

# NEWSLETTER

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# Contents

<b>EDITORIAL NOTE .....</b>	<b>4</b>
<b>FROM THE LITERATURE .....</b>	<b>6</b>

## Editorial Note

Bilthoven, 3 April 2023

Dear colleague,

I hope you are doing well. According to the calendar it is already spring, but until now the weather in the Netherlands was more like fall than spring. Hopefully it will soon become more spring-like everywhere.

As always, we have been, and still are, busy with the Proficiency Tests:

In November 2022 the **PT on typing of *Salmonella*** was organised, containing an obligatory part on serotyping of *Salmonella*, and a voluntary part on cluster analysis. The evaluation of the serotyping results was performed in January/February 2023 and on 1 March 2023 the participants received their own results as well as the interim summary report containing the results of all participants. The interim summary report is also available at the EURL-*Salmonella* website: <https://www.eurlsalmonella.eu/documenten/interim-summary-report-eurl-salmonella-pt-serotyping-2022> Two participants did not meet the level of good performance and a follow-up study is currently organised. In addition to the obligatory serotyping part, this PT included also a part on cluster analysis. The results on this (optional) part of the PT are under evaluation and will be reported separately in the coming months.

Currently the **combined PT for Food-Feed on detection of *Salmonella* in seeds** is performed. The deadline for reporting the results of this PT is on 19 April 2023. In this PT, NRLs-*Salmonella* analysing food samples as well as NRLs-*Salmonella* analysing animal feed samples participate.

In March 2023 we were informed that the SMP (Single Market Programme Regulation) Work Programme for 2023-2024 was adopted by the European Commission in the second half of February 2023. The formal call to the EURLs to submit their **work programmes for 2023-2024** is expected by the end of April 2023. Unfortunately the grant agreements for 2023-2024, for all EURLs, are not expected to take place before the end of 2023. In January 2023, the EURL-*Salmonella* discussed the draft work programme for 2023-2024 with the desk officer at DG SANTE. As a result of this discussion it was decided that this year's workshop will again be an **online workshop in May**. The invitation for this workshop has been sent to the NRLs-*Salmonella* early March 2023, with a deadline for registration by early April 2023. Suggestions for presentations at this workshop are still welcome.

Before the end of February 2023, we drafted the technical and financial **reports about the activities of the EURL-*Salmonella* performed in 2021-2022**. The reports are currently under evaluation at HaDEA and DG SANTE.

As you may know, the EURL-*Salmonella* is member of the **Inter-EURLs working group on NGS**, existing in total of 8 microbiological EURLs. This working group has drafted several guidance documents for application of NGS, which are published at the EURLs' websites. By the end of 2022 and early 2023 several guidance documents have been updated. The guidance documents can be found (and downloaded) at: <https://www.eurlsalmonella.eu/publications/analytical-methods> - Next Generation Sequencing (NGS).

In addition to drafting guidance documents, the Inter-EURLs WG NGS will also organise a joint training on NGS in June 2023, at the premises of EURL-*Salmonella* (Bilthoven, the Netherlands). The invitation to apply for this training, together with information about the training and a draft agenda, was sent to the NRLs by the end of March 2023. The deadline for application is 17 April 2023.

For the standardisation of methods for *Salmonella*, currently two ISO working groups are active:

**ISO/TC34/SC9 – WG9** (ISO 6579-1 'Detection of *Salmonella*'); This working group was re-activated to complete the performance characteristics of ISO 6579-1 for all relevant product categories and to consider the comments to ISO 6579-1:2017 from the systematic review of 2022. The first meeting of the re-activated WG9 was organised as virtual meeting in the end of March 2023. At this meeting the comments received from the systematic review were discussed as well as the steps to be taken to obtain the missing performance characteristics. The planned activities of WG9 will be presented at the annual meeting of ISO/TC34/SC9 in June 2023.

**ISO/TC34/SC9 – WG10** (draft ISO/TS 6579-4 'Identification of monophasic *Salmonella* Typhimurium by PCR'). A virtual meeting of this working group was organised in February 2023 and at this meeting the results of the interlaboratory study (ILS) for determination of the performance characteristics were presented, as well as the 4<sup>th</sup> draft version of ISO/DTS 6579-4. After this meeting, the 5<sup>th</sup> draft of ISO/DTS 6579-4 was prepared and distributed to the members of WG10 for comments until the second half of April 2023. As a result of this commenting round and when necessary, the document will be updated for launching the voting of ISO/DTS 6579-4 among the members of ISO/TC34/SC9. This will be the last voting round for this document. If the comments from SC9 are not too substantial, the document may be finished for final publication by the end of 2023/early 2024. Additionally, the results of the methods evaluation study as well as of the ILS will also be summarised in more detail in a report which we are currently drafting.

Best wishes,  
Kirsten Mooijman  
Coordinator EURL-*Salmonella*

## From the Literature

### *Salmonella*-related Literature from Scopus: January – March 2023

**González-Torres, B., González-Gómez, J.P., Ramírez, K., Castro-del Campo, N., González-López, I., Garrido-Palazuelos, L.I., Chaidez, C., Medrano-Félix, J.A.**  
*Population structure of the Salmonella enterica serotype Oranienburg reveals similar virulence, regardless of isolation years and sources*  
(2023) *Gene*, 851, art. no. 146966, .

ABSTRACT: *Salmonella enterica* serotype Oranienburg is a multi-host, ubiquitous, and prevalent Non-typhoidal *Salmonella* (NTS) in subtropical rivers, particularly in sediments; little studied so far possible the adaptation and establishment of this microorganism based on its genetic content. This study was focused on the first five genomes of *S. Oranienburg* in sediments through whole-genome sequencing (WGS) and 61 river water genomes isolated in previous studies. Results showed an open pangenome with 5,594 gene clusters (GCs), and the division of their categories showed; 3,303 core genes, 741 persistent genes, 1,282 accessory genes, and 268 unique genes. Additionally, it showed three main subclades within the same serotype and showed a conserved genetic content, suggesting the display of different adaptation strategies to its establishment. Nine genes for antimicrobial resistance were detected: *aac* (6') - *ly*, *H-NS*, *golS*, *marA*, *mdsABC*, *mdtK*, and *sdiA*, and a mutation in the *parC* gene p. T57S generating a resistance. In addition, virulence genes and pathogenicity islands (SPI's) were analyzed, finding 92 genes and an identity above 80 % in the SPI's 1 to 5, and the centisomes 54 and 63. The environmental strains of *S. Oranienburg* do not represent a concern as multidrug resistance (MDR) bacterium; however, virulence genes remain a potential health risk. This study contributes to understanding its adaptation to aquatic environments in Mexico. ISSN: 03781119

**Su, Z., Wei, S., Shi, X., Wang, X., Zhang, L., Bu, X., Xu, H., Liu, Y., Jin, M., Pang, B., Zhao, C.**

*Smartphone-assisted colorimetric detection of Salmonella typhimurium based on the catalytic reduction of 4-nitrophenol by  $\beta$ -cyclodextrin-capped gold nanoparticles*  
(2023) *Analytica Chimica Acta*, 1239, art. no. 340672, .

ABSTRACT: *Salmonella typhimurium* (*S. typhimurium*) is one of the most common pathogens in the environment, such as in drinking water and soil. Herein, an on-site detection method was developed by combining silver-coated magnetic nanoparticles (Fe<sub>3</sub>O<sub>4</sub>@Ag NPs) with the  $\beta$ -cyclodextrin-capped gold nanoparticles ( $\beta$ -CD-Au NPs) to achieve sensitive detection of *S. typhimurium*. After they formed a sandwich structure in the presence of *S. typhimurium*, the 4-nitrophenol was reduced to 4-aminophenol based on the nitro-reductase activity of  $\beta$ -CD-Au NPs. The naked eyes were able to observe the color change from yellow to colorless. Under optimal conditions, the detection range of *S. typhimurium* was 10–107 CFU mL<sup>-1</sup>, and the limit of detection (LOD) was 10 CFU mL<sup>-1</sup>. The total detection time was 90 min, showing satisfactory performance in real samples. We combined a smartphone app with the colorimetric method, making it possible to semi-quantitatively detect *S. typhimurium* by analyzing the grey value. In conclusion, this assay detects *S. typhimurium* in environmental samples, offering an accurate and sensitive detection method without sophisticated equipment. ISSN: 00032670

**Lee, M.D., Pedroso, A.A., Maurer, J.J.**

*Bacterial composition of a competitive exclusion product and its correlation with product efficacy at reducing Salmonella in poultry*  
(2023) *Frontiers in Physiology*, 13, art. no. 1043383, .

ABSTRACT: The mature intestinal microbiome is a formidable barrier to pathogen colonization. Day-old chicks seeded with cecal contents of adult hens are resistant to colonization with *Salmonella*, the basis of competitive exclusion. Competitive exclusion products can include individual microbes but are commonly undefined intestinal communities taken from adult animals and in commercial production is amplified in fermentator and sold commercially in freeze dried lots. While superior to single and multiple species probiotics, reducing *Salmonella* colonization by multiple logs, undefined products have limited acceptance because of their uncharacterized status. In this study, the bacterial composition of the master stock, preproduction seed stocks and commercial lots of a poultry competitive exclusion product, was defined by 16S rRNA sequence analysis, targeting the 16S rRNA variable region (V1-V3). The samples contained a diversity of genera (22–52 distinct genera) however, the commercial lots displayed less

diversity compared to the seeds and the master stock. Community composition varied between seeds and the master stock and was not a good predictor of potency, in terms of log<sub>10</sub> reduction in *Salmonella* abundance. While there was significant correlation in composition between seeds and their commercial lots, this too was not a good predictor of potency. There was linear correlation between unclassified Actinobacteria, Peptococcus, and unclassified Erysipelotrichaceae, and *Salmonella* abundance ( $r^2 > .75$ ) for commercial seeds. However, upon review of the literature, these three genera were not consistently observed across studies or between trials that examined the correlation between intestinal community composition and *Salmonella* prevalence or abundance. Copyright ISSN: 1664042X

**Yao, S., LiBrizzi, B.R., Chen, H.**

*Heating temperature and water activity of alfalfa seeds affect thermal inactivation of Salmonella and maintaining seed viability*

(2023) *International Journal of Food Microbiology*, 384, art. no. 109975, .

ABSTRACT: Sprouts have been involved in many outbreaks of salmonellosis where seeds were identified as the likely source of contamination. This study aimed to develop an effective heat treatment that could achieve a >5-log reduction of *Salmonella* inoculated on alfalfa seeds while maintaining seed viability and vigor. Effects of seeds' water activity (aw) and heat treatment temperature on *Salmonella* inactivation and seed viability were determined. Alfalfa seeds were dip-inoculated with a four-strain *Salmonella* cocktail and dried to aw of 0.05–0.20. The inoculated seeds were then placed in sealed glass tubes and heated at 65.9, 71.0, and 76.6 °C for up to 180 h. Increasing aw of seeds greatly improved thermal inactivation of *Salmonella*. For example, to achieve a >5-log reduction of *Salmonella* on seeds, treatment times of 140 and 60 h at 71.0 °C were required for aw of 0.1 and 0.2, respectively. Treatment temperature also greatly affected inactivation of *Salmonella* on alfalfa seeds. For example, to achieve a >5-log reduction of *Salmonella* on seeds with aw of 0.2, treatment times of 180 and 60 h were required for temperatures of 65.9 and 71.0 °C, respectively. Seeds' aw was critical for preserving seed viability. When seeds were treated at 71.0 °C for 60 h, increasing aw from 0.1 to 0.2 decreased the sprout yield ratio from 103.9 % to 73.7 %. Treatment of seeds with aw of 0.1 at 71.0 °C was found to be optimum for achieving a desirable *Salmonella* inactivation level while maintaining seed viability, resulting in 4.2 and 6.0 log reductions of *Salmonella* and yield ratios of 100.7 % and 96.1 % after 100- and 140-h treatments, respectively. This optimum heat treatment was compared with the traditional 20,000-ppm chlorine wash in terms of *Salmonella* inactivation and preservation of seed viability and found to be a far superior disinfection method. The chlorine treatment achieved 1.8 and 2.0 log reductions of *Salmonella* and yield ratios of 70.9 % and 65.1 % after 15- and 20-min treatments, respectively. ISSN: 01681605

**Topalcengiz, Z., Friedrich, L.M., Danyluk, M.D.**

*Salmonella transfer potential between tomatoes and cartons used for distribution*

(2023) *Journal of Food Protection*, 86 (1), art. no. 100016, .

ABSTRACT: Corrugated fiberboard boxes (cartons) can be reused during fresh market tomato packing and repacking. The fate of *Salmonella* on the new, used, and dirty tomato packaging cartons, and *Salmonella* transfer between tomatoes and new, used, and dirty packaging cartons was assessed. Mature green tomatoes or blank cartons were spot inoculated with cocktail of rifampicin-resistant *Salmonella* strains before touching cartons/tomatoes at 0, 1, or 24 h postinoculation. Tomatoes were placed on new, used, and dirty carton squares (5 by 5 cm) for 0, 1, and 7 days of contact at 12°C and 25°C with a relative humidity value of 85%. Transfer coefficients (TCs) were calculated for all conditions. *Salmonella* populations decreased following inoculation by 2-3 log units during 24 h drying regardless of storage temperature; the presence of debris enhanced survival at 12° C. In general, the highest transfer rates occurred with wet inoculum. The highest *Salmonella* transfer was calculated for wet inoculated tomatoes with 7 days of contact time at 25°C (TC = 14.7). Increasing contact time decreased TCs for new cartons, but increased TCs for used and dirty cartons. Regardless of carton condition or storage temperature, a greater population of *Salmonella* was transferred from tomatoes to cartons than from cartons to tomatoes. *Salmonella* transfer between tomatoes and cartons is highly dependent on moisture, with increased levels of moisture increasing transfer, highlighting the importance of harvesting and packing dry tomatoes. ISSN: 0362028X

**Kempf, F., Cordoni, G., Chaussé, A.-M., Drumo, R., Brown, H., Horton, D.L., Paboef, F., Denis, M., Velge, P., La Ragione, R., Kerouanton, A.**

*Inflammatory Responses Induced by the Monophasic Variant of Salmonella Typhimurium in Pigs Play a Role in the High Shedder Phenotype and Fecal Microbiota Composition*

(2023) *mSystems*, 8 (1), .

**ABSTRACT:** Pigs infected with *Salmonella* may excrete large amounts of *Salmonella*, increasing the risk of spread of this pathogen in the food chain. Identifying *Salmonella* high shedder pigs is therefore required to mitigate this risk. We analyzed immune-associated markers and composition of the gut microbiota in specific-pathogen-free pigs presenting different shedding levels after an oral infection with *Salmonella*. Immune response was studied through total blood cell counts, production of anti-*Salmonella* antibodies and cytokines, and gene expression quantification. Total *Salmonella* shedding for each pig was estimated and hierarchical clustering was used to cluster pigs into high, intermediate, and low shedders. Gut microbiota compositions were assessed using 16S rRNA microbial community profiling. Comparisons were made between control and inoculated pigs, then between high and low shedders pigs. Prior to infection, high shedders had similar immunological profiles compared to low shedders. As soon as 1 day postinoculation (dpi), significant differences on the cytokine production level and on the expression level of several host genes related to a proinflammatory response were observed between high and low shedders. Infection with *Salmonella* induced an early and profound remodeling of the immune response in all pigs, but the intensity of the response was stronger in high shedders. In contrast, low shedders seroconverted earlier than high shedders. Just after induction of the proinflammatory response (at 2 dpi), some taxa of the fecal microbiota were specific to the shedding phenotypes. This was related to the enrichment of several functional pathways related to anaerobic respiration in high shedders. In conclusion, our data show that the immune response to *Salmonella* modifies the fecal microbiota and subsequently could be responsible for shedding phenotypes. Influencing the gut microbiota and reducing intestinal inflammation could be a strategy for preventing *Salmonella* high shedding in livestock. Copyright ISSN: 23795077

**Elpers, L., Lüken, L., Lange, F., Hensel, M.**

*Factors Required for Adhesion of Salmonella enterica Serovar Typhimurium to Lactuca sativa (Lettuce)*

(2023) *Microbiology Spectrum*, 11 (1), .

**ABSTRACT:** *Salmonella enterica* serovar Typhimurium is a major cause of foodborne gastroenteritis. Recent outbreaks of infections by *S. enterica* serovar Typhimurium are often associated with non-animal-related food, i.e., vegetables, fruits, herbs, sprouts, and nuts. One main problem related to the consumption of fresh produce is the minimal processing, especially for leafy green salads. In this study, we focused on butterhead lettuce (*Lactuca sativa*) to which *S. enterica* serovar Typhimurium adheres at higher rates compared to *Valerianella locusta*, resulting in prolonged persistence. Here, we systematically analyzed factors contributing to adhesion of *S. enterica* serovar Typhimurium to *L. sativa* leaves. Application of a reductionist, synthetic approach, including the controlled surface expression of specific adhesive structures of *S. enterica* serovar Typhimurium, one at a time, enabled the identification of relevant fimbrial and nonfimbrial adhesins, the O-antigen of lipopolysaccharide, the flagella, and chemotaxis being involved in binding to *L. sativa* leaves. The analyses revealed contributions of Lpf fimbriae, Sti fimbriae, autotransported adhesin MisL, T1SS-secreted BapA, intact lipopolysaccharide (LPS), and flagella-mediated motility to adhesion of *S. enterica* serovar Typhimurium to *L. sativa* leaves. In addition, we identified BapA as a potential adhesin involved in binding to *V. locusta* and *L. sativa* leaf surfaces. **IMPORTANCE** The number of produce-associated outbreaks by gastrointestinal pathogens is increasing and underlines the relevance to human health. The mechanisms involved in the colonization of, persistence on, and transmission by, fresh produce are poorly understood. Here, we investigated the contribution of adhesive factors of *S. enterica* serovar Typhimurium in the initial phase of plant colonization, i.e., the binding to the plant surface. We used the previously established reductionist, synthetic approach to identify factors that contribute to the surface binding of *S. enterica* serovar Typhimurium to leaves of *L. sativa* by expressing all known adhesive structures by remote control expression system. ISSN: 21650497

**Pardos de la Gandara, M., Fournet, N., Bonifait, L., Lefèvre, S., Chemaly, M., Grastilleur, C., Cadel-Six, S., Fach, P., Pignault, A., Brisabois, A., Jourdan-Da Silva, N., Weill, F.-X.**

*Countrywide multi-serotype outbreak of Salmonella Bovismorbificans ST142 and monophasic Salmonella Typhimurium ST34 associated with dried pork sausages in France, September 2020\* to January 2021*

(2023) *Euro surveillance : bulletin European sur les maladies transmissibles = European communicable disease bulletin*, 28 (2), .

**ABSTRACT:** The French National Reference Centre for *Escherichia coli*, *Shigella* and *Salmonella* (FNRC-ESS) detected two human clusters of 33 cases (median age: 10 years;



17 females) infected by *Salmonella enterica* serotype Bovismorbificans, ST142, HC5\_243255 (Enterobase HierCC-cgMLST scheme) in September-November 2020 and of 11 cases (median age: 11 years; seven males) infected by *S. enterica* serotype 4,12:i:-, ST34, HC5\_198125 in October-December 2020. Epidemiological investigations conducted by Santé publique France linked these outbreaks to the consumption of dried pork sausages from the same manufacturer. *S. Bovismorbificans* and *S. 4,12:i:-* were isolated by the National Reference Laboratory from different food samples, but both strains were identified in a single food sample only by qPCR. Three recalls and withdrawals of dried pork products were issued by the French general directorate of food of the French ministry for agriculture and food in November 2020, affecting eight supermarket chains. A notification on the European Rapid Alert System for Food and Feed and a European urgent enquiry on the Epidemic Intelligence Information System for Food and Waterborne Diseases and Zoonoses (EPIS-FWD) were launched. No cases were reported outside France. Outbreaks caused by multiple serotypes of *Salmonella* may go undetected by protocols in standard procedures in microbiology laboratories. ISSN: 15607917

**Song, W.-J.**

*Effect of culture method on storage, plasma, and dry heat treatment resistance of Salmonella enterica serovar Typhimurium on black pepper*  
(2023) *Letters in Applied Microbiology*, 76 (1), art. no.ovac021, .

ABSTRACT: The purpose of this study was to determine the effect of the culture method on the resistance of *Salmonella Typhimurium* in low water activity foods to storage, plasma, and dry heat. Whole black peppers were used as the model food. *S. Typhimurium* cultured in liquid broth (tryptic soy broth) or solid agar (tryptic soy agar) and inoculated on whole black pepper was stored or treated with cold plasma or dry heat. Inactivation of *S. Typhimurium* cultured in liquid medium was higher in all the treatments. Liquid-cultured *S. Typhimurium* showed higher DPPP = O (diphenyl-1-pyrenylphosphine oxide) values compared to the solid-cultured *S. Typhimurium* after plasma or dry heat treatment. Furthermore, the unsaturated fatty acid and saturated fatty acid ratio (USFA/SFA) was significantly ( $P < 0.05$ ) reduced from 0.41 to 0.29 when *S. Typhimurium* was cultured on solid agar. These results suggested that the use of food-borne pathogens cultured on solid agar is more suitable for low water activity food pasteurization studies. ISSN: 02668254

**Applegate, S.F., Englishbey, A.K., Stephens, T.P., Sanchez-Plata, M.X.**

*Development and Verification of a Poultry Management Tool to Quantify Salmonella from Live to Final Product Utilizing RT-PCR*  
(2023) *Foods*, 12 (2), art. no. 419, .

ABSTRACT: The United States Department of Agriculture Food Safety and Inspection Service (USDA FSIS) does not maintain a zero-tolerance policy for *Salmonella* in poultry and poultry products, despite being a known food safety hazard throughout the poultry industry. In 2016, USDA FSIS established performance standards for a 52-week moving window with the maximum acceptable percent positive for comminuted turkey (325 g sample) at 13.5% (7 of 52 samples). Based upon FSIS verification sampling results from one 52-week moving window, the *Salmonella* prevalence for each poultry establishment in category 1 (below limit), 2 (meeting limit), or 3 (exceeding limit) are published for public viewing. Moreover, many poultry producers continue to have post-intervention samples test positive. Therefore, the use of quantification would be more valuable to determine the efficacy of process control interventions, corrective actions, and final product Log CFU/g of *Salmonella* to make rapid, within shift, food safety decisions. Therefore, the objectives of these studies are to develop, verify, and validate a rapid and reliable quantification method utilizing RT-PCR to enumerate *Salmonella* in the poultry industry from flock to final product and to utilize the method in an application study. BAX® System SalQuant® is an application of the BAX® System Real-Time PCR Assay for *Salmonella* to enumerate low levels of *Salmonella* with shortened enrichment times. Curve development encompassed inoculating poultry matrix samples at four levels with an ATCC strain of *Salmonella*, with three biological replicates per inoculation level, and five technical replicates being run on the BAX® System for various timepoints, gathering the data, and creating a linear-fit equation. A linear-fit equation was provided for each timepoint. The ideal timepoint, based on the statistical parameters surrounding the equation ( $R^2 > 0.80$ ,  $\text{Log RMSE} < 0.60$ , and enumerable range 0.00 to 4.00 Log CFU/mL (g)) that most accurately estimate *Salmonella* compared to most probable number (MPN), was chosen to be utilized for further studies. ISSN: 23048158

**Porto, Y.D., Fogaça, F.H.D.S., Andrade, A.O., da Silva, L.K.S., Lima, J.P., da Silva, J.L., Vieira, B.S., Cunha Neto, A., Figueiredo, E.E.D.S., Tassinari, W.D.S.**

*Salmonella* spp. in Aquaculture: An Exploratory Analysis (Integrative Review) of Microbiological Diagnoses between 2000 and 2020 (2023) *Animals*, 13 (1), art. no. 27, .

**ABSTRACT:** The present study aimed to characterize, through descriptive statistics, data from scientific articles selected in a systematic integrative review that performed a microbiological diagnosis of *Salmonella* spp. in aquaculture. Data were obtained from research articles published in the BVS, Scielo, Science Direct, Scopus and Web of Science databases. The selected studies were published between 2000 and 2020 on samples of aquaculture animal production (fish, shrimp, bivalve mollusks, and other crustaceans) and environmental samples of aquaculture activity (farming water, soil, and sediments). After applying the exclusion criteria, 80 articles were selected. Data such as country of origin, categories of fish investigated, methods of microbiological diagnosis of *Salmonella* spp., sample units analyzed and most reported serovars were mined. A textual analysis of the word cloud and by similarity and descending hierarchical classification with the application of Reinert's algorithm was performed using R® and Iramuteq® software. The results showed that a higher percentage of the selected articles came from Asian countries (38.75%). Fish was the most sampled category, and the units of analysis of the culture water, muscle and intestine were more positive. The culture isolation method is the most widespread, supported by more accurate techniques such as PCR. The most prevalent *Salmonella* serovars reported were *S. Typhimurium*, *S. Weltevreden* and *S. Newport*. The textual analysis showed a strong association of the terms "Salmonella", "fish" and "water", and the highest hierarchical class grouped 25.4% of the associated text segments, such as "aquaculture", "food" and "public health". The information produced characterizes the occurrence of *Salmonella* spp. in the aquaculture sector, providing an overview of recent years. Future research focusing on strategies for the control and prevention of *Salmonella* spp. in fish production are necessary and should be encouraged. ISSN: 20762615

**Castronovo, C., Agozzino, V., Schirò, G., Mira, F., Di Bella, S., Lastra, A., Antoci, F., Pennisi, M., Giudice, E., Guercio, A.**

*Evaluation of the Antimicrobial Resistance of Different Serotypes of Salmonella enterica from Livestock Farms in Southern Italy* (2023) *Applied Sciences (Switzerland)*, 13 (1), art. no. 442, .

**ABSTRACT:** The antimicrobial susceptibility profiles of *Salmonella* spp. isolated from livestock production systems in Sicily were determined. The antibiotic sensitivity of isolated *Salmonella* spp. and broad-spectrum beta-lactamase strains were assessed by detecting  $\beta$ -lactamases blaCTX-M IV, TEM, and OXA SHV, and  $\beta$ -lactamases blaCMY II, CTX-M I, CTX-M II, and DHA. In total, 93.3% of *Salmonella* spp. strains showed multi-drug resistance (MDR). A total of seven serotypes (i.e., *Salmonella* Infantis, *S. Typhimurium* (monophasic), *S. Derby*, *S. Hadar*, *S. salamae*, *S. houtenae*, *S. Cardoner*) showed high resistance values (R) (100–47%) to sulfonamides, tetracyclines, diaminopyrimidines, penicillins, and quinolones. The gene for  $\beta$ -lactamase blaTEM was found in *S. Typhimurium* (monophasic) and *S. Derby*, isolated from swine meat and feces samples; *S. Hadar* isolated from an insect sample; *S. salamae* isolated from an abrasive sponge on swine skin; *S. houtenae* isolated from chicken skin samples; and *S. Cardoner* isolated from a chicken meat sample. The gene blaCTX-M I was found in *S. Infantis* isolated from a chicken meat sample. The results gathered in the current study suggest that the resistance to antibiotics is continuously increasing. This represents a worrying perspective since they should be usually used as the last option for therapy against bacterial infections. ISSN: 20763417

**Lessard, M., Talbot, G., Bergeron, N., Lo Verso, L., Morissette, B., Yergeau, É., Matte, J.J., Bissonnette, N., Blais, M., Gong, J., Wang, Q., Quessy, S., Guay, F.**

*Weaning diet supplemented with health-promoting feed additives influences microbiota and immune response in piglets challenged with Salmonella* (2023) *Veterinary Immunology and Immunopathology*, 255, art. no. 110533, .

**ABSTRACT:** The aim of this study was to evaluate the potential of micronutrients and feed additives to modulate intestinal microbiota and systemic and mucosal immune responses in weaned pigs infected with *Salmonella*. At weaning, 32 litters of 12 piglets each were allocated to four dietary treatments: 1) control diet (CTRL), 2) CTRL supplemented with chlortetracycline (ATB), 3) CTRL supplemented with a cocktail of feed additives (CKTL); and 4) CKTL diet containing bovine colostrum in replacement of spray-dry animal plasma (CKTL+COL). The CKTL supplement included cranberry extract, encapsulated carvacrol and yeast-derived products and an enriched selenium and vitamin premix. Three weeks after weaning, four pigs per litter were orally inoculated with *Salmonella* Typhimurium DT104. Half of them were euthanized 3 days post-infection (dpi) and the other half, 7 dpi. The expression of IL6, TNF, IL8, monocyte chemoattractant protein 1 (MCP1), IFNG,

cyclooxygenase 2 (COX2), glutathione peroxidase 2 (GPX2) and  $\beta$ -defensin 2 (DEFB2) showed a peaked response at 3 dpi ( $P < 0.05$ ). Results also revealed that DEFB2 expression was higher at 3 dpi in CTRL and CKTL groups than in ATB ( $P = 0.01$  and  $0.06$ , respectively) while GPX2 gene was markedly increased at 3 and 7 dpi in pigs fed CKTL or CKTL+COL diet compared to CTRL pigs ( $P < 0.05$ ). In piglets fed CKTL or CKTL+COL diet, intestinal changes in microbial communities were less pronounced after exposure to *Salmonella* compared to CTRL and progressed faster toward the status before *Salmonella* challenge (AMOVA  $P < 0.01$ ). Furthermore, the relative abundance of several families was either up- or down-regulated in pigs fed CKTL or CKTL+COL diet after *Salmonella* challenge. In conclusion, weaning diet enriched with bovine colostrum, vitamins and mixture of feed additives mitigated the influence of *Salmonella* infection on intestinal microbial populations and modulate systemic and intestinal immune defences. ISSN: 01652427

**Roasto, M., Bonardi, S., Mäesaar, M., Alban, L., Gomes-Neves, E., Vieira-Pinto, M., Vågsholm, I., Elias, T., Lindegaard, L.L., Blagojevic, B.**

*Salmonella enterica* prevalence, serotype diversity, antimicrobial resistance and control in the European pork production chain

(2023) *Trends in Food Science and Technology*, 131, pp. 210-219.

**ABSTRACT:** Background: A risk assessment conducted by EFSA identified *Salmonella enterica* (*Salmonella*) as a high-risk hazard at the EU level in the context of meat inspection of swine. Despite pork being considered an important source of *S. Typhimurium* and its monophasic variant, Regulation (EC) No 2073/2005 does not set criteria for specific *Salmonella* serotypes. Enforcing specific criteria for *Salmonella* target serotypes could result in a reduction in the prevalence of *Salmonella* in the pork production chain, as has happened in broiler flocks. Scope and approach: This study gives an overview of *Salmonella enterica* in the European pork chain, discussing prevalence, serotype diversity, antimicrobial resistance and epidemiological importance during the last 20 years. Additionally, future trends and recommendations regarding control of *Salmonella* in the European pork production chain are introduced. Key findings and conclusions: The highest proportions of *Salmonella*-positive samples were observed at the fattening pig farm level, whereas the prevalence of *Salmonella* on pig carcasses was much lower. Among epidemiologically important serotypes, isolates of *S. Typhimurium*, and its monophasic variant were found to be resistant to ampicillin, sulfamethoxazole, streptomycin and tetracycline. Future *Salmonella* control in the pork production chain can preferably be conducted through a risk-based meat safety assurance system. In conclusion, a fit-for-purpose strategy applied to the pork production chain and adapted to the national epidemiological situation can deliver acceptable consumer safety. ISSN: 09242244

**Goni, J.I., Hendrix, K., Kritchevsky, J.**

*Recovery of Salmonella bacterial isolates from pooled fecal samples from horses*

(2023) *Journal of Veterinary Internal Medicine*, 37 (1), pp. 323-327.

**ABSTRACT:** Background: It is important to determine if a horse is shedding *Salmonella* spp., but a complete culture series can be cost prohibitive. Objectives: Determine the optimal pooling technique to maintain high sensitivity of *Salmonella* spp. culture using spiked samples, and then demonstrate the efficacy of this protocol on clinical submissions. Hypothesis: Pooled fecal samples are as sensitive as 5 individual cultures for the detection of *Salmonella* shedding. Animals: A single *Salmonella*-negative horse from the university herd, and 19 hospitalized horses. Methods: *Salmonella*-free fecal samples were spiked with different amounts of *Salmonella* spp. (102, 103, 104, and 105 colony forming units [cfu]) and homogenized to evaluate pooled samples. Five individual fecal samples were collected from 19 hospitalized horses. Ten-gram aliquots of each individual sample were combined to make a pooled sample. Both individual and pooled samples were cultured for *Salmonella* spp. The identity of bacterial isolates was confirmed by matrix-assisted laser desorption-ionization time of flight mass spectrometry. Results: A 102 cfu concentration of *Salmonella* spp. could be recovered from a spiked *Salmonella*-free fecal sample. Homogenization protocols indicated that the addition of 20 mL of broth to the pooled sample improved recovery, whereas homogenization time did not. Of the 19 horses tested, 5 were positive for *Salmonella*. In all instances, *Salmonella* spp. were recovered from the fecal pool as well as individual samples. Conclusions and Clinical Importance: Pooling of 5 fecal samples for *Salmonella* culture is a sensitive and cost-effective diagnostic approach to detect horses that are shedding the organism. ISSN: 08916640

**McMillan, E.A., Berrang, M.E., Read, Q.D., Rasamsetti, S., Richards, A.K., Shariat, N.W., Frye, J.G.**

*Buffered Peptone Water Formulation Does Not Influence Growth of pESI-positive Salmonella enterica Serovar Infantis*

(2023) *Journal of Food Protection*, 26 (2), art. no. 100033, .

**ABSTRACT:** *Salmonella enterica* is a major cause of human foodborne illness and is often attributed to poultry food sources. *S. enterica* serovar *Infantis*, specifically those carrying the pESI plasmid, has become a frequently isolated serotype from poultry meat samples at processing and has caused numerous recent human infections. In 2016, the USDA-Food Safety and Inspection Service changed the official sampling method for raw poultry products from BPW to using neutralizing BPW (nBPW) as the rinsing agent in order to prevent residual antimicrobial effects from acidifying and oxidizing processing aids. This change was contemporaneous to the emergence of pESI-positive ser. *Infantis* as a prevalent serovar in poultry, prompting some to question if nBPW could be selecting for this prevalent serovar. We performed two experiments: a comparison of ser. *Infantis* growth in BPW versus nBPW, and a simulation of regulatory sampling methods. We found that when inoculated into both broths, ser. *Infantis* initially grows slightly slower in nBPW than in BPW but little difference was seen in abundance after 6 h of growth. Additionally, the use of nBPW to simulate poultry rinse sample and overnight cold shipping to a regulatory lab did not affect the survival or subsequent growth of ser. *Infantis* in BPW. We concluded that the change in USDA-FSIS methodology to include nBPW in sampling procedures has likely not affected the emergence of *S. ser. Infantis* as a prevalent serovar in chicken and turkey meat product samples. ISSN: 0362028X

**Oscar, T.P.**

*Poultry Food Assess Risk Model for Salmonella and Chicken Gizzards: I. Initial Contamination*

(2023) *Journal of Food Protection*, 26 (2), art. no. 100036, .

**ABSTRACT:** The Poultry Food Assess Risk Model (PFARM) project was initiated in 1995 to develop data collection and modeling methods for simulating the risk of salmonellosis from poultry food produced by individual production chains. In the present study, the Initial Contamination (IC) step of PFARM for *Salmonella* and chicken gizzards (CG) was conducted as a case study. *Salmonella* prevalence (Pr), number (N), and serotype/zoonotic potential (ZP) data (n = 100) for one sample size (56 g) of CG were collected at meal preparation (MP), and then Monte Carlo simulation (MCS) was used to obtain data for other sample sizes (112, 168, 224, 280 g). The PFARM was developed in Excel and was simulated with @Risk. Data were simulated using a moving window of 60 samples to determine how *Salmonella* Pr, N, and ZP changed over time in the production chain. The ability of *Salmonella* to survive, grow, and spread in the production chain and food, and then cause disease in humans was ZP, which was based on U. S. Centers for Disease Control and Prevention data for salmonellosis. Of 100 CG samples tested, 35 were contaminated with *Salmonella* with N from 0 to 0.809 (median) to 2.788 log per 56 g. *Salmonella* serotype Pr per 56 g was 16% for Kentucky (ZPmode = 1.1), 9% for *Infantis* (ZPmode = 4.4), 6% for *Enteritidis* (ZPmode = 5.0), 3% for *Typhimurium* (ZPmode = 4.9), and 1% for *Thompson* (ZPmode = 3.7). Results from MCS indicated that *Salmonella* Pr, N, and ZP among portions of CG at MP changed ( $P \leq 0.05$ ) over time in the production chain. Notably, the main serotype changed from Kentucky (low ZP) to *Infantis* (high ZP). However, the pattern of change for *Salmonella* Pr, N, and ZP differed over time in the production chain and by the statistic used to characterize it. Thus, a performance standard (PS) based on *Salmonella* Pr, N, or ZP at testing or MP will likely not be a good indicator of poultry food safety or risk of salmonellosis. ISSN: 0362028X

**Bertelloni, F., Bresciani, F., Cagnoli, G., Scotti, B., Lazzerini, L., Marcucci, M., Colombani, G., Bilei, S., Bossù, T., De Marchis, M.L., Ebani, V.V.**

*House Flies (Musca domestica) from Swine and Poultry Farms Carrying Antimicrobial Resistant Enterobacteriaceae and Salmonella*

(2023) *Veterinary Sciences*, 10 (2), art. no. 118, .

**ABSTRACT:** The house fly (*Musca domestica*) is a very common insect, abundantly present in farm settings. These insects are attracted by organic substrates and can easily be contaminated by several pathogenic and nonpathogenic bacteria. The aim of this survey was to evaluate the presence of *Salmonella* spp. and other Enterobacteriaceae in house flies captured in small-medium size farms, located in Northwest Tuscany, Central Italy, and to evaluate their antimicrobial resistance; furthermore, isolates were tested for extended spectrum  $\beta$ -lactamase and carbapenems resistance, considering the importance these antimicrobials have in human therapy. A total of 35 traps were placed in seven poultry and 15 swine farms; three different kinds of samples were analyzed from each trap, representing attractant substrate, insect body surface, and insect whole bodies. Enterobacteriaceae were isolated from 86.36% of farms, 82.87% of traps, and 60.95% of

samples; high levels of resistance were detected for ampicillin (61.25% of resistant isolates) and tetracycline (42.5% of resistant isolates). One extended spectrum  $\beta$ -lactamase producer strain was isolated, carrying the blaTEM-1 gene. *Salmonella* spp. was detected in 36.36% of farms, 25.71% of traps, and 15.24% of samples. Five different serovars were identified: Kentucky, Kisarawe, London, Napoli, and Rubislaw; some isolates were in R phase. Resistance was detected mainly for ampicillin (31.21%) and tetracycline (31.21%). House flies could represent a serious hazard for biosecurity plans at the farm level, carrying and sharing relevant pathogenic and antimicrobial resistant bacteria. ISSN: 23067381

**Alves da Cunha Valini, G., Arnaut, P.R., Barbosa, L.G., de Azevedo, P.H.A., Melo, A.D.B., Marçal, D.A., Campos, P.H.R.F., Hauschild, L.**

*A Simple Assay to Assess Salmonella Typhimurium Impact on Performance and Immune Status of Growing Pigs after Different Inoculation Doses*  
(2023) *Microorganisms*, 11 (2), art. no. 446, .

ABSTRACT: *Salmonella Typhimurium* is the most frequent serovar in pigs and causes infections in humans. However, the dosage used for experimentation is not well defined. The present study aimed to evaluate a dosage for oral inoculation with *Salmonella Typhimurium* to assess immunological and growth performance alterations in pigs. Gilts were randomly allocated into one of three experimental treatments: no *Salmonella Typhimurium* inoculation (Basal), or oral inoculation of  $1 \times 10^8$  or  $1.5 \times 10^8$  colony-forming units of *Salmonella Typhimurium*. Growth rate, rectal temperature, and fecal *Salmonella* shedding were recorded. Blood samples were taken. Inoculated pigs shed the bacteria for up to 7 days, but no differences were observed between the groups. No differences were observed in rectal temperature, body weight, or average daily feed intake. However, reductions in average daily gain (-17 and -22%) and feed efficiency (-14 and -20%) were observed in pigs inoculated with  $1 \times 10^8$  and  $1.5 \times 10^8$  colony-forming units, respectively. The hemoglobin and hematocrit concentrations increased in challenged pigs compared to Basal pigs. The oral dosage of  $1.5 \times 10^8$  colony-forming units of *Salmonella Typhimurium* is suitable for activating the immune system of pigs and assessing the impact of *Salmonella* on pig performance. ISSN: 20762607

**Anis, N., Bonifait, L., Quesne, S., Baugé, L., Chemaly, M., Guyard-Nicodème, M.**  
*Simultaneous Detection of Salmonella spp. and Quantification of Campylobacter spp. in a Real-Time Duplex PCR: Myth or Reality?*

(2023) *Pathogens*, 12 (2), art. no. 338, .

ABSTRACT: In Europe, there is a process hygiene criterion for *Salmonella* and *Campylobacter* on broiler carcasses after chilling. The criterion gives indicative contamination values above which corrective actions are required by food business operators. The reference methods for verifying compliance with the criterion for *Salmonella* and *Campylobacter* are international standards EN ISO 6579-1 (2017) and EN ISO 10272-2 (2017), respectively. These methods are time-consuming and expensive for food business operators. Therefore, it would be advantageous to simultaneously detect *Salmonella* spp. and quantify *Campylobacter* in the same analysis, using the same sample after the pre-enrichment step for *Salmonella* recovery. A duplex PCR for *Salmonella* detection and *Campylobacter* spp. enumeration was developed. Considering the method as a whole, the LOD and LOQ for *Campylobacter* enumeration were slightly over the limit of 3 log CFU/g set by the process hygiene criterion. A comparison of the duplex PCR method developed with the ISO method on artificially contaminated bacterial suspensions and on naturally contaminated samples demonstrated a good correlation of the results for *Campylobacter* enumeration when the duplex PCR was performed on samples taken before or after the pre-enrichment step, but revealed a slight bias with a large standard deviation resulting in widely spaced limits of agreement. ISSN: 20760817

**Plumb, I.D., Brown, A.C., Stokes, E.K., Chen, J.C., Carleton, H., Tolar, B., Sundararaman, P., Saupe, A., Payne, D.C., Shah, H.J., Folster, J.P., Friedman, C.R.**  
*Increased Multidrug-Resistant Salmonella enterica I Serotype 4,[5],12:i:- Infections Associated with Pork, United States, 2009–2018*  
(2023) *Emerging Infectious Diseases*, 29 (2), pp. 314-322.

ABSTRACT: Reports of *Salmonella enterica* I serotype 4,[5],12:i:- infections resistant to ampicillin, streptomycin, sulphamethoxazole, and tetracycline (ASSuT) have been increasing. We analyzed data from 5 national surveillance systems to describe the epidemiology, resistance traits, and genetics of infections with this *Salmonella* strain in the United States. We found ASSuT-resistant *Salmonella* 4,[5],12:i:- increased from 1.1% of *Salmonella* infections during 2009–2013 to 2.6% during 2014–2018; the proportion of *Salmonella* 4,[5],12:i:- isolates without this resistance pattern declined from 3.1% to

2.4% during the same timeframe. Among isolates sequenced during 2015–2018, a total of 69% were in the same phylogenetic clade. Within that clade, 77% of isolates had genetic determinants of ASSuT resistance, and 16% had genetic determinants of decreased susceptibility to ciprofloxacin, ceftriaxone, or azithromycin. Among outbreaks related to the multidrug-resistant clade, 63% were associated with pork consumption or contact with swine. Preventing *Salmonella* 4,[5],12:i:- carriage in swine would likely prevent human infections with this strain. ISSN: 10806040

**Hong, Y., Ji, R., Wang, Z., Gu, J., Jiao, X., Li, Q.**

*Development and application of a multiplex PCR method to differentiate Salmonella enterica serovar Typhimurium from its monophasic variants in pig farms (2023) Food Microbiology, 109, art. no. 104135, .*

**ABSTRACT:** *Salmonella enterica serovar Typhimurium monophasic variants (Salmonella 4,[5],12:i:-)* has increased dramatically, causing human salmonellosis and colonization in pigs. With a difference to *S. Typhimurium*, the monophasic variants of *S. Typhimurium* lose the gene cassettes encoding the second phase flagellin. To establish a rapid method to detect and differentiate the two serotypes, we analyzed the published 679 genomes of *S. Typhimurium* and its monophasic variants and found that no *Salmonella* 4,[5],12:i:- strains carry both *fljB* and *hin* genes. Therefore, we established a novel multiplex PCR method using the *fljB-hin* region and *mdh* gene as target sequences to detect and differentiate both serotypes. This method can be used to specifically detect both serotypes with a detection limit for DNA concentration at 10 pg/μL. In addition, the PCR assay successfully differentiated 36 *S. Typhimurium* isolates from 62 isolates of monophasic variants preserved in our laboratory from 2009 to 2017, which corresponds to the whole-genome-based serotyping results. Application of the multiplex PCR method to 60 fecal samples from a pig farm identified 11.7% (7/60) of *S. Typhimurium* monophasic variants, which is consistent with the whole-genome-based serotyping results. The multiplex PCR assay is a rapid and precise method for the detection of *S. Typhimurium* monophasic variants from samples across food production chains. ISSN: 07400020

**Zhang, Y., Liao, X., Feng, J., Liu, D., Chen, S., Ding, T.**

*Induction of viable but nonculturable Salmonella spp. in liquid eggs by mild heat and subsequent resuscitation (2023) Food Microbiology, 109, art. no. 104127, .*

**ABSTRACT:** *Salmonella* spp. is one of the leading causes of foodborne outbreaks worldwide. *Salmonella* spp. has been associated with a variety of food sources, particularly egg products. They can enter a viable but nonculturable (VBNC) state in response to harsh stress. VBNC cells still retain membrane integrity and metabolic activity, which may pose health risks. However, the formation mechanism and resuscitation ability of VBNC cells are not well understood. In this work, *Salmonella* spp. cocktails, including *Salmonella enterica* serovar Newport and *Salmonella enterica* serovar Enteritidis, in liquid egg products was induced into a VBNC state by mild heat treatment, a commonly used method to inhibit the growth of pathogenic in liquid egg industry. Mild heat induced VBNC cells were found to resuscitate in liquid egg yolk (LEY) and liquid whole egg (LWE), but they failed to recover in liquid egg white (LEW). In addition, a certain number of cells remained as VBNC state after in vitro digestion. The membrane vesicle (MV) protein encoding gene *pagC*, two-component system encoding genes *phoP/Q* and sigma factor encoding gene *rpoS* were highly expressed in VBNC cells compared with the culturable counterparts. The results of this study can contribute to a better understanding of the health risks associated with *Salmonella* spp. in VBNC state and provide a theoretical basis for formation mechanism of VBNC state. ISSN: 07400020

**Serra-Castelló, C., Possas, A., Jofré, A., Garriga, M., Bover-Cid, S.**

*High pressure processing to control Salmonella in raw pet food without compromising the freshness appearance: The impact of acidulation and frozen storage (2023) Food Microbiology, 109, art. no. 104139, .*

**ABSTRACT:** The trend of feeding dogs and cats with raw pet food claiming health benefits poses health concerns due to the occurrence of pathogenic bacteria. High pressure processing (HPP) allows the non-thermal inactivation of microorganisms, preserving the nutritional characteristics with minimal impact on organoleptic traits of food. The present study aimed to evaluate and model the effect of HPP application (450–750 MPa for 0–7 min) on the inactivation of *Salmonella*, endogenous microbiota and colour of raw pet food formulated with different concentrations of lactic acid (0–7.2 g/kg) as natural antimicrobial. Additionally, the effect of a subsequent frozen storage of pressurized product was assessed. *Salmonella* inactivation ranged between 1 and 9 log, depending on the combination of conditions. According to the polynomial model obtained, the effect of

pressure was linear, while a quadratic term was also included for holding time (depicting the occurrence of a resistant tail at ca. 4–6 min). The effect of lactic acid was dependent on the pressure level, being most relevant for treatments below 600 MPa. Frozen storage after HPP prevented the pathogen recovery and caused a further *Salmonella* inactivation enhanced by lactic acid in most of the treatments. Endogenous microbial groups were significantly reduced by HPP to below the detection level in several conditions. In general, little effect of HPP on the instrumental colour parameters was observed, except for a slight increase in lightness, which was hardly appreciable from visual observation. High pressure processing emerges as a relevant technology for the control of *Salmonella* spp. and to manage the microbiological safety of raw pet food. The mathematical model can be used as decision support tool to design safer raw pet food, while keeping the desired freshness appearance of the products. ISSN: 07400020

**Cargnel, M., Filippitzi, M.-E., Van Cauteren, D., Mattheus, W., Botteldoorn, N., Cambier, L., Welby, S.**

*Assessing evidence of a potential Salmonella transmission across the poultry food chain (2023) Zoonoses and Public Health, 70 (1), pp. 22-45.*

**ABSTRACT:** Enhanced *Salmonella* surveillance programmes in poultry were implemented in all European Member States, with minimum prevalence targets for a list of targeted serotypes to safeguard food and public health. Based on the Belgian *Salmonella* surveillance programme and focusing on poultry, the overarching aim of this study was to highlight possible *Salmonella* transmissions across the food chain (FC). For this purpose, firstly, the prevalence patterns of *Salmonella* (targeted and the most prevalent non-targeted) serotypes along the FC were described over time. Secondly, the effectiveness of the control measures against vertical transmission (breeders to 1-day-old broiler and layer chicks) was indirectly assessed by looking into the odds of targeted serotypes detection. Thirdly, it was appraised if *Salmonella* prevalence can significantly increase during broilers and layers production. In addition, it was tested if being tested negative at the end of production in broilers when tested positive at the entrance is serotype dependent (targeted vs. non-targeted serotypes). Results showed that, firstly, the prevalence patterns of the listed serotypes were inconstant over time and across the FC. Secondly, the odds of *Salmonella* targeted serotype detection in 1-day-old broiler and in 1-day-old layer flocks were lower than in breeder flocks while, thirdly, infection during broiler and layer production can lead to significant increase in positivity in subsequent samples. Finally, being infected by a targeted or by non-targeted serotype at the entrance of the flock poorly reflects the *Salmonella* status at the end of production. Note that this study did not make a distinction between the different sources of contamination and the effects of sampling methods and isolation methods should be subject to further investigation. ISSN: 18631959

**Salam, F., Lekshmi, M., Prabhakar, P., Kumar, S.H., Nayak, B.B.**

*Physiological characteristics and virulence gene composition of selected serovars of seafood-borne Salmonella enterica (2023) Veterinary World, 16 (3), pp. 431-438.*

**ABSTRACT:** Background and Aim: All serotypes of *Salmonella enterica* are considered potentially pathogenic. However, the nontyphoidal *Salmonella* (NTS) serotypes vary considerably in terms of pathogenicity and the severity of infections. Although diverse serotypes of NTS have been reported from tropical seafood, their sources, physiological characteristics, and virulence potentials are not well understood. This study aimed to compare the physiological characteristics of selected serovars of *Salmonella* from seafood and investigate possible variations in the distribution of known genes within the pathogenicity islands. Materials and Methods: A series of biochemical tests, including carbohydrate fermentation and amino acid decarboxylation tests were performed to physiologically compare the isolates. The genetic characterization with respect to putative virulence genes was done by screening for genes associated with *Salmonella* pathogenicity island (SPI) I-V, as well as the toxin- and prophage-associated genes by polymerase chain reaction. Results: Irrespective of serotypes, all the isolates uniformly harbored the five SPIs screened in this study. However, some virulence genes, such as the *avrA*, *sodC*, and *gogB* were not detected in all *Salmonella* isolates. The biochemical profiles of *Salmonella* serotypes were highly conserved except for variations in inositol fermentation and citrate utilization. All the isolates of this study were weak biofilm formers on polystyrene surfaces. Conclusion: The pathogenicity profiles of environmental NTS isolates observed in this study suggest that they possess the virulence machinery necessary to cause human infections and therefore, urgent measures to contain *Salmonella* contamination of seafood are required to ensure the safety of consumers. ISSN: 09728988

**Zwilling, J.D., Whitham, J., Zambrano, F., Pifano, A., Grunden, A., Jameel, H., Venditti, R., Gonzalez, R.**

*Survivability of Salmonella Typhimurium (ATCC 14208) and Listeria innocua (ATCC 51742) on lignocellulosic materials for paper packaging (2023) Heliyon, 9 (3), art. no. e14122, .*

**ABSTRACT:** Lignocellulosic materials are widely used for food packaging due to their renewable and biodegradable nature. However, their porous and absorptive properties can lead to the uptake and retention of bacteria during food processing, transportation, and storage, which pose a potential risk for outbreaks of foodborne disease. Thus, it is of great importance to understand how bacteria proliferate and survive on lignocellulosic surfaces. The aim of this research was to compare the growth and survivability of *Salmonella Typhimurium* and *Listeria innocua* on bleached and unbleached paper packaging materials. Two different paper materials were fabricated to simulate linerboard from fully bleached and unbleached market pulps and inoculated with each bacterium at high bacterial loads (107 CFU). The bacteria propagated during the first 48 h of incubation and persisted at very high levels ( $>107$  CFU/cm<sup>2</sup>) for 40 days for all paper and bacterium types. However, the unbleached paper allowed for a greater degree of bacterial growth to occur compared to bleached paper, suspected to be due to the more hydrophobic nature of the unbleached, lignin-containing fibers. Several other considerations may also alter the behavior of bacteria on lignocellulosic materials, such as storage conditions, nutrient availability, and chemical composition of the fibers. ISSN: 24058440

**Kalchayanand, N., Wang, R., Brown, T., Wheeler, T.L.**

*Efficacy of Short Thermal Treatment Time Against Escherichia coli O157:H7 and Salmonella on the Surface of Fresh Beef (2023) Journal of Food Protection, 26 (3), art. no. 100040, .*

**ABSTRACT:** Thermal treatment interventions consistently provide effective pathogen reductions. However, the cost of maintaining high temperature of 95°C in order to raise the surface temperature of carcasses to 82°C is very expensive. Therefore, beef processors need to identify thermal application times and temperatures that optimize the treatment effects with less maintenance cost. The objectives of this study were to determine the efficacy of hot water or steam at 71°C for 6 s and cascade e-ion plasma treatment for 2 s in reducing pathogens on the surface of fresh beef compared to the thermal treatment at 82°C for 15 s. Hot water at 71°C for 6 s reduced *Escherichia coli* O157:H7 and *Salmonella* by 2.38 and 2.48 log CFU/cm<sup>2</sup>, while steam treatment at 71°C for 6 s reduced *E. coli* O157:H7 and *Salmonella* by 2.94 and 3.06 log CFU/cm<sup>2</sup>, respectively. Cascade e-ion plasma treatment for 2 s reduced *E. coli* O157:H7 on surface of fresh beef by 1.89 log CFU/cm<sup>2</sup>. The findings indicate that short treatment time with appropriate temperature could serve as an effective carcass intervention to improve the safety of fresh beef. ISSN: 0362028X

**Alves, V.V., Arantes, L.C.R.V., de Barros Moreira Filho, A.L., da Silva Teixeira, M., da Silva, E.F.A., de Mesquita Souza Saraiva, M., de Lucena, R.B., Givisiez, P.E.N., de Oliveira, C.J.B., de Freitas Neto, O.C.**

*Effect of diets containing commercial bioactive compounds on Salmonella Heidelberg infection in broiler chicks (2023) Brazilian Journal of Microbiology, 54 (1), pp. 571-577.*

**ABSTRACT:** *Salmonella Heidelberg* (SH) is responsible for economic losses in poultry farming and food infections in humans and is a serious public health problem. Recently, there has been an increase in the frequency of isolation of this serotype in batches of broilers raised in Brazil. It is necessary to find new ways to help control this pathogen. The present study aimed to evaluate the effect of diets containing the compound Original XPC, which is a prebiotic-like fermented compound (PFC), and/or Sangrovit, which is a sanguinarine-based phytobiotic (SAN), on SH infection in broiler chicks. For this purpose, SH colonization in the cecum and its invasion into the spleen and liver were evaluated, as were the histopathological changes caused in these organs. The lowest cecal SH counts were observed in birds that ingested SAN, followed by those fed PFC ( $P < 0.05$ ), with no added effect when the two bioproducts were used together (SAN + PFC). The mean SH and liver spleen counts did not differ between groups ( $P > 0.05$ ). In general, birds from all groups challenged with SH showed similar macroscopic changes, such as hemorrhagic areas, hepatomegaly, and splenomegaly, such changes being more intense in the infected control group. The microscopic changes observed in the liver included hepatocyte congestion, heterophil infiltration in the sinusoid capillaries, areas of necrosis, and mononuclear inflammation. In the cecum, heterophilic infiltrate and thickening of the lamina propria were observed. In the ileum, the most common changes were congestion and thickening of the lamina propria and atrophy of the villi and crypts. The microscopic



changes were less intense in the supplemented birds than the infected control group, and those supplemented with SAN developed the least changes. As ideal conditions for histomorphometric parameters of the ileum, the villus:crypt ratio in birds should be high, the villi should be long, and the crypts should be shallow. In the present study, higher mean heights and villus areas were observed in uninfected control and SAN group birds, and the crypt depth was lower in birds in the negative control group. The lowest villus:crypt ratio was observed in the birds of the infected control group. Although additional studies are needed, the preliminary results of the current investigation indicated that the addition of bioproducts, especially SAN, to the diet of birds helped to control SH infection, reducing its count in the cecum and improving overall and intestinal health. ISSN: 15178382

**Belo, N.O., de Angeli Dutra, D., Rodello, D., Crispim, N.P.C.C., Silva, A.S.G., Coelho, H.L.G., Cunha, J.L.R., Martins, N.R.S., Braga, E.M.**

*Detection of Salmonella spp. in wild and domestic birds in an anthropized ecotone between the Cerrado and the Amazon Forest in Brazil*

*(2023) Brazilian Journal of Microbiology, 54 (1), pp. 565-569.*

**ABSTRACT:** Emergence of zoonotic infectious diseases represent one of the main threats to people worldwide. To properly understand and prevent zoonoses is fundamental to study their epidemiology and the possibility of spillover events, especially for commercially intensive domestic animals and humans. Here, we studied 210 wild birds from the "Ipucas" region, which consists of fragments of the Amazon Forest interspersed with fragments of the "Cerrado" that is subject to seasonal flooding and 75 domestic birds from neighboring poultry farming. Then, we molecularly diagnosed *Salmonella* and *Chlamydia* from wild birds and poultry. Among the wild birds, four were diagnosed with *Chlamydia psittaci* and 23 with *Salmonella* spp., while we detected 15 poultry infected by *Salmonella* spp. and no poultry with *C. psittaci*. We highlighted the common infections of wild and domestic birds in an anthropologically modified environment and potential spillover of *Salmonella* pathogens among wild and livestock birds. Those infections can harm the health of native and domestic species. ISSN: 15178382