NEWSLETTER

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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

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EURL *Salmonella*

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Contents

EDITORIAL NOTE **4**

CONTRIBUTION OF THE EURL-*SALMONELLA* **6**

EURL-*SALMONELLA* ACTIVITIES FORESEEN IN 2026 6
TIMETABLE EURL-*SALMONELLA* PROFICIENCY TEST FOOD 2026 DETECTION OF *SALMONELLA* IN A FOOD MATRIX 7

FROM THE LITERATURE **8**

Editorial Note

Bilthoven, 8 January 2026

Dear colleagues,

First of all, I would like to **wish you all a very good and healthy 2026**! I hope you had a nice time during the Christmas break and found some time to relax.

In the Newsletter of December 2024, I started the editorial note with the information about the relocation of our institute (RIVM) to a new building in Utrecht. I almost feel ashamed to say that we are still located in the (old) building in Bilthoven and that according to current information it is quite likely that the relocation will take place this year (2026, that is). We will wait and see. Anyway, we look forward to a continuation of the nice cooperation with all NRLs-*Salmonella* in the new year!

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**. Please find an overview of this planning on page 6 of this Newsletter.

You can see in this planning that the first Proficiency Test (PT) organised this year, is for detection of *Salmonella* in a food matrix. The timetable for this **EURL-*Salmonella* PT Food 2026** was shared with the NRLs in December 2025 and can be found in this Newsletter as well (page 7).

Additionally we have planned the **EURL-*Salmonella* workshop** to be organised as an hybrid meeting on 12 and 13 May 2026 in Zaandam, the Netherlands. Information and the link to the registration form was shared with the NRLs-*Salmonella* early December 2025. The deadline for onsite registration is 15 January and for online registration 10 April 2026.

Another activity which is planned for the first part of 2026 is the **joint training course of the inter EURLs Working Group on NGS**. This year the training will be organised at the premises of the EURL-AMR in Denmark in June 2026. Soon more details about this training will be shared with all NRLs of the 8 EURL/NRL networks.

In August/September 2025 we organised the **EURL-*Salmonella* PT Typing 2025**, for serotyping of *Salmonella*. The deadline for reporting the results was 3 October 2025. The results have been analysed and the interim summary report was shared with the participants and published at the EURL-*Salmonella* website in November 2025. We are happy to notice that all participants scored a good performance in this PT. Please find here the link to interim summary report: https://www.eurlsalmonella.eu/en/documenten/interim-summary-report-eurl-salmonella-pt-serotyping-2025

Already in fall 2024, as you may know, the Commission implementing Regulation (EU) 2024/2463 was published, 'laying down analytical methods applicable to official controls performed for the verification of compliance of food business operators with Regulation (EC) No 2073/2005'. With publication of this Regulation, it became permitted to use **alternative, validated methods** for the official control of foodstuffs. Up to now, we prescribed the use of EN ISO 6579-1 for the detection of *Salmonella* in our PTs. Alternative methods could be used in addition, but the assessment of the performance was based upon the results found with EN ISO 6579-1. However, if NRLs-*Salmonella* use alternative, validated methods for the official control of (food/feed/veterinary) samples, we will, from now on, also use the results of these methods for assessment of the performance of the NRLs in the PTs. Mind that the alternative method has to be

properly validated in accordance with EN ISO 16140-2 and in case of a proprietary method, it shall be certified by an independent certification body. If an alternative method is used, we will ask to report the reference to the validation report and (if relevant) to the certificate. If this information can not be supplied, we can not assess the performance of the NRL-*Salmonella* when using this alternative method in the PT.

In fall 2025, the following EURL-*Salmonella* reports were published:

Diddens, R.E. and Mooijman, K.A, 2025. EURL-*Salmonella* Combined Proficiency Test food-feed 2025. Detection of *Salmonella* in flaxseed. National Institute for Public Health and the Environment, Bilthoven, the Netherlands. RIVM Report 2025-0038. https://www.rivm.nl/bibliotheek/rapporten/2025-0038.pdf

Mooijman, K.A. The 30th EURL-*Salmonella* workshop; 20 May 2025, Online. National Institute for Public Health and the Environment, Bilthoven, the Netherlands. RIVM Report 2025-0039. https://www.rivm.nl/bibliotheek/rapporten/2025-0039.pdf

Best wishes,
Kirsten Mooijman
Coordinator EURL-*Salmonella*

Contribution of the EURL-*Salmonella*

EURL- *Salmonella* activities foreseen in 2026

Date(s)	Activity
16 March – 15 April 2026	EURL-*Salmonella* Proficiency Test Food 2026; Detection of *Salmonella* in a food matrix.
12 & 13 May 2026	Hybrid EURL-*Salmonella* workshop, Zaandam, the Netherlands
June 2026	Joint Training Course of the inter EURLs Working Group on NGS in Denmark.
September – October 2026	EURL-*Salmonella* Proficiency Test primary production stage (PPS).
November 2026 – January 2027	EURL-*Salmonella* Proficiency Test Typing; Serotyping and (optional) WGS Cluster analysis.

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

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	Monday **16 March 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 23 March 2026**	**Start performance of the Proficiency Test.**
16	Wednesday **15 April 2026** at the latest	Deadline for completing the result form: **15 April 2026** (23:59h CET) After this deadline the result form will be closed.
	May 2026	Summary of results

If you have questions about this Proficiency Test, please contact:
Robin Diddens
E-mail: EURLSalmonella@rivm.nl
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: October – December 2025

Brait, V., Böff, L., Zmarlak-Feher, N.M., Silva, N.J.-D., Mazzilli, S., de la Gandara, M.P., Moura, A., Mossong, J., Ernst, C., Ragimbeau, C., Pijnacker, R., Lanzl, M., Brandal, L.T., Lange, H., Stephan, R., Biggel, M., Raess, M., Daniel, O., Spackova, M., Clarke, C., Cormican, M., Colgan, A., Garvey, P., McKeown, P., Dryselius, R., Karamehmedovic, N., Grilc, E., Trkov, M., Pirš, M., Brown, D., Browning, L., Hoban, A., Godbole, G., Painset, A., Anne Chattaway, M.A., Vainio, A., Rimhanen-Finne, R., Fischer, J., Lamparter, M.C., Mattheus, W., Commans, F., Grginić, A.G., Mlinaric, I., Pem-Novosel, I., Filipovic, S.K., Ferencak, I., Jurić, D., Niskanen, T., Jernberg, C., Rizzi, V., Sarno, E., Kornschober, C., Wolfsbauer, A., Werber, D., Simon, S., Gymoese, P., Ethelberg, S., Müller, L., Maritschnik, S., Meinen, A., Pietsch, M.
Insights into recurring multi-country outbreaks of Salmonella Strathcona associated with tomatoes, Europe, 2011 to 2024
(2025) Eurosurveillance, 30 (41), art. no. 2500224
ABSTRACT: Notifications of Salmonella Strathcona infections increased in Europe in 2023 prompting a multi-country outbreak investigation. We aimed to describe the epidemiology of S. Strathcona infections in 17 European countries 2011–2024, investigate the genetic relatedness of S. Strathcona isolates and identify the vehicle. Cases were persons residing in the study area and with a laboratory-confirmed S. Strathcona infection 2011–2024. Confirmed cases had a S. Strathcona isolate clustering with the outbreak reference strain in core genome multilocus sequence typing (cgMLST) within 7 allelic differences (AD) and possible cases within 8–13 AD. Probable cases had an epidemiological link to a confirmed case and non-outbreak cases had an isolate > 13 AD from the outbreak reference strain. Since 2011, 662 S. Strathcona infections have been identified: 469 confirmed, 161 probable, 13 possible and 19 non-outbreak cases. Median age of the cases was 34 years (IQR: 19–58 years) and 306 (47.5%) were notified in 2023–2024. Most sequenced isolates (469/496; 94.5%) were highly genetically related (≤ 7 AD) over time and across countries, compatible with a common source. Epidemiological and traceback investigations identified small tomatoes from Sicily as the suspect food vehicle. Stringent control measures at the source are needed to stop the contamination and prevent future cases.
ISSN: 1025496X

Wongwigkarn, J., Kucharoenphaibul, S., Sitthisak, S., Thummeepak, R., Cheewapat, R., Nimanussornkul, K., Khongfak, S., Tasanapak, K.
Molecular detection of virulence genes and antibiotic resistance profiles in Salmonella spp. contaminated on food-contact surfaces in restaurant settings
(2025) ScienceAsia, 51 (5), art. no. 2025089
ABSTRACT: This study investigates the prevalence, virulence genes, and antimicrobial resistance profiles of Salmonella spp. isolated from food contact surfaces and food handlers in local restaurants in northern Thailand. Salmonella, a prominent foodborne pathogen, can thrive under diverse conditions, leading to the contamination of various food products and causing illnesses. It is acknowledged as a prominent foodborne pathogen. A total of 650 samples were collected, resulting in the identification of 21 Salmonella belonging to serogroups B (52.38%), D (14.30%), A, C1, E1 (each 9.52%), and C2 (4.76%). Virulence gene analysis revealed that Salmonella group B isolates possessed the highest number of virulence genes, with up to 12 per isolate, including commonly detected genes such as msgA, sopB, and sif A. A significant correlation between specific virulence genes and antibiotic resistance was observed. Of the Salmonella isolates recovered in this study, 43% were identified as multidrug-resistant (MDR). Among these MDR strains, 78% were isolated from the hands of food handlers, while the remaining originated from kitchen surfaces. The combined threat posed by these Salmonella strains is underscored by the presence of multiple virulence genes and elevated levels of antibiotic resistance. Effective control measures, including stringent hygiene practices, regular cleaning and sanitization of kitchen equipment, and the implementation of Hazard Analysis and Critical Control Points (HACCP) systems, are essential to minimize contamination risk and prevent the spread of harmful pathogens. Ongoing surveillance and antimicrobial resistance monitoring

programs are crucial for managing the threat of MDR Salmonella in restaurant environments. ISSN: 15131874

ECDC and EFSA
Prolonged multi-country outbreak of Salmonella Strathcona ST2559 linked to consumption of tomatoes in the European Union/European Economic Area – first update, 23 October 2025
(2025) EFSA Journal, 23 (10), art. no. e9740
ABSTRACT: A prolonged cross-border outbreak of Salmonella Strathcona ST2559 is ongoing in the European Union/European Economic Area (EU/EEA). From 2023 to 30 September 2025, 437 confirmed cases of S. Strathcona ST2559 were identified in 17 EU/EEA countries (205 additional cases since the first rapid outbreak assessment published on 12 November 2024): Austria (76), Croatia (3), Czechia (11), Denmark (12), Estonia (2), Finland (5), France (43), Germany (113), Ireland (6), Italy (123), Luxembourg (5), the Netherlands (5), Norway (4), Slovakia (6), Slovenia (10), Spain (3) and Sweden (10). Cases have also been reported in the United Kingdom (73), Canada (10) and the US (24). The most visited country among travel-related cases was Italy. Tomatoes remain the primary food vehicle in several investigations for this prolonged multi-country outbreak. In 2025, new outbreak investigations in Austria identified small tomatoes from Sicily (Italy) as the source of infection, as was the case for the 2023 outbreak in Austria and the 2024 outbreak in Italy. The same conclusion was reached for a historical S. Strathcona ST2559 outbreak in Denmark in 2011. In response, comprehensive investigations have been carried out by the food safety authority in Italy. The detection of S. Strathcona in a sample of irrigation water collected at the site of a tomato producer in Sicily confirmed the role of the environment in tomato contamination. These findings also highlighted the need for a multi-disciplinary strategy integrating environmental assessments to mitigate the risk of Salmonella contamination. This need is also confirmed by the detection of the outbreak strain in other matrices connected with aquatic environments. To prevent new cases from occurring, further investigations should be undertaken to verify whether tomatoes from Sicily are the vehicle of infection and to guide effective control measures during the (pre)harvest period, including irrigation water sources. © European Centre for Disease Prevention and Control, European Food Safety Authority, 2025.

Lewis, S.E., Cawthraw, S.A., Wales, A.D., Rawlins, M., Brown, D., Ring, I., Huby, T., Sandu, C., Jinks, R., Snow, L.C., Wyllie, S., Mackintosh, A., Smith, R.P., Evans, S., Martelli, F.
Salmonella in the slaughter sheep population in England and Wales
(2025) Journal of Applied Microbiology, 136 (10), art. no. lxaf244
ABSTRACT: Aims A survey of Salmonella in sheep caecal content samples was undertaken in England and Wales in 2023. Methods Over 9 months, repeated sampling was conducted in 12 abattoirs that represented 28% of national annual sheep throughput with good geographical coverage. Samples of caecal content were obtained from 1228 sheep at abattoirs and cultured for Salmonella spp. Results Salmonella was isolated from 104 (8.5%) samples, with 21 isolations (1.7%) of Salmonella Typhimurium. The most commonly isolated serovar (80 samples, 6.5%) was the sheep-adapted Salmonella enterica subspecies diarizonae serovar 61: k:1,5,(7), which has low zoonotic potential. Modelling estimated the mean annual Salmonella prevalence to be 10.5% (95% CI 8.5%–13.0%). Multivariate logistic regression indicated that the likelihood of Salmonella isolation was significantly associated with animal age, with the odds of a sheep over 12 months old yielding Salmonella being significantly greater than for those under 12 months (OR 7.2, $P < 0.001$). For serovars of public health importance, particularly S. Typhimurium, the analysis was limited by the small number of isolations, but univariate analysis indicated a significant association between over-12-month animals and the likelihood of isolating S. Typhimurium, similar to overall Salmonella isolation risk. Conclusions Our study has assessed Salmonella carriage among sheep presented for slaughter and intended for the food chain and found 8.5% of samples positive. It provides an improved understanding of the prevalence, distribution, and subtypes of Salmonella in slaughter sheep of different ages, indicating that older sheep were more often associated with isolation of Salmonella. ISSN: 13645072

Siceloff, A.T., Shariat, N.W.
Optimizing Salmonella Recovery From Commercial Poultry Environmental Samples With Selective Preenrichment
(2025) Journal of Food Protection, 88 (11), art. no. 100627
ABSTRACT: The current culture-based methods for detecting Salmonella are time and resource-intensive, as it can take between three to five days with preenrichment and

selective enrichment steps. Previous work by our group has shortened this process by combining novobiocin and selective ingredients from Rappaport-Vassiliadis (RV) (malachite green; 0.1 g/L) and tetrathionate (TT) (bile salts; 1 g/L) to BPW in parallel, creating an all-encompassing selective preenrichment step. In this study, we sought to validate the use of selective preenrichment on commercial poultry live production samples, as the increased presence of background bacteria may limit Salmonella recovery. Two pairs of boot sock samples were collected from 35 houses, representing 17 different commercial broiler or breeder farms (n = 70 samples). The samples were cultured under selective preenrichment conditions in parallel with standard nonselective preenrichment (BPW), followed by selective enrichment (RV, TT). Additionally, molecular enumeration was performed to quantify the amount of Salmonella present in each sample. Overall, Salmonella was found in 74% (52/70) of samples collected, and selective preenrichment and selective enrichment conditions each recovered Salmonella in 14/17 farms. The average quantity per sample was greater in those recovered with selective preenrichment (5.2 log<inf>10</inf> CFU/sample) than those that were not (3.0 log<inf>10</inf> CFU/sample; p = 0.01, Welch two-sample t-test). CRISPR-SeroSeq was used to determine the relative frequency of Salmonella serovars in each sample and culture condition. The proportion of multiserovar populations observed in the selective preenrichment conditions (53%, 29/55) was not significantly different from those in selective enrichment conditions (56%, 39/70; p = 0.1, McNemar's chi-squared test). These findings suggest that increasing the selectivity of the Salmonella preenrichment step could eliminate the need for a subsequent selective enrichment, thus reducing the time to Salmonella isolation by 24 h. ISSN: 0362028X

Rakover, A., Ødeskaug, L.E., Lund, H., Lange, H., Kaupang, K., Skjerdal, T.O., Jensvoll, L., Bergsjö, B., Katsiouleri, P., Veneti, L., Naseer, U., Brandal, L.T., Johannessen, G., Berglund, T., Røed, M.H., Falk, M., Astrup, E., Madslien, E., Woods, M., Bruvik, T., Laird, T.S., Lavoll, S.B., Heradstveit, P.L., Berg, T.C.
A large outbreak of multiple Salmonella serovars linked to alfalfa sprouts in Norway, October to December 2024
(2025) Infection, 53 (5), pp. 2125 - 2134
ABSTRACT: Purpose: This study investigates a nationwide Salmonella outbreak in Norway during October–December 2024 involving four different serovars—S. Newport, S. Typhimurium, S. Kisarawe, and S. Kinondoni. The investigation aimed to assess the outbreak's scope, identify the source, and implement control measures. Methods: Epidemiological analyses included trawling and targeted questionnaires, a matched case–control study, and grocery receipt analysis. Whole-genome sequencing (WGS) determined genetic links between Salmonella isolates from human cases, food, and environmental samples. Traceback investigations identified potential contamination sources. Results: A total of 230 cases (69% female, median age: 48 years) were identified, with 33% requiring hospitalization. Sprout consumption was reported by 69% of cases interviewed through trawling or targeted questionnaires. Grocery receipts were collected from some of the cases, and half of these had purchased sprouts. A matched case–control study found cases to be associated with consumption of sprouts (penalized adjusted odds ratio of 3.13). WGS established genetic links between clinical, food, and environmental isolates, identifying alfalfa sprouts as the outbreak source. Traceback investigations identified potential risk associated with seeds from an Italian supplier, previously associated with two Salmonella outbreaks in Norway in 2024 and multiple outbreaks across the European Union. The Italian supplier reported negative findings for Salmonella in their self-monitoring checks on seeds sent to Norway. Control measures included product withdrawal, seed batch quarantine, and public health advisories. Conclusion: This multi-serovar outbreak highlights the public health risks associated with consumption of raw sprouts and emphasizes the need for improved detection methods and stricter regulations to prevent future outbreaks. ISSN: 03008126

Kosola, M., Markkula, A., Rimhanen-Finne, R., Lundén, J.
Bootstrap simulation of the effect of food control inspections on the number of Campylobacter and Salmonella infections and means to increase effectiveness of inspections
(2025) Food Control, 176, art. no. 111404
ABSTRACT: Food control inspections are performed to ensure food safety. Inspections have been demonstrated to decrease non-compliance with food safety legislation but quantified knowledge regarding the effect of inspections on the incidence of foodborne illnesses is scarce. We used bootstrap simulation to estimate the effect that changes in the compliance level of food establishments would have on Campylobacter and Salmonella incidences in Finland and examined means to improve the effectiveness of food control inspections. We

estimated that if the compliance level of food establishments in all 62 food control units in Finland were in the range of the top half of the units, domestic Campylobacter infections would decrease by 12.1 % and Salmonella infections by 12.4 %. We demonstrated that item-specific inspection grades are associated with 1) the non-compliance correction percentage and 2) the percentage of inspections in which certain inspection items—mainly those related to temperature management [cold-stored foodstuffs ($\rho = 0.34$, $p = 0.01$), management of shelf life and sale period of product ($\rho = 0.27$, $p = 0.03$)] and actions of personnel [hygiene of work practices used by personnel ($\rho = 0.43$, $p = 0.001$), work clothes ($\rho = 0.33$, $p = 0.01$)]—were inspected. Shorter verbal descriptions of the inspection findings correlated with increased correction of some non-compliances, including non-compliances in chilling, adequacy of the own-check plan, cleanliness of the working utensils and equipment, and reception of foodstuffs. Food control units that experience difficulties in the correction of non-compliances should be supported to increase effectiveness of food control. ISSN: 09567135

Georgalis, L., Tsagkaropoulou, T., Karatzas, K.A.G., Fernández Escámez, P.S., Garre, A.
Stress response variability can cause up to 3-fold increase in the thermal resistance of Salmonella strains
(2025) International Journal of Food Microbiology, 442, art. no. 111347
ABSTRACT: The variability in the bacterial stress response has received plenty of attention during the last years, partly due to its relevance to microbial risk assessment. Although the microbial response is affected by numerous variability sources, previous studies focused mostly on strain variability (inherent differences between strains of the same bacterial species) under optimal growth conditions. Here, we analyze a variability source relatively unexplored within microbial risk assessment: stress response variability. This refers to physiological differences due to prior exposure to stressful environments. Namely, we studied the impact of sub-optimal pre-culture conditions or the application of an acid shock on the thermal resistance of two strains of Salmonella (a reference strain and a highly heat resistant one). We observed that stress response variability is strain dependent. The heat resistance of the reference strain had a significant increase in heat resistance (up to 3-fold increase), whereas the conditions tested resulted in a reduction of thermal resistance with respect to control conditions (up to 2-fold reduction). Considering that magnitude of these changes are comparable to strain variability, and that stress response variability might be common throughout the food supply chain, this study evidences the need to study this phenomenon further in order to incorporate it into quantitative microbial risk assessments. ISSN: 01681605

Mantovam, V.B., dos Santos, D.F., Giola Junior, L.C., Landgraf, M., PINTO, U.M., Todorov, S.D.
Listeria monocytogenes, Salmonella spp., and Staphylococcus aureus: Threats to the Food Industry and Public Health
(2025) Foodborne Pathogens and Disease, 22 (12), pp. 809 - 824
ABSTRACT: Foodborne pathogens have always been of public health concern and represent safety issues for food processors. These pathogens develop new ways to overcome antibiotics, survive in different environmental conditions, and the ability to reproduce in many hostile environments configure them as serious health hazards. Considering the huge number of microorganisms, three bacterial representatives were selected to provide a better knowledge about the question of which one is the worst enemy for humans, from the food industry point of view, taking into consideration their multiplication specificity, virulence, and resistance. As we constantly are exposed to these pathogens in our nutritional habits, this overview aims to summarize the most relevant characteristics associated with the pathogenicity, clinical symptoms and most importantly, how deadly Listeria monocytogenes, Salmonella spp., and Staphylococcus aureus can be in the hospital and the food industry, by comparing among them. Overall, the microbiological knowledge clearly suggests that while all three pathogens are dangerous, L. monocytogenes presents the highest risk of death due to their ability to cause severe complications in vulnerable populations as it presents a range of virulence factors that facilitate evasion of the immune system and cytological effects. Additionally, it shows great resistance to standard food processing and preservation techniques, making it one of the most difficult pathogens to control. Understanding the risks and characteristics of these foodborne pathogens is essential for implementing effective control measures to prevent their occurrence in food products and to promote public health. ISSN: 15353141

Zhang, J., Ebosa, O., Diarra, M., Nadon, C., McAllister, T., Sparling, R., Narváez-Bravo, C.

Genomic Drivers of Biofilm Formation in Salmonella Enteritidis and S. Kentucky from Poultry Production
(2025) Microorganisms, 13 (11), art. no. 2473
ABSTRACT: Salmonella Enteritidis (SE) remains a leading cause of human illness worldwide, and its persistence in poultry environments might be partially attributed to their ability to form biofilm. This study compared the biofilm capacity of 15 SE and 24 Salmonella Kentucky (SK) isolates from poultry products and processing facilities to uncover genetic factors driving biofilm heterogeneity. Biofilm formation and curli/cellulose production were evaluated at 20–22 °C. Genomic analyses included phylogenetic reconstruction, comparative system profiling, SNP variation, and BLASTp v2.17.0 comparisons. Phenotypic assays showed that most SE isolates (73%) were strong biofilm formers, while the majority of SK isolates (62%) failed to form biofilms, despite many carrying the complete curli–cellulose gene set and other biofilm-associated genes. Genomic analysis identified 124 biofilm-related genes, 108 of which were conserved across all isolates, and revealed 24 variants with potential functional impact. Mutations in cellulose biosynthesis (bcs) genes were linked to weaker biofilms, whereas nonsynonymous variants in tol family genes may impair flagellar biosynthesis and matrix stability. These findings demonstrate that genetic variation, not just gene presence, shapes biofilm phenotypes and highlight key molecular targets that may explain why SE persists in poultry production while SK is less successful.

Tekin, Y., Yazgan, H., Güven Gökmen, T.G., Gungor, N., Uprak, N.S.
Integrated Analysis of Salmonella Infantis in Chicken Meat: Epidemiological Surveillance, Antibiotic Resistance, and Potential Bioactive Control Agents
(2025) Pathogens, 14 (11), art. no. 1178
ABSTRACT: Salmonella species isolated from chicken meat pose an increasing threat to public health. According to ECDC data, salmonellosis cases have shown a significant upward trend in many European countries between 2019 and 2023, almost reaching pre-pandemic levels. EFSA reported 77,486 confirmed human cases in the EU in 2023. This corresponds to a notification rate of 18 cases per 100,000 people, compared to 15.4 cases per 100,000 in 2022. This study evaluated the prevalence of Salmonella spp., antimicrobial resistance (AMR) profiles, and the effectiveness of natural biological preservatives in raw chicken meat obtained from retail outlets in Southeast Turkey. Among 100 samples analyzed according to ISO 6579-1:2017, suspicious colonies were detected after selective enrichment in XLD and n = 3 isolates were confirmed to be Salmonella enterica subsp. enterica serovar Infantis by real-time PCR. Disk diffusion tests performed in accordance with EUCAST showed that all isolates were resistant to beta-lactam, tetracycline, trimethoprim, sulfonomid and aminoglycoside groups. All isolates were classified as multidrug-resistant. PCR detected blaTEM-1 (all isolates), aphA1-IAB (all isolates), aadA1 (two isolates), and sul1 (all isolates), while tetA/tetB genes were not detected. Among the natural compounds tested, carvacrol showed the strongest antimicrobial activity (MIC 1.56 µL/mL; MBC 3.125–6.25 µL/mL; inhibition zones 32–35 mm). Eugenol showed moderate effects with higher MIC/MBC values (3.125–6.25 µL/mL/12.25 µL/mL), while α-terpineol was effective only at higher concentrations. These findings are consistent with the global increase in Salmonella Infantis and AMR, supporting carvacrol followed by eugenol and α-terpineol as promising natural alternatives for controlling MDR Salmonella spp. in food safety applications.

Teunis, G., Dallman, T.J., Zając, M., Skarżyńska, M., Petrovska, L., Pista, A., Silveira, L., Clemente, L., Thépault, A., Bonifait, L., Kérouanton, A., Chemaly, M., Álvarez Sánchez, J., Söderlund, R., Nielsen, E.M., Anne Chattaway, M., Burgess, K., Byrne, W., Zomer, A.L., van den Beld, M., Hendrickx, A.P.A., Franz, E., Pires, S., Hald, T., Mughini-Gras, L.
Attributable sources of the five most prevalent non-typhoidal Salmonella serovars across ten European countries
(2025) Journal of Infection, 91 (5), art. no. 106632
ABSTRACT: Non-typhoidal Salmonella is the second most frequently reported zoonotic pathogen in the European Union and European Economic Area. Most human infections are caused by serovars Enteritidis and Typhimurium. Genomic characterisation of Salmonella isolates from humans and animals has become a routine public health surveillance tool in many countries. In this study, the relative contributions of several potential sources of human infection of the five frequently reported Salmonella serovars were estimated using machine-learning methods based on a large, cross-sectional collection of genomes from human cases, and animal and environmental sources, across ten European countries. To define the population structure, core-genome Multilocus Sequence Typing was performed. A supervised machine-learning approach was applied for source attribution in the form of a

Random Forest classifier. The source and country attribution models achieved moderate accuracy (F1=0.6–0.9), which is lower than in previous studies using machine-learning on Whole Genome Sequencing data. However, attributions of human clinical isolates to different sources were generally in line with previous findings for these five serovars. While the lack of clonality in some sources hindered their prediction, it is also likely that certain sources (e.g., pets) do not serve as major contributors to human infection. Therefore, in most cases attributing these sources to the livestock species they are typically associated with, is likely appropriate. Country attributions showed that substantial human cases are attributable to countries other than their own, indicating geographical interrelatedness of sources. This highlights the value of internationally harmonised Salmonella-control policies in the food production chain. ISSN: 01634453

Phayakka, P., Vongkamjan, K., Khrongsee, P., Subramaniam, K., Mordmueng, A., Pelyuntha, W.
Detection, Genomic Characterization, and Antibiotic Susceptibility of Salmonella Anatum SPBM3 Isolated from Plant-Based Meat
(2025) Foods, 14 (21), art. no. 3710
ABSTRACT: Plant-based meat (PBM) products have rapidly grown in popularity due to increasing consumer demand for sustainable, ethical, and health-oriented food alternatives. However, these novel products may pose microbiological risks similar to traditional meats, including contamination by Salmonella spp. In this study, PBM samples (n = 63), including raw products (ground pork, mushroom, and burger) and cooked products (chicken tender, chicken breast, nugget, and beef), were collected from local retail markets in Bangkok, Thailand. The prevalence of Salmonella spp. was assessed by calculating the proportion of confirmed positive samples relative to the total number of PBM products tested. Additionally, the genomic characteristics and antibiotic susceptibility of Salmonella isolated from PBM were also investigated. From the result, Salmonella enterica was detected in 2.44% (1/41) of raw PBM samples, whereas no contamination was observed in cooked PBM products (0/22). Serovar identification revealed the isolate to be S. Anatum. Whole genome sequencing (WGS) analysis revealed the genome of S. Anatum SPBM3 consisted of 4,726,256 base pairs with 52.15% GC content, encoding 4717 coding sequences (CDS). Pangenomic analyses placed S. Anatum SPBM3 within a distinct sub-cluster closely related to pathogenic Salmonella strains previously reported, confirming its identity as part of the S. enterica lineage. The genome harbored 67 antimicrobial resistance genes, 5 prophage elements, and 305 key virulence determinants. Phenotypically, the isolate exhibited susceptibility to most tested antibiotics but showed intermediate resistance to streptomycin, ciprofloxacin, and colistin. Our findings highlight the potential microbial risks associated with PBM products and emphasize the importance of genomic surveillance to ensure food safety and public health protection as dietary preferences evolve toward non-traditional food matrices.

Patch, C.A., Larsen, K.M., Armstrong, C.M., Kanrar, S., Michaelides, A.M., Chakraborty, P., Harper, K., Devlin, V., Martin, L., Lunna, A., Blackwell, H.L., Nguyen, S.C., Penny, A., Etter, A.J.
Prevalence, Risk Factors, and Human Health Implications of Salmonella enterica and Campylobacter spp. in Vermont Backyard Poultry
(2025) Zoonoses and Public Health, 72 (7), pp. 654 - 668
ABSTRACT: Introduction: Backyard poultry (BYP) are increasingly linked to cases of campylobacteriosis and salmonellosis. Methods: Between 2022 and 2024, soiled bedding samples from 70 BYP farms were tested for Campylobacter spp. and/or Salmonella enterica. Results: Nine farms (12.86%) had at least one sample positive for S. enterica, while 19.05% (12/63) tested positive for Campylobacter spp. We sequenced 54 S. enterica isolates from eight farms in this sample and four farms from previous sampling in 2021 (n = 12 total farms) to determine the genetic characteristics of S. enterica from backyard poultry. Salmonella Schwarzengrund was the most common serovar (33%; 18/54) found, followed by Kentucky (16.7%; 9/54) and serovars Hadar (14.8%; 8/54) and Enteritidis (14.8%; 8/54). Though over half of isolates (51.9%; 28/54) exhibited no predicted genotypic or phenotypic resistance to antimicrobials, some serovars such as Salmonella Hadar were resistant to multiple antimicrobials. Four isolates had intermediate phenotypic resistance to ciprofloxacin and two were resistant to ampicillin. Conclusions: In summary, the frequency of Campylobacter and Salmonella in BYP populations of Vermont may pose a significant public health risk. Although the rate of antimicrobial resistance was low among S. enterica isolates, resistance to medically important antibiotics was observed, and isolate serovars aligned with serovars implicated in human illness in Vermont.
ISSN: 18631959

Huneau-Salaün, A., Le Bouquin-Leneveu, S., Chemaly, M.
Salmonella Control Programme in France: Factors Influencing the Detection of Salmonella in Laying Hen Flocks From 2013 to 2021
(2025) Zoonoses and Public Health, 72 (7), pp. 628 - 636
ABSTRACT: Introduction: Salmonellosis is the second leading foodborne illness in the European Union. Eggs are still an important source of Salmonella despite an EU-harmonised control programme in laying hen flocks. The objective of our study was to identify the characteristics related to poultry house (location, type of housing system) and sampling (sampler, type and number of samples, date) associated with the detection of Salmonella target serovars (STS) in France (S. enteritidis, S. typhimurium, three monophasic variants of S. typhimurium and S. Kentucky). Methods: For the first time since the implementation of the EU target prevalence in 2010, we compiled the results of bacteriological detection of Salmonella in French laying hen flocks (108,718 sampling events carried out in 4744 poultry houses). The risk of STS detection was modelled using a mixed logistic regression model taking into account repeated sampling at the poultry house level. Results: An STS was isolated from 737 sampling events (0.68%). Caged flocks had a higher risk (odds ratio (OR) = 1.6, 95% confidence interval [1.2–2.0]) of testing positive compared with on-floor, organic or free-range flocks. The risk of detecting STS was higher when sampling was carried out by the competent authority (CA) (OR = 2.62, [2.2–3.1]) relative to food business operators (FBO), in relation to the risk-based sampling strategy used by the CA. A higher risk of STS detection was associated with taking six samples or more per sampling (OR = 2.8 [2.0–4.0]). A spatial gradient of risk was also described, running from the north-west to the south-east regions of France, in addition to seasonal (third quarter of the year: 2.8 [2.2–3.5], fourth quarter: 2.4 [1.9–3.0], relative to the first quarter) and annual effects (2016: 1.7 [1.2–2.5], 2020: 2.1 [1.5–2.9], 2021: 2.0 [1.4–2.8], relative to 2013). Conclusions: Our findings are of interest for improving sampling protocols for Salmonella detection in laying hen farms. ISSN: 18631959

Parker, E.M., Mollenkopf, D.F., Li, C., Ballash, G.A., Wittum, T.E.
Pet treats, Salmonella, and antimicrobial resistance; a One Health problem
(2025) Preventive Veterinary Medicine, 244, art. no. 106622
ABSTRACT: Zoonotic pathogens, including Salmonella and antimicrobial resistant bacteria, may contaminate the food or treats consumed by our pets. These may directly impact the health of the pets or may be transferred to humans who are in close contact. To better understand the potential risk, we purchased 505 pet treats from pet and farm supply stores, grocery stores, and online retailers in the U.S. over a period of 16 months to identify and characterize Salmonella and Enterobacterales resistant to Highest Priority Critically Important Antimicrobials. We used selective media to detect Salmonella and bacteria resistant to colistin, carbapenems, fluoroquinolones, and 3rd and 4th generation cephalosporins. Four pig ear treats from Brazil were positive for Salmonella, with serotypes, Muenchen, Derby, Agona and Regent. We found that S. Muenchen and S. Derby were closely related to clinical and environmental isolates from the U.S., Canada, Venezuela, and Colombia. We detected three colistin resistant isolates, Klebsiella pneumoniae, Escherichia coli, and Enterobacter hormaechei, all from pig ear treats from Brazil, harboring the mcr-1.18 resistance gene on identical IncX4 plasmids. In addition, we recovered one carbapenem resistant E. coli harboring both bla<inf>KPC-2</inf> and bla<inf>NDM-5</inf> from a “bully stick”. We found that treats originating from North America and treats purchased in grocery stores had a lower risk of contamination with bacteria resistant to the antimicrobials tested. Outreach and extension activities are needed to increase awareness of the risks of contaminated pet treats and to highlight the importance of hand hygiene when feeding and interacting with pets. ISSN: 01675877

Cataldo, N., Schwensohn, C., Kirchner, M., Jenkins, E., Jemaneh, T., Seelman, S., Dey, M., Hamblin, C., Brillhart, D., Goodman, A., Nolte, K., Baker, A., Jackson, T., Literman, B., Bell, R.L., Hawkins, T., Gieraltowski, L., Salter, M., Viazis, S.
An Investigation of an Outbreak of Salmonella Newport Infections Linked to Melons from Southwest Indiana—United States, 2023
(2025) Foodborne Pathogens and Disease, 22 (12), pp. 825 - 833
ABSTRACT: The Food and Drug Administration (FDA), the Centers for Disease Control and Prevention (CDC), and state health and regulatory partners have investigated outbreaks of Salmonella enterica serovar Newport and Typhimurium infections in 2012, 2020, 2022, and 2023 linked to cantaloupes and/or watermelons from Southwest Indiana. In 2023, an outbreak of Salmonella Newport infections included 11 ill people and five hospitalizations reported in six states. The FDA and CDC collaborated with state partners to investigate the outbreak. The traceback investigation did not identify a single point of convergence for cantaloupe or watermelon. Products and environmental samples collected by the FDA and

state partners from farms, public land, distributors, and points of service yielded isolates of multiple Salmonella serovars, including Salmonella Typhimurium and Salmonella Newport, that matched by whole genome sequencing to the 2020, 2022, and 2023 outbreak strains. Due to limitations with the traceback investigation and lack of convergence, a specific type of melon or source of contamination was not identified. However, the laboratory findings and historical outbreak information provided additional evidence to support a finding of ongoing contamination issues for cantaloupes and watermelons grown in Southwest Indiana. This is the fourth outbreak of salmonellosis confirmed to be linked to cantaloupes and/or watermelons from this area since 2012. These outbreaks of reoccurring and persisting strains of Salmonella illustrate the urgent need to determine the source, pathway, and extent of environmental contamination in the melon-growing region of Southwest Indiana and for outreach and education to help promote practices to reduce the contamination of melons. ISSN: 15353141

R., Petrin, S., Gallo, A., G., Salaris, S., Alfano, D., Morena, C., Serluca, G., Balestrieri, A., Proroga, Y.T.R., A., De Vita, S., Della Rotonda, M., de Nicola, D., Barco, L., Galiero, G.
European multinational outbreak of Salmonella Umbilo linked to rocket salad and baby spinach traced to buffalo farms in Italy, 2024 to 2025
(2025) Veterinary Research, 56 (1), pp. 233
ABSTRACT: Following RASFF Alert 2024.7033 (Salmonella Umbilo in rocket from Italy), an investigation was conducted on three buffalo farms in Salerno, Southern Italy, located near the horticultural company implicated in the production of contaminated rocket salad and baby spinach linked to the outbreak. Salmonella Umbilo was isolated from faecal samples of buffalo calves in one of the three farms, and whole-genome sequencing confirmed a genetic match with the outbreak strain. Irrigation channels positioned close to animal housing were identified as potential contamination pathways. Corrective measures were promptly implemented to minimise the risk of further contamination. ISSN: 09284249

Laisnez, V., Vusirikala, A., Nielsen, C.S., Cantaert, V., Delbrassinne, L., Mattheus, W., Verhaegen, B., Delamare, H., Jourdan-Da-Silva, N., Lachmann, R., Simon, S., Cormican, M., Garvey, P., McKeown, P., Stephan, R., Brown, D., Browning, L., Hoban, A., Larkin, L., Schroeder, M., Anne Chattaway, M., Painset, A., Smith, R., Cabrey, P., Horlbog, J., Nuësch-Inderbinen, M., Bor¨jesson, S., Karamehmedovic, N., Dryselius, R., Martínez, A.A., Herrera-León, S., Martínez, C.V., Grilc, E., Trkov, M., T Brandal, L., Lange, H., van den Beld, M., Pijnacker, R., Mossong, J., Vergison, A., Ragimbeau, C., Scavia, G., Lucarelli, C., Villa, L., Moore, O., Lenahan, M., Eble, D., Schmid, J., Ladewig, B., Falkenhors, G., White, E.D., Gymoese, P., Müller, L., Daniel, O., Spackova, M., Misfeldt, C., O Forrest, R., Audistere, R., Jaramillo, V., Hammami, N., Kornschober, C., Pardos de la Gandara, M.P., Jernberg, C., Takkinen, J., Balasegaram, S., van Cauteren, D.
Key role of whole genome sequencing in resolving an international outbreak of monophasic Salmonella Typhimurium linked to chocolate products
(2025) BMC Infectious Diseases, 25 (1), art. no. 242
ABSTRACT: Background: In February 2022, the United Kingdom (UK) detected a cluster of monophasic Salmonella Typhimurium based on whole genome sequencing (WGS). Subsequently, several countries reported cases belonging to this cluster. Epidemiological, microbiological and traceability investigations pointed toward a chocolate food business operator (FBO) in Belgium. We describe the magnitude of the outbreak, investigations performed and control measures taken. Methods: Cases were ascertained based on internationally agreed case definitions and interviewed about food consumption prior to disease onset. Analytical epidemiological studies were conducted by the UK and Ireland. The Belgian food safety authority (FSA) coordinated microbiological and traceability investigations. Results: A total of 456 cases (61% female), belonging to two genetically different WGS clusters, in 14 countries of the European Union, the UK, Switzerland, Canada and the United States were linked to the outbreak, between December 2021 and June 2022. 87% of cases were younger than 10 years. Brand A chocolate eggs, marketed for children, were reported as consumed by 168 cases (80%) with information. Analytical studies in the UK and Ireland showed a significantly higher odds of disease associated with consumption of brand A chocolate products. Retrospective investigations by the FSA revealed that routine samples (raw materials, intermediate, semi-finished and finished products as well as environmental and rinse oil samples) taken by the FBO linked to the Brand A products between December 2021 and January 2022 had tested positive for salmonella. Nine isolates were submitted to EnteroBase and matched with human isolates from both WGS clusters. The authorization for production was temporarily withdrawn on 8 April 2022 and all products of brand A were recalled worldwide, followed by a decrease in

cases. Conclusions: A multi-country salmonellosis outbreak linked to chocolate occurred in the months before Easter 2022. International collaboration between stakeholders from epidemiological, microbiological and food safety entities with rapid sharing of WGS results from human and nonhuman isolates were key in containing the outbreak. Implementation of routine WGS on human and nonhuman isolates will strengthen public health responses to future outbreaks. The magnitude of the outbreak underlines the importance of timely and open communication of FBOs to FSAs in case of salmonella detection. ISSN: 14712334

Graziosi, G., Cirasella, L., Lupini, C., D'Annunzio, G., Catelli, E., Romboli, C., Siclari, C., Perulli, S., Fiorentini, L., Tosi, G., Bassi, P., Mescolini, G.
Unveiling a Salmonella Enteritidis Outbreak in an Italian Meat Rabbit Farm: Histopathological Features and Epidemiological Investigation
(2025) Animals, 15 (24), art. no. 3642
ABSTRACT: This study documents an outbreak of Salmonella enterica serovar Enteritidis (SE) on a commercial meat rabbit farm in Italy. Following the observation of increased mortality in kits and severe enteric symptoms across all age groups, SE was first isolated in early March 2024. A diagnostic and epidemiological investigation was subsequently undertaken to characterize the anatomo-histopathological features in deceased rabbits and to identify the source and transmission dynamics of the infection. Between March and December 2024, a total of 1550 rectal swabs from live rabbits, 60 environmental samples, and 168 carcasses were collected and subjected to microbiological analysis. SE-positivity rates ranged from 8.4% to 36.3%, depending on the sample type considered. Co-infections with Pasteurella multocida, Escherichia coli, and Staphylococcus spp. were also detected. Gross and histological lesions in SE-positive rabbits included fibrinonecrotizing enterocolitis, hepatosplenomegaly, and renal damage such as suppurative nephritis and tubulorrhexis. Despite the implementation of enhanced biosecurity protocols, SE re-emerged over time and across different pens. Given the zoonotic potential of SE, the outbreak described underscores the need for rabbit-specific Salmonella control programs to safeguard both animal and public health.

Bivona, M., De Bene, A.F., Russini, V., De Marchis, M.L., Di Domenico, I., Riccardi, F., Senese, M., Gasperetti, L., Campeis, F., Di Blasi, L., Carfora, V., Middei, B., Cordaro, G., Adreani, G., Marconi, P., Bossù, T.
One Health Investigation of a Household Salmonella Thompson Outbreak in Italy: Genomic and Epidemiological Characterization of an Emerging Serotype
(2025) Pathogens, 14 (12), art. no. 1285
ABSTRACT: Salmonella is a Gram-negative enteric bacterium responsible for the foodborne and waterborne disease salmonellosis, which was the second most reported foodborne gastrointestinal infection in humans in the European Union in 2023. Animals represent the principal reservoir of this pathogen, with animal-derived food products serving as the main route of transmission to humans. In a household context, having numerous animals can be a crucial factor for contracting Salmonella spp. infection. In the present study, we report a case of a familiar outbreak of Salmonella Thompson that occurred in 2024 in central Italy, involving an infant and the companion animals (a dog, a cat and ten birds) of the family's farm. To support the epidemiological investigations, antimicrobial susceptibility testing and whole-genome sequencing (WGS) were conducted on strains from the human case and from animals. Eleven strains were isolated in total, from fecal samples collected from the child and the animals at different times. WGS confirmed the genetic relatedness between human and animal isolates, supporting the hypothesis of a shared source of infection, but genes or plasmid involved in antibiotic resistance were not found. Moreover, AST revealed that isolates were fully susceptible to major antimicrobial classes tested. Despite being an uncommon serotype, the involved Salmonella Thompson serovar 6,7: k:1,5 O:7 (C1) demonstrated a high pathogenic potential, emphasizing the need for vigilance even toward serotypes not typically associated with major public health concerns. Moreover, these findings underscore the critical need for an integrated One Health approach to effectively monitor, prevent, and control zoonotic infections.

Smith, J.C., Siceloff, A.T., Shirazi, S.M., Bell, R.L., Shariat, N.W.
A two-year study of Salmonella in four natural watersheds highlights the need for increased environmental Salmonella surveillance to close the One Health loop
(2025) Applied and Environmental Microbiology, 91 (12)
ABSTRACT: Salmonella enterica is a leading bacterial cause of foodborne illness, often transmitted through contaminated food and water. Improved food handling has led to considerable reductions of Salmonella contamination in meat and poultry products; this does not wholly contribute to decreased salmonellosis incidence, highlighting the need to definealternative reservoirs and transmission pathways. In this study, we collected

samples from four distinct watersheds over 24 months to characterize Salmonella serovar diversity and utilized phylogenetic approaches, along with proximal land use analyses, to identify relationships between environmental reservoirs and hosts. Across 19 sites, including animal agriculture, suburban, and forested areas, 10 L water samples were collected (n = 456), and cultured for Salmonella, followed by whole genome sequencing of isolates and deep serotyping of positive samples. Overall prevalence was 69% (314/456), and generalized linear mixed models showed that compared to proximal land use, seasonal weather patterns, including precipitation and humidity, significantlyinfluencedrecovery and complexity. Antimicrobial resistance was detected in 11% (33/314) of isolates, with 21% (7/33) classifiedas multidrug resistant. CRISPR-SeroSeq identified37 serovars, and multiserovar populations were detected in 89% (229/258) of positive samples with sequencing data, averaging 3.7 serovars/sample. Comparison with national food animal production monitoring showed limited serovar overlap, with serovar Rubislaw dominating water samples but absent in agricultural data sets. Collectively, these results demonstrate extensive serovar diversity within Salmonella populations in freshwater systems, including clinically relevant serovars, and emphasize the need to develop a robust surveillance platform for source attribution and, ultimately, prevention of future outbreaks.
ISSN: 00992240

Okur, I., Sullivan, G., Stratton, J., Chaves, B.D., Wang, B.
Thermal Inactivation of Salmonella in Not-Ready-to-Eat Breaded Stuffed Chicken Products Using an Air Fryer: Impact on Safety, Quality, and Texture
(2025) Journal of Food Science, 90 (12), art. no. e70780
ABSTRACT: ABSTRACT: Multiple Salmonella outbreaks in the United States have been associated with undercooked not-ready-to-eat (NRTE) breaded stuffed chicken products, which require thorough cooking to ensure pathogen inactivation. Despite manufacturers' safe handling instructions, increasing consumer use of air fryers for these products poses potential food safety risks when no validated cooking guidelines are currently available. This study evaluated Salmonella inactivation and quality changes in NRTE breaded stuffed chicken cooked in two air fryer types (basket and oven-style) across three temperatures (176.7°C/350°F, 190.6°C/375°F, and 204.4°C/400°F) and five time points (10-30 min). Results demonstrated that basket-type air fryers achieved USDA-FSIS recommended 7-log Salmonella reductions and target internal temperatures (>74°C) faster than oven-type models: at 25 min (176.7°C/350°F), 20 min (190.6°C/375°F), and 20 min (204.4°C/400°F) versus 30, 30, and 25 min, respectively, for oven-type units. Color analysis revealed decreasing L* (lightness) and b* (yellowness) values with increasing time/temperature, while a* (redness) values remained higher than control cooking samples. Texture measurements showed MORS force increased with longer processing times. Based on microbiological, color, and texture analysis, specific conditions most closely matched control cooking results: oven-type air frying at 176.7°C (350°F) for 30 min and basket-type air frying at 176.7°C (350°F) for 25 min. These findings provide critical data for developing science-based cooking guidelines for air-fried NRTE stuffed chicken products, addressing an important food safety gap in consumer practices. Further research should validate these parameters across additional product formulations and air fryer models. ISSN: 00221147

Holden, N., Barak, J.
Microbe-plant interactions of Escherichia coli and Salmonella
(2025) EcoSal Plus, 13 (1)
ABSTRACT: Escherichia coli and non-typhoidal Salmonella enterica are capable of persisting and growing in a wide range of environments. Although best known for their interactions and pathogenic phenotypes in warm-blooded animal hosts, they can be located in a diversity of hosts and habitats. This capability has led to foodborne illness arising from multiple sources, including crop plants. It raises key questions about the bacterial traits and adaptations that permit this degree of flexibility. By describing plant features and the associated environments, we illustrate the underlying physiological basis that enables E. coli, including Shiga toxin-producing E. coli, and S. enterica to colonize plant hosts. We follow the distinct stages of the interactions and the different considerations to understand how they will play out and the resulting outcome for the bacteria. Knowledge of the processes involved lays the foundation for understanding and managing real-life scenarios in agriculture and food production and allows predictions for the bacterial responses in the plant environment under changing climatic conditions.

Simó-Martínez, M.S., Marco-Fuertes, A., Galán-Relaño, Á., Astorga, R.J., Marín, C., Valero Diaz, A., Vega, S.

Prevalence and Antimicrobial Resistance Patterns of Salmonella in Asymptomatic Horses in Eastern Spain: A One Health Perspective
(2025) Animals, 15 (23), art. no. 3413
ABSTRACT: (1) Background: Salmonella are zoonotic pathogens, and rising antimicrobial resistance (AMR) amplifies their public health impact. Asymptomatic horses can act as reservoirs, contributing to environmental contamination and interspecies transmission. This study aimed to estimate the prevalence of Salmonella and characterize AMR patterns in healthy horses from eastern Spain. (2) Methods: Faecal samples from 95 asymptomatic horses were collected once daily over five consecutive days (475 samples in total) and processed under for Salmonella detection. Epidemiological information was obtained through owner questionnaires, and associations with Salmonella shedding were analyzed using generalized linear models. Antimicrobial susceptibility was assessed by minimum inhibitory concentration assays following the European Committee on Antimicrobial Susceptibility Testing (EUCAST) criteria. (3) Results: Salmonella was detected in 25.3% of horses (24/95), with S. Enteritidis, S. Johannesburg, and S. Virchow as the most frequent serotypes. A significant association was observed between proximity of manure storage and bacterial detection ($p < 0.001$). Among 24 isolates of Salmonella, 88.9% were resistant to at least one antimicrobial, and 50% exhibited multidrug resistance. The highest resistance rates were against sulfamethoxazole and gentamicin, followed by ciprofloxacin and tigecycline. (4) Conclusions: Healthy horses can act as silent carriers of multidrug-resistant Salmonella, highlighting the need for surveillance, strengthened biosecurity, and prudent antimicrobial use within a One Health framework.

Alsaaod, M., Stevens, M.J.A., Cernela, N., Horlbog, J., Stephan, R., Albini, S.
Retrospective Analysis of Persistent Clonal Salmonella enterica Strains of Various Serovars in Commercial Swiss Broiler Farms
(2025) MicrobiologyOpen, 14 (6), art. no. e70149
ABSTRACT: Detection of Salmonella Enteritidis (SE) and S. Typhimurium (STm) in broiler holdings is regulated by European and Swiss law to ensure public health. Persistence of Salmonella in broiler houses may jeopardize this goal. The aim of this study was to analyze whether non-SE/STm isolated from boot socks were of clonal origin. Four Salmonella serovars from 11 broiler houses from 10 Swiss farms were selected: S. Infantis, S. Livingston and S. Welikade (meat integration A) and S. enterica subsp. enterica 13,23:i:- (integration B). The genetic relationship was evaluated by whole-genome sequencing (WGS) and core genome multilocus sequence typing (cgMLST)-based tree analysis, with a cluster being defined as < 8 cg alleles differences. The isolates of S. Infantis and S. Livingston, respectively, were shown to belong to the same serovar-specific clusters (range: 1–7 cg alleles differences), suggesting that the Salmonella strains persisted in the respective broiler houses. S. Welikade, however, showed 8–11 cg alleles differences among isolates, indicating either a reintroduction of similar but not clonal strains into the houses due to insufficient biosecurity, or the evolution of a persistent strain. Remarkably, all isolates of S. 13,23:i:- from integration B from 2013 to 2024 were clonal, suggesting dispersal and persistence in the broiler integration. The clonality of analyzed strains suggests that Salmonella can persist on farms or integration level despite disinfection after each production cycle. Hence, improved farm and vehicle cleaning and disinfection practices are essential to ensure that the next flock is not exposed to non-SE/STm Salmonella serovars.

Li, L., Zhou, Y., Chousalkar, K., McWhorter, A.
Phenotypic and genotypic investigation into the survival of Salmonella Typhimurium and Salmonella Hessarek in eggs at different storage temperatures
(2025) Food Research International, 222, art. no. 117795
ABSTRACT: Salmonella (S.) Hessarek is an emerging serotype with limited characterisation compared to S. typhimurium. Recent S. Hessarek-related foodborne outbreaks linked to the consumption of egg products have raised concerns about this pathogen. However, little is known about its survival capabilities in egg-related environments or genomic features. This study compared their survival potential under 5 °C, 15 °C, and 25 °C over 28 days, and characterised the genomic features of S. typhimurium and S. Hessarek through whole-genome sequencing. Both strains showed significantly lower bacterial loads in eggshell crushes at 5 °C than at 15 °C or 25 °C, and egg internal contents were Salmonella-positive when contaminated eggs were stored at 15 °C and 25 °C, which may pose a greater risk of contamination at unrefrigerated temperatures. Both strains share core pathways related to genetic information processing, environmental information processing, signalling and cellular processes, and carbohydrate metabolism, supporting their persistence under diverse conditions. However, the absence of some genes in S. Hessarek that are associated with motility and anaerobic metabolism may partially explain its reduced ability

to adapt to dry or nutrient-scarce environments on the eggshells, compared to S. typhimurium. Overall, S. typhimurium and S. Hessarek possessed genomic and phenotypic traits that allow them to persist in different egg components under various conditions, though they appeared to show differences in their survivability. Further studies are essential to explore the differences in their survival mechanisms and whether their virulence potential will be influenced by incubating at 15 °C or less in different egg components. ISSN: 09639969

Solaiman, S., Meeks, E., Hines, I., Zheng, J., Hoffmann, M.
Transcriptome alteration induced by desiccation stress in Salmonella enterica subsp. enterica serovar Agona
(2025) Food Research International, 221, art. no. 117548
ABSTRACT: Salmonella Agona (S. Agona) is a foodborne pathogen that caused recurrent multistate outbreaks associated with cereal in 1998 and 2008, underscoring the endurance of Salmonella in low-moisture food (LMF). The whole genome sequencing revealed that it persisted in the LMF industry for a decade, then resurfaced as a virulent strain and caused outbreak. In this study, we aimed to determine the molecular mechanism of survival of S. Agona in LMF and its impact on phenotypes. RNA-seq was used to compare the adaptability of this pathogen in an extreme environment. There were 1114 differentially expressed genes (DEGs) in S. Agona in response to desiccation stress (Padj < 0.01, |log2FoldChange| >1), with 646 downregulated and 468 upregulated. Functional analysis of downregulated DEGs revealed that most of the genes were associated with metabolic pathways, followed by translation, suggesting slower growth in the surviving population. We observed that virulence genes, including those associated with the Salmonella Pathogenicity Island, were not expressed initially, but showed upregulation after 24 h. Among the upregulated operons/genes, kdp/ccm/tisB were directly associated with growth and metabolism. kdp has the regulatory function to reduce replication, ccm is associated with reducing the consumption of molecular oxygen, and tisB with persister formation. We knocked out three operons/gene and assessed the surviving capability of mutants under desiccation stress. An approximate 1–2 log reduction (P > 0.05) was noticed in the mutant's survival compared with wild type. This transcriptome data suggests that S. Agona survives in low-moisture food by conserving energy, lowering metabolism, and reducing replication. ISSN: 09639969

Liu, Z., Liu, Y., He, J., Pei, X., Lin, Y., Magnani, M., Liu, D., Ding, T., Feng, J.
Milkfat influences thermal tolerance and biofilm formation of Salmonella Typhimurium during pasteurization
(2025) Food Research International, 221, art. no. 117538
ABSTRACT: The bacterial contamination and failure of pasteurization are leading threats to the safety of dairy productions. Milk contains a large quantity of fat which supports bacterial growth but its influence on pasteurization efficacy and biofilm formation remains poorly understood. In this study, we first demonstrate that the inactivation of Salmonella during pasteurization is significantly less effective in whole milk compared to skim milk, with the D-value increasing from 0.60 min in skim milk to 0.67 min in whole milk (P = 0.0047). In whole milk, Salmonella biofilms form greater biomass and display a distinct architecture from biofilms in skim milk. Specifically, Salmonella in whole milk was embedded within the extracellular polymeric substances (EPS), while cells in skim milk biofilms were sparsely distributed. Raman spectroscopy showed that biofilms formed in whole milk possess a distinctly higher lipid content. Therefore, we hypothesized that the thermal tolerance of Salmonella in whole milk was directly linked to its physical interaction with milkfat. Confocal laser scanning microscopy showed an increase from 26.1 % to 86.1 % of the fraction of Salmonella co-localizing with milkfat after 12 h of incubation in whole milk. Lipase treatment (200 units/mL) on whole milk reduced biofilm formation and improved the efficacy of thermal inactivation. Our findings demonstrate the milkfat acts as a physical scaffold, facilitating bacterial aggregation and the formation of a protective, lipid-rich biofilm matrix enhancing Salmonella survival during pasteurization. These insights should inform pasteurization strategies of high-fat dairy products to ensure food safety. ISSN: 09639969

Barik, P., Ahmed, S., Biswas, P., Mondal, S., Sahu, A., Nath, S., Mohan, U., Babu, S., Arumugam, S., Mallick, A.I.
Comparative analysis of the oral and injectable form of heat-inactivated Salmonella Enteritidis vaccine efficacy in commercial chickens
(2025) Microbe (Netherlands), 9, art. no. 100549

ABSTRACT: Salmonella enterica subsp. enterica serovar Enteritidis (Salmonella Enteritidis) is a non-typhoidal Salmonella (NTS), a facultatively anaerobic, Gram-negative bacteria commonly residing in the intestines of chickens, cattle, rodents, reptiles, and amphibians. Specifically, Salmonella Enteritidis causes salmonellosis in chickens, characterised by weakness, reduced appetite, stunted growth, and diarrhoea. Although both live and inactivated vaccines are currently used in poultry, they present several drawbacks. While live vaccines generally are more effective at stimulating strong immune responses, they carry the risk of reverting to virulence. In contrast, inactivated or killed vaccines are safer but often elicit weaker immune responses, requiring multiple booster doses and adjuvants to achieve protective immunity. These limitations highlight the need for improved vaccine strategies that are both safe and highly immunogenic. To develop a safer and more practical vaccine strategy against salmonellosis in commercial chickens, we evaluated the immunogenicity and protective efficacy of a heat-inactivated whole-cell S. Enteritidis (SE) vaccine. Two routes of vaccine administration were chosen, oral and injectable, to compare their efficacy using a prime-boost regimen. We demonstrated that oral administration of the heat-inactivated vaccine elicited stronger mucosal antibody responses than the injectable route. Moreover, orally vaccinated birds were significantly protected against challenge infection without adverse effect on gut health. These findings indicate that the mucosal (oral) delivery of heat-inactivated S. Enteritidis vaccine can represent a promising and safe approach for developing an effective vaccine against salmonellosis in commercial chickens.

Muslin, C., Salas-Brito, P., Coello, D., Morales-Jadán, D., Viteri-Dávila, C., Coral, M.
Salmonella prevalence and serovar distribution in reptiles: a systematic review and meta-analysis
(2025) Gut Pathogens, 17 (1), art. no. 52
ABSTRACT: Background: Reptiles are recognized as reservoirs of Salmonella bacteria, and the expansion of the global pet reptile trade has led to reptile-associated salmonellosis emerging as a significant public health concern. To characterize the risk posed by reptiles as a source of Salmonella transmission to humans, we conducted the first comprehensive meta-analysis to estimate the worldwide prevalence of Salmonella in both wild and captive reptiles and identify the primary factors influencing this prevalence. Results: We systematically reviewed publications reporting the prevalence of Salmonella spp. intestinal isolation in reptiles, published between 1986 and 2023, across the PubMed, Scopus and Web of Science databases. The 179 studies included examined a total of 23,411 reptiles from 56 countries across all continents, with 49.9% being free-ranging animals and 48.4% living in captivity, mainly from zoos, pet shops, or households. The overall pooled prevalence of Salmonella spp. in reptiles was estimated at 30.4% (95% confidence interval, CI: 27.4–33.6%). Notably, significant variations in Salmonella spp. colonization rates were observed across different reptile taxa, with snakes exhibiting the highest prevalence at 63.1% (95%CI: 57.4–68.4%), followed by lizards at 33.6% (95%CI: 28.6–39.0%), and turtles and crocodiles with similar rates of 11.2% (95%CI: 8.8–14.2%) and 10.5% (95%CI: 5.7–18.6%), respectively. Furthermore, significant differences in Salmonella spp. prevalence were observed across different reptile families within each taxon. The data suggest that captivity is a contributing factor to Salmonella spp. colonization, as captive reptiles showed significantly higher prevalence rates (37.8%, 95%CI: 34.3–41.4%) compared to their wild counterparts (14.8%, 95%CI: 11.0-19.6%). Additionally, we found that the inclusion of pre-enrichment and selective enrichment steps in culture broths significantly improved the sensitivity of both culture-based and PCR-based Salmonella detection methods. Importantly, the study revealed that reptiles primarily carried Salmonella enterica subspecies enterica, responsible for most human salmonellosis cases. Of particular concern, several human-pathogenic Salmonella serovars of public health relevance, such as Enteritidis, Typhimurium and Newport, were identified among the 10 most common serovars colonizing reptiles. Conclusions: Collectively, these findings highlight the substantial health threat posed by reptiles as a source of human Salmonella infection and may inform the development of policies and strategies for prevention and public education to mitigate the risk of reptile-associated salmonellosis.

Guo, C., Xie, Y., Zhang, Y., Tu, T., Wang, L.
Fate of Salmonella, Escherichia coli, and Listeria monocytogenes in dark leafy green vegetable juice at different storage temperatures
(2025) Food Microbiology, 132, art. no. 104854
ABSTRACT: Dark leafy green vegetables (DLGVs), including kale, chard, and collard greens, have gained increasing attention for their rich nutrient profiles and health benefits, driving the development of derivative products such as dark leafy green vegetable juices (DLGVJs). However, fresh DLGVJs are susceptible to contamination by foodborne

pathogens due to inadequate hygiene, improper handling, and cross-contamination. Additionally, temperature abuse during storage and distribution may further compromise their safety. This study investigated the fate of Salmonella, pathogenic Escherichia coli, and Listeria monocytogenes in non-acidified and acidified kale, chard, and collard greens juices when being stored at 4, 10, and 23 °C. Changes in pH and indigenous microbial populations (total aerobic plate count [APC]) were also assessed. Results showed that pH remained stable in acidified DLGVJs at all temperatures, while significant pH declines were observed in non-acidified juices at elevated temperatures. The growth rate of APC increased with rising temperatures, with greater increases observed in non-acidified juices. At 4 °C, all pathogens survived in all juices for over 168 h. At 23 °C, growth of pathogens was observed, particularly in non-acidified chard juice. Temperature abuse could compromise the food safety benefit brought by acidification. Based on results from DMFit, the Baranyi and Roberts model effectively described the fate of most pathogens with R2 ranging from 0.474 to 0.997. These findings highlight the importance of acidification and temperature management in maintaining the microbial safety of DLGVJs and provide insights for developing food safety guidelines to mitigate food safety risks associated with fresh DLGVJs. ISSN: 07400020

Pegueros-Valencia, C.A., Lucero-Mejía, J.E., Hernández-Iturriaga, M., Godínez-Oviedo, A.
Assessing Salmonella enterica biofilm formation in frequent scenarios of chicken handling in domestic kitchen environments
(2025) Food Microbiology, 132, art. no. 104849
ABSTRACT: Home kitchens are major sources of foodborne illnesses. This study evaluated Salmonella enterica biofilm formation (BF) in common chicken handling scenarios in domestic kitchens (CHSDK). An online survey identified the most frequent CHSDK. Based on the results, three S.enterica (Anatum, Saintpaul, and Typhimurium) were assessed for their attachment on plastic, glass, and stainless-steel surfaces with chicken residues, with or without raw chicken microbiota (RCM), at 25 °C. BF was evaluated by measuring pathogen growth and biopolymer production over three days. Survey results showed plastic was the predominant material for cutting boards (47.8 %), and cookware was used for raw (40.3 %) and cooked (59.6 %) chicken, followed by glass,21.5 %, and 31.2 %, respectively. Knives (79.1 %) were the main utensils for cutting raw chicken. Regarding the attachment, S.enterica strains were significantly lower in the presence of RCM (2.3 ± 0.7 logCFU/cm2) compared to its absence (5.4 ± 0.4logCFU/cm2) ($p < 0.05$). A full-factorial ANOVA showed that strain, surface, RCM, and the RCM-surface interaction significantly affected both, pathogen growth within biofilms and biopolymer production ($p < 0.05$). The interaction showed that the greatest difference in pathogen growth occurred on stainless steel, with 1.31 ± 0.73logCFU/cm2 in the absence and 0.23 ± 0.76 logCFU/cm2 in the presence of RCM. For biopolymer, the largest difference was on glass, 0.52 ± 0.26 and 0.37 ± 0.15 OD595nm. Anatum had the highest attachment, Typhimurium the greatest growth, and Saintpaul the highest biopolymer production, regardless of the surface and presence/absence of RCM. These findings suggest that S.enterica can persist in biofilms under CHSDK, highlighting the risk of cross-contamination not only through immediate contact, but also through BF over time. ISSN: 07400020

Gaspari, S., Akkermans, S., Buysse, I., van Impe, J.F.M.
Studying the defensive role of monoculture and polyculture gut microbiota against Salmonella enterica: An in vitro case study
(2025) Food Microbiology, 132, art. no. 104798
ABSTRACT: Salmonellosis is the second most reported gastrointestinal infection in Europe and a leading cause of foodborne outbreaks. Interactions between individual bacterial species and Salmonella enterica have been extensively studied under in vitro conditions. However, the role of diverse gut microbial communities in a more intestine-like environment remains underexplored. Therefore, this study aimed to examine how both monoculture and polyculture gut microbiota communities interact with one of the main foodborne pathogens, S. enterica, within an in vitro system designed to simulate the human gastrointestinal environment. Species from four representative gut bacterial genera were tested in mono-, co- and polycultures, i.e., Bacteroides, Bifidobacterium, Escherichia, and Lactiplantibacillus. The results revealed that Escherichia coli had a strong inhibitory effect on Salmonella growth within all microbial communities. Moreover, Bifidobacteria protected Salmonella, helping it resist inhibitory influences within the community. Furthermore, higher community complexity correlated with a greater reduction in the pathogen's cell density. These findings emphasize the importance of assessing gut microbial complexity and its interactions with S. enterica in a physicochemically

representative in vitro environment, as understanding these dynamics is crucial for improving food microbiology and safety, particularly in mitigating foodborne infections and enhancing the effectiveness of food safety. ISSN: 07400020

Kaboudari, A., Aliakbarlu, J.
Effects of freezing period and meat juice model type on the survival, hydrophobicity, and acid resistance of Listeria monocytogenes and Salmonella Typhimurium
(2025) BMC Microbiology, 25 (1), art. no. 321
ABSTRACT: Background: The survival of food-borne pathogenic bacteria in food processing environments and increasing their resistance to antimicrobials is one of the most crucial challenges in food safety. The present study aimed to investigate the effects of freezing period (0–60 days) and meat juice model (beef, mutton, and goat juices) on the survival, hydrophobicity, and acid resistance of Listeria monocytogenes and Salmonella Typhimurium. Methods: The survival of L. monocytogenes and S. Typhimurium in different meat juice models during the freezing period (0, 1, 2, 3, 4, 7, 14, 21, 30, and 60 days) was determined by colony counting method. The cell surface hydrophobicity of the bacteria was measured by bacterial adhesion to hydrocarbon assay. Changes in the bacterial resistance to acetic acid and lactic acid were evaluated by determining minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC). Results: The survival of both bacteria was significantly higher in mutton juice than in other juices ($p < 0.05$). The survival rate of L. monocytogenes in freezing conditions was higher than that of S. Typhimurium. The amount of hydrophobicity was increased during the freezing period, and the highest increase was observed in the mutton juice. The increase in hydrophobicity of S. Typhimurium was higher than L. monocytogenes. The acid resistance of both bacteria, especially L. monocytogenes, was increased with increasing freezing time. Conclusion: Freezing stress and meat juice model type could change the survival, hydrophobicity, and acid resistance of L. monocytogenes and S. Typhimurium. The mutton juice model showed the highest protective effect on both bacteria during the freezing period. Meanwhile, the bacteria inoculated in the mutton juice model exhibited significantly higher hydrophobicity than those in other meat juices. The acid resistance of L. monocytogenes was significantly increased, especially in the mutton juice model, at the end of the freezing period. ISSN: 14712180

Cao, Q., Jia, C., Zhou, H., An, H., Huang, C., Wu, X., Kang, X., Huang, Y., Fang, F., Li, Y., Yue, M.
An adult chicken mortality case investigation: coinfection by Salmonella Indiana and Kentucky
(2025) Animal Diseases, 5 (1), art. no. 14
ABSTRACT: Coinfection, the simultaneous invasion of multiple pathogens into a single host, is a critical but understudied area, especially in the farm animal sector. We report a unique and unusual fatal case of coinfection with S. Indiana and S. Kentucky, which has rarely been studied in the literature and could hold potential importance for veterinary clinics. In silico analysis revealed that all the isolates exhibited extensive multidrug resistance. By analyzing the plasmids, two replicons, IncHI2 and IncHI2A, were detected in S. Indiana, whereas no plasmids were detected in S. Kentucky. Chicken embryo lethality assays demonstrated that both S. Indiana and S. Kentucky caused 100% mortality by the third day post infection, significantly exceeding the lethality of the control strains. These findings emphasize the high pathogenic potential of these serovars, especially S. Indiana, which carries the cdtB gene encoding typhoid toxin, further confirming its increased pathogenicity. Overall, our results underscore the urgent need to improve biosecurity measures to mitigate the risk of coinfections involving multidrug-resistant Salmonella strains in poultry production environments. ISSN: 27310442