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Prevalence of antimicrobial resistance in Campylobacter spp. and Salmonella spp. in Switzerland 2007–2022: a retrospective observational study

Frederik Jung[1], Deborah R. Vogt[2], Roger Stephan[3], Andreas Kronenberg[4], Adrian Egli[1,2], and the Swiss Antibiotic Resistance Centre ANRESIS[4]

1 Institute of Medical Microbiology, University of Zurich, Zurich, Switzerland; 2 Department of Clinical Research, University of Basel, University Hospital Basel, Basel, Switzerland; 3 Institute for Food Safety and Hygiene, Swiss National Reference Centre for Enteropathogenic 10 Bacteria and Listeria (NENT), Vetsuisse, University of Zurich, Zurich, Switzerland; 4 Swiss Centre for Antibiotic Resistance, University of Bern, Berne, Switzerland

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Correspondence
Prof. Adrian Egli, MD PhD
aegli[at]imm.uzh.ch

Summary

BACKGROUND: In Switzerland, acute infectious diarrhoea is frequently caused by Campylobacter spp. and Salmonella spp. The rise of antimicrobial resistance complicates treatment and underscores requirements for continuous surveillance. We aimed to analyse the development of antimicrobial resistance in Campylobacter spp. and Salmonella spp. isolated from human samples in Switzerland over time.

METHODS: We conducted a retrospective observational analysis using the ANRESIS database, covering the period from January 2007 to December 2022. The study included 47,498 Campylobacter spp. isolates and 5964 Salmonella enterica isolates. Antimicrobial resistance was categorised according to CLSI or EUCAST. Descriptive statistical analyses were performed to explore resistance over time, focusing on pathogens and invasive versus non-invasive isolates.

RESULTS: The majority of Campylobacter isolates were Campylobacter jejuni (80.4%) and Campylobacter coli (7%). Resistance to ciprofloxacin in Campylobacter jejuni increased from 38% in 2007 to 81% in 2022. Resistance to doxycycline and tetracycline also rose sharply between 2012 and 2014, reaching approximately 37% by 2022. Resistance to macrolides remained consistently low (<1%) throughout the study period. Campylobacter coli exhibited higher resistance levels compared to Campylobacter jejuni, with notable increases in resistance to ciprofloxacin (73%) and macrolides (approximately 15%) by 2022.

Non-typhoidal Salmonella accounted for 95.4% of all Salmonella isolates, with serovars Enteritidis (32%) and Typhimurium (15%) being most prevalent. Resistance to ciprofloxacin/norfloxacin was observed in about 10% of isolates, with an increase noted around 2013–2014. High resistance levels were found for amoxicillin/ampicillin (23%) and gentamicin (70%), while resistance to third- and fourth-generation cephalosporins and carbapenems remained low (<1%). A decline in nitrofurantoin resistance was also observed over time.

CONCLUSIONS: The increasing prevalence of antimicrobial resistance in Campylobacter spp. and Salmonella spp. in Switzerland emphasises the critical need for ongoing surveillance and judicious antibiotic use.

Introduction

Acute infectious diarrhoea is a prevalent illness globally and in Switzerland, attributed to different gastrointestinal pathogens, including *Campylobacter* spp. and *Salmonella* spp., which are among the most relevant bacteria associated with foodborne diseases [1-3]. Nutritional risk behaviours have linked *Campylobacter* spp. infections to seasonal traditions, such as consumption of fondue with chicken meat in Switzerland or Germany during the holiday season [4]. In Switzerland, the Federal Office of Health documents approximately 7000–8000 cases of *Campylobacter* and 1200–

1500 *Salmonella* infections every year with a typical seasonal pattern [5]. It is estimated that the total Swiss healthcare costs resulting from Campylobacteriosis amount to €29–45 million annually [6].

Some episodes with *Campylobacter* spp. and *Salmonella* spp. infections may progress to bacteraemia and sepsis. This happens more commonly in susceptible populations, such as the elderly, young children or in the presence of comorbidities [1, 7]. Invasive infection is associated with substantial morbidity and mortality [8]. Besides pathogen-associated virulence, antimicrobial resistance is an increasing concern for both species [9-11]. A recent Swiss study included genomes of 340 *Campylobacter jejuni* isolates over 18 years and revealed high genetic diversity, with recurring multilocus sequence types (ST) and clonal complexes linked to antimicrobial resistance. The increasing prevalence of quinolone and tetracycline resistance was associated with specific genomic mutations in the *gyrA* (T86I) and *tet(O)* genes, alongside the discovery of a novel chromosomal cassette carrying multiple resistance genes, highlighting the pathogen's evolving genomic adaptations [12]. Macrolides and fluoroquinolones are the preferred medications for the treatment of potentially infectious diarrhoea when pharmacological intervention is necessary [13].

The emergence of antimicrobial resistance also emphasises the need for accurate and rapid pathogen identification and resistance profiling for effective patient management. Identification of the infection source is critical for foodborne pathogens, especially as there is barely any direct human-to-human transmission. The "One Health" approach, recognising the interconnection between human, animal and environmental health, is critical in locating sources of infection and antimicrobial resistance spread [14, 15]. The complexity highlights the benefit of coordinated and collaborative efforts among farms, veterinarians, medical professionals and public health experts to devise and implement strategies to mitigate resistance development [16].

A critical aspect of such coordinated efforts is access to antimicrobial resistance data. The ANRESIS (Swiss Centre for Antibiotic Resistance) platform is Switzerland's national surveillance programme for antibiotic resistance and consumption [17]. ANRESIS provides a wealth of antibiotic susceptibility test results from a network of human and veterinary laboratories, covering a substantial proportion of the Swiss population. ANRESIS currently includes around 40 human and 10 veterinary laboratories. The goals of this network are to continuously monitor antibiotic resistance, to provide reliable data for research and public health and to support national strategies aimed at controlling resistant pathogens. Using ANRESIS data, we can facilitate comprehensive trend analyses and inform public health strategies to combat the spread of, for example, resistant foodborne pathogens in Switzerland [34].

We aimed to analyse the development of antimicrobial resistance in *Campylobacter* spp. and *Salmonella* spp. isolates from diseased humans in Switzerland over a 15-year time span. As a secondary endpoint, we compared resistance patterns between invasive isolates.

Methods

Study design

We conducted a retrospective observational study, focusing on antimicrobial resistance and associated metadata collected on the ANRESIS platform. We reutilised these anonymised data for our research project after approval by the ANRESIS board. The study spans data collected from January 2007 to December 2022.

Our objectives are structured to methodically investigate (i) the prevalence and (ii) the dynamics of antimicrobial resistance in *Campylobacter* spp. and *Salmonella* spp. We focused on pathogen distribution over time and profiles in invasive isolates.

We carried out quantitative analyses of categorical resistance frequencies, leveraging statistical models to explore correlations with sample origin.

The ethics of our study were evaluated and approved by the Nordwest- und Zentralschweiz Ethics Committee (BASEC Nr. Req 2018-00728 and 2020-00033). For the analysis, we only used anonymised data.

Data collection

We accessed the data including *Campylobacter* spp. and *Salmonella* spp. isolates originating from human samples and tested for antimicrobial susceptibility across the whole ANRESIS database. We treated repeat isolates and differentiated infection episodes according to a predetermined principle. Duplicates (same microorganism, same patient) within 92 days were excluded from analysis.

The individual samples are the relevant unit for the analysis of *Campylobacter* and *Salmonella* species distribution (objective A). Each sample is considered a separate infection event. The separate antibiotic tests are the relevant unit for the analyses of antibiotic resistance (objectives B and C). The dataset includes 13 identified *Campylobacter* species (and subspecies), plus samples with identification to the genus level only (*Campylobacter* sp.).

The objectives of this study are:

– To describe the frequency distribution of all included *Campylobacter* species and *Salmonella* species over time.
– To describe the temporal trends of antibiotic resistance of *Campylobacter* spp. and *Salmonella* spp.
– To describe the antibiotic resistance profiles of *Campylobacter* spp. and *Salmonella* spp. in invasive samples.

For *Campylobacter* spp., we started with a set of 47,498 isolates from 46,458 patients, including 143,588 antimicrobial susceptibility tests. We excluded isolates with species other than *Campylobacter jejuni* or *Campylobacter coli*. In the final analysis, we ended up with data of 41,559 isolates from 40,709 patients including 126,798 antibiotic susceptibility tests (figure 1). For *Salmonella* spp., we started with a set of 9,389 isolates from 8,136 patients, including 104,711 antibiotic susceptibility tests. Isolates without identification of the serovar or serogroup ("*Salmonella* species", "*Salmonella* subsp. *enterica*" and "*Salmonella* subsp. *enterica* monophasic") were assigned to the group of non-typhoidal *Salmonella* and were excluded from further analysis (figure 2).

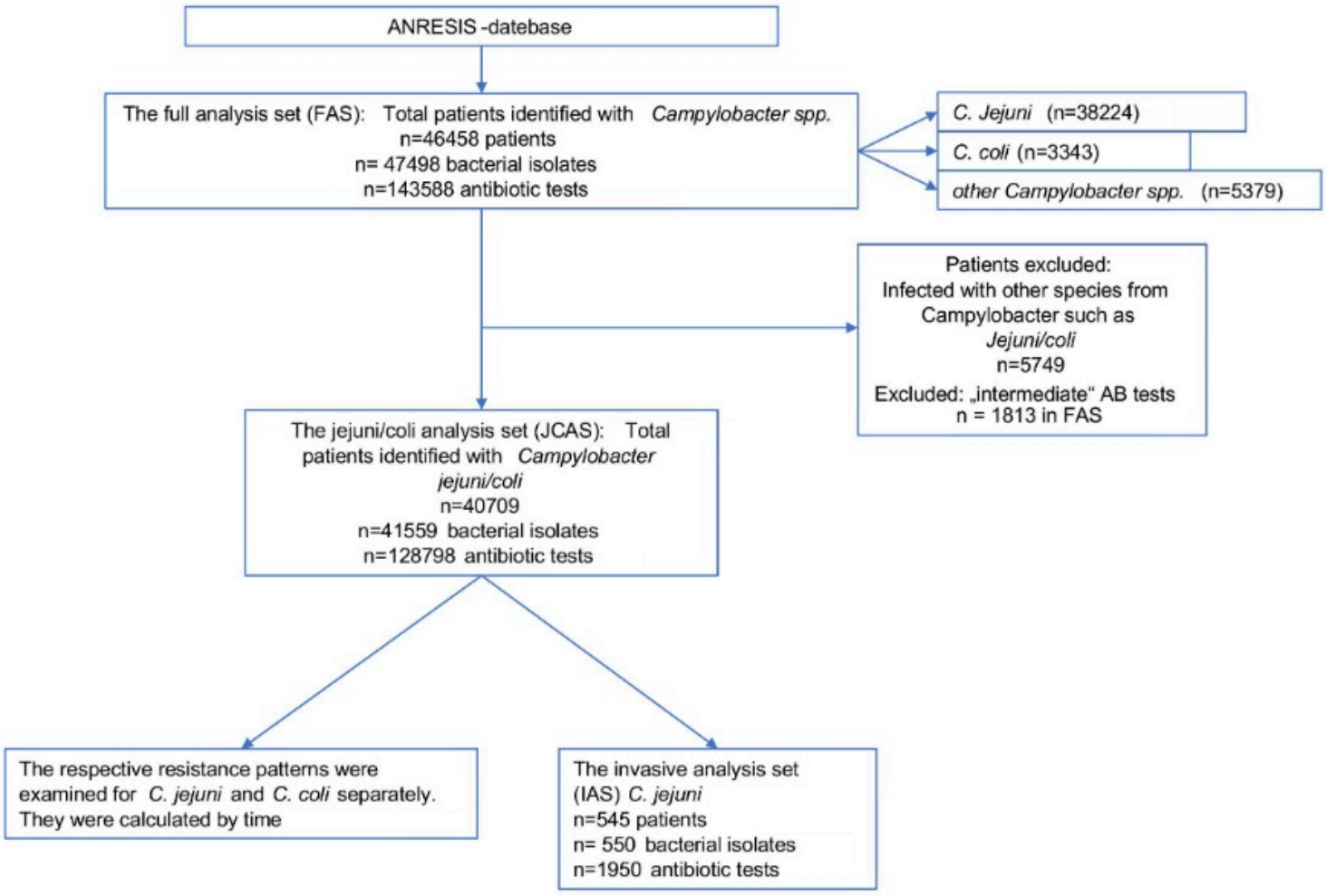


Figure 1: Flowchart of Campylobacter spp. analysed.

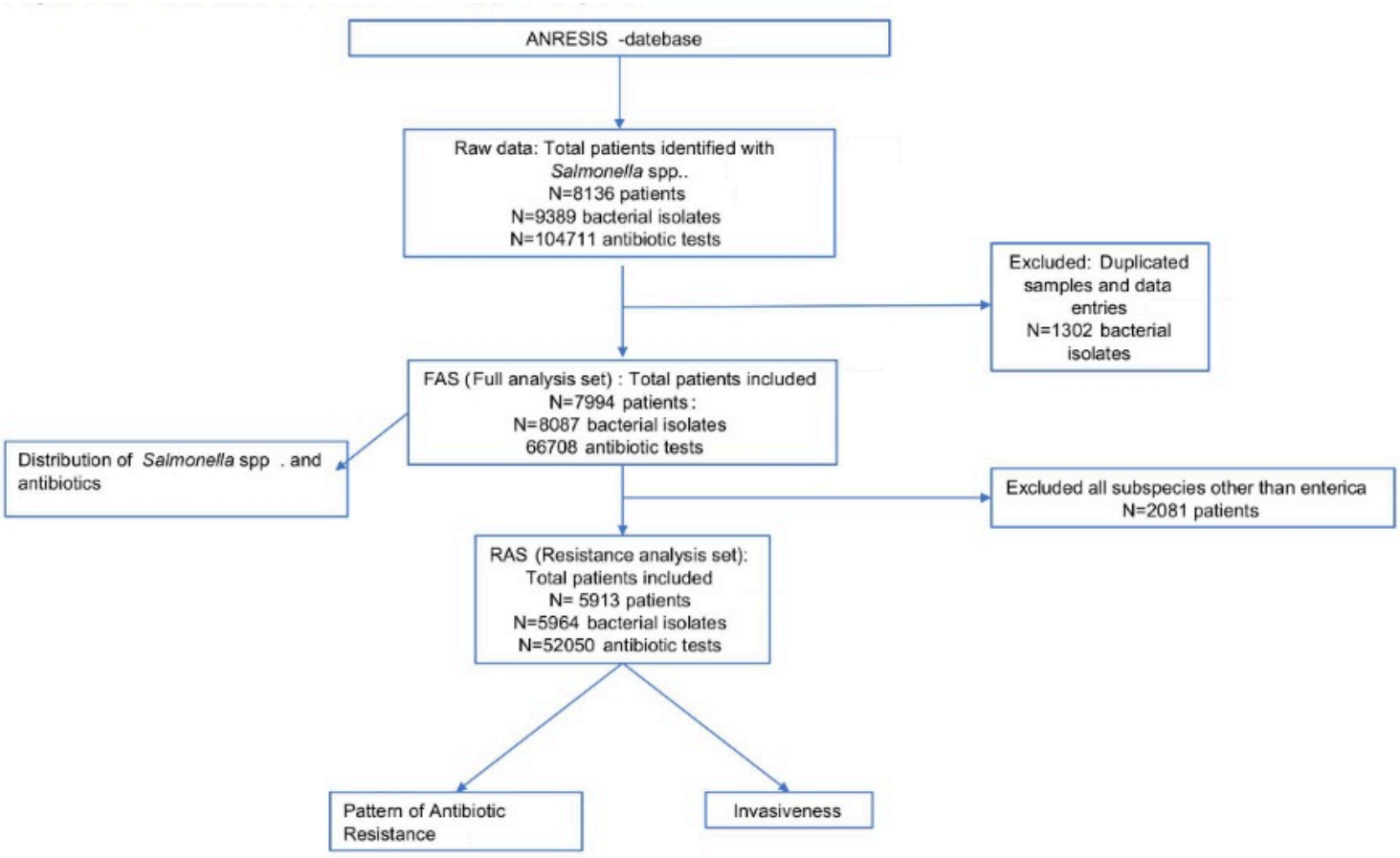


Figure 2: Flowchart of Salmonella spp. analysed.

Antibiotic resistance

Antimicrobial susceptibility testing was performed according to the guidelines of the Clinical and Laboratory Standards Institute (CLSI) or the European Committee on Antimicrobial Susceptibility Testing (EUCAST). Most laboratories switched from CLSI to EUCAST breakpoints between 2011 and 2013 [18]. The categories “intermediate” and “susceptible” were combined into “nonresistant”.

Invasiveness

Invasive isolates were defined as samples from primarily sterile body sites, including blood cultures, cerebrospinal fluid and deep tissue, in contrast to non-sterile body sites such as stool or skin.

Statistical analysis

The outcome of primary interest is antibiotic resistance (binary variable). Results of the antibiotic susceptibility tests (original variable “DELIVERED_QUALITATIVE_RES”) are categorised as “susceptible” (can be treated with the antibiotic), “intermediate” (may be treatable with the antibiotic, but may require adjusted dosage) or “resistant” (cannot be treated with the antibiotic). The categories “intermediate” and “susceptible” were combined into “nonresistant”. “Invasiveness” (binary variable, derived from original variable “LOCATION_IS_STERILE”) indicates whether the sample originates from a sterile site (abscess, blood culture, biopsy, bone, lung, device, peritoneal fluid, pleural fluid, synovial fluid, cerebrospinal fluid, urine punction, “urine-sing-cath”) or not.

All analyses are descriptive and exploratory in nature. Relative resistance was calculated as the number and proportions of resistant isolates in relation to tested isolates. Proportions are indicated with exact 95% confidence intervals calculated using the Pearson-Clopper method. These analyses are based on the JCAS (The jejuni/coli analysis set) and RAS (Resistance analysis set).

All analyses were conducted using the statistical software package R, version 4.3.1 [19].

Results

Within all *Campylobacter* spp., *Campylobacter jejuni* dominated with 38,224 (80.4%) isolates. *Campylobacter coli* consisted of 3343 (7%) isolates. In the older data from 2007 to 2011, we noted that 5379 (39.9%) isolates were without classified species. All *Campylobacter non-jejuni* and *non-coli* species were rare. Of these, *Campylobacter fetus* was the most abundant species with a median of 17 isolates per year.

Within all *Salmonella* spp., we focused our analysis on the *Salmonella enterica* dataset and included 5964 isolates from 5913 patients with a total of 52,050 antibiotic susceptibility tests. In total, 277 (4.6%) of the *Salmonella enterica* isolates were identified as typhoidal *Salmonella*. Among *Salmonella enterica* serovars, Enteritidis is the most prevalent at 32% and Typhimurium at 15%. We noted an increase in the number of non-typhoidal *Salmonella* by more than 50% from 2015 (n = 343) to 2022 (n = 534), especially with serovars other than Enteritidis or Typhimurium, while typhoidal *Salmonella* counts have stayed low and steady.

Overall antibiotic resistance patterns

Changes in EUCAST breakpoint values for several antibiotics have led to significant shifts in reported resistance patterns. However, these changes result solely from breakpoint revisions rather than bacterial adaptation. (A comprehensive overview of the EUCAST breakpoints used in this study can be found in the Excel file provided as supplementary material.)

Figure 3 shows the percentage of resistant *Campylobacter jejuni* isolates of frequently tested antibiotics.

We observed an increase in resistance over time for quinolones from 38% (95% CI: 34.8–41.4) in 2007 to 80.9% (95% CI: 79.1–82.5) in 2022.

For doxycycline and tetracycline, we observed a particular sharp rise between 2012 and 2014, starting with 9.3% (95% CI: 5.7–14.8) and 18.2% (95% CI: 14.9–22.1), respectively, in 2007 and ending with 37% (95% CI: 33.6–40.5) and 36.7% (95% CI: 33.1–40.4), respectively, in 2022. Resistances to azithromycin, clarithromycin and erythromycin were stable over time, at around 1%.

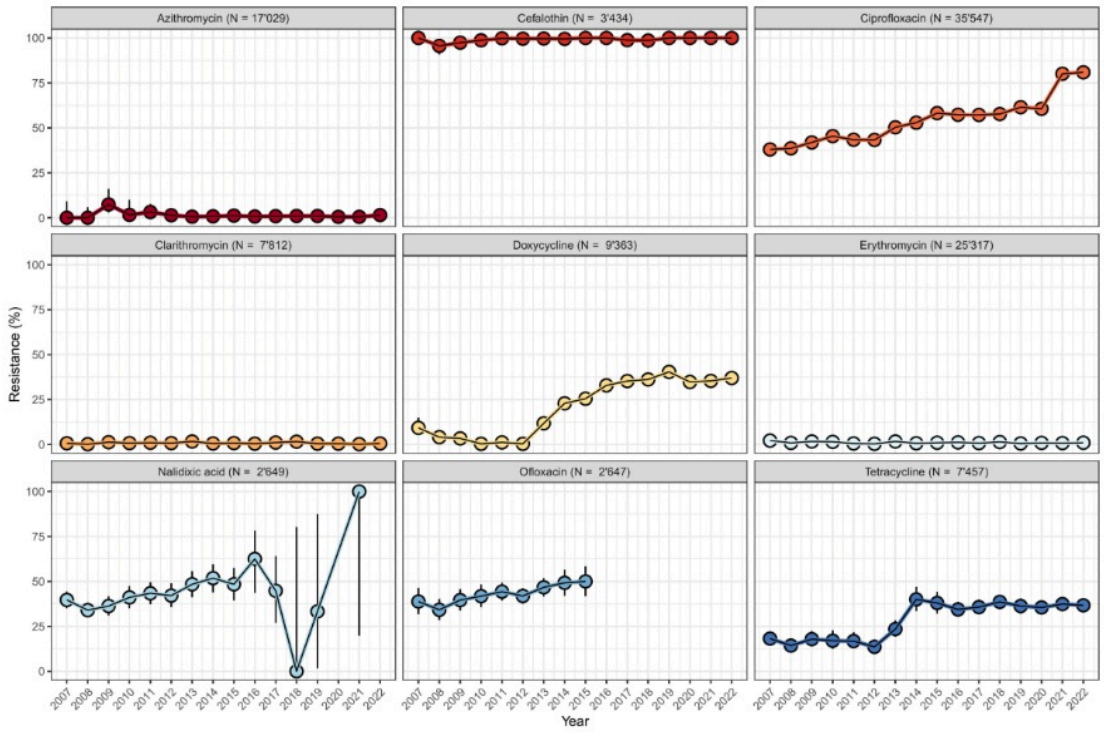


Figure 3: Antimicrobial resistance in Campylobacter jejuni. Antimicrobial resistance (% of resistant isolates) according to year. Error bars indicate 95% confidence intervals. n = number of isolates analysed in the observation period.

Supplementary figure 3 depicts the resistance patterns of *Campylobacter coli* against frequently tested antibiotics. The resistance profile of Campylobacter coli largely mirrored that of Campylobacter jejuni, albeit with generally higher resistance levels. During the entire period examined, the resistance rates observed were as follows: clarithromycin at 17.3% (95% CI: 14.3–20.7), azithromycin at 13% (95% CI: 11.3–14.9) and erythromycin at 14.3% (95% CI: 12.8–15.8). A slight increase in these resistance rates can be observed over time. An upward trajectory in resistance levels, particularly for ciprofloxacin (73.3% [95% CI: 71.7–74.9]), was observed. We noted an increasing resistance to ciprofloxacin starting in 2010, with a marked rise in 2022.

Figure 4 shows the percentage of resistant *Salmonella enterica* isolates of frequently tested antibiotics. Cefotaxime, ceftazidime, ceftriaxone and cefepime showed an average resistance of 1% (95% CI: 0.8–1.2). There were high levels of resistance against amoxicillin/ampicillin, at 23.4% (95% CI: 22.4–24.5), and virtually no resistance observed against ertapenem, imipenem and meropenem, 0% (95% CI: 0–0.1). Ciprofloxacin/norfloxacin showed resistance of 9.9% (95% CI: 9.3–10.6). We noted an increase in 2013 and 2014. The temporal trends also revealed a notable decline in azithromycin, clarithromycin and erythromycin resistance, transitioning from complete resistance to none.

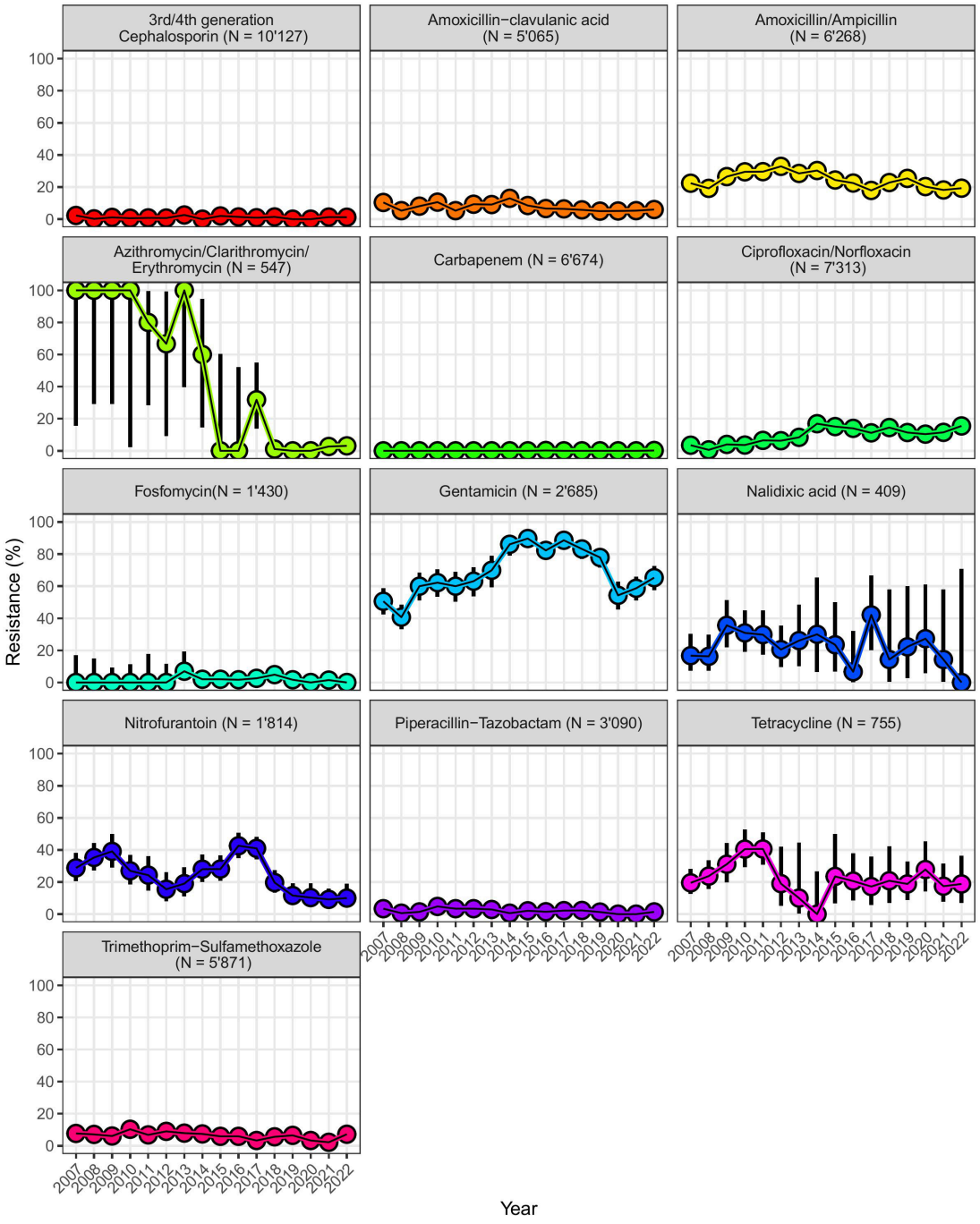


Figure 4: Antimicrobial resistance of Salmonella spp. Antimicrobial resistance (% of resistant isolates) according to year. Error bars indicate 95% confidence intervals. n = number of isolates analysed in the observation period.

Resistance to gentamicin was most pronounced, at 70.4% (95% CI: 68.6–72.1). Resistance to fosfomycin was lower, at 2% (95% CI: 1.3–2.8). Over the entire study period, 480 of 1,814 isolates tested for nitrofurantoin were resistant (26.5%; 95% CI: 24.4–28.6%).

Overall rates of resistance averaged over the total measured period were slightly higher in typhoidal *Salmonella*.

Antibiotic resistance in invasive isolates

For *Campylobacter*, 550 isolates from invasive sites (blood culture, fluid, biopsy, swab and swab/biopsy) were collected from 545 patients. A total of 1950 antibiotic test results were available. Our analysis showed that the resistance rates observed in invasive *Campylobacter jejuni* closely match those identified in the broader dataset. In 2020–2022, recommended azithromycin showed resistance of 1.5% (95% CI: 1.2–1.9) for non-invasive and 0% (95% CI: 0–6.5) for invasive isolates. For ciprofloxacin, the non-invasive and invasive isolates showed 74.1% (95% CI: 73.1–75) and 55.6% (95% CI: 51.1–60) resistance, respectively.

For *Salmonella enterica*, a majority (n = 4640, 78%) of the isolates were sourced from the gastrointestinal tract, followed by blood culture (n = 833, 14%). Figure 2 did not show a clear upward trajectory of antimicrobial resistance. The strong fluctuation in *Salmonella* with azithromycin/clarithromycin/erythromycin resistance is due to the very low number of tests performed up to 2017.

The resistance rates are slightly increased for the invasive ones.

Discussion

Increasing resistance trends highlight challenges in infection management

The data presented illustrate a clear upward trajectory of antimicrobial resistance for some of the antibiotics tested in *Campylobacter* spp. and *Salmonella* spp., across a time span of over a decade and a half in Switzerland. Although *Campylobacter jejuni* remains the most frequently encountered species, and certain *Salmonella enterica* serovars continue to dominate, the broader trend indicates that resistance to several commonly used antibiotics is increasing. These observations highlight the complexity of controlling foodborne infections in both clinical and public health settings. A critical interpretation of these findings suggests that evolving resistance patterns are likely driven by multiple factors, including antibiotic consumption in human and veterinary medicine, as well as the transmission dynamics within and between animal reservoirs. Despite variations in clinical practice and public health policies among European countries, Switzerland's data largely echo international trends, where fluoroquinolone and tetracycline resistance in *Campylobacter* and reduced fluoroquinolone susceptibility in *Salmonella* are documented worldwide [12, 20, 21]. The modest but persistent presence of macrolide resistance, particularly in *Campylobacter coli*, further emphasises that complacency about these agents is risky. Even if current macrolide resistance levels appear relatively low, vigilant surveillance and judicious prescribing are key to preventing the rapid emergence of resistance in this critical drug class. Due to excessively high resistance rates, testing of nalidixic acid and ofloxacin declined substantially from 2015 onwards [22].

Implications of rising antimicrobial resistance for treatment and surveillance

From a clinical standpoint, these trends challenge some traditional empirical therapies. For instance, the high rate of fluoroquinolone resistance in *Campylobacter* increasingly limits the utility of these agents as first-line treatments, leaving macrolides as a mainstay for severe infections. Similarly, for *Salmonella*, the finding that resistance to fluoroquinolones is steadily inching upwards has direct therapeutic repercussions, particularly for invasive disease in high-risk populations. Meanwhile, other antibiotics, such as fosfomycin and nitrofurantoin, remain useful in particular contexts (e.g. urinary tract infections), yet their routine application to gastrointestinal or systemic disease is limited [23, 24]. This scenario highlights the importance of context-specific prescribing and the need to maintain a diverse arsenal of treatment options that remain effective. Another dimension of concern is the potential underestimation of the actual burden of resistant infections [25]. Surveillance data are almost exclusively drawn from individuals who seek medical care and from laboratories that participate in national reporting systems. Mild or self-limited cases of gastroenteritis often go untested, and the data are further shaped by the diagnostic habits and reporting thresholds of participating institutions [26]. Consequently, the current estimates may represent only the tip of the iceberg, and true community-level resistance rates might be different. This underreporting can lead to an attenuation of public health responses if policy decisions rely strictly on these laboratory-confirmed cases.

The One Health approach as a key strategy in the fight against antibiotic resistance

The observed differences in antimicrobial resistance profiles between *Campylobacter jejuni* and *Campylobacter coli* have broader ecological and economic implications. In agricultural settings, the selective pressures from prophylactic and therapeutic antibiotic use in livestock can propagate resistant strains that contaminate food products or the environment [27, 28]. Integrating veterinary surveillance data on *Campylobacter* and *Salmonella* with human clinical isolates would provide more robust evidence to guide interventions aimed at reducing resistance across the entire chain of transmission. Such an integrated, multidisciplinary framework, commonly referred to as the One Health approach, recognises that improving agricultural practices, ensuring responsible antibiotic use in veterinary medicine and promoting safe food handling are complementary and essential strategies for addressing antimicrobial resistance.

Future challenges and opportunities in diagnostics and therapy

Looking ahead, several areas merit further investigation. First, there is a need to unravel the genetic underpinnings of emerging resistance mechanisms within these pathogens, which may reveal opportunities for novel diagnostics or antimicrobial agents [16, 28, 29]. Second, more extensive testing of alternative antibiotics, such as macrolides in *Salmonella* or newer drug classes, can identify additional therapeutic options and mitigate the risk of overdependence on a narrow range of agents. A problem could be increasing evaluation with panel PCRs. Here, reference laboratories may need to test a representative sample set throughout the country. Third, expanding the surveillance network to include more outpatient clinics, private laboratories and veterinary settings would help capture a broader cross-section of the population and provide more-representative data on resistance dynamics.

Changed resistance trends due to the switch from CLSI to EUCAST thresholds

Although this study provides valuable insights into antimicrobial resistance trends in Campylobacter and Salmonella, it nevertheless has several limitations. First, the data stem from a retrospective observational analysis of laboratory-confirmed cases; consequently, underreporting of milder or self-limiting infections is inevitable, and community-level resistance rates may be different than estimated. Second, the shift from CLSI to EUCAST breakpoints during the study period may have artificially influenced observed resistance trends [18].

An example of this is the revision of EUCAST breakpoint values for several antibiotics. These adjustments primarily took place in 2013–2015 and in 2021. As a result, reported resistance patterns have changed significantly. However, this is solely due to the modification of breakpoint values and not to an actual adaptation of the bacteria [30-33].

Methodological strengths and limitations of surveillance data

Fourth, the dataset relies on results reported by a network of participating laboratories, each potentially using different testing panels or methodologies (e.g. the choice of specific antibiotic discs or automated systems), which can introduce heterogeneity.

Finally, although the surveillance system captures a large portion of hospitalised cases, it also includes a growing number of outpatient samples, making it more representative of the broader Swiss population compared to many other countries. This strengthens the generalisability of our findings, as ANRESIS provides a comprehensive overview that covers both inpatient and outpatient settings.

Joint action is key to containing antibiotic-resistant pathogens

In conclusion, this study adds to a growing body of evidence that foodborne bacterial pathogens in Switzerland, while comparatively low in some forms of resistance relative to global hotspots, are nonetheless trending towards more problematic resistance profiles. Coordinated and sustained efforts involving clinicians, microbiologists, veterinarians, farmers and policymakers are vital to preserve the effectiveness of existing antibiotics and to safeguard public health. A strong commitment to prudent antibiotic stewardship, alongside comprehensive surveillance that spans humans, animals and the environment, offers the best path forward for containing the spread of resistant *Campylobacter* and *Salmonella* strains.

Data availability statement

The raw data of the study can be provided upon request.

Notes

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https://www.anresis.ch/de/antibiotikaresistenz/laboratorien

Author contributions: AE designed the study, discussed the data, edited the first version manuscript and follow-up version; FJ wrote the draft, analysed the data and conducted the literature review; AK continually provided content and structural input throughout the entire process and was also the contact person and head of the ANRESIS database. DRV planned and performed the data analysis and edited the manuscript; RS was involved in the idea and the first steps of the work and edited the manuscript.

Use of AI: During the revision of this manuscript, the authors used ChatGPT (OpenAI) to assist with English language editing and phrasing. All suggested changes were reviewed and approved by the authors, who take full responsibility for the content of the manuscript.

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Potential competing interests

All authors have completed and submitted the International Committee of Medical Journal Editors form for disclosure of potential conflicts of interest. No potential conflict of interest related to the content of this manuscript was disclosed.

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Supplementary file

A comprehensive overview of the EUCAST breakpoints used in this study can be found in the Excel file available for download as a separate file at https://doi.org/10.57187/4615.

Appendix

Table S1: Selection criteria for isolates included in the study

Scenario	Criteria for Selection
Multiple isolates per patient within 92 days	Select the first isolate (earliest date). Later isolates are considered duplicates and discarded.
Multiple isolates per patient on the same day	1. If both resistant and sensitive findings for the same antibiotic, select the resistant finding.
	2. If classified as both inpatient and outpatient, select the isolate from inpatient.
	3. If isolates are from both invasive and non-invasive sites, select the isolate from the invasive site.
Multiple isolates per patient more than 92 days apart	Treat as two separate episodes. Select:
	The first isolate of the first episode (earliest date).
	The first isolate of the second episode (earliest date more than 92 days after the earliest date of the first episode).
	If multiple isolates per episode or on the same day, follow the criteria above for selection.

Table S2: EUCAST Clinical Breakpoint Tables v. 14.0, valid from 2025-01-01

Campylobacter jejuni and *Campylobacter coli* and *Salmonella spp.*: ***[33]***

A comprehensive overview of the EUCAST breakpoints used in this study can be found in the Excel file provided as Supplementary Material.

Table S3: Resistance pattern in years 2020-2022 regarding antibiotics according to *Campylobacter* invasive.

invasive.fac	antibiotic	n	res	prop.out
non-invasive	Azithromycin	5758	89	1.5 [1.2, 1.9]
non-invasive	Cefalothin	418	418	100 [99.1, 100]
non-invasive	Ciprofloxacin	7883	5839	74.1 [73.1, 75]
non-invasive	Clarithromycin	1632	30	1.8 [1.2, 2.6]
non-invasive	Doxycycline	2594	962	37.1 [35.2, 39]
non-invasive	Erythromycin	6135	128	2.1 [1.7, 2.5]
non-invasive	Nalidixic acid	2	2	100 [15.8, 100]
non-invasive	Tetracycline	2201	849	38.6 [36.5, 40.6]
invasive	Azithromycin	55	0	0 [0, 6.5]
invasive	Cefalothin	6	6	100 [54.1, 100]
invasive	Ciprofloxacin	149	101	67.8 [59.6, 75.2]
invasive	Clarithromycin	39	0	0 [0, 9]
invasive	Doxycycline	29	13	44.8 [26.4, 64.3]
invasive	Erythromycin	162	3	1.9 [0.4, 5.3]
invasive	Nalidixic acid	1	1	100 [2.5, 100]
invasive	Tetracycline	100	35	35 [25.7, 45.2]

Table S4: Resistance pattern in years 2020-2022 regarding antibiotics according to *Salmonella* invasive.

invasive.fac	antibiotic	n	res	prop.out
non-invasive	3rd/4th generation Cephalosporin	1965	17	0.9 [0.5, 1.4]
non-invasive	Amoxicillin-clavulanic acid	1049	60	5.7 [4.4, 7.3]
non-invasive	Amoxicillin/Ampicillin	1344	264	19.6 [17.5, 21.9]
non-invasive	Azithromycin/Clarithromycin/Erythromycin	295	6	2 [0.7, 4.4]
non-invasive	Carbapenem	1219	1	0.1 [0, 0.5]
non-invasive	Ciprofloxacin/Norfloxacin	1406	162	11.5 [9.9, 13.3]
non-invasive	Fosfomycin	280	1	0.4 [0, 2]
non-invasive	Gentamicin	396	223	56.3 [51.3, 61.3]
non-invasive	Nalidixic acid	7	1	14.3 [0.4, 57.9]
non-invasive	Nitrofurantoin	249	23	9.2 [5.9, 13.5]
non-invasive	Piperacillin-Tazobactam	495	2	0.4 [0, 1.5]
non-invasive	Tetracycline	93	22	23.7 [15.5, 33.6]
non-invasive	Trimethoprim-Sulfamethoxazole	1287	51	4 [3, 5.2]
invasive	3rd/4th generation Cephalosporin	466	5	1.1 [0.3, 2.5]
invasive	Amoxicillin-clavulanic acid	136	5	3.7 [1.2, 8.4]
invasive	Amoxicillin/Ampicillin	185	30	16.2 [11.2, 22.3]
invasive	Azithromycin/Clarithromycin/Erythromycin	12	1	8.3 [0.2, 38.5]
invasive	Carbapenem	371	0	0 [0, 1]
invasive	Ciprofloxacin/Norfloxacin	184	38	20.7 [15, 27.2]
invasive	Fosfomycin	35	1	2.9 [0.1, 14.9]
invasive	Gentamicin	98	72	73.5 [63.6, 81.9]
invasive	Nalidixic acid	14	3	21.4 [4.7, 50.8]
invasive	Nitrofurantoin	28	4	14.3 [4, 32.7]
invasive	Piperacillin-Tazobactam	128	1	0.8 [0, 4.3]
invasive	Tetracycline	21	2	9.5 [1.2, 30.4]
invasive	Trimethoprim-Sulfamethoxazole	172	12	7 [3.7, 11.9]

Figure S1: FAS (the full analysis set): Frequency distribution over years for isolates that could only be determined to the genus level (***C. species***)

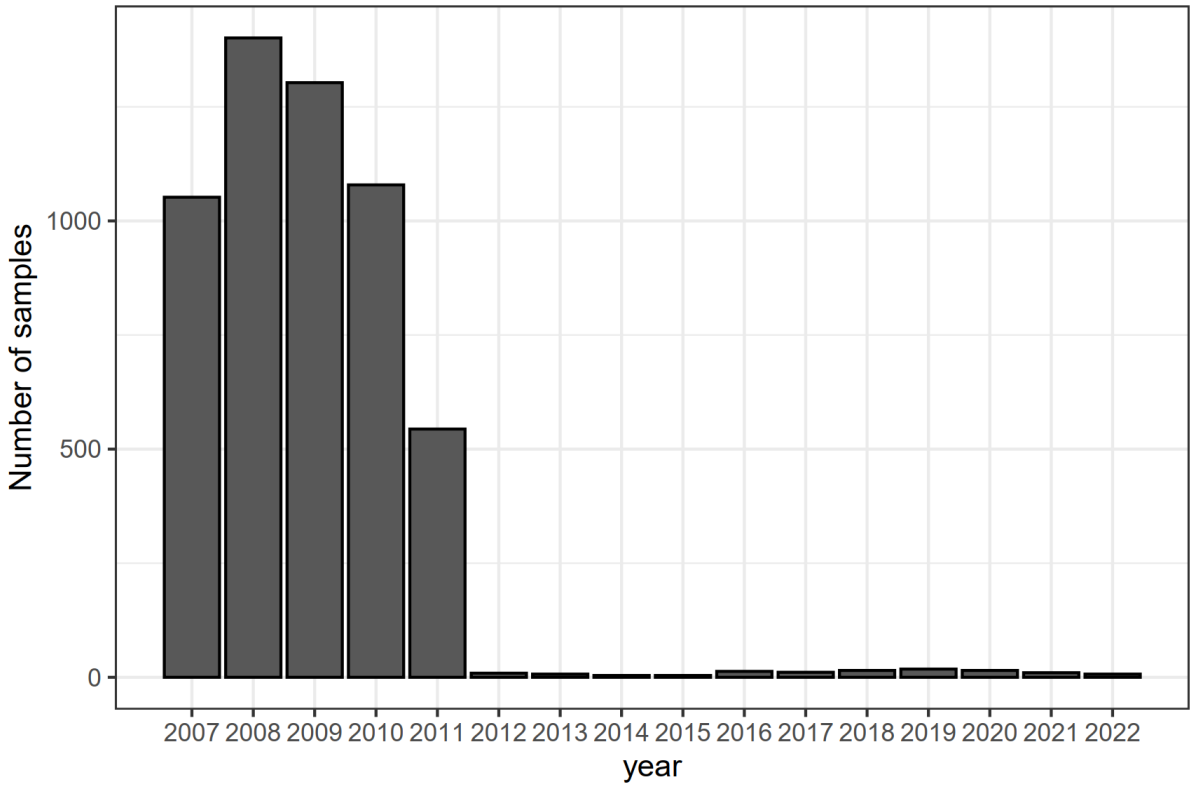


Figure S2: Distribution of typhoidal and *non-typhoidal Salmonella* isolates over time. Please note that y-axes differ between the plots´

Salmonella enterica

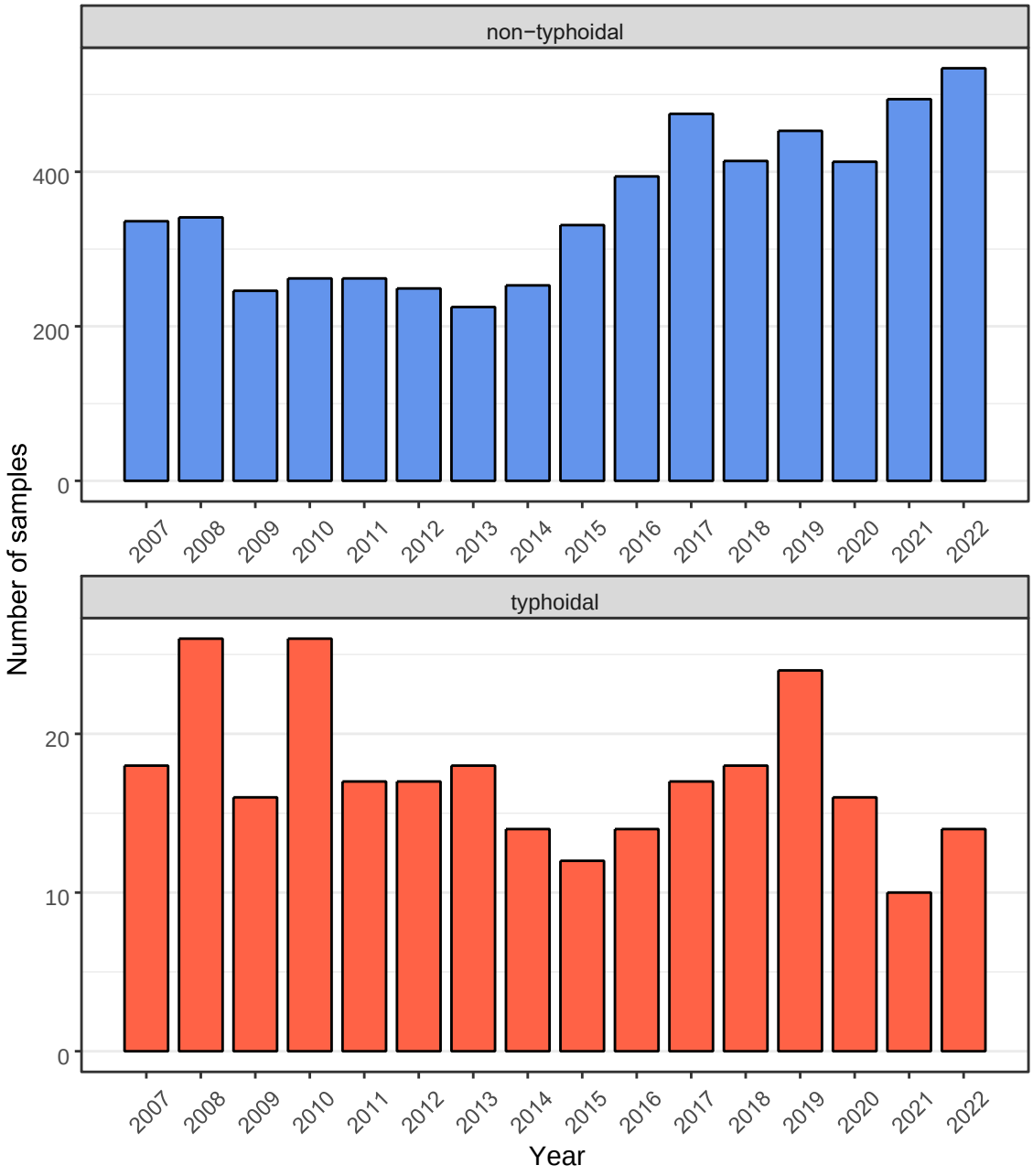


Figure S3: Antibiotic resistance of *C. coli* (% of resistant isolates) according to year. Error bars indicate 95% confidence intervals.

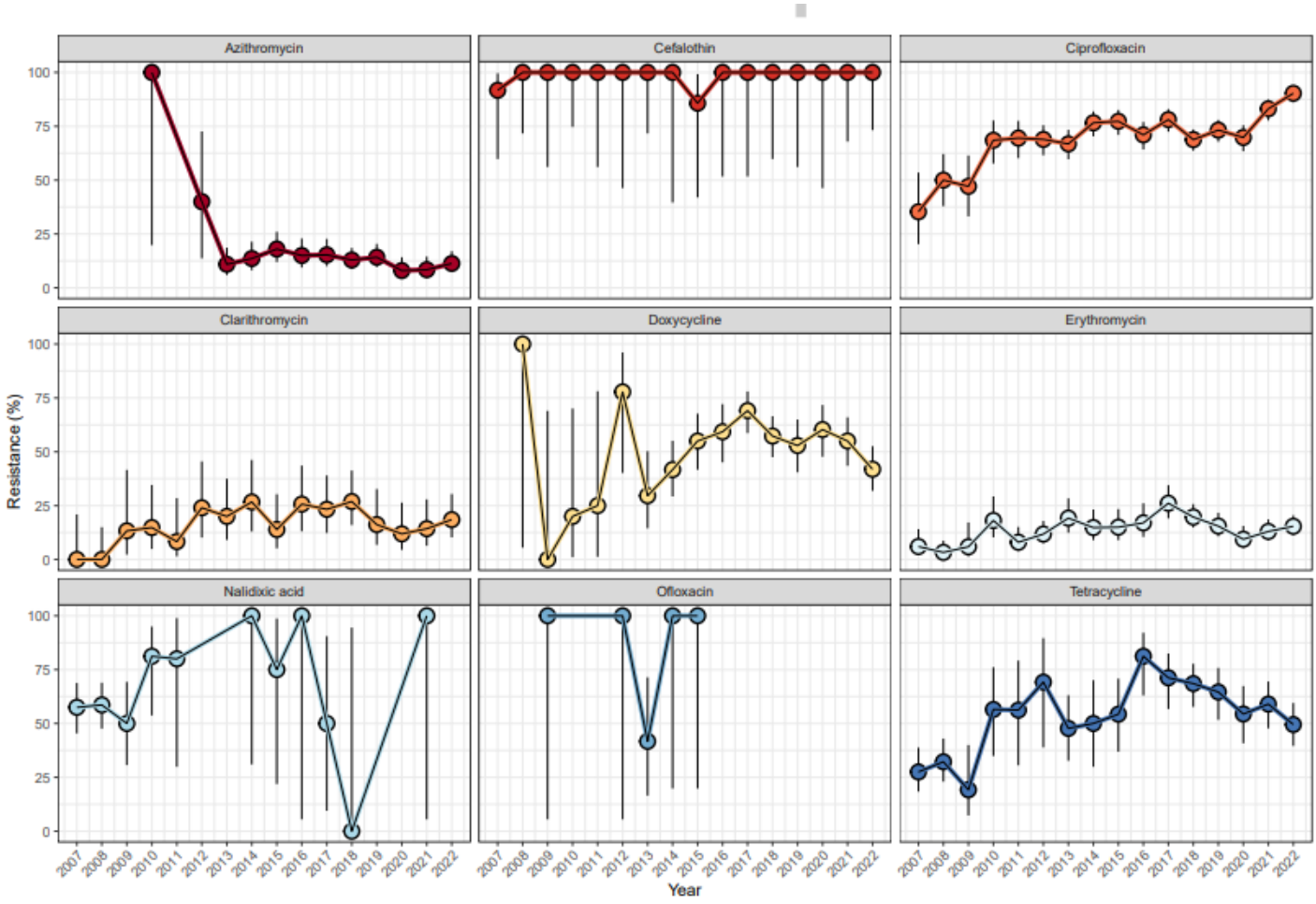
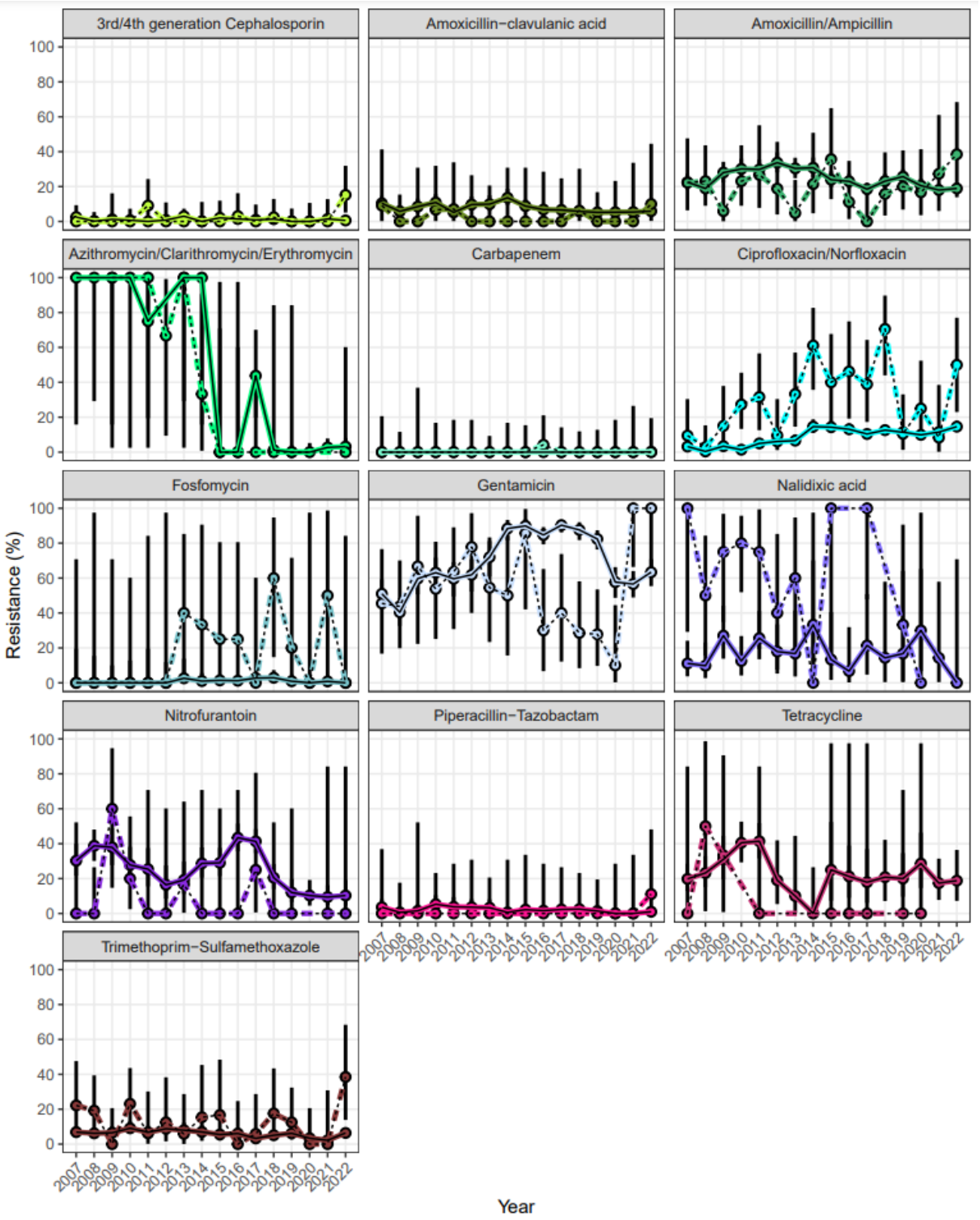


Figure S4: Antibiotic resistance of *Salmonella* spp. *non-typhoidal and typhoidal* (% of resistant isolates) according to year. Error bars indicate 95% confidence intervals.



solid line = non-typhoidal
dashed line = typhoidal