 5, 10, 15, 20, 30, 40, or 50 min. Results showed that mutants with a defective *lpa* or *zapC* significantly affected the survival of *Salmonella* in peanut products during heat treatments. Significantly, a higher reduction in *Salmonella* population was observed in regular peanut butter, followed by natural and reduced-fat peanut spreads. The study provides new insight into one of the molecular mechanisms underlying the thermal tolerance of *Salmonella enterica*.

ISSN: 20367473

Barbarulo S., Rampacci E., Primavilla S., Stefanetti V., Passamonti F.

Characterization of Salmonella spp. Isolates from European Hedgehogs (Erinaceus europaeus) in Italy: Serotypes and Antimicrobial Susceptibility Profiles

(2026) *Antibiotics*, 15 (1), art. no. 46

ABSTRACT: Background: Wildlife is increasingly recognized as an important component in the epidemiology of zoonotic pathogens. *Salmonella* spp., a leading cause of foodborne disease worldwide, can circulate across human, domestic animal, and environmental interfaces. European hedgehogs (*Erinaceus europaeus*), a synanthropic species frequently inhabiting urban and peri-urban areas, may act as reservoirs or sentinels for *Salmonella*. Objectives: The aim of this study was to investigate the prevalence, serotype distribution, and antimicrobial susceptibility profiles of *Salmonella* spp. isolated from European hedgehogs admitted to wildlife rehabilitation centers in Italy. Methods: Fecal samples were collected from 100 European hedgehogs housed in five wildlife rehabilitation centers located in four Italian regions. *Salmonella* spp. were isolated using standard bacteriological methods, serotyped according to the Kaufmann–White–Le Minor scheme, and tested for antimicrobial susceptibility by broth microdilution for ampicillin, enrofloxacin, and sulfamethoxazole-trimethoprim. Minimum inhibitory concentrations (MICs) were interpreted following CLSI guidelines. Results: *Salmonella* spp. was isolated from 30% of the animals sampled. Four serovars were identified, with *S. Enteritidis* (50%) and *S. Typhimurium* (36.7%) being the most prevalent, followed by *S. Agona* (10%) and *S. Chester* (3.3%). Antimicrobial susceptibility testing revealed a high level of susceptibility, with 90% of isolates sensitive to all tested antibiotics. One *S. enteritidis* strain showed resistance to enrofloxacin and sulfamethoxazole–trimethoprim, while two isolates exhibited intermediate susceptibility to enrofloxacin. Conclusions: The detection of *Salmonella* serovars commonly associated with human infections in European hedgehogs highlights the potential role of this species in the ecology of zoonotic *Salmonella*. Although

antimicrobial resistance levels were low, the presence of resistant and intermediate strains underscores the importance of continued surveillance. Despite some limitations related to the study design and sample representativeness, these results support the need for further large-scale investigations, reinforcing the need for integrated One Health surveillance strategies. ISSN: 20796382

Wang J., Lu S., Lian H., Yang Y., Huang W., Yuan Q., Kong X., Meilang J., Xiang Y., Zhang X., Zuo H., Li M., Pei X.

A Stratified Genomic Framework for Salmonella Serotype Prediction: Evaluation of MLST, SeqSero, SeqSero2, SeqSero2S, and SISTR in Southwest China
(2026) *Journal of Visualized Experiments*, 2026-January (227), art. no. e69117

ABSTRACT: Accurate serotyping of *Salmonella* is essential for effective surveillance and outbreak investigation, as serotype diversity directly impacts pathogenicity and public health risk assessment. However, conventional slide agglutination methods are limited by poor reproducibility, labor intensity, and high costs, which hinder their application in high-throughput monitoring programs. To address these limitations, we developed and validated a genomic workflow integrating Multilocus Sequence Typing (MLST), the *Salmonella* In Silico Typing Resource (SISTR), SeqSero, SeqSero2, and SeqSero2S for serotype prediction using whole-genome sequencing data. This protocol was evaluated through a multicenter analysis of 315 *Salmonella* isolates collected from food and human sources in Southwest China. The findings of this study demonstrated significantly higher concordance among genomic approaches (up to 100%/99.1%/90.1% in the training set and 100%/97.1%/93.1% in the validation set for SISTR/MLST/SeqSero2S, respectively) compared to traditional serotyping. The workflow includes recommendations for selecting appropriate prediction methods based on surveillance context, emphasizing MLST and SeqSero2S for routine monitoring, SeqSero2S for rapid screening, and SISTR with core genome MLST for outbreak investigations. This approach facilitates the integration of genomic serotyping into public health practice, reducing reliance on traditional serology and improving reproducibility and scalability in *Salmonella* monitoring programs. ISSN: 1940087X

Miranda H.N.C.M., dos Santos A.J.F., Almeida K.D.S., Ribeiro-Júnior J.C.

Main Salmonella serotypes in free-range Amazon broiler chicken farms: Comparison between collection methods and seasonal period in tropical regions
(2026) *Research in Veterinary Science*, 198, art. no. 105987

ABSTRACT: Broiler chicken raised in semi-closed or completely free-range systems are challenged by more environmental variables that can compromise the biosecurity and microbiological quality and safety of the final product from this type of production. This study investigated *Salmonella* serotypes in Brazilian Amazon free-range broiler chicken farms in a tropical climate region, comparing the efficacy of the official collection methods of poultry sheds (drag swabs, footpads, and cecal feces) and the rainy and dry seasons typical of the region. Specific qualitative microbiological cultures, confirmation of identity by genus-specific PCR (*invA*), and determination of *Salmonella* serotypes by real-time PCR were performed on all free-range poultry farms in Tocantins, North Brazil. In total, 935 suggestive isolates were recovered using the three collection methods in both seasons, of which 90 (9.5 %) were positive for *invA*. There were no significant differences ($p > 0.05$) between the collection methods or between the rainy and dry seasons. *Salmonella* Mbandaka, S. Panama, and S. Javiana were identified on different free-range poultry farms. Although the main serotypes of importance in poultry and public health were not identified, according to Brazilian regulations, the results did not compromise the processing of batches for fresh trade, reinforcing the need to support surveillance programs, animal health defense, and epidemiological measures of a one-health approach to control the pathogen in the chain of free-range broiler chickens raised in tropical climate regions. ISSN: 00345288

Martínez-González N.E., García-Frutos R., Martínez-Chávez L., Domínguez-Bustos F.O., Díaz-Patiño C.J., Gutiérrez-González P.

Postharvest reduction of Salmonella on Hass avocado epicarp by hot water immersion and evaluation of fruit quality

(2026) *International Journal of Food Microbiology*, 444, art. no. 111444

ABSTRACT: *Salmonella* contamination of fresh produce, including avocados, poses a significant public health concern. Effective postharvest interventions are needed to reduce pathogen loads without compromising fruit quality. This study evaluated the efficacy of hot water (HW) immersion (70 or 80 °C for 1, 2, and 4 min) in reducing loosely (LA) and strongly attached (SA) *Salmonella* cells on Hass avocado epicarp, and its effect on background microbiota and fruit quality. Whole avocados, inoculated or uninoculated, were

stored at 25 °C for 72 h before being washed and treated by HW immersion. The LA and SA cells of Salmonella, aerobic plate count (APC), and yeasts and molds (YM) were enumerated on avocado epicarp. Hot water immersion was equally effective ($P > 0.05$) in removing LA and SA cells of Salmonella and background microbiota. Temperature and immersion time significantly influenced Salmonella reductions ($P < 0.05$), with 80 °C for 4 min being the most effective, achieving 5.1 and 4.8 log CFU/avocado reductions for LA and SA. Immersion time did not significantly affect ($P > 0.05$) the reductions in background microbiota. Treatments at 80 °C yielded the greatest APC and YM reductions ($P < 0.05$), with maximum reductions of 3.5 and 4.3 for LA, and 3.7 and 4.2 for SA. No significant differences ($P > 0.05$) were observed in pulp color, firmness, total fat content, or flavor between HW-treated and untreated samples. These results support the use of HW immersion as a postharvest decontamination strategy that enhances microbial safety while maintaining avocado pulp quality. ISSN: 01681605

De Witte L., De Reu K., Van der Eycken M., Van Raemdonck J., Botteldoorn N., Van Immerseel F., Rassaert G.

Guess Who's Back: Persistence and Circulation of Salmonella Infantis on Broiler Farms with a History of Contamination
(2026) *Foods*, 15 (2), art. no. 339

ABSTRACT: For several years, *Infantis* was the most common Salmonella serovar circulating in the Belgian broiler sector and persisting on broiler farms. To gain insight into its prevalence and circulation on broiler farms in Belgium, five farms (14 flocks) with a *S. Infantis* contamination history were monitored during two consecutive production rounds. In total, ten sampling events were conducted using moist sponge sticks after cleaning and disinfection, during the delivery of the one-day-old chicks and during production until slaughter or until positive for *S. Infantis*. Salmonella presence on samples was determined based on the ISO 6579:2017 standard, and the isolated strains were typed using PFGE. The results showed that current cleaning and disinfection practices were unable to completely remove *S. Infantis* from the farms. Cleaning equipment (3 out of 9 sample times) and the floor (5 out of 10 sample times) were particularly contaminated. Furthermore, external environmental samples were also frequently contaminated (e.g., mortality containers, concrete driveway). During production, 12 of the 28 sampled flocks were colonized with *S. Infantis* after one week, indicating that *S. Infantis* quickly spreads throughout the broiler house, which raises the hypothesis that feeding and/or drinking water systems play a critical role in the circulation of the bacteria. This study gives insights into the circulation and difficulty of controlling *S. Infantis* in persistently contaminated broiler farms, highlighting the importance of thorough cleaning and disinfection and biosecurity. ISSN: 23048158

de Lucena F.A., Schaffner D.W., da Silva R.T., de Paiva Anciens Ramos G.L., dos Santos Franco A.J., Alvarenga V.O., Baldwin C., de Souza Pedrosa G.T., Magnani M
Survival of Salmonella enterica in chocolate formulated with contaminated coconut flakes, raisins, and cocoa nibs under varying temperature and humidity conditions
(2026) *International Journal of Food Microbiology*, 445, art. no. 111505

ABSTRACT: This study evaluated the survival of *Salmonella enterica* in chocolate formulated with artificially contaminated coconut flakes, raisins, and cocoa nibs, under varying storage conditions. The products were stored for 120 days at controlled temperatures (7, 14, and 25 °C) and relative humidity (RH) levels (65 %, 85 %, and 100 %). After 120 days of storage at 7 °C, *S. enterica* populations remained around 3.5 log CFU/g in chocolates containing coconut flakes and raisins, while levels were below the detection limit (<1.7 log CFU/g) in chocolate containing cocoa nibs, regardless of RH. At 14 °C and 100 % RH, *S. enterica* counts dropped below the detection threshold after 108, 99, and 66 days for chocolates with coconut flakes, cocoa nibs, and raisins, respectively. Temperature and RH significantly influenced *S. enterica* survival dynamics. Both linear and quadratic effects of temperature and RH were significant in chocolate with contaminated coconut flakes. Linear temperature and quadratic RH coefficients were significant in chocolate with raisins. Only temperature (both linear and quadratic terms) significantly affected survival in chocolate with cocoa nibs, while RH had no significant effect. The fastest declines in *S. enterica* counts were observed at 85 % RH. Slower reductions were observed at 65 % and 100 % RH for the same temperature conditions, regardless of the chocolate ingredients. The fitted predictive models demonstrated strong explanatory power, with R^2 values of 0.94, 0.88, and 0.84 for chocolates containing coconut flakes, raisins, and cocoa nibs, respectively. These findings contribute to risk assessment frameworks and provide critical insights for developing targeted control strategies to mitigate *S. enterica* persistence in low-moisture chocolate products. ISSN: 01681605

Małaszczuk M., Pawlak A., Wernecki M., Bugla-Płoskońska G.

Comparative Identification of Rare Salmonella Serovars from Snakes in Poland Using Slide Agglutination and Genomic Analysis, Including a Putatively Novel Serovar IIIb 38:z₁₀:z₆ (2026) Applied Sciences (Switzerland), 16 (1), art. no. 437

ABSTRACT: Featured Application: This study highlights the proven need to apply complementary methods—genetic prediction and slide agglutination—for reliable identification of rare or atypical *Salmonella* serovars. *Salmonella* is a globally important pathogen and one of the World Health Organization and One Health priority organisms. Reptiles represent environmental reservoirs of *Salmonella* serovars that can cause reptile-associated salmonellosis (RAS) in humans. Due to distinct biochemical features and uncommon O and H antigen variants, reptile-associated isolates may be difficult to identify using standard microbiological diagnostics. This study analyzed 62 *Salmonella* isolates obtained from wild and kept snakes in Poland. Samples originated from *Natrix natrix*, *N. tessellata*, *Coronella austriaca*, *Zamenis longissimus*, *Elaphe dione* and *Nerodia fasciata* species. Serovar prediction using SeqSero1.2 was compared with classical slide agglutination. Seventeen serovars were confirmed, with *S. enterica* subsp. *diarizonae* (IIIb) 38:r:z being the most frequent. For seven isolates, molecular and serological results were inconsistent. Among three isolates from *Coronella austriaca* predicted as IIIb 38:z₁₀:z₅₀, three distinct second-phase flagellar phenotypes were detected. Slide agglutination confirmed the presence of serovar 38:z₁₀:z₆, which has not been previously listed in the White-Kauffmann-Le Minor scheme or described in the scientific literature. The findings highlight the utility of genetic serovar prediction while emphasizing the need for continuous validation, particularly for the identification of rare or atypical *Salmonella* serovars associated with reptiles. ISSN: 20763417

Mutlu M., Incili G.K., Calicioglu M.

Survival of Staphylococcus aureus, Listeria monocytogenes, and Salmonella spp. in traditional Tomas cheese during the ripening at different temperatures (2026) Food and Bioprocess Processing, 155, pp. 124 - 133

ABSTRACT: This study aimed to investigate the viability of *Listeria monocytogenes*, *Staphylococcus aureus*, and *Salmonella* spp. in Tomas cheese produced by traditional methods and ripened at 4 °C and 10 °C. Fresh Tomas cheese samples were inoculated with a cocktail of *Staphylococcus aureus*, *Listeria monocytogenes*, and *Salmonella* spp. (approximately 4.0–5.0 log₁₀ CFU/g) and then pressed into plastic jars and stored at 4 °C and 10 °C. Chemical and microbiological analyses of the cheese were performed on days 0, 7, 15, 30, 45, 60, 90, and 120. At the end of the ripening period, the mean reductions in pathogen counts in the groups stored at 4 °C and 10 °C were 4.54 and 3.15 log₁₀ CFU/g for *Salmonella* spp. ($p < 0.001$), 1.59 and 1.75 log₁₀ CFU/g for *Staphylococcus aureus*, and 2.92 and 3.06 log₁₀ CFU/g for *Listeria monocytogenes*, respectively. The total viable counts (TVC), psychrotrophic bacteria, *Lactobacillus* spp., *Lactococcus* spp., *Enterococcus* spp., proteolytic bacteria, lipolytic bacteria, mold and yeast counts remained within the 4–7 log₁₀ CFU/g range with only slight fluctuations during the ripening period, and no significant differences were detected between the groups at the two storage temperatures. As a result, although *Staphylococcus aureus*, *Salmonella* spp., and *Listeria monocytogenes* counts decreased at two both ripening temperatures (4 °C and 10 °C) by the end of the ripening period, the data suggest that these pathogenic microorganisms may still pose a potential food safety risk to public health in Tomas cheese. ISSN: 09603085

Fröder H., Lorusso A.B., Martinez G.S., de Macedo R.E.F.

Rapid detection of Salmonella Enteritidis and S. Typhimurium serotypes and characterization of flagellar variants using real-time PCR (2026) Food Microbiology, 133, art. no. 104900

ABSTRACT: The wide diversity of *Salmonella* serotypes poses challenges for traditional serotyping methods, which are labor-intensive and unsuitable for high-throughput testing, particularly in food safety contexts. Hence, this study aimed to develop and validate a real-time PCR method for detecting *Salmonella* spp., identifying the major public health serotypes (*S. Enteritidis* and *S. Typhimurium*), and differentiating monophasic *S. Typhimurium* variants. The method demonstrated high specificity and sensitivity, with 100 % inclusivity and 96.8 % exclusivity. Novel primers targeting fljB-hin allowed effective differentiation of monophasic variants, while dual biomarkers (STM4492 and STM2755) improved *S. Typhimurium* detection accuracy. Compared to conventional serotyping, the method showed excellent concordance ($\kappa = 1.00$, $p < 0.01$) and reduced turnaround time to under 2 h without requiring post-PCR processing. The inclusion of short amplicons (<200 bp) ensures efficiency and compatibility with fast cycling protocols. This validated,

open-access assay offers a reliable and cost-effective molecular alternative for food safety monitoring, especially in settings with limited infrastructure. ISSN: 07400020

Van der Voort M., Castelijm G.A.A., Stassen J.H.M.

Identification of Salmonella Infantis persistence in poultry products in the Netherlands with a role for the pESI plasmid

(2026) *Letters in Applied Microbiology*, 79 (1), art. no. ovag006

ABSTRACT: As *Salmonella* is known to be able to persist in processing environments, we investigated whether the detection of *Salmonella* clusters from retail poultry can be linked to a persistent source. A total of 69 *Salmonella* *Infantis* isolates from retail poultry products from four different producers between 2008 and 2020 were sequenced and their sensitivity to antibiotics was determined. The six phylogenetic clusters spanning multiple months identified by sequence analysis indicate persistence of *Salmonella*. In addition, the pESI megaplasmid, which is known to harbor a diversity of resistance and persistence factors, was identified in 53 of the 69 isolates. The pESI plasmid was shown to be more prevalent among more recent strains and was shown to be present in isolates from five out of six clusters. The identification of clusters by whole genome sequencing analyses helps to identify persistent strains, as was shown in this study for *S. Infantis*. Moreover, the detection of pESI in these *S. Infantis* isolates suggests that pESI has a role in persistence and thus in the further spread and increased prevalence of *S. Infantis*. ISSN: 02668254

Piña-Iturbe A., Tichy-Navarro D., Miranda-Riveros J., Navarrete M.J., Moreno-Switt A.I.

Emergent Salmonella enterica serovar Infantis forms a monophyletic lineage shaped by geographic structuring

(2026) *International Journal of Food Microbiology*, 446, art. no. 111536

ABSTRACT: Multidrug-resistant *Salmonella* *Infantis* carrying pESI-like megaplasmids have disseminated worldwide representing a serious threat to public health. Previous studies have investigated its population structure and temporal dynamics above the continental level. However, their conclusions were constrained by limited datasets and sampling biases. To address these issues, we analyzed all publicly available *Salmonella* *Infantis* genomes to characterize its global population structure and phylogeographic dispersal. We selected a non-redundant dataset of 14,010 genomes representing the temporal, geographic, isolation source, and genomic diversity of *Salmonella* *Infantis* from 77 countries across five continents, collected from 1910 to 2024. Phylogenomic analyses showed that emergent megaplasmid-positive *Salmonella* *Infantis* forms a monophyletic lineage with significant geographic structuring. The megaplasmid-positive lineage was inferred to have originated in Western Asia around 1990, followed by multiple introductions into Europe and a single transmission to South America which resulted in the dissemination of this pathogen to Northern America, and from there to the rest of the continent. Multiple recent transmission events of the American lineage to all continents were observed, driving the dispersal of the bla CTX-M-65 gene encoding extended-spectrum β -lactamases. Moreover, genomic evidence also suggests that the emergence of ESBL-producing strains in parts of Asia and Africa may be associated with poultry trading from the Americas. Our findings underscore the urgent need for integrating global human, animal, and environmental surveillance data with population genomic analyses to contain the threats posed by ESBL-producing *Salmonella* *Infantis*. ISSN: 01681605

Pulido-Villamarín A., Vesga F.-J., Venegas C., Rodríguez-Cordero D., Matiz-Villamil A., Barrientos I., Chamorro-Tobar I.C., Caicedo J.P., Ariza B., Gomez S., Bermudez L.S., Carrascal-Camacho A.K., Aranda-Silva M., David Olaya E.

Prevalence of Escherichia coli and Salmonella spp. in Colombian Pig Production Settings: A One Health Perspective Study

(2026) *Veterinary Sciences*, 13 (2), art. no. 189

ABSTRACT: Zoonotic pathogens in swine production can negatively impact both human and animal health, with the environment serving as a potential transmission vehicle. Therefore, this study aimed to determine the prevalence of *Escherichia coli* and *Salmonella* spp. in the Colombian swine production chain using the One Health approach. Samples were collected from nine farms and two slaughterhouses in the departments of Antioquia, Cundinamarca, Valle del Cauca, and Meta. The analyzed samples included water, feed, pig and worker feces, organic material in treatment (manure treated and compost), and pig carcasses. These samples were analyzed using standard microbiological methods and the Molecular Detection System (MDS). The results showed *Salmonella* spp. prevalence rates of 15.47% in pigs, 9.4% in feed, 8.47% in water, and 2.56% in organic material. For *E. coli* O157, prevalence rates were 25.71% in pigs, 10% in feed, 22.22% in water, and 33.33% in organic material. The high prevalence and bacterial loads in water suggest it is

a critical reservoir and a potential primary source of contamination in the production chain. Although these pathogens were not detected in workers, the zoonotic risk remains. Additionally, the prevalence of haemolytic enterotoxigenic *E. coli* (ETEC), a major swine pathogen, was 40.1%. This study emphasizes the need to improve biosecurity and farm management practices to reduce the risk of environmental transmission, thereby minimizing public, occupational, and animal health risks. Implementing water treatment protocols and improving organic waste management are recommended to limit the spread of bacterial contamination. These actions are based on the 'One Health' approach, recognizing that animal health and ecosystem integrity are indivisible pillars of human health. ISSN: 23067381

Thames H.T., Pokhrel D., Sukumaran A.T., Dinh T.T.T.N., Schilling M.W., White S., Ramachandran R., Macklin K., Zhang L.

Environmental stress modulates expression of biofilm-related genes in Salmonella
(2026) *Journal of Applied Microbiology*, 137 (2), art. no. lxag018

ABSTRACT: Aims Biofilms formed by *Salmonella* are a significant concern in the poultry industry due to their role in pathogen persistence. However, there is a lack of data observing the expression of biofilm related genes in different *Salmonella* serovars. The aim of this study was to investigate the expression patterns of key biofilm-associated genes across three *Salmonella* serovars, namely *Salmonella* Typhimurium, Kentucky, and Reading, throughout their biofilm growth cycles. Methods and results The expressions of *csgD*, *bapA*, *bcsA*, *adrA*, and *luxS* were analyzed in cultures representing different biofilm growth phases: 12 h and 24 h planktonic cells, 4-day old biofilms, and 5-day old biofilms under nutrient deprivation. The findings from this study revealed that only *S. Reading* exhibited upregulation of these genes at the 24 h planktonic stage at a maximum of 9.58-fold. In contrast, a downregulation of all five genes was noted in the 4-day old biofilms for all serovars. Most notably, *bapA* was downregulated by 3765-fold in *S. Typhimurium*. Upon subjecting the biofilms to nutrient deprivation, there was a notable recovery in the activity of these genes across all serovars with the exception of *csgD* in *S. Typhimurium*. Conclusion These results suggest that expression of biofilm-associated genes is stimulated by nutrient availability even at biofilm maturity and may vary among different serovars. ISSN: 13645072

Cano P.W., Tondo E.C., Malheiros P.D.S.

Salmonella Inactivation During the Preparation of Omelets, Poached Eggs, and Scrambled Eggs

(2026) *Journal of Food Safety*, 46 (1), art. no. e70053

ABSTRACT: Salmonellosis remains a significant public health concern, often linked to egg consumption. This study evaluated *Salmonella* inactivation in omelets, scrambled eggs, and poached eggs. Egg yolks were contaminated with a *Salmonella* cocktail and incubated at 37°C for 24 h, achieving approximately 8 log CFU/g. These eggs were used to prepare omelets in a frying pan for 5–7 min, testing different cooking times due to the lack of a standard. Scrambled eggs were cooked on direct heat for 3–8 min, followed by 1 min off the heat. Poached eggs were cooked in boiling water for up to 8 min, following Le Cordon Bleu recipes. *Salmonella* survivors were quantified on xylose lysine deoxycholate (XLD) agar and confirmed by ISO 6579:2022. Scrambled eggs and omelets showed *Salmonella* levels below the limit of enumeration after 5 min of cooking, when fully coagulated. However, poached eggs made with refrigerated eggs required longer cooking to achieve equivalent *Salmonella* inactivation compared with those at room temperature. Eggs stored at room temperature (28°C) showed a mean reduction of 7.4 log CFU/g after 5 min, whereas, eggs stored at 5°C achieved a similar 7.6 log CFU/g reduction only after 7 min. At 5 min, the difference in *Salmonella* inactivation between poached eggs prepared from room-temperature and refrigerated eggs was 4.4 log CFU/g. These results demonstrate that lower egg storage temperature delays heat penetration and requires longer cooking to achieve equivalent microbial reduction, emphasizing the importance of controlling both initial contamination level and cooking time, especially for poached eggs with partially coagulated yolks considered ready-to-eat. ISSN: 01496085

Li Y., Wu Y., Xia K., Zheng K., Sun L., Liang J., Hong Y., Li Z., Ma Y., Qin X., Dong Q., Wang X.

Effects of simulated food processing stresses on antibiotic resistance in Salmonella Typhimurium

(2026) *Food Research International*, 226, art. no. 118179

ABSTRACT: Antibiotic resistance in *Salmonella enterica* poses a growing food safety concern. Sublethal environmental stresses during food processing, storage, and transportation may influence bacterial resistance phenotypes. This study investigated the

effects of simulated food processing stresses including heat, refrigeration, freezing, acid, and alkaline conditions on the survival and antibiotic resistance of *S. Typhimurium*. The mechanisms underlying antibiotic resistance changes were further explored using scanning electron microscopy (SEM), extracellular ATP content quantification, and analysis of resistance-related and stress response gene expression. The results demonstrated that the antibiotic resistance in *S. Typhimurium* was influenced by both the type and duration of stress exposure. Resistance to aminoglycoside and β -lactam antibiotics increased following heat and cold stresses, whereas fluoroquinolone and β -lactam resistance was more prominent under acidic and alkaline conditions. Prolonged exposure to thermal or cold stress led to a time-dependent enhancement of resistance levels. SEM observations and elevated extracellular ATP levels after heat treatment revealed significant outer membrane disruption and cellular content leakage, suggesting increased membrane permeability. These membrane changes, along with transcriptional alterations such as the upregulation of resistance genes (e.g., *bla*TEM) and stress response regulators (*dnaK*), as well as the downregulation of porin-encoding genes (*ompF*), likely contributed to the observed resistance changes. Overall, the findings underscore the potential of food chain-associated environmental stresses to induce adaptive responses and promote antibiotic resistance in *S. Typhimurium*. This highlights the importance of considering such effects during food processing, transportation, and storage, to support improved microbial risk management and safeguard public health. ISSN: 09639969

Rocha J.S., Lepaus B.M., Domingos M.M., Bernardes P.C., de São José J.F.B.

Study of the Factors Involved in the Adhesion Process of Salmonella enterica Enteritidis, Escherichia coli, and Staphylococcus aureus to the Surface of Apple, Arugula, Cucumber, and Strawberry

(2026) *Foods*, 15 (3), art. no. 449

ABSTRACT: Bacterial contamination of fresh produce remains a global food safety concern, with pathogens such as *Salmonella*, *Escherichia coli*, and *Staphylococcus aureus* frequently implicated in foodborne outbreaks. Understanding the physicochemical factors involved in bacterial adhesion to fresh produce surfaces is essential for developing effective sanitization strategies. This study evaluated the influence of surface roughness, hydrophobicity, thermodynamic free energy, and temperature on pathogen adhesion to apple, arugula, cucumber, and strawberry. Surface roughness varied significantly among produce types (2.51–5.86 μm), with arugula exhibiting the highest values. Hydrophobicity assessments revealed discrepancies between qualitative (contact angle-based) and quantitative (free energy-based) methods: while all produce were classified as hydrophobic qualitatively, strawberry was hydrophilic by quantitative analysis. All bacterial species tested were hydrophilic qualitatively, but *E. coli* showed hydrophobic character quantitatively. Thermodynamic predictions of adhesion ($\Delta G_{\text{adhesion}}$) did not predict observed adhesion bacterial counts (5.07–6.20 log CFU·g⁻¹), with substantial bacterial attachment occurring even when thermodynamically unfavorable (positive $\Delta G_{\text{adhesion}}$), indicating that biological factors override physicochemical interactions. Temperature deeply influenced adhesion, with 25 °C promoting 0.3–3.5 log CFU·g⁻¹-higher bacterial counts than 7 °C across all combinations (p-value ≤ 0.05). These findings demonstrate that bacterial adhesion to fresh produce is multifactorial, with temperature as the dominant controllable factor, and highlight the need for integrated sanitation approaches combining physical and chemical treatments applied before refrigerated storage. ISSN: 23048158

Houser K.E.

Multicounty Outbreak of Salmonella Agbeni Linked to Ice in a Cooler at a County Fair – Illinois, August 2024

(2026) *MMWR Recommendations and Reports*, 75 (7), pp. 93 - 97

ABSTRACT: On August 5, 2024, the Brown County (Illinois) Health Department (BCHD) was informed by the county sheriff that numerous potential jurors being screened for an upcoming trial had reported recently experiencing a gastrointestinal illness. One week later, on August 12, a laboratory-confirmed case of *Salmonella enterica* serotype Agbeni infection was reported to BCHD by the Illinois Department of Public Health. Investigation by BCHD identified seven laboratory-confirmed and six probable cases of *S. enterica* serotype Agbeni illness across five Illinois counties. All persons who became ill had attended the Brown County fair in rural Illinois during July 30–August 4 and reported drinking beer served from a cooler in the fair’s beer tent. No other common food or environmental exposures were identified. The cooler containing the beer was reused for multiple days and not cleaned. A generative artificial intelligence tool (ChatGPT 4.0, OpenAI; 2024) was used to assist with hypothesis generation during the investigation, supplementing traditional epidemiologic methods and contributing to identification of a

shared, nonfood vehicle of transmission. This outbreak highlights the role of standardized hygiene protocols for cooler sanitation and beverage storage and handling at public events.
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Caulcrick-Grimes M., Loeck B.K.D., Homola P., Fu T.-J., Burgos J., Schoelen D., Litterman R., Ladines E., Buchholz A., Tung G., Smith N., Buss B.F., Jansen L., Palacios A., McCutchen E., Wetzel C., McClellan H., Andrews C., Wright E., Pearson E., Waldron A., Loeffler J., Orthahn D., Kreil K., Schwensohn C., Viazis S.

An investigation of an outbreak of Salmonella Typhimurium infections linked to alfalfa sprouts – United States, 2022

(2026) *Food Control*, 181, art. no. 111654

ABSTRACT: In 2022, the U.S. Food and Drug Administration (FDA), Centers for Disease Control and Prevention (CDC), and state and local public health and regulatory agencies investigated an outbreak of Salmonella Typhimurium infections linked to alfalfa sprouts. A total of 63 ill people were reported in eight states, including ten hospitalizations.

Interviews of ill people identified raw alfalfa sprouts as the vehicle of interest. A traceback investigation, including eight points of service in three states, identified a single grower as the source of the alfalfa sprouts. An inspection by FDA and Nebraska Department of Agriculture at the grower identified deviations from food safety standards and violations to FDA's produce safety regulation, including failure to follow the production batch testing requirements. The grower voluntarily recalled four lots of raw alfalfa sprouts. Retail sprout samples collected by state and local officials and sprouts and alfalfa seed samples collected by FDA during inspections at the grower and distributor all tested negative. The epidemiologic, traceback, and inspectional evidence supported the conclusion that alfalfa sprouts from the single grower were the source of illnesses. Whole genome sequencing data from Australian clinical isolates, after the outbreak concluded, supported that contaminated seed was the likely source of sprout contamination. Rapid response and collaborative efforts by federal, state, and local public health officials helped identify the outbreak source and implement the necessary control measures for preventing further illnesses. Established food safety requirements are necessary to reduce foodborne illnesses associated with the production of sprouts for human consumption. ISSN: 09567135

Guyard-Nicodème M., Payen C., Larivière-Gauthier G., Mompelat S., Quesne S., Anis N., Bonifait L., Guillier L., Keita A., Bougeard S., Fravallo P., Chemaly M.

Co-inoculation of broilers by Campylobacter and Salmonella: effect on colonization, cecal microbiota, and serum metabolome

(2026) *Microbiology spectrum*, 14 (3), pp. e0110225

ABSTRACT: Campylobacteriosis and salmonellosis are the leading bacterial zoonoses in Europe, with poultry meat being the primary source of human contamination. Although both Campylobacter and Salmonella bacteria can coexist asymptotically in chickens, their reciprocal impact remains underexplored. An in vitro study showed that Campylobacter jejuni survival was positively affected by the presence of Salmonella, but no data are available on this interaction in the animal gut. In this study, an in vivo investigation was carried out to explore the dynamics between Campylobacter and Salmonella colonization in chickens. The results revealed that both Salmonella and Campylobacter maintained significantly higher levels of colonization in the ceca throughout the experiment when co-inoculated compared to when inoculated alone. Additionally, changes in the microbiota were associated with each pathogen inoculated alone, but the simultaneous presence of Campylobacter and Salmonella induced specific modulations that could possibly explain this phenomenon. Significant differences were found in the serum metabolome of the contaminated groups, and partial least squares discriminant analysis models enabled the discrimination of contaminated animals from controls using these metabolic signals. Furthermore, possible links between variations in the microbiota and variations in the metabolome were identified. IMPORTANCE This study demonstrates a synergistic effect between Salmonella and Campylobacter jejuni in the gut during co-infection in chickens, leading to an increased presence of both pathogens, as well as unique microbiota and metabolome changes. These findings underscore the importance of considering co-infection in poultry control measures and highlight the complex interplay between pathogens, microbiota, and metabolism.

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Wenderlein J., Stroehlein A.J., Pietsch M., Simon S., Szabo I., Malorny B., Lamparter M.C., Fischer J.

Salmonella's lost phenotype: Implications of sequence-based serotyping on the characterization of lipopolysaccharide-deficient Salmonella isolates

(2026) *Microbiology Spectrum*, 14 (3), pp. 1 - 16

ABSTRACT: *Salmonella* serotyping is shifting from slide agglutination toward whole-genome sequencing (WGS). While WGS allows for comprehensive analyses, phenotypic information about lipopolysaccharide-deficient ("LPS-rough") isolates obtained from slide agglutination is lost. This discrepancy represents a challenge for *Salmonella* control in livestock because in the European Union, LPS-rough *Salmonella* isolated from food-producing animals that are untypable using slide agglutination alone are not subject to control measures, whereas isolates of certain serovars in certain matrices would be, when based on geno-serotyping. Here, we provide an account of the relevance of this phenotype in the context of routine diagnostics and food safety by characterizing the occurrence, diversity, and isolation matrices of LPS-rough isolates among non-human *Salmonella enterica* subsp. *enterica* isolates from Germany. Using available WGS data, we examined phylogenetic relationships and associations with certain genomic features. On average, 5% of isolates exhibited an LPS-rough phenotype across 46 serovars, but clonal distribution of this phenotype along the food chain was not evident. LPS-rough isolates were more commonly found in *S. Choleraesuis* isolated from wild boar and in *S. Typhimurium* isolated from pork products, compared with other matrices. We also found associations with two virulence factors, an AMR gene, and a plasmid marker. The present work lays the foundation for future research into the role of certain matrices, environments, or genomic factors in the development of LPS-rough *Salmonella* isolates and will facilitate the elucidation of the genomic basis of this phenotype, which may improve recommendations regarding risk management and control measures. **IMPORTANCE** The present work highlights some of the challenges associated with the recent shift from serology- to sequence-based typing of *Salmonella enterica* serovars and provides a national perspective on the presence and relevance of the lipopolysaccharide-deficient ("LPS-rough") phenotype in samples obtained from food, animals, and the environment, including considerations regarding the choice of typing method. We provide evidence that clonal distribution of isolates with this phenotype is unlikely, but that certain environments may favor its development, and certain genomic factors may increase survival rates of LPS-rough isolates when exposed to environmental stressors. These findings could have important implications for regulations regarding the surveillance and management of *Salmonella* isolated from food, feed, and animals in the future, in particular in the context of using different typing methods, and warrant further detailed research. ISSN: 21650497

Adriaansens D.L.L., van den Berg O.E., Lanzl M.I., van der Weijden C., van Dommelen M., Nagel K., Batstra-Blokpoel J., Brandwagt D.A.H., van der Zwaluw K., Mooijman K., van Hoek A.H.A.M., Mans-Poulie J., van den Beld M., Castelijm G., Koene M., Slegers-Fitz-james I.A., Franz E., Pijnacker R.

The role of contaminated eggshells used in poultry feed in a diffuse nationwide outbreak of Salmonella Enteritidis, the Netherlands, 2023 to 2025

(2026) *Eurosurveillance*, 31 (9), art. no. 2500603

ABSTRACT: We describe a large and prolonged outbreak of *Salmonella* Enteritidis in the Netherlands. Between June 2023 and September 2025, we identified 227 outbreak cases (110 males, 114 females, three with missing information of sex; median age 43 years). Outbreak cases were individuals whose isolates belonged to the outbreak cluster based on whole genome sequencing (WGS) using single-linkage clustering with a threshold of ≤ 5 allelic differences, since June 2023. A case-control study focussing on egg consumption was conducted, alongside trace-back and trace-forward investigations. Findings of the case-control study confirmed the existence of two WGS subclusters: subcluster A linked to barn eggs (adjusted odds ratio (aOR)=5.8; 95% confidence interval (CI): 2.11–15.99) and subcluster B linked to organic eggs (aOR=63.6; 95% CI: 6.04–670.55). Isolates from 14 laying hen farms and eggshells were linked to the outbreak, suggesting the outbreak had multiple sources. Inadequate processing of contaminated eggshells before their use in poultry feed was most probably contributing to the spread and length of the outbreak. Measures to improve raw material control for animal feed were implemented, contributing to a decline in case numbers. However, since the outbreak likely had multiple sources, new cases continue to be detected, especially in subcluster B. ISSN: 1025496X

de Aguiar G.A., da Silva D.G., Arruda L.P., Petri F.A.M., Storino G.Y., Rabelo I.P., Nogueira G.S., Lopes B.T., Nunes C.C., Pires G.P., Ferreira G.C., Santos G.F., Sanches T.V.C., Braga E.R., de Oliveira L.G.

Experimental Salmonella Typhimurium infection in pigs

(2026) *Journal of Veterinary Diagnostic Investigation*, 38 (2), pp. 265 - 267

ABSTRACT: The genus *Salmonella*, particularly *Salmonella enterica* subsp. *enterica* serovars *Choleraesuis* and *Typhimurium*, poses significant challenges to swine production and leads to economic losses from conditions such as septicemia and enterocolitis. We evaluated the effects of experimental infection with *Salmonella Typhimurium* on clinical

signs and anatomopathologic outcomes in pigs. Twenty 90-d-old pigs were divided into 2 groups: G1 received an oral inoculum of 10⁸ cfu of *Salmonella* Typhimurium; G2 served as a control. Pigs were monitored clinically for 30 d; postmortem examinations and microbiologic analyses were conducted. No significant differences were found in rectal temperature or weight between groups; however, diarrhea episodes were noted in the challenged group starting on day 5 post-inoculation. Isolates of *Salmonella* Typhimurium were detected intermittently in the challenged group; all positive samples came from pigs without diarrhea. Macroscopic lesions in G1 pigs included button-shaped ulcers in the ileocecal region, enlarged or hemorrhagic mesenteric lymph nodes, and hyperplasia of lymphoid tissue in the colon. ISSN: 10406387