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Editorial Note

Bilthoven, 3 October 2025

Dear colleagues,

I hope you all had a good and relaxing summer break. Our summer period was a bit busier than usual, due to the rescheduling of two Proficiency Tests from autumn to summer 2025. After all, this new schedule would not have been necessary because the relocation of our institute to the new building was postponed again. However, we already started the new schedule before we were told about this new delay. A definite date for the relocation is still not known and we therefore can not yet foresee the effect on the planning of our activities in 2026. For the time being we stick to the 'normal' planning of our activities in 2026. As soon as more information is available about the relocation to the new building and the potential effect on our planning, we will send you an update.

In June/July 2025 we organised the **EURL-*Salmonella* PT Primary Production Stage (PPS) 2025**, for detection of *Salmonella* in chicken faeces. The samples were sent to the NRLs on 2 June 2025 and the deadline for reporting the results was 4 July 2025. The results have been analysed and the interim summary report was shared with the participants and published at the EURL-*Salmonella* website by the end of July 2025: https://www.eurlsalmonella.eu/en/documenten/interim-summary-report-eurl-salmonella-pt-pps-2025 In this PT, 34 of the 35 participants scored a good performance. One participant did not fulfill all criteria for good performance and the EURL is in contact with this NRL to discuss the next step(s).

From 11 August until 3 October 2025, the **EURL-*Salmonella* PT Typing 2025** was organised. Due to the reschedule of the PTs, this years' PT Typing contained only the obligatory part on serotyping of *Salmonella*. As soon as all results are reported by the NRLs, we will start with the analyses of the data and drafting of the report.

Currently, we also started brainstorming about the choice of the matrix and the planning of the **EURL-*Salmonella* PT Food 2026**. As soon as more details are available we will let you know.

I am happy to inform you that this Newsletter also contains a **contribution of an NRL-*Salmonella***. The NRL-*Salmonella* in France has performed a study on the influence of 'lag time' between adding the sample to the pre-enrichment broth and starting the incubation of the pre-enrichment broth on the detection of *Salmonella*. A summary of this interesting study is included on the next pages of this Newsletter.

Best wishes,
Kirsten Mooijman
Coordinator EURL-*Salmonella*

Contribution NRL-*Salmonella*-France

Influence of the time interval before pre-enrichment on *Salmonella* detection accuracy

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Introduction

Despite various control measures, salmonellosis remains the second leading cause of foodborne bacterial illness in Europe, highlighting the need for continuous surveillance and improved prevention strategies throughout the food production chain. *Salmonella* is known to cause a wide range of infections in both humans and animals, with the primary source of infection being the consumption of contaminated food, particularly poultry products. Given its potential to cause serious health issues, the detection and control of *Salmonella* are key priorities in public health and food safety efforts. Currently, in France, three standards are commonly used for *Salmonella* detection: NF U 47-100, NF U 47-101 and NF EN ISO 6579-1 (2017). All these standards require, as a first step, a pre-enrichment phase lasting 18 hours ± 2 hours. This incubation period may pose a challenge for the laboratory workflow and operational organization, especially when large amounts of samples need to be investigated. Therefore, the aim of this study is to investigate the impact of a “lag time” between adding the sample to the pre-enrichment broth and starting the incubation of the pre-enrichment broth on the detection of *Salmonella*.

Method

At the National Reference Laboratory for *Salmonella* (NRL) in France, the NF U 47-100 standard is used for the detection of *Salmonella* in fecal samples. This document specifies the French horizontal method based upon NF EN ISO 6579-1:2017, applicable to samples from the primary production stage such as animal faeces, dust, and swabs. The French standard outlines a pre-enrichment step using buffered peptone water (BPW). The test portion is inoculated into BPW at ambient temperature and then incubated at 37 °C ± 2 °C for 18 h ± 2 h. This is followed by a selective enrichment step using two enrichment media: modified semi-solid Rappaport-Vassiliadis (MSRV) agar and Muller-Kauffmann tetrathionate novobiocin broth (MKTTn broth). Both the MSRV agar and the MKTTn broth are incubated at 41,5 °C for 24 h.

In this study, different conditions were tested prior to the incubation phase of the pre-enrichment step, to assess their impact on *Salmonella* detection (Table 1): Inoculation of 25 g chicken faeces, free from specific pathogenic organisms, with five different *Salmonella* serovars: *S.* Enteritidis, *S.* Typhimurium, *S.* Virchow, *S.* Infantis or *S.* Hadar. Each condition was performed in triplicate:

- Inoculation at varying concentrations: ranging from 1,3 to 50,3 cfu/test portion.

- Each chicken faeces sample of 25 g was added to 225 ml BPW and subjected to various “lag times” prior to incubation at 37 °C ± 2 °C for 18 h ± 2 h: 45 min, 90 min, 4 h, 6 h.
- Storage at different temperatures during the “lag time”: room temperature (21 °C) and 4 °C.

Results and discussion

As part of the analysis, the total aerobic count of the non-inoculated chicken faeces was enumerated, following the NF EN ISO 4833-1, to assess the impact of the amount of background flora on the *Salmonella* detection. The concentrations of the two different chicken faeces batches used, ranged from 6,1 × 10^8 to 9,5 × 10^9 cfu/mL. The detection levels of *Salmonella* remained consistent for all serotypes tested, indicating that the detection method is robust and reliable regardless of the serotype (Table 1).

As previously documented in the literature (Bonifait *et al.*, 2018), *Salmonella* detection in fecal samples was negatively correlated with the *Salmonella* concentration in the samples (Figure 1). Specifically, samples inoculated with low concentrations of *Salmonella* spp. and in presence of high amounts of background flora, showed reduced detection rates. This finding underscores the challenges of detecting low-level contamination of pathogens in complex biological matrices such as animal faeces.

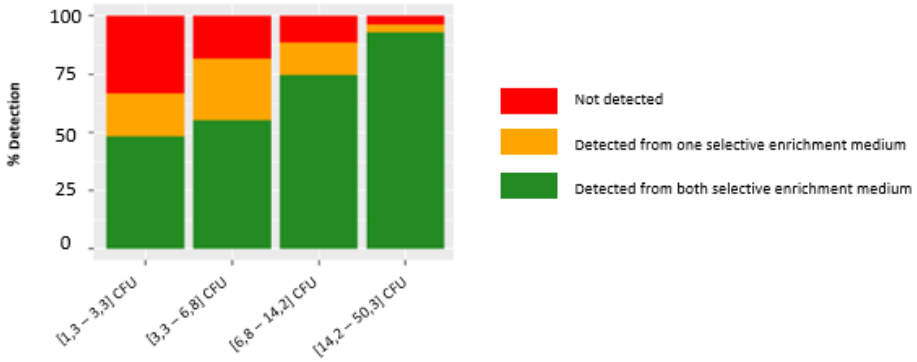

Figure 1 Influence of Salmonella concentration on the percentage of chicken faeces samples testing positive for Salmonella *according to NF U 47-100, regardless of the* Salmonella *serovar tested*

Furthermore, application of the non-parametric “Kruskal-Wallis” test demonstrated a statistically significant impact ($p<0,05$) of the pre-incubation “lag time” on the detection of *Salmonella* (Kruskal W. H. & Wallis W. A.).

Independently of the contamination level of *Salmonella*, the data indicated (Table 1) that detection rates were higher when samples experienced a “lag time” of 45 minutes, 90 minutes or 4 hours at ambient temperature, compared to those subjected to a 6 hour “lag time” at either cold conditions (4 °C) or ambient conditions (21 °C).

Notably, a 6 hour pre-incubation “lag time” at ambient temperature led to a substantial decrease in *Salmonella* detection, with recovery rates dropping to 50% (Figure 2A). Incubation of samples after a 6 hour “lag time” at 21 °C, resulted in a significant rate of non-detection for those containing less than 5 cfu *Salmonella* per test portion (Figure 2B). This effect can be mitigated by storing the ‘BPW-samples’ in the refrigerator (4°C) instead of at room temperature. Additionally, the impact of lag-time and temperature is less severe for samples with higher initial concentrations of *Salmonella* (approximately 10 cfu, Figure 2C). Still, these findings underscore the critical importance of restricting the delay between adding the sample to BPW and starting the incubation.

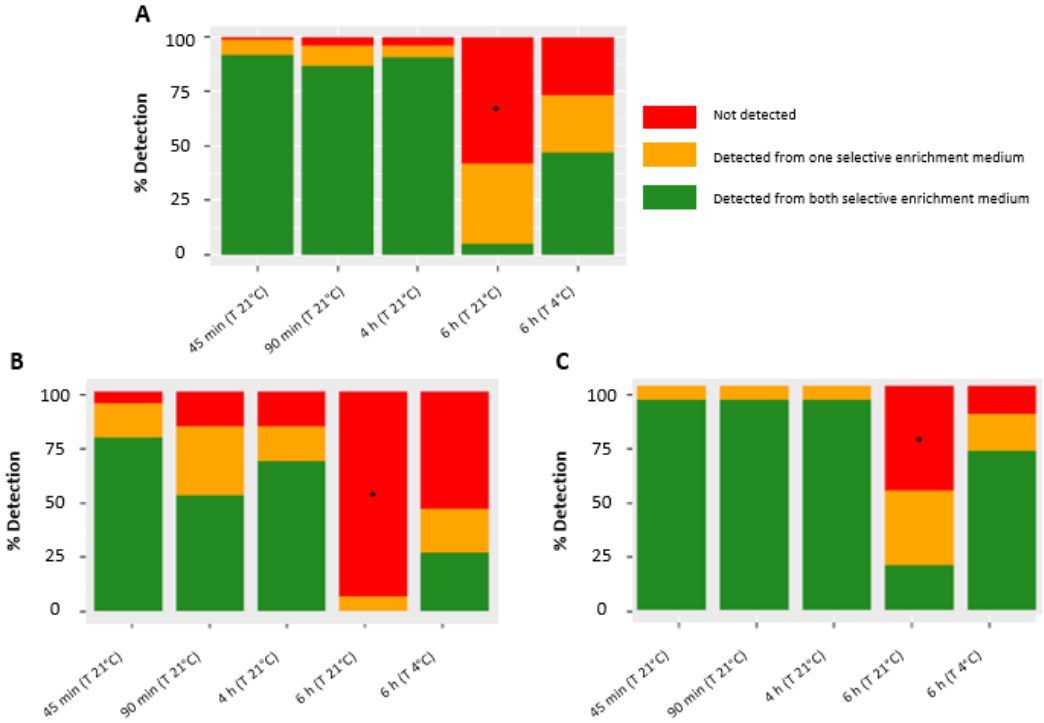

Figure 2: Pre-incubation "lag time" on the detection of Salmonella *in chicken faeces samples : (A) regardless of the serovar and the contamination level (*=p < 0.05) ; (B) for samples with a low concentration of* Salmonella *(1,3 to 3,3 cfu); (C) for samples contaminated with 6,8 to 14,2 cfu* Salmonella *per test portion.*

Conclusions

These results show that prolonged lag periods (more than 4h) of the pre-enrichment broth, after the sample has been added to BPW but before incubation, can adversely affect the detection of *Salmonella.* It is therefore important to limit this "lag time" to ensure optimal detection sensitivity, particularly when dealing with low *Salmonella* loads in complex matrices such as animal faeces. It may be important to add this information to the standard method(s) for detection of *Salmonella*, by indicating that once the sample is added to BPW, the pre-enrichment broth shall be placed in the incubator as soon as possible, e.g. within less than 4 h.

References

Bonifait L., Le Gall F., Baugé L. and Chemaly M. (2018) Detection of *Salmonella* spp. from samples at the primary production level: better understandings for a better analysis. Symposium Salmonella and Salmonellosis (I3S). 24 to 26 September 2018. Saint-Malo, France.

Kruskal W. H. & Wallis W. A. (1952). Use of ranks in one-criterion variance analysis. Journal of the American Statistical Association, 47(260), 583–621.

Table 1 Salmonella *detection in artificially contaminated chicken faeces samples, after different lag times and temperatures of the samples in BPW, following* NF U 47-100

N°	Lag temp	Serovar	Lag time	CFU	Detection	N°	Lag temp	Serovar	Lag time	CFU	Detection	N°	Lag temp	Serovar	Lag time	CFU	Detection
1	RT	Enteritidis	45 min	1,8	2	116	RT	Virchow	45 min	1,6	2	231	RT	Infantis	45 min	3,0	2
2	RT	Enteritidis	45 min	1,9	2	117	RT	Virchow	45 min	1,5	2	232	RT	Infantis	45 min	5,4	2
3	RT	Enteritidis	45 min	1,6	2	118	RT	Virchow	45 min	2,5	1	233	RT	Infantis	45 min	5,4	1
4	RT	Enteritidis	45 min	3,6	2	119	RT	Virchow	45 min	3,3	2	234	RT	Infantis	45 min	6,2	2
5	RT	Enteritidis	45 min	3,8	2	120	RT	Virchow	45 min	3,0	2	235	RT	Infantis	45 min	10,8	2
6	RT	Enteritidis	45 min	3,3	2	121	RT	Virchow	45 min	5,0	2	236	RT	Infantis	45 min	10,9	1
7	RT	Enteritidis	45 min	7,2	2	122	RT	Virchow	45 min	6,6	2	237	RT	Infantis	45 min	12,3	2
8	RT	Enteritidis	45 min	7,5	2	123	RT	Virchow	45 min	6,0	2	238	RT	Infantis	45 min	21,5	2
9	RT	Enteritidis	45 min	6,5	2	124	RT	Virchow	45 min	10,0	2	239	RT	Infantis	45 min	21,8	2
10	RT	Enteritidis	45 min	14,5	2	125	RT	Virchow	45 min	13,2	2	240	RT	Infantis	45 min	24,7	2
11	RT	Enteritidis	45 min	15,0	2	126	RT	Virchow	45 min	12,1	2	241	RT	Infantis	45 min	43,0	2
12	RT	Enteritidis	45 min	13,0	2	127	RT	Virchow	45 min	20,0	2	242	RT	Infantis	45 min	43,6	2
13	RT	Enteritidis	45 min	29,0	2	128	RT	Virchow	45 min	26,3	2	243	RT	Infantis	45 min	49,3	2
14	RT	Enteritidis	45 min	30,0	2	129	RT	Virchow	45 min	24,3	2	244	RT	Infantis	90 min	2,7	0
15	RT	Enteritidis	45 min	26,0	2	130	RT	Virchow	90 min	1,3	1	245	RT	Infantis	90 min	2,7	1
16	RT	Enteritidis	90 min	1,8	2	131	RT	Virchow	90 min	1,6	1	246	RT	Infantis	90 min	3,0	0
17	RT	Enteritidis	90 min	1,9	1	132	RT	Virchow	90 min	1,5	2	247	RT	Infantis	90 min	5,4	2
18	RT	Enteritidis	90 min	1,6	2	133	RT	Virchow	90 min	2,5	1	248	RT	Infantis	90 min	5,4	2
19	RT	Enteritidis	90 min	3,6	2	134	RT	Virchow	90 min	3,3	2	249	RT	Infantis	90 min	6,2	2
20	RT	Enteritidis	90 min	3,8	2	135	RT	Virchow	90 min	3,0	2	250	RT	Infantis	90 min	10,8	2
21	RT	Enteritidis	90 min	3,3	2	136	RT	Virchow	90 min	5,0	2	251	RT	Infantis	90 min	10,9	2
22	RT	Enteritidis	90 min	7,2	2	137	RT	Virchow	90 min	6,6	2	252	RT	Infantis	90 min	12,3	2
23	RT	Enteritidis	90 min	7,5	2	138	RT	Virchow	90 min	6,0	2	253	RT	Infantis	90 min	21,5	2
24	RT	Enteritidis	90 min	6,5	2	139	RT	Virchow	90 min	10,0	2	254	RT	Infantis	90 min	21,8	2
25	RT	Enteritidis	90 min	14,5	2	140	RT	Virchow	90 min	13,2	2	255	RT	Infantis	90 min	24,7	2
26	RT	Enteritidis	90 min	15,0	2	141	RT	Virchow	90 min	12,1	2	256	RT	Infantis	90 min	43,0	2
27	RT	Enteritidis	90 min	13,0	2	142	RT	Virchow	90 min	20,0	2	257	RT	Infantis	90 min	43,6	2
28	RT	Enteritidis	90 min	29,0	2	143	RT	Virchow	90 min	26,3	2	258	RT	Infantis	90 min	49,3	2

N°	Lag temp	Serovar	Lag time	CFU	Detection	N°	Lag temp	Serovar	Lag time	CFU	Detection	N°	Lag temp	Serovar	Lag time	CFU	Detection
29	RT	Enteritidis	90 min	30,0	2	144	RT	Virchow	90 min	24,3	2	259	RT	Infantis	4 h	2,7	2
30	RT	Enteritidis	90 min	26,0	2	145	RT	Virchow	4 h	1,3	1	260	RT	Infantis	4 h	2,7	2
31	RT	Enteritidis	4 h	1,8	0	146	RT	Virchow	4 h	1,6	2	261	RT	Infantis	4 h	3,0	2
32	RT	Enteritidis	4 h	1,9	1	147	RT	Virchow	4 h	1,5	2	262	RT	Infantis	4 h	5,4	2
33	RT	Enteritidis	4 h	1,6	0	148	RT	Virchow	4 h	2,5	1	263	RT	Infantis	4 h	5,4	2
34	RT	Enteritidis	4 h	3,6	2	149	RT	Virchow	4 h	3,3	2	264	RT	Infantis	4 h	6,2	2
35	RT	Enteritidis	4 h	3,8	2	150	RT	Virchow	4 h	3,0	2	265	RT	Infantis	4 h	10,8	2
36	RT	Enteritidis	4 h	3,3	2	151	RT	Virchow	4 h	5,0	2	266	RT	Infantis	4 h	10,9	2
37	RT	Enteritidis	4 h	7,2	2	152	RT	Virchow	4 h	6,6	2	267	RT	Infantis	4 h	12,3	2
38	RT	Enteritidis	4 h	7,5	2	153	RT	Virchow	4 h	6,0	2	268	RT	Infantis	4 h	21,5	2
39	RT	Enteritidis	4 h	6,5	2	154	RT	Virchow	4 h	10,0	2	269	RT	Infantis	4 h	21,8	2
40	RT	Enteritidis	4 h	14,5	2	155	RT	Virchow	4 h	13,2	2	270	RT	Infantis	4 h	24,7	2
41	RT	Enteritidis	4 h	15,0	2	156	RT	Virchow	4 h	12,1	2	271	RT	Infantis	4 h	43,0	2
42	RT	Enteritidis	4 h	13,0	2	157	RT	Virchow	4 h	20,0	2	272	RT	Infantis	4 h	43,6	2
43	RT	Enteritidis	4 h	29,0	2	158	RT	Virchow	4 h	26,3	2	273	RT	Infantis	4 h	49,3	2
44	RT	Enteritidis	4 h	30,0	2	159	RT	Virchow	4 h	24,3	2	274	RT	Infantis	6 h	2,9	1
45	RT	Enteritidis	4 h	26,0	2	160	RT	Virchow	6 h	1,7	0	275	RT	Infantis	6 h	2,9	0
46	RT	Enteritidis	6 h	1,7	0	161	RT	Virchow	6 h	1,7	0	276	RT	Infantis	6 h	2,9	0
47	RT	Enteritidis	6 h	1,7	0	162	RT	Virchow	6 h	1,7	0	277	RT	Infantis	6 h	5,8	1
48	RT	Enteritidis	6 h	1,7	0	163	RT	Virchow	6 h	3,4	0	278	RT	Infantis	6 h	5,8	1
49	RT	Enteritidis	6 h	3,4	0	164	RT	Virchow	6 h	3,4	0	279	RT	Infantis	6 h	5,8	0
50	RT	Enteritidis	6 h	3,4	0	165	RT	Virchow	6 h	3,4	0	280	RT	Infantis	6 h	11,5	1
51	RT	Enteritidis	6 h	3,4	1	166	RT	Virchow	6 h	6,8	0	281	RT	Infantis	6 h	11,5	0
52	RT	Enteritidis	6 h	6,8	1	167	RT	Virchow	6 h	6,8	1	282	RT	Infantis	6 h	11,5	0
53	RT	Enteritidis	6 h	6,8	0	168	RT	Virchow	6 h	6,8	1	283	RT	Infantis	6 h	17,3	1
54	RT	Enteritidis	6 h	6,8	0	169	RT	Virchow	6 h	10,2	0	284	RT	Infantis	6 h	17,3	0
55	RT	Enteritidis	6 h	10,3	0	170	RT	Virchow	6 h	10,2	1	285	RT	Infantis	6 h	17,3	0
56	RT	Enteritidis	6 h	10,3	1	171	RT	Virchow	6 h	10,2	2	286	4 °C	Enteritidis	6 h	2,4	0
57	RT	Enteritidis	6 h	10,3	0	172	RT	Hadar	45 min	2,3	2	287	4 °C	Enteritidis	6 h	2,4	2
58	RT	Typhimurium	45 min	2,5	2	173	RT	Hadar	45 min	3,1	2	288	4 °C	Enteritidis	6 h	2,4	2
59	RT	Typhimurium	45 min	2,4	2	174	RT	Hadar	45 min	2,8	1	289	4 °C	Enteritidis	6 h	4,9	0

N°	Lag temp	Serovar	Lag time	CFU	Detection	N°	Lag temp	Serovar	Lag time	CFU	Detection	N°	Lag temp	Serovar	Lag time	CFU	Detection
60	RT	Typhimurium	45 min	1,8	2	175	RT	Hadar	45 min	4,6	2	290	4 °C	Enteritidis	6 h	4,9	1
61	RT	Typhimurium	45 min	5,0	2	176	RT	Hadar	45 min	6,3	2	291	4 °C	Enteritidis	6 h	4,9	1
62	RT	Typhimurium	45 min	4,7	2	177	RT	Hadar	45 min	5,6	2	292	4 °C	Enteritidis	6 h	9,7	1
63	RT	Typhimurium	45 min	3,5	2	178	RT	Hadar	45 min	9,3	2	293	4 °C	Enteritidis	6 h	9,7	2
64	RT	Typhimurium	45 min	10,0	2	179	RT	Hadar	45 min	12,6	2	294	4 °C	Enteritidis	6 h	9,7	2
65	RT	Typhimurium	45 min	9,4	2	180	RT	Hadar	45 min	11,2	2	295	4 °C	Enteritidis	6 h	11,1	2
66	RT	Typhimurium	45 min	7,0	2	181	RT	Hadar	45 min	18,5	2	296	4 °C	Enteritidis	6 h	11,1	2
67	RT	Typhimurium	45 min	20,0	2	182	RT	Hadar	45 min	25,2	2	297	4 °C	Enteritidis	6 h	11,1	2
68	RT	Typhimurium	45 min	18,8	2	183	RT	Hadar	45 min	22,3	2	298	4 °C	Typhimurium	6 h	2,7	0
69	RT	Typhimurium	45 min	14,2	2	184	RT	Hadar	45 min	37,0	2	299	4 °C	Typhimurium	6 h	2,7	1
70	RT	Typhimurium	45 min	40,0	2	185	RT	Hadar	45 min	50,3	2	300	4 °C	Typhimurium	6 h	2,7	2
71	RT	Typhimurium	45 min	37,6	2	186	RT	Hadar	45 min	44,6	2	301	4 °C	Typhimurium	6 h	5,4	0
72	RT	Typhimurium	45 min	28,3	2	187	RT	Hadar	90 min	2,3	2	302	4 °C	Typhimurium	6 h	5,4	1
73	RT	Typhimurium	90 min	2,5	2	188	RT	Hadar	90 min	3,1	0	303	4 °C	Typhimurium	6 h	5,4	2
74	RT	Typhimurium	90 min	2,4	1	189	RT	Hadar	90 min	2,8	2	304	4 °C	Typhimurium	6 h	10,8	1
75	RT	Typhimurium	90 min	1,8	2	190	RT	Hadar	90 min	4,6	2	305	4 °C	Typhimurium	6 h	10,8	1
76	RT	Typhimurium	90 min	5,0	2	191	RT	Hadar	90 min	6,3	2	306	4 °C	Typhimurium	6 h	10,8	2
77	RT	Typhimurium	90 min	4,7	2	192	RT	Hadar	90 min	5,6	2	307	4 °C	Typhimurium	6 h	12,5	2
78	RT	Typhimurium	90 min	3,5	2	193	RT	Hadar	90 min	9,3	2	308	4 °C	Typhimurium	6 h	12,5	2
79	RT	Typhimurium	90 min	10,0	2	194	RT	Hadar	90 min	12,6	2	309	4 °C	Typhimurium	6 h	12,5	2
80	RT	Typhimurium	90 min	9,4	1	195	RT	Hadar	90 min	11,2	2	310	4 °C	Virchow	6 h	1,7	0
81	RT	Typhimurium	90 min	7,0	2	196	RT	Hadar	90 min	18,5	2	311	4 °C	Virchow	6 h	1,7	0
82	RT	Typhimurium	90 min	20,0	2	197	RT	Hadar	90 min	25,2	2	312	4 °C	Virchow	6 h	1,7	0
83	RT	Typhimurium	90 min	18,8	2	198	RT	Hadar	90 min	22,3	2	313	4 °C	Virchow	6 h	3,3	1
84	RT	Typhimurium	90 min	14,2	2	199	RT	Hadar	90 min	37,0	2	314	4 °C	Virchow	6 h	3,3	1
85	RT	Typhimurium	90 min	40,0	2	200	RT	Hadar	90 min	50,3	2	315	4 °C	Virchow	6 h	3,3	2
86	RT	Typhimurium	90 min	37,6	2	201	RT	Hadar	90 min	44,6	2	316	4 °C	Virchow	6 h	6,7	0
87	RT	Typhimurium	90 min	28,3	2	202	RT	Hadar	4 h	2,3	2	317	4 °C	Virchow	6 h	6,7	1
88	RT	Typhimurium	4 h	2,5	2	203	RT	Hadar	4 h	3,1	2	318	4 °C	Virchow	6 h	6,7	2
89	RT	Typhimurium	4 h	2,4	2	204	RT	Hadar	4 h	2,8	2	319	4 °C	Virchow	6 h	9,5	2
90	RT	Typhimurium	4 h	1,8	0	205	RT	Hadar	4 h	4,6	2	320	4 °C	Virchow	6 h	9,5	2

N°	Lag temp	Serovar	Lag time	CFU	Detection	N°	Lag temp	Serovar	Lag time	CFU	Detection	N°	Lag temp	Serovar	Lag time	CFU	Detection
91	RT	Typhimurium	4 h	5,0	2	206	RT	Hadar	4 h	6,3	2	321	4 °C	Virchow	6 h	9,5	2
92	RT	Typhimurium	4 h	4,7	2	207	RT	Hadar	4 h	5,6	2	322	4 °C	Hadar	6 h	3,0	1
93	RT	Typhimurium	4 h	3,5	2	208	RT	Hadar	4 h	9,3	2	323	4 °C	Hadar	6 h	3,0	1
94	RT	Typhimurium	4 h	10,0	2	209	RT	Hadar	4 h	12,6	1	324	4 °C	Hadar	6 h	3,0	2
95	RT	Typhimurium	4 h	9,4	2	210	RT	Hadar	4 h	11,2	2	325	4 °C	Hadar	6 h	6,1	1
96	RT	Typhimurium	4 h	7,0	2	211	RT	Hadar	4 h	18,5	2	326	4 °C	Hadar	6 h	6,1	1
97	RT	Typhimurium	4 h	20,0	2	212	RT	Hadar	4 h	25,2	2	327	4 °C	Hadar	6 h	6,1	2
98	RT	Typhimurium	4 h	18,8	2	213	RT	Hadar	4 h	22,3	2	328	4 °C	Hadar	6 h	12,3	1
99	RT	Typhimurium	4 h	14,2	2	214	RT	Hadar	4 h	37,0	2	329	4 °C	Hadar	6 h	12,3	2
100	RT	Typhimurium	4 h	40,0	2	215	RT	Hadar	4 h	50,3	2	330	4 °C	Hadar	6 h	12,3	2
101	RT	Typhimurium	4 h	37,6	2	216	RT	Hadar	4 h	44,6	2	331	4 °C	Hadar	6 h	16,1	2
102	RT	Typhimurium	4 h	28,3	2	217	RT	Hadar	6 h	2,9	0	332	4 °C	Hadar	6 h	16,1	2
103	RT	Typhimurium	6 h	1,7	0	218	RT	Hadar	6 h	2,9	0	333	4 °C	Hadar	6 h	16,1	2
104	RT	Typhimurium	6 h	1,7	0	219	RT	Hadar	6 h	2,9	0	334	4 °C	Infantis	6 h	2,7	0
105	RT	Typhimurium	6 h	1,7	0	220	RT	Hadar	6 h	5,8	1	335	4 °C	Infantis	6 h	2,7	0
106	RT	Typhimurium	6 h	3,3	1	221	RT	Hadar	6 h	5,8	1	336	4 °C	Infantis	6 h	2,7	0
107	RT	Typhimurium	6 h	3,3	1	222	RT	Hadar	6 h	5,8	0	337	4 °C	Infantis	6 h	5,5	0
108	RT	Typhimurium	6 h	3,3	0	223	RT	Hadar	6 h	11,7	0	338	4 °C	Infantis	6 h	5,5	0
109	RT	Typhimurium	6 h	6,7	1	224	RT	Hadar	6 h	11,7	0	339	4 °C	Infantis	6 h	5,5	1
110	RT	Typhimurium	6 h	6,7	1	225	RT	Hadar	6 h	11,7	2	340	4 °C	Infantis	6 h	10,9	0
111	RT	Typhimurium	6 h	6,7	1	226	RT	Hadar	6 h	17,5	0	341	4 °C	Infantis	6 h	10,9	0
112	RT	Typhimurium	6 h	10,0	1	227	RT	Hadar	6 h	17,5	1	342	4 °C	Infantis	6 h	10,9	0
113	RT	Typhimurium	6 h	10,0	1	228	RT	Hadar	6 h	17,5	1	343	4 °C	Infantis	6 h	12,4	2
114	RT	Typhimurium	6 h	10,0	2	229	RT	Infantis	45 min	2,7	2	344	4 °C	Infantis	6 h	12,4	2
115	RT	Virchow	45 min	1,3	1	230	RT	Infantis	45 min	2,7	0	345	4 °C	Infantis	6 h	12,4	2

RT: Room temperature = ambient condition

CFU : inoculation level of Salmonella *in the 25 g chicken faeces sample*

2: Salmonella was detected from both selective enrichment medium ; 1: Salmonella was detected from one selective enrichment medium ; 0: Salmonella was not detected

From the Literature

Salmonella-related Literature selection from Scopus: July – September 2025

O.E., van den Berg, Oda E., D.L., Adriaansens, Dana Ll, M.I., Lanzl, Maren I., K.A., Mooijman, Kirsten A., A.H.A.M.H.A.M., van Hoek, A. H. A. M. H.A.M., D.A.H., Brandwagt, Diederik A.H., S., Feenstra-Gols, S., J., Mans-Poulie, Joline, P.Y., Dop, Petra Y., I.A., Slegers-Fitz-James, Ife A.
Ongoing increase in autochthonous Salmonella Enteritidis infections, the Netherlands, June 2023 to June 2025
(2025) Eurosurveillance, 30 (30), art. no. pii=2500536
ABSTRACT: Salmonella Enteritidis (SE) cases in humans have increased in the Netherlands, from an annual average of 281 (2017–2019) to 427 in 2023, 401 in 2024 and 209 in 2025 (January–June). This rise is paralleled by a 2.5-fold increase in SE-positive laying hen flocks. Genomic surveillance shows numerous small clusters, suggesting a diffuse transmission rather than a single point-source outbreak, which complicates outbreak investigations. Coordinated interventions in the laying hen sector are urgently needed to mitigate public health risks. ISSN: 15607917, 1025496X

E., Weinstein, Eva, K., Lamba, Katherine, C., Bond, Christian, V., Peralta, Vi, M., Needham, Michael, S.W., Beam, Stephen W., F., Arroyo, Francine, D., Kiang, David, Y., Chen, Yishi, S., Shah, Seema
Outbreak of Salmonella Typhimurium Infections Linked to Commercially Distributed Raw Milk — California and Four Other States, September 2023-March 2024
(2025) Morbidity and Mortality Weekly Report, 74 (27), pp. 433 - 438
ABSTRACT: Unpasteurized (raw) milk has been linked to foodborne illness outbreaks caused by Escherichia coli bacteria and certain species of Brucella, Campylobacter, Cryptosporidium, and Salmonella. In October 2023, the County of San Diego Health and Human Services Agency notified the California Department of Public Health (CDPH) of eight cases of salmonellosis in persons who reported consuming brand A raw milk, produced exclusively by dairy farm A. A total of 171 outbreak-associated Salmonella Typhimurium cases were identified through review of standardized salmonellosis case report forms and a search of PulseNet, CDC's national molecular subtyping network for enteric disease surveillance, followed by administration of a dairy-focused supplementary questionnaire. Most cases (98%) were identified in California; one case each was identified in four other states. Among the 171 cases, 120 (70%) cases and 18 (82%) of the cases requiring hospitalization were among children and adolescents aged <18 years. Among 159 patients confirmed to be infected with the outbreak strain, 55 (70%) of those with exposure data consumed brand A raw milk or heavy cream. Four of 40 samples collected from dairy farm A, retail stores, and patients' homes, including raw milk and raw milk cheese aged for 60 days, tested positive for the outbreak strain of S. Typhimurium by whole-genome sequencing. Dairy farm A voluntarily recalled raw milk and raw heavy cream 1 week after the initial outbreak identification. Commercially distributed raw dairy products have the potential to cause large and widespread infectious disease outbreaks. Public health authorities should continue to raise awareness of the risks associated with consuming raw dairy products, especially by persons at increased risk for severe disease from enteric pathogens, including children. ISSN: 01492195, 1545861X

X., Fan, Xuetong, J.B., Gurtler, Joshua B., J., Baik, Jessica, C.M., Garner, Christina M., B.T., Vinyard, Bryan T.
Effectiveness of UVC-Assisted Fenton Reaction Wash-Based System to Inactivate Salmonella Typhimurium, Escherichia coli O157:H7, and Listeria monocytogenes on Cherry Tomatoes
(2025) Journal of Food Protection, 88 (8), art. no. 100555
ABSTRACT: The Fenton reaction results when hydrogen peroxide (H2O2) interacts with the ferrous ion, producing highly antimicrobial hydroxyl free radicals ([rad]OH). In this study, a UVC-assisted Fenton reaction was tested against cocktails of Salmonella Typhimurium, E. coli O157:H7, and Listeria monocytogenes, inoculated onto cherry tomatoes. Inoculated cherry tomatoes were subjected to 2% H2O2wash, 1 mM Fe3+ wash, or exposed to UVC during washing, and simultaneously in the following combinations: H2O2+ Fe3+, H2O2+ UVC, or H2O2+ Fe3+ + UVC for 2 min at ambient temperature (~20 °C). In addition,

[rad]OH were measured using the methylene blue dye test, after combining Fenton reaction components in water. Results revealed that H2O2 alone, or in combination, reduced significantly higher populations of the three bacterial pathogens, when compared with water wash alone. The H2O2+ Fe3+ + UVC treatment inactivated 5.24 ± 1.17 log CFU Salmonella/fruit, which was significantly ($P < 0.05$) greater than those reduced by Fe3+ or UVC alone. However, the reduction was not statistically significant when compared to H2O2, H2O2+ Fe3+, or H2O2+ UVC. Similarly, the combinations did not inactivate significantly ($P > 0.05$) more E. coli O157:H7 and L. monocytogenes than individual H2O2 or UVC treatments, with reductions of 2.31–3.20 and 1.96–3.17 log CFU/fruit, respectively, although [rad]OH were produced in water during the H2O2+ Fe3+ + UVC treatments. Overall, our results demonstrate that UVC-assisted Fenton washing does not consistently exhibit advantages over individual H2O2 or UVC treatments during cherry tomato washing to inactivate foodborne pathogens, presumably due to the inability of short-lived hydroxyl radicals to reach the bacteria on tomatoes.
ISSN: 19449097, 0362028X

N.Y., Viktorovna, Novik Yana, S.P., Tiwari, Sita Prasad, B., Dixit, Baleshwari, M.T., Evgenievna, Mironova Tatyana, C.V., Sergeevna, Cherepushkina Victoria, A., Nikolaevich, Afonyushkinvasily, K.M., Vyacheslavovna, Korneva Marina, D.N., Victorovna, Davydova Natalia, Y.E., Evgenievna, Yurchenko Elizaveta
A cross-sectional study to understand the correlation among Salmonella enterica infection and Lactobacillus reuteri concentration in fecal samples of post weaning piglets and their association in causation of diarrhea
(2025) Indian Journal of Animal Sciences, 95 (4), pp. 286 - 290
ABSTRACT: Interaction among host gut microbiome and disease-causing organisms play an important role in the establishment of infection. Considering it, the relationship between the concentration of Lactobacillus reuteri and the level of Salmonella infection was assessed in the feces of post weaning piglets, in reference to diarrheic (sick) and healthy piglets. Eighty fecal samples from piglets (40-50 days of age) of eight different pig farms were examined. Piglets were classified as sick (diarrhea) and healthy (norm) by Indikal indicator paper method. Fecal samples were processed for the extraction of genomic DNA of Lactobacilli and Salmonella and subjected to real-time PCR to detect concentration of microorganisms in the sample. The results indicated that Salmonella infection did not directly affect the development of post weaning diarrheal syndrome in piglets. Positive correlation between the presence of L. reuteri and the PCR prevalence of salmonellosis in piglets was puzzling, since this contradicts a lot of literature data. The relationship between opportunistic intestinal microbiota and Lactobacilli of normal microflora is more complex under conditions of long-term coevolution. The probiotics based on L. reuteri may be more effective, provided that there was no long-term adaptation of Salmonella to Lactobacilli of this species. ISSN: 03678318

L., van Hulzen, Landen, J.E., Pietri, Jose E.
Salmonella Typhimurium Infection and Excretion Following Sublethal Exposure to Insecticidal Bait in the German Cockroach Vector
(2025) ACS Infectious Diseases, 11 (7), pp. 1968 - 1974
ABSTRACT: The German cockroach, Blattella germanica, is a widespread indoor pest and a vector of enteric human pathogens, including Salmonella enterica serovar Typhimurium (S. Typhimurium). Insecticidal baits are the most commonly used tools to control these cockroaches in built environments. Sublethal exposure to insecticidal baits has been a major driver of adaptive evolution, leading to physiological resistance to insecticides and behavioral aversion to glucose in some cockroach populations. Here, we conducted the first study investigating the effects of sublethal bait exposure on human pathogen biology in B. germanica. Our results show that a sublethal exposure to bait containing the common insecticide indoxacarb can increase susceptibility to subsequent infection by ingested S. Typhimurium in surviving cockroaches within the same generation. Interestingly, increased susceptibility to infection after sublethal bait exposure was cockroach strain dependent and did not increase the rate of shedding of the pathogen in excreta. These findings establish for the first time a potential link between a common anthropogenic intervention used to control this prevalent indoor pest and its capacity to maintain pathogens. In doing so, our work reveals a possible unintended consequence of failed pest control efforts. That is, some cockroach populations may become inadvertently more adept at maintaining pathogens due to sublethal exposure to baits stemming from existing insecticide resistance. Additional studies should further investigate this phenomenon to determine its extent and impact. ISSN: 23738227

L., Barre, Léna, F., Guillier, Florence, B., Lombard, Bertrand, C., Danan, Corinne, J.A., Hennekinne, Jacques Antoine, B., Constantin, Boris, R., Le Neve, Romain, S., Nguyen, Sandrine, A., Boubetra, Abdelkader, M.M., Chemaly, Marianne Monsour
Interlaboratory proficiency tests to assess the analytical competency of French official control laboratories for the analysis of Listeria monocytogenes, Salmonella spp. and coagulase-positive staphylococci in food
(2025) International Journal of Food Microbiology, 438, art. no. 111218
ABSTRACT: A common interlaboratory proficiency testing scheme in food microbiology was organised yearly in France from 2019 to 2021 by the three National Reference Laboratories for Listeria monocytogenes, Salmonella spp. and coagulase-positive staphylococci (CPS). This proficiency testing scheme aimed to assess the performance of French official control laboratories for the detection and enumeration of these three major foodborne pathogenic bacteria covered by European regulations on microbiological criteria for foodstuffs. An average of 65 laboratories participated in the proficiency test (PT) each year, using either reference or validated alternative methods. For each PT, ten samples for detection and four samples for enumeration per pathogen were sent to each participant. Over the three years, the PT results demonstrated the ability of the laboratory network to detect L. monocytogenes and Salmonella spp., as well as to enumerate L. monocytogenes and CPS in food matrices. These PTs showcased the robustness of the official laboratory network and provided an opportunity to give scientific and technical advices in case of discrepancy results, representing an efficient tool for quality improvement of the analyses performed by the laboratory network. ISSN: 01681605, 18793460

D.A., Ekunseitan, Deji Abiodun, S.H., Harrison, Scott H., I.M., Ogunade, Ibukun Michael, Y.O., Fasina, Yewande O.
Influence of Different Litter Regimens on Ceca Microbiota Profiles in Salmonella-Challenged Broiler Chicks
(2025) Animals, 15 (14), art. no. 2039
ABSTRACT: A 14-day study was conducted to evaluate the effect of litter type (dirty litter, DL; fresh litter, FL) and Salmonella Enteritidis SE challenge (no challenge, NC; challenge, SE) on the growth performance and cecal microbial composition of neonate chicks. Day-old chicks (n = 240, Ross 708 male) were allocated to a 2 × 2 factorial design consisting of four treatments: chicks raised on dirty litter (CONDL), chicks raised on fresh litter (CONFL); and chicks raised on litter types similar to CONDL and CONFL but inoculated with 7.46 × 108 CFU SE/mL at d 1 (CONDLSE and CONFLSE). The performance indices measured included body weight (BW), body weight gain (BWG), feed intake (FI), mortality, and feed conversion ratio (FCR). Cecal SE concentration was assessed on d 3 and 14, and ceca were collected from chicks on day 14 for DNA extraction. The Illumina Miseq platform was used for microbiome analysis of the V3–V4 region of the 16S rRNA gene. The interaction of litter type and SE influenced FCR and FI. CONDL recorded the poorest FCR (1.832). FI was highest and similar in CONFLSE, CONDL, and CONDLSE (0.655, 0.692, and 0.677, respectively). Cecal SE concentration was significantly reduced in CONDLSE at d 3 and 14. Alpha diversity was higher ($p < 0.05$) in the DL compared to that in NC. Beta diversity showed a separation ($p < 0.05$) between the DL and the FL. Comparative tree analysis revealed 21 differential significant genera, with 14 prevalent in the DL and 7 in the FL, specifically, bacteria genera such as Lactobacillus, Clostridia_vadinBB60_group, Lachnospira, Oscillospiraceae UCG_005, and Marvinbryantia, which play significant roles relating to improved growth performance, metabolic homeostasis within the gut, energy metabolism, and short-chain fatty acid (SCFA) utilization. Our results concluded that litter management regimen differentially alters the microbiome of chicks, which accounts for the improved performance and exclusion of pathogens in the study. ISSN: 20762615

E., Skrzypiec, Ewelina, M., Skarżyńska, Magdalena, M., Zając, Magdalena, R., Kwit, Renata, A., Lalak, Anna, A., Śmiałowska-Węglińska, Aleksandra, E., Mikos-Wojewoda, Emilia, P., Pasim, Paulina, W., Koza, Weronika, D., Wojdat, Dominika
Surveillance of Salmonella Serovars in the Food Chain in Poland: A Five-Year Review (2016–2020)
(2025) Pathogens, 14 (7), art. no. 712
ABSTRACT: (1) Background: Understanding the distribution of Salmonella serovars in food, animals, and their environments is crucial for identifying infection sources and monitoring pathogen prevalence in the food chain. This study analysed Salmonella serovars in Poland from 2016 to 2020, focusing on their epidemiological significance. (2) Methods: Isolation of Salmonella was carried out following PN-EN ISO 6579 standards, and serotyping was performed using the White–Kauffmann–Le Minor scheme. A total of 7104 isolates were collected from food-producing animals, their environments, food of animal origin, feedingstuffs, and fertilisers. (3) Results: A total of 175 serovars were identified, with S.

Enteritidis (n = 2905; 40.9%), S. Infantis (n = 1167; 16.4%), and S. Typhimurium (n = 360; 5.1%) being the most prevalent. Species-specific patterns were observed: S. Enteritidis dominated in chickens, ducks, and cattle; S. Kentucky in turkeys; S. Typhimurium in geese; and monophasic S. Typhimurium in pigs. S. Enteritidis and S. Infantis were most frequent in food of animal origin, especially broiler meat. In feedingstuffs, S. Agona was predominant, while fertilisers mostly contained S. Derby and S. Infantis. (4) Conclusions: The study highlights the source-dependent variety of Salmonella serovars and the importance of serotyping in tracing infection routes and preventing the spread of pathogens. Identifying the most common serovars supports the development of targeted preventive measures, including improved biosecurity, hygiene, and management practices to enhance food safety. ISSN: 20760817

R.K., Gast, Richard K., J.S., Garcia, Javier S., R., Guraya, Rupa, D.R., Jones, Deana R., D.M., Karcher, Darrin M.
Environmental contamination and horizontal transmission of Salmonella Enteritidis among experimentally infected layer pullets in indoor cage-free housing
(2025) Poultry Science, 104 (7), art. no. 105236
ABSTRACT: The persistence and transmission of the egg-associated pathogen Salmonella Enteritidis in laying flocks are significantly influenced by the poultry housing environment. The present study assessed environmental contamination and horizontal transmission of S. Enteritidis within groups of layer pullets in cage-free housing after infection just before the age of sexual maturity. In each of 3 trials, 144 pullets were transferred from a rearing facility at 15 wk of age and randomly distributed between 2 isolation rooms simulating commercial cage-free barns with perches and nest boxes (72 birds/room). One wk after placement in the containment facility, a proportion of the 72 pullets in each room were orally inoculated with approximately 6 × 107 cfu of S. Enteritidis: 1/3 in trial 1, 1/6 in trial 2, and 1/12 in trial 3. At 2 wk post-inoculation in each trial, samples of liver, spleen, and intestinal tract were collected from 40 uninoculated (contact-exposed) birds in each room for bacteriologic culturing to detect horizontal transmission of S. Enteritidis. At 6 intervals between inoculation and necropsy, 5 types of environmental samples (wall dust swab, nest box swab, perch swab, flooring substrate drag swab, and flooring substrate composite) were collected and cultured for S. Enteritidis. The overall frequencies of S. Enteritidis recovery from both environmental samples and internal organs from contact-exposed pullets after initial oral inoculation of 1/3 of the birds in each room (97 % and 75 %, respectively) were significantly greater than after initial infection of 1/6 of the birds (78 % and 58 %), and S. Enteritidis recovery from birds inoculated at a 1/12 proportion (10 % of environmental samples and 18 % of organs) was significantly lower than from the 1/6 inoculation group. Flooring substrate composites were the most efficient environmental sample type for all 3 trials combined (72 % positive), providing significantly better S. Enteritidis recovery than the least efficient samples (flooring substrate drag swabs; 53 % positive). These data suggest that a high frequency of environmental contamination may be an important contributor to horizontal transmission of S. Enteritidis infections among pullets in cage-free housing. ISSN: 00325791, 15253171

C.M., Sia, Cheryll M., J.S., Pearson, Jaclyn S., B.P., Howden, Benjamin P., D.A., Williamson, Deborah A., D.J., Ingle, Danielle J.
Salmonella pathogenicity islands in the genomic era
(2025) Trends in Microbiology, 33 (7), pp. 752 - 764
ABSTRACT: Serovars of Salmonella are significant bacterial pathogens and are leading contributors to the global burden of diarrhoeal disease. Salmonella pathogenicity islands (SPIs) are essential for the survival and success of this genus, enabling colonisation, invasion, and survival in hostile environments. While genomics has transformed efforts to understand the evolution, dissemination, and antimicrobial resistance of members, its use to explore virulence determinants that contribute to the pathogenicity of specific organisms and severity of infection remains varied. Here, we discuss the importance of SPIs to the evolution of Salmonella, the implications in the shift of identification of SPIs from molecular microbiology to genomic-based approaches, and examine current efforts to explore the distribution and prevalence of SPIs in large-scale datasets of Salmonella genomes.
ISSN: 0966842X, 18784380

D.G., Belay, Dagim G., J.V., Olsen, Jakob Vesterlund
Economic Impacts of Salmonella Dublin in Dairy Farms: Panel Evidence From Denmark
(2025) Agricultural Economics (United Kingdom), 56 (4), pp. 666 - 693
ISSN: 15740862, 01695150

S., Kiener, Shannon, E., Smith, Emily, N., Singh, Neha, S.M., Nemser, Sarah M., K., Hettwer, Karina, M.R., Miller, Megan R., A., Tkachenko, Andriy, S., Uhlig, Steffen, R.M., Reddy, Ravinder M.
Determination of limit of detection and relative limit of detection of Salmonella in raw pet food matrices using Salmonella bacteriological analytical manual methods
(2025) Journal of Microbiological Methods, 232-234, art. no. 107116
ABSTRACT: Each year, there are multiple Salmonella recalls due to contaminated pet food products. Routine testing of finished products requires reliable, quick, and sensitive detection methods. In this study we comparatively evaluated the sensitivity of a culture-based reference method and two alternative methods, which are based on LAMP and PCR principles. The evaluation was performed in multiple trials using challenging pet food matrices, which were tested after various storage time intervals to better address the reliability of the methods. Raw freeze-dried treats, kibble, and patties were individually inoculated with Salmonella Typhimurium at fractional and high inoculation levels. Raw freeze-dried treats and kibble were inoculated at 0, 1, 3, 5, 7 and 10 CFU/25 g and raw patties were inoculated at 0, 1, 3, 5, 7, 10 and 30 CFU/25 g. For the culture method, the level of detection (LOD<inf>50</inf>) values were 0.9, 1.1, and 3.7 CFU/25 g for freeze-dried treats, kibble, and patties respectively. The calculated relative level of detection (RLOD) values were close to 1 CFU/25 g, indicating that LAMP and PCR methods have similar LOD<inf>50</inf> values to the culture method. It was also confirmed that the alternative LAMP and PCR methods can provide reliable results within 24 h that match the reference culture method. Faster response times are invaluable when responding to potential pet food product contamination. ISSN: 01677012, 18728359

Y., Zhao, Yuying, G., Li, Guohui, Q., Li, Quan, H., Shi, Huoying
Identification and evaluation of cross-protection efficiency of the conserved antigens of Salmonella Enteritidis
(2025) Vaccine, 62, art. no. 127622
ABSTRACT: Salmonella, a major foodborne zoonotic pathogen, threatens global poultry production and public health. While inactivated vaccines exhibit limited efficacy and live attenuated vaccines raise safety concerns due to risks of virulence reversion, subunit vaccines represent a safer and more targeted alternative. However, existing subunit vaccines against Salmonella provide limited cross-serotype protection. To address this challenge, OmpC, OmpD, OmpF (outer membrane proteins), SseB (a Type III secretory system secretory protein), and FliC (flagellin) were selected as five conserved antigens of Salmonella Enteritidis (S. enteritidis) for evaluation of their immune protective efficacy in this work. Our data showed that all antigens exhibited strong humoral and cell-mediated immune responses specific to each antigen, significantly reducing mortality and bacterial burdens following S. enteritidis challenge compared to infected controls. Notably, the SseB subunit vaccine demonstrated promising but serovar-dependent protection, inducing partial cross-reactive opsonophagocytic antibody (OPA) responses against Salmonella serovars. Protection experiments revealed divergent efficacy: 66.7 % survival against homologous S. enteritidis versus limited 33.3 % survival against heterologous S. typhimurium challenge. Both groups exhibited significantly reduced bacterial colonization and mitigated histopathological damage. These findings position SseB as a key candidate for serovar-specific subunit vaccines, laying the groundwork for multivalent approaches targeting conserved virulence machinery. ISSN: 0264410X, 18732518

F.L.L., Leite, Fernando Lopes L., P.H.E., Arruda, Paulo H.E., B., Ford, Brianna, D., Jordan, Dianna, L., Giménez-Lirola, Luis, J.C., Mora-Díaz, Juan Carlos, D., Bradshaw, David, S.M.D., Bearson, Shawn Michelle Dunkin
Oral live bivalent Salmonella vaccine reduces clinical disease, colonization and fecal shedding of multidrug resistant Salmonella enterica serovar I 4,[5],12:i:-
(2025) Vaccine, 62, art. no. 127540
ABSTRACT: Salmonella enterica serovar I 4,[5],12:i:- is currently the most common serovar identified in U.S. swine clinical cases and is prevalent worldwide. This serovar also ranks among the leading causes of human foodborne salmonellosis and is the most frequently identified multidrug-resistant (MDR; resistance to ≥3 antimicrobial classes) Salmonella serovar in the U.S. Given its importance to both swine health and food safety, the current study evaluated the efficacy of a commercial vaccine containing live attenuated Salmonella enterica serovars Typhimurium and Choleraesuis in pigs challenged with MDR Salmonella I 4,[5],12:i:-. Pigs vaccinated with a single oral dose exhibited significantly reduced diarrhea and lower body temperatures following challenge compared to non-vaccinated pigs (n = 20/group). During the 14-days post-challenge, vaccinated pigs also demonstrated significantly reduced fecal shedding and up to a 2.3-log reduction in intestinal tissue colonization, as well as a significant reduction in the number of pigs

colonized, compared to non-vaccinated pigs. Furthermore, weight gain was significantly higher in vaccinated pigs compared to non-vaccinated pigs after challenge. Collectively, these results demonstrate that vaccination significantly reduces clinical disease, fecal shedding, and tissue colonization following challenge with MDR Salmonella I 4,[5],12:i:-, revealing the vaccine to be an effective pre-harvest tool to improve both animal health and food safety. ISSN: 0264410X, 18732518

A.F., Nugraha, Asep Firman, W.P., Rahayu, Winiati Pudji, A.B., Sitanggang, Azis Boing
The prevalence of Salmonella contamination in beef and beef products: A systematic review and meta-analysis
(2025) BIO Web of Conferences, 186, art. no. 01015
ABSTRACT: Salmonella continues to be a leading global foodborne pathogen, posing significant threats to public health, economic stability, and food safety systems. This systematic review and meta-analysis aimed to determine the global prevalence of Salmonella in beef and its products, guided by the PRISMA 2020 framework, to ensure transparency and rigor. Relevant studies were retrieved from scientific databases using targeted keywords, with the inclusion criteria focused on empirical data regarding Salmonella prevalence in beef and beef products. Of the 629 initially identified articles, 51 comprising 72 datasets met the inclusion criteria. Data extraction included variables such as sample size, detection method, and prevalence rates, which were synthesized to generate pooled prevalence estimates. The analysis revealed an overall Salmonella prevalence of 9.73% (95% CI: 6.66%-13.28%) across 106,666 samples, with a higher prevalence in beef products (13.71%) than in raw beef (9.30%). Regional disparities were observed, with the highest prevalence observed in Asia and the lowest in Europe and South America. This study confirms the need for targeted interventions, improved processing hygiene, robust monitoring systems, and public awareness campaigns to mitigate Salmonella contamination risks, ultimately contributing to enhanced food safety standards globally and aligned with the Sustainable Development Goals.
ISSN: 22731709, 21174458

K., Patil, Kavita, M., Adhikari, Manita, P.M., Rubinelli, Peter M., J.C., Acuff, Jennifer C.
A Salmonella enterica Surrogate for Future Validation Studies for Nonfat Dried Milk and Low-Moisture Food Environments
(2025) Journal of Food Protection, 88 (9), art. no. 100578
ABSTRACT: Low-moisture food persistent bacterial populations (LMF PBPs) may be responsible for pathogen harborage in LMF processing environments, resulting in outbreaks and recalls. To address this issue, industry requires a surrogate to understand the survivability of LMF PBP and perform in-plant validation studies to reduce the level of this pathogen to an acceptable level. Hygienic controls for the LMF industry must be tailored to different equipment, environments, and food types. In-plant validations with a surrogate would assist with evaluating the efficacy of sanitation protocols that eliminate LMF PBPs and harborage. This study explored surrogates for Salmonella LMF PBP to provide tools for challenge studies to eliminate LMF PBPs from stainless-steel surfaces. Three surrogates (Escherichia coli MP 26, Enterococcus faecium, Pediococcus acidilactici) were evaluated for similarity to a Salmonella LMF PBP in nonfat dried milk (NFDM) formed on stainless steel coupons stored at 30% or 70% relative humidity (RH) at 25 °C. Coupons were prepared with a previously established method to form an LMF PBP (0.5 g of NFDM, 0.4 mL culture). Microbial survival was enumerated at intervals (0, 1, 3, 5, and 7 days) using standard plating techniques. An ANOVA and Tukey's HSD tests were used to compare log reductions to identify suitable surrogates. E. faecium exhibited higher survival trends that were most similar to Salmonella, with no significant differences in log reductions ($p > 0.05$). In contrast, E. coli surrogate panel and P. acidilactici showed significantly greater reductions, making them unsuitable surrogate candidates for Salmonella. Matrices and RH interactions influenced survival, but E. faecium consistently mirrored Salmonella behavior. E. faecium was similar but hardier than Salmonella LMF PBPs and could be used in processing environments for challenging and validating sanitation protocols. ISSN: 19449097, 0362028X

L., Xiaoli, Lingzi, P.P., Huth, Paula Pennell, C., Sherman, Cassandra, D., Wroblewski, Danielle, S., Anderson, Stacy, L., Ferraro, Lindsey, D., Jones, Dee, M., Slaughter, Molly, B.R., Morningstar, Brenda R., T.A., Mackie, Tonya A.
Reoccurring Salmonella Cotham Outbreak Linked to Pet Bearded Dragons - United States, 2024
(2025) Morbidity and Mortality Weekly Report, 74 (31), pp. 474 - 479

ABSTRACT: In April 2024, CDC's PulseNet identified a cluster of seven Salmonella Cotham cases from five states. Isolates were highly related by whole genome sequencing (WGS), and one patient reported contact with a pet bearded dragon. CDC initiated a multistate investigation and as of December 10, 2024, an additional 19 cases had been identified, for a total of 26 confirmed cases from 13 states; state public health partners identified one probable case in an additional state for a total of 27 cases. Eighteen of 25 cases (72%) were among persons who reported contact with a bearded dragon or lizard. Children aged <5 years, especially infants, were disproportionately affected, accounting for 17 (65%) of the 26 confirmed cases; most had bearded dragons in the home without direct animal contact. WGS of two bearded dragon specimens collected in 2024 and three bearded dragon specimens collected during 2012-2014 confirmed genetic relatedness of this rare Salmonella strain and continued circulation among commercially sold bearded dragons. CDC implemented a One Health approach in response, working with pet industry representatives to disseminate information about biosecurity best practices to bearded dragon suppliers and retailers. Investigators contacted a common bearded dragon supplier identified in the traceback investigation to share biosecurity and prevention recommendations. CDC used social media and a website investigation notice to inform the public, recommending that caregivers prevent young children from indirect reptile contact by restricting reptiles from roaming freely, separating reptiles and supplies from food preparation areas, and washing hands and changing clothes after handling reptiles and before holding infants. ISSN: 01492195, 1545861X

B.M., Whitney, Brooke M., A., Palacios, Alexandra, B., Warren, Benjamin, D.A., Kautter, Donald A., E.A., Grant, E. Ashley, A.J., Crosby, Alvin J., S.L., Seelman, Sharon L., L., Walerstein, Lindsay, J., Mangia, Julia, A.W., Pightling, Arthur W.
An Investigation of Salmonella Senftenberg Illnesses in the United States Linked to Peanut Butter—2022
(2025) Foodborne Pathogens and Disease, 22 (9), pp. 635 - 642
ABSTRACT: In 2022, the U.S. Food and Drug Administration (FDA), the Centers for Disease Control and Prevention (CDC), and state partners conducted a sample-initiated investigation of a multistate outbreak of Salmonella Senftenberg illnesses linked to peanut butter. Twenty-one illnesses and four hospitalizations were reported in 17 states, with a significant epidemiological signal for peanut butter from Firm A. Whole genome sequence (WGS) data from a Salmonella-positive environmental swab sample collected at Firm A in 2010 yielded the outbreak strain that was a match to the WGS data from the 2022 clinical isolates. Lot code information collected from patients indicated Firm A's facility in Kentucky as a common manufacturing source, and FDA and state partners initiated an inspection. In 2021, Firm A installed two new roasters with at least one of the cooling air supply vents leaking, allowing unfiltered air and rainwater to enter the cooling section after the roasting process. Investigators noted the limitations of Firm A's finished product testing program to identify contamination. Investigative partners from five states collected and analyzed 14 product samples, and FDA collected 205 environmental swabs, and all were negative. Although the exact source and route of the contamination were not determined, epidemiological and traceback evidence confirmed peanut butter consumed by patients was produced by Firm A. Firm A voluntarily recalled all implicated products and provided a plan for corrective actions and restart to FDA. This was the first major domestic investigation of a multistate-foodborne illness outbreak linked to peanut butter since 2012. This investigation demonstrates the importance of caution with reliance on finished product testing, taking appropriate corrective actions when detection occurs, and potential benefits for industry to incorporate WGS as a tool in their environmental monitoring program. ISSN: 15567125, 15353141

I., Matle, Itumeleng, D.M., Pfukenyi, Davies Mubika, N., Maphori, Nozipho, N., Moatshe, Nkagiseng, T., Nkabinde, Thabo, A., Motaung, Annah, T., Schmidt, Tracy, E.M., Seakamela, Emmanuel M., M.F., Mwanza, Mulunda Feza, L., Ngoma, Lubanza
Monitoring, surveillance, antimicrobial resistance and genetic diversity analysis of non-typhoidal Salmonella in South Africa from 1960–2023 from animal and animal products
(2025) PLOS ONE, 20 (8 August), art. no. e0329061
ABSTRACT: Salmonellosis remains one of the most frequently reported foodborne diseases globally, with the highest burden in low-resource areas. The millions of deaths caused by Nontyphoidal Salmonella (NTS) infections emphasize the urgent need for timely, detailed, and evidence-based interventions to effectively manage and monitor NTS burdens. This study retrospectively analyzed 1,028 NTS isolates from animals, the environment, and food products in South Africa, collected between 1960 and 2023. Among the 102 serotypes identified, S. Heidelberg, isolated only between 2000−2009 and 2020−2023, accounted for 94.3% of isolations during the latter period, suggesting a recent shift in Salmonella

epidemiology in the region. The highest resistance rates were observed for cefoxitin (65.7%), cephalothin (62.8%), and tetracycline (59.8%), with a significant increase in resistance to several antibiotics, including ceftriaxone and aztreonam, from 2010−2023. Genetic analysis revealed that S. Gallinarium had the highest prevalence of antibiotic resistance genes, such as tetA (71.4%), qnrA (64.3%), cat1 (64.3%), bla<inf>PSE</inf> (57.1%), and both bla<inf>CMY-2</inf> and qnrB at 50%. The bla<inf>PSE</inf> and bla<inf>SHV</inf> genes were strongly associated with ceftriaxone resistance in S. Dublin isolates, while bla<inf>PSE</inf> and qnrS were linked to chloramphenicol resistance in S. Enteritidis and S. Dublin isolates. Additionally, 87% of the virulence genes screened were present in over 50% of the serotypes, indicating increased adaptability and potential shifts in disease dynamics. The rise in antimicrobial resistance, driven by antimicrobial misuse, horizontal gene transfer, and biofilm formation, could alter serotype dynamics and changing disease epidemiology. This trend underscores the urgent need for effective antimicrobial stewardship and surveillance to combat the spread of antibiotic resistance in Salmonella populations. ISSN: 19326203

T.P., Oscar, Thomas Patrick
Poultry Food Assess Risk Model for Salmonella and Chicken Gizzards: IV. Consumer Response Step
(2025) Journal of Food Safety, 45 (4), art. no. e70026
ABSTRACT: A Poultry Food Assess Risk Model (PFARM) for Salmonella and chicken gizzards was developed and published in four steps because of its complexity. In the present study, outputs from the first three steps were combined to predict consumer responses of no response, infection, illness, hospitalization, and death. The PFARM found that salmonellosis (illness, hospitalization, or death) was a rare event (15 cases per 100,000 consumers) that occurred by random chance when multiple risk factors occurred together. Sensitivity analysis indicated that the risk factors for salmonellosis were cross-contamination and growth on lettuce, Salmonella serotype and number at consumption, buffering capacity of the meal, and consumer health and immunity. Scenario analysis indicated that initial Salmonella prevalence, number, and serotype changed ($p \leq 0.05$) over time in the simulated production chain but were poor indicators of salmonellosis because they did not consider the identified risk factors for salmonellosis. Based on lessons learned in the COVID-19 pandemic, the economics of salmonellosis, and the results of the current study, it was concluded that the best indicator of poultry food safety was the PFARM prediction of the cases of severe salmonellosis (hospitalization and death) per lot (1000 kg) of chicken gizzards. Interestingly, cases of severe salmonellosis per lot of chicken gizzards did not change across time in the production chain despite significant changes in Salmonella prevalence, number, and serotype at final product testing. This may explain why the current approach to poultry food safety is not reducing rates of foodborne salmonellosis. ISSN: 17454565, 01496085

A., Abrego, Alejandra, B., Wiseman, Barry, S.E., Gragg, Sara Elizabeth
Summarizing the Current knowledge and Existing Knowledge Gaps for Preharvest and Postharvest Salmonella Contamination in Pork
(2025) Journal of Food Protection, 88 (10), art. no. 100609
ABSTRACT: Pork production is one of the most important industries in the world, and ensuring safety in the production chain is crucial for public health. Salmonella presence in pigs and pork products is a significant challenge within the pork industry. Salmonella can contaminate the production chain at any stage, from the farm sites to harvest and final product processing. Different strategies can be used to mitigate Salmonella on the farm and during transportation, lairage, and postharvest; however, despite ongoing improvement of these interventions, many knowledge gaps remain and must be addressed. This review summarizes what is currently published in the literature regarding Salmonella contamination in pigs and pork, including the efficacy of common interventions, and highlights critical knowledge gaps at each production stage. Research recommendations to control Salmonella and enhance food safety and public health are also described herein. ISSN: 19449097, 0362028X

Z., Topalcengiz, Zeynal, S., Chandran, Sahaana, F., Torko, Francis, K.E., Gibson, Kristen E.
Recovery of Salmonella and Listeria monocytogenes from Nonporous Surfaces Based on Surface Sampler Type
(2025) Journal of Food Protection, 88 (10), art. no. 100599
ABSTRACT: Surface sampling devices ranging in material composition and size can be used in environmental monitoring programs. This study aimed to compare the bacterial recovery efficiency of surface samplers on stainless steel (SS) and polypropylene (PP) surfaces.

Separate cocktails of Listeria monocytogenes and Salmonella enterica strains were spot inoculated (1 mL; 40 spots × 25 µL) on SS and PP surfaces at high (7 log) and low (4 log) concentrations. A cellulose sponge sampler, polyurethane foam sponge sampler, and polyolefin nonwoven fabric sampler were utilized for bacteria recovery from SS and PP surfaces at two surface areas: 1× [929 cm2 (144 in2)] and 2× [1858 cm2 (288 in2)]. The effect of prewet volume (5 mL, 10 mL) on bacteria recovery from PP and SS was also investigated with the nonwoven fabric sampler at high inoculum level and 1× surface area. Three experimental trials were conducted totaling 336 samples, and recovery percentages were based on the CFU recovered divided by the initial CFU added to each surface. Statistical analysis was performed to determine whether sampler type, pathogen type, inoculum concentration, surface type, and surface area were significant predictors of recovery percentage. A significant five-way interaction (P = 0.0015) was observed between the predictor variables; therefore, no conclusions can be made regarding the main effects. The recovery percentage of L. monocytogenes was significantly higher than Salmonella from PP surfaces across all three sampler types. For the nonwoven fabric sampler, the 5 mL prewet volume yielded significantly higher recovery (P ≤ 0.05) for both bacteria combined at 10.66% (95% CI: 9.93, 11.44) compared to 3.09% (95% CI: 2.71, 3.52) recovery with the 10 mL prewet volume. However, the effect of volume on recovery depended on the interaction between surface type and inoculum level.
ISSN: 19449097, 0362028X

X., Liu, Xiyang, E.M., Grasso-Kelley, Elizabeth M., A., Lee, Alvin, L., Warda, Lilybell, N.M., Anderson, Nathan M.
Salmonella spp. Inactivation During Hot Air Drying of Apples: Influence of Temperature, Bed Depth, and Air Velocity
(2025) Journal of Food Protection, 88 (10), art. no. 100597
ABSTRACT: Dried fruit has been linked to recalls and outbreaks due to microbiological hazards. While most drying processes are optimized for product quality, microbiological safety may not always be prioritized. The food industry is required to validate process preventive controls to ensure they significantly minimize or prevent microbial hazards. This study aimed to evaluate the combined effects of temperature, drying bed depth, and air velocity on the inactivation of Salmonella on apple cubes. A cocktail of six Salmonella serovars was inoculated onto fresh Gala apple cubes (~0.256 cm3). A single layer of Salmonella-inoculated apple cubes was dyed red and placed atop un-inoculated cubes in a drying chamber to achieve final bed depths of 5.1, 8.9, or 12.7 cm. Apple cubes were dried at 88, 104, or 120 °C with air velocities of 2.10, 2.95, or 3.82 m/s. At multiple time points (n ≥ 5), samples were collected from the inoculated, dyed apple cubes on the top layer for water activity measurement and Salmonella enumeration. Across all drying conditions, an initial stable stage of apple a<inf>w</inf> and Salmonella populations was observed with varying durations followed by a rapid decrease in both. The overall effect of drying temperature, bed depth, and air velocity on microbial inactivation followed a consistent pattern: Higher temperature reduced the drying time required to achieve comparable Salmonella reductions as elevated product temperature enhanced microbial inactivation. Similarly, lower bed depth allowed the thinner apple layers to reach higher temperatures more rapidly, accelerating microbial reduction. Increased air velocity shortened the constant-rate drying period, promoted a faster temperature increase in the apple cubes, and resulted in higher lethality within a shorter drying period. Although a 5-log reduction of Salmonella was achieved at the end of drying under all but one condition, the reductions were reached at varying endpoint water activity levels. ISSN: 19449097, 0362028X

K., Lillepold, Kate, N., Karamehmedovic, Nadja, I., Bujila, Ioana, A., Ohlson, Anna, J., Nederby-Öhd, Joanna, I., Hall, Ingela, G., Ockborn, Gunilla, M., Lindblad, Mats, I., Galanis, Ilias, M., Rehn, Moa
Multi-cluster outbreak of Salmonella Typhimurium sequence type 36 linked to alfalfa sprouts, Sweden, August-November 2024
(2025) Epidemiology and Infection, 153, art. no. e108
ABSTRACT: Salmonella Typhimurium sequence type (ST) 36 is a rare sequence type in Sweden. During August-November 2024, 100 cases of Salmonella Typhimurium ST36 were reported nationwide. The highest proportions of cases were observed among individuals aged 0-10years (17%) and 41-50years (20%), with females representing 65% of the total cases. Microbiological analysis of the S. Typhimurium ST36 isolates identified nine clusters and five individual strains clustering within 53 single-nucleotide polymorphisms. A matched case-control study found cases to be associated with the consumption of alfalfa sprouts (adjusted odds ratio=8.94, 95% CI: 2.96-27.1). Trace-back investigation identified seeds used by two alfalfa sprout producers in Sweden as the likely source of the outbreak, although microbiological analysis of sprouted alfalfa seeds from the producers did not

detect Salmonella. However, continued international investigations further implicated seeds sourced from the same origin, supporting that alfalfa seeds were the ultimate source of the Swedish outbreak. Our investigation and findings indicate that alfalfa sprouts may contain Salmonella and thus pose a health risk to consumers. We emphasize the need for primary producers of alfalfa seeds and sprouts to identify and prevent possible contamination points. ISSN: 09502688, 14694409

A., Kaushik, Abhishek, N.K., Kumra Taneja, Neetu Kumra, K., Chauhan, Komal, H.S., Oberoi, Harinder Singh
Dynamics of mono and dual-species biofilms of Escherichia coli and Salmonella Typhimurium: Interspatial interactions and novel inhibition strategies
(2025) International Journal of Food Microbiology, 440, art. no. 111280
ABSTRACT: Multi-species biofilms in the food industry present significant global health risks, contributing to frequent outbreaks, diseases, and fatalities. This study aimed to characterize the mono- and dual-species biofilms formed by invasive food isolates Escherichia coli EMC17 and Salmonella typhimurium SMC25, focusing on microbial load variations, interspecies interactions, and the exploration of a combinatorial inhibition strategy for biofilm disruption. The highest biofilm density was observed in dual-species cultures at equal inoculum after 96 h, as confirmed by Crystal Violet assay and exopolysaccharide (EPS) production (72 μg/ml). Dual-species biofilms showed total bacterial counts of 7.29 log<inf>10</inf> CFU/cm2 for E. coli EMC17 and 5.95 log<inf>10</inf> CFU/cm2 for S. Typhimurium SMC25, with both strains exhibiting strong multidrug resistance (MDR), as indicated by MAR indices of 0.46 and 0.38, respectively. Epifluorescence and confocal laser microscopy revealed synergistic interactions during dual-species biofilm development, further supported by principal component analysis, which highlighted distinct growth patterns between mono- and dual-species biofilms. Specifically, mono-species biofilms of E. coli EMC17 had a biovolume of 56.70 ± 1.36 μm3/μm2 at 96 h, whereas dual-species biofilms reached 62.61 ± 1.38 μm3/μm2. Additionally, dual-species biofilm-associated cells exhibited significantly enhanced adhesion (16.40 %) and invasion (2.07 %) potential compared to the mono-species biofilms. Furthermore, a combinatorial inhibition strategy using quercetin and citric acid demonstrated synergistic activity against the MDR strains, with fractional inhibitory concentration index (FIC) of <0.5. These findings offer new insights into the dynamics of dual-species biofilms, emphasizing the potential of phytochemical-citric acid combinations as promising alternatives to traditional antibiotics in biofilm management.
ISSN: 01681605, 18793460

J.S., Seixas, Julia Silva, S.M., Hernández, Sonia Maria, K.F., Christie, Katherine F., W.A., Norfolk, William A., R.S., Rozier, Ralph Scott, E.A., Kurimo-Beechuk, Elizabeth A., L.A., Hoopes, Lisa A., M.J., Yabsley, Michael J., E.K., Lipp, Erin K.
Salmonella infections in white ibis nestlings in urban areas as a result of environmental contamination reveal a potential health risk to humans and animals
(2025) Journal of the American Veterinary Medical Association, 263 (9), pp. 1077 - 1084
ABSTRACT: Salmonella is an important zoonotic pathogen of wildlife and humans. Adult white ibis (Eudocimus albus), an abundant bird in urbanized landscapes in Florida, have a high Salmonella prevalence (26%). Salmonella surveillance of nestlings improves our understanding of transmission and infection dynamics and disease risks. To determine Salmonella epidemiology in ibis nestlings, 2 studies were conducted. First, 24 free-living ibis chicks were captured for an experimental infection trial to evaluate susceptibility and clinical outcome. Most (58%) were shedding Salmonella at capture, but prevalence decreased to zero. After there were no Salmonella detections for 5 weeks, the chicks were inoculated with 106 Salmonella Typhimurium. Seven had evidence of inoculation: 3 of 7 (42.8%) shed at 1 day following inoculation and 1 of 7 (14.2%) at 5 days following inoculation. Only 1 bird developed clinical signs for approximately 24 hours. Second, the Salmonella prevalence between free-living nestlings from 1 urban and 2 natural rookeries were compared. Weekly sampling from hatch until fledging revealed Salmonella shedding up to 22 days. Salmonella prevalence was higher in the urban nestlings. Thirty-two serotypes were detected; Salmonella Rubislaw and Salmonella Reading were the most common, and 19% and 13% of serotypes were in the top 10 and 20 responsible for human cases in the US, respectively. These studies show an absence of clinical disease with Salmonella infection in young birds and the demographic and anthropogenic factors that impact Salmonella shedding, relevant at the human-wildlife interface. An important aspect of Salmonella epidemiology is environmental persistence, which is addressed in a companion Currents in One Health by Perez et al, AJVR, June 2025. This record is sourced from MEDLINE/PubMed, a database of the U.S. National Library of Medicine
ISSN: 1943569X, 00031488

G., de Lorenzi, Giorgia, Y., Gherpelli, Yuri, E., Scaltriti, Erika, C., Bracchi, Chiara, M., Vinci, Massimiliano, L., Bolzoni, Luca, S., Pongolini, Stefano, P., Bonilauri, Paolo, P., Bassi, Patrizia, I., Barbieri, Ilaria
Antimicrobial resistance in Salmonella enterica serovar Choleraesuis isolated from pigs in northern Italy
(2025) Research in Veterinary Science, 193, art. no. 105773
ABSTRACT: Salmonella enterica subspecies enterica serovar Choleraesuis (S. Choleraesuis) is a pathogen known to cause severe systemic infections in pigs and occasionally in humans. Despite the relevance of S. Choleraesuis due to its re-emergence in pig herds in recent years in the EU, little is known about its antibiotic resistance profile. The aim of this study was to evaluate the antimicrobial susceptibility of 188 S. Choleraesuis strains isolated from clinically diseased pigs in Northern Italy between 2022 and 2024. Antimicrobial susceptibility testing to a panel of antimicrobials was evaluated using the Minimal Inhibitory Concentration (MIC) method according to CLSI procedures. Phenotypic resistances to sulfisoxazole (90.2 %), ampicillin (85.0 %), enrofloxacin (83.5 %), florfenicol (73.9 %), tetracycline (71.3 %), trimethoprim-sulfamethoxazole (59.1 %) and flumequine (44.2 %) were the most frequently observed in the S. Choleraesuis population. Among the 188 strains, 59 isolates of S. Choleraesuis displaying multidrug-resistant (MDR) profiles were subject to Whole Genome Sequencing in order to detect possible genetic determinants responsible for the observed MDR profiles and to evaluate the correspondence between the observed phenotypic resistance to antimicrobials and the in-silico prediction. The most frequently detected genetic determinants in the MDR isolates were blaTEM-1B, tet(A), floR, sul2 and sul1. A strong agreement between phenotypic and genotypic resistance for ampicillin, florfenicol, tetracycline and sulfamethoxazole was observed, while low agreement was observed for colistin and trimethoprim-sulfamethoxazole. While similar investigations have been extensively conducted for other Salmonella serotypes, data on antimicrobial resistance in S. Choleraesuis are still limited. Therefore, further studies are needed to better understand antimicrobial resistance in this serotype. ISSN: 00345288, 15322661

J.A., Byrd, James Allen, S., Faust, Sarah, D.Y., Caldwell, Denise Y., C.L., Swaggerty, Christina L., K.J., Genovese, Kenneth James, M.H., Kogut, Michael H., A.V., Carlson, Anna V., C.N., Johnson, Casey N., T.L., Poole, Toni L., K.N., Norman, Keri N.
Recovery of Salmonella from alternative anatomical sites after an oral challenge with three different Salmonella serotypes in turkeys
(2025) Poultry Science, 104 (9), art. no. 105406
ABSTRACT: The poultry cecum is considered the “gold standard” for detecting Salmonella in poultry because it has the largest concentration of Salmonella in the bird. The current study investigated alternative anatomical sampling locations for detecting Salmonella in preharvest turkeys. In this study, 36-day-old turkeys were challenged with a cocktail of Salmonella Heidelberg, S. Reading, and S. Infantis by oral gavage (N = 78). The birds were sampled on Day 0-, 6-, 9- and 12-days post-challenge. Across all serotypes, total Salmonella recovery from the different anatomical locations was significantly higher in samples taken from the cloaca, crop, vent feathers, and foot pad samples when compared to the cecal samples ($P < 0.05$). Similarly, Salmonella results for individual serotypes demonstrated a higher recovery of S. Reading and S. Infantis within the cloaca, and vent feathers samples compared to the ceca. Salmonella Heidelberg recovery was significantly higher in the joints, and bone marrow when compared to the cecal samples. Study results demonstrate that Salmonella can spread systemically in turkeys without demonstrated morbidity and can be recovered at other anatomical locations at higher rates than found in ceca. In addition, Salmonella serotypes translocated differently within the bird and can be recovered at different anatomical locations. ISSN: 00325791, 15253171