



Characteristics of antibiotic resistance of non-typhoidal *Salmonella* circulating in the Russian Federation in the period from 2019 to 2022

Anastasia S. Pavlova[✉], Konstantin V. Kuleshov, Natalia E. Krutova,
Anna N. Guseva, Alexandr T. Podkolzin

Central Research Institute of Epidemiology, Moscow, Russia

Abstract

Introduction. Non-typhoidal *Salmonella* make a significant contribution to the incidence of enteric infections and are characterized by an increasing proportion of strains resistant to antimicrobial agents (AMAs), including the first choice antibiotics (cephalosporins III and fluoroquinolones).

The **purpose** of the study is to assess the phenotypic resistance of *Salmonella* to various classes of AMAs and determine the relationship between the phenotypic resistance, serotype, source of isolation and nature of incidence.

Materials and methods. We studied 752 representative strains of *Salmonella* of 2494 strains isolated from various sources (clinical samples, food products, environment) received from 59 regions of Russia in the period from 2019 to 2022. The phenotypic resistance to 22 antibiotics of 11 CLSI classes of AMAs was assessed by broth microdilution method (minimum inhibitory concentration). The diversity of resistance profiles of *Salmonella* serotypes was compared using the Shannon index.

Results. The dominant position in terms of isolation frequency is occupied by the serotypes *Salmonella* Enteritidis, S. Infantis, S. Muenchen, S. Typhimurium, S. Bovismorbificans, which accounted for 64.4% of the studied strains. 543 (72.2%) strains showed resistance to at least one of the tested antibiotics; 193 (25.7%) strains were characterized by multidrug resistance phenotype (MDR). Resistance to AMA classes was characterized by the following distribution: quinolones (61.3%), tetracyclines (28.1%), penicillins (19.1%), β -lactam combination agents (18.6%), folate pathway antagonists (16, 5%), phenicols (10.1%), aminoglycosides (5.6%), cepheims (4.7%), monobactams (4.4%), lipopeptides (3.9%). No penem-resistant strains have been identified. The features of *Salmonella* resistance by AMA classes are shown to depend on the sources of isolation, the *Salmonella* serotype and the nature of the incidence (outbreak and sporadic).

Conclusions. Monitoring of phenotypic antibiotic resistance is an important tool for epidemiological surveillance in order to prevent the spread of bacterial resistance to AMAs.

Keywords: phenotypic resistance, *Salmonella enterica*, antibiotics, *Salmonella* serotypes, sources of isolation

Ethics approval. The study was conducted with the informed consent of the patients. The research protocol was approved by the Ethics Committee of the Central Research Institute of Epidemiology (protocol No. 83, June 26, 2018).

Funding source. The study was conducted as part of the industry research program of Rospotrebnadzor for the period 2021-2025. (№ НИОКТР АААА-А21-121011990054-5).

Conflict of interest. The authors declare no apparent or potential conflicts of interest related to the publication of this article.

For citation: Pavlova A.S., Kuleshov K.V., Krutova N.E., Guseva A.N., Podkolzin A.T. Characteristics of antibiotic resistance of non-typhoidal *Salmonella* circulating in the Russian Federation in the period from 2019 to 2022. *Journal of microbiology, epidemiology and immunobiology*. 2023;100(5):287–301.

DOI: <https://doi.org/10.36233/0372-9311-451>

EDN: <https://www.elibrary.ru/tmxvam>

Научная статья

<https://doi.org/10.36233/0372-9311-451>

Характеристика антибиотикорезистентности нетифоидных сальмонелл, циркулирующих на территории Российской Федерации в период с 2019 по 2022 год

Павлова А.С.[✉], Кулешов К.В., Крутова Н.Е., Гусева А.Н., Подколзин А.Т.

Центральный научно-исследовательский институт эпидемиологии Роспотребнадзора, Москва, Россия

Аннотация

Введение. Нетифоидные сальмонеллы вносят значительный вклад в заболеваемость кишечными инфекциями и характеризуются возрастанием доли штаммов, резистентных к антимикробным препаратам (АМП), в том числе к современным препаратам выбора (цефалоспорины III и фторхинолоны).

Цель работы — оценка фенотипической резистентности сальмонелл к различным классам АМП и определение связи между фенотипической резистентностью, серотипом, источником изоляции и характером заболеваемости.

Материалы и методы. Исследованы 752 неповторяющихся штамма сальмонелл из 2494 штаммов, выделенных из различных источников (клинический материал, пищевые продукты, окружающая среда), поступивших из 59 регионов России в период с 2019 по 2022 г. Фенотипическая резистентность к 22 антибиотикам из 11 CLSI-классов АМП оценена методом серийных разведений в бульоне (минимальная подавляющая концентрация). Проведено сравнение разнообразия профилей резистентности серотипов сальмонелл с использованием индекса Шеннона.

Результаты. Доминирующее положение по частоте изоляции занимают серотипы *Salmonella* Enteritidis, S. Infantis, S. Muenchen, S. Typhimurium, S. Bovismorbificans, на которые приходилось 64,4% исследованных штаммов. Устойчивость по меньшей мере к одному из тестируемых антибиотиков проявляли 543 (72,2%) штамма, множественной лекарственной устойчивостью характеризовались 193 (25,7%) штамма. Резистентность к классам АМП характеризовалась следующим распределением: хинолоны (61,3%), тетрациклины (28,1%), пенициллины (19,1%), β-лактамы комбинированные препараты (18,6%), антагонисты фолатного пути (16,5%), фениколы (10,1%), аминогликозиды (5,6%), цефемы (4,7%), монобактамы (4,4%), липопептиды (3,9%). Резистентных штаммов к пенициллинам не выявлено. Показаны особенности резистентности сальмонелл по классам АМП в зависимости от источников выделения, серотипа сальмонелл и характера заболеваемости (групповая и спорадическая).

Выводы. Мониторинг фенотипической антибиотикорезистентности является важным инструментом эпидемиологического надзора в целях профилактики распространения резистентности бактерий к АМП.

Ключевые слова: фенотипическая резистентность, *Salmonella enterica*, антибиотики, серотипы сальмонелл, источники выделения

Этическое утверждение. Исследование проводилось при добровольном информированном согласии пациентов. Протокол исследования одобрен Этическим комитетом ЦНИИ Эпидемиологии Роспотребнадзора (протокол № 83 от 26.06.2018).

Источник финансирования. Авторы заявляют об отсутствии внешнего финансирования при проведении исследования.

Конфликт интересов. Авторы декларируют отсутствие явных и потенциальных конфликтов интересов, связанных с публикацией настоящей статьи.

Для цитирования: Павлова А.С., Кулешов К.В., Крутова Н.Е., Гусева А.Н., Подколзин А.Т. Характеристика антибиотикорезистентности нетифоидных сальмонелл, циркулирующих на территории Российской Федерации в период с 2019 по 2022 год. *Журнал микробиологии, эпидемиологии и иммунобиологии*. 2023;100(5):287–301.

DOI: <https://doi.org/10.36233/0372-9311-451>EDN: <https://www.elibrary.ru/tmxvam>

Introduction

Non-typhoidal strains of *Salmonella enterica* subsp. *enterica* (hereafter referred to as non-typhoidal *Salmonella*) make a significant contribution to the incidence of enteric infections in the world [1, 2]. These strains of *Salmonella* is responsible for 99% of cases of salmonellosis in humans and animals and remains relevant in the formation of outbreak incidence, ranking 3rd (after acute intestinal infection of viral etiology) by the number outbreaks with the fecal-oral chain of transmission of the infection¹. Despite the downward trend in the incidence in recent years, salmonellosis is still the most frequently reported foodborne zoonosis in Russia. According to the dynamics of incidence in Russia from 2019 to 2021, the incidence rate decreased 1.8 times and amounted to 13.61 per 100 thousand population, while in 2022 it was 17.1 per 100 thousand population¹.

Uncomplicated salmonellosis, as a rule, does not require antibacterial therapy, but it is indicated for the treatment of invasive and severe forms, as well as patients of high-risk groups² (infants, elderly people and patients with weakened immune systems) [3, 4]. For a long time, the commonly used antimicrobial agents (AMAs) were chloramphenicol, ampicillin, and trimethoprim-sulfamethoxazole [5, 6], but in recent years, resistance to these AMAs has increased significantly [7].

Currently, the recommended the first choice antibiotics in the treatment of severe and generalized forms of salmonellosis are third-generation cephalosporins and fluoroquinolones^{3,4}. These AMAs are included in the list of mandatory monitoring for *Salmonella* according to the guidelines of the World Health Organization. The percentage of ciprofloxacin-resistant *Salmonella* strains isolated from humans increased from 12.0% in 2017 to 19.7% in 2020, according to the latest report from the Global Antimicrobial Resistance and Use Surveillance System (GLASS).⁵ At the same time, the percentage of detection of extended-spectrum β -lactamase-producing strains, although remaining at a low level, tends to increase [8].

Monitoring of circulating strains and determination of their AMA resistance profiles are necessary to better understand the epidemiological situation, develop national strategies to eradicate resistant strains,

and develop preventive measures to avoid the formation of reservoirs of infection. At the same time, the organization of monitoring should be based on the One Health principle, which engage close interaction and coordination of different areas. In particular, the organization of monitoring of the phenotypic and molecular genetic characteristics of *Salmonella* both in the human population and in different branches of agriculture, which is especially important to ensure food safety [9].

Comparative analysis of data on antibiotic bacterial resistance of *Salmonella* obtained in Russia in different years involves certain difficulties. One of the main reasons is continuously changing interpretation criteria and methodological approaches to testing for antibiotic bacterial resistance. These changes are occurring around the world, making it difficult to conduct an objective analysis [10]. According to previous studies, the percentage of non-typhoidal *Salmonella* strains resistant to various AMA classes varied significantly across different regions of Russia in different years. Resistance to aminoglycosides was shown by 1–2% to 53.1% of strains, to quinolones — from 0.0% to 59.2%, to penicillins — from 26.4% to 42.0% [11–14]. Another important factor is the limited number of studies in Russia reflecting a comprehensive analysis of the phenotypic resistance of non-typhoidal *Salmonella* strains in terms of the diversity of sources and geography of isolation, as well as the serotype diversity.

The **purpose** of this study was to assess the phenotypic resistance of *Salmonella* to various AMA classes and to determine the relationship between the phenotypic resistance and such parameters as serotype, isolation source and the nature of the incidence (outbreak and sporadic) at which the strains were isolated.

Materials and Methods

Selection of isolates and microbiological studies

In 2019–2022, 2494 strains of non-typhoidal *Salmonella* isolated in 59 regions of Russia from various sources were studied. Among them, 1355 isolates were obtained during the investigation of 113 cases of outbreak incidence of salmonellosis from people and suspected infection transmission factors (food and environment), 1139 isolates were obtained in single cases of salmonellosis from food and the environment. The study was conducted with the informed consent of the patients. The research protocol was approved by the Ethics Committee of the Central Research Institute of Epidemiology (protocol No. 83, June 26, 2018).

The studied strains were preliminary cultured to obtain individual colonies on MacConkey medium (CONDA Pronadisa). The species identity was established using biochemical identification systems API[®] 20E (bioMérieux).

¹ On the state of sanitary and epidemiological well-being of the population in the Russian Federation in 2022: State report. Moscow; 2023.

² Plumb I., Fields P., Bruce B.B. Salmonellosis (Non-typhoidal). CDC Yellow Book; 2024. Travel-Related Infectious Diseases. URL: <https://wwwnc.cdc.gov/travel/yellowbook/2020/travel-related-infectious-diseases/salmonellosis-non0typhoidal> (access date 7/9/2023).

³ Clinical guidelines. Salmonellosis in adults. M.; 2021.

⁴ The WHO Essential Medicines List Antibiotic Book: improving antibiotic AWaRe (Draft for consultation). Geneva; 2022.

⁵ Global antimicrobial resistance and use surveillance system (GLASS) report 2022. Geneva; 2022.

Serological identification

Serological identification of *Salmonella* was carried out using standardized methods according to the Kaufman–White classification scheme with diagnostic polyclonal sera (PETSAL) and monoclonal sera (Sifin).

Genetic typing

Genetic typing was carried out according to the international standardized protocol using restriction enzymes *XbaI* and *BlnI* [15].

Determination of phenotypic resistance

Among all analyzed strains ($n = 2494$), 1522 isolates (61.0%; 95% confidence interval (CI) 59.1–62.9) were determined to be susceptible to AMAs (729 strains from loci of outbreak incidence and 793 from sporadic cases of detecting *Salmonella*) by broth microdilution method with determining the minimum inhibitory concentration of the antibiotic on plates G-I and G-II Mikrolatest®SensiLaTest MIC (Erba Lachema). *Escherichia coli* strain (ATCC 25922) was used as a control strain. The spectrum of AMAs by class, according to the Clinical and Laboratory Standards Institute (CLSI) classification⁶, included:

- penicillins: ampicillin, piperacillin;
- β -lactam combination agents: ampicillin/sulbactam, piperacillin/tazobactam;
- cepheems: cefazolin, cefuroxime, cefotaxime, ceftazidime, cefepime;
- monobactams: aztreonam;
- penems: meropenem, ertapenem;
- aminoglycosides: gentamicin, netilmicin, amikacin, tobramycin;
- lipopeptides: colistin;
- folate pathway antagonists: trimethoprim/sulfamethoxazole;
- quinolones: ciprofloxacin;
- phenicols: chloramphenicol;
- tetracyclines: tetracycline, tigecycline.

The results of susceptibility tests were interpreted in accordance with the current European Committee on Antibiotic Susceptibility Testing criteria (EUCAST v. 13.0). If a strain showed resistance to at least one antibiotic of a certain class, then the strain was considered resistant to this class.

Due to the lack of interpretation of the minimum inhibitory concentrations of cefazolin, cefuroxime, netilmicin, and tigecycline for *Salmonella* spp., data on these AMAs were not taken into account in the study. The interpretation for tetracycline and chloramphenicol was assessed using epidemiological cut-

off values (ECOFF). In addition, following the World Health Organization recommendations, the ECOFF value of $>8 \mu\text{g/ml}$ was established for colistin when testing *Salmonella* strains belonging to the serotypes S. Enteritidis and S. Dublin⁷.

Strategy for identifying of representative strains and assessing the diversity of resistance profiles

Representative strains were those strains that were characterized by a unique combination of such characteristics as serotype, isolation date, isolation site, isolation source, AMA resistance profile, and genetic subtype. Each event of outbreak incidence, regardless of the isolation source, was represented by one strain or several strains, if strains differing in one or more characteristics were identified within the outbreak. If there was no genetic subtype for a strain, it was not taken into account in the spectrum of characteristics.

To analyze the diversity of resistance profiles of *Salmonella* spp., we used the Shannon diversity index (H). The significance of the difference in Shannon index values (p -level of significance) between two groups of strains, each of which was characterized by a set of resistance profiles with certain frequencies of occurrence, was assessed using modified parametric Student's t -test — Hutcheson's t -test [16].

The 95% CI for the proportion of detected strains according to various criteria was calculated using the BinomCI function according to the Wilson method using the DescTools library package of the R software.

Results

Patterns and characteristics of resistance of *Salmonella* circulating in Russia

Among 1522 isolates tested for antibiotic susceptibility in 2019–2022, 752 representative strains belonging to 69 serotypes were selected. Of these, 153 strains belonged to loci of outbreak incidence and included *Salmonella* strains isolated both from people ($n = 121$) and from suspected sources ($n = 32$), and 599 strains were from sporadic cases of salmonellosis (Table 1). Sporadic strains were divided into three groups according to isolation sources: sporadic incidence — strains isolated from humans ($n = 270$), from food ($n = 239$) and the environmental samples — from various water bodies and wastewater ($n = 90$).

543 (72.2%) strains were resistant to at least one of the tested antibiotics, and 193 (25.7%) strains were characterized by multidrug resistance (MDR). The majority of strains with the MDR phenotype ($n = 120$) were resistant to 4–6 AMA classes, and 6 strains were characterized by the maximum spectrum of resistance — 10 AMA classes out of 11 tested (see **Supplemen-**

⁶ Clinical and Laboratory Standards Institute (CLSI). Performance Standards for Antimicrobial Susceptibility Testing. 31st ed. CLSI supplement M100 Clinical and Laboratory Standards Institute, USA, 2021.

⁷ Integrated Surveillance of Antimicrobial Resistance in Foodborne Bacteria: Application of a One Health Approach. Geneva; 2017.

Table 1. Distribution of *S. enterica* serotypes in outbreaks and in sporadic cases of *Salmonella* isolation

Serotype (number of outbreaks)	Number of strains	Percentage of strains, %	95% CI
Outbreak cases			
<i>S. Enteritidis</i> (103)	138	90,2	84,4–93,9
<i>S. Abony</i> (2)	5	3,3	1,4–7,4
<i>S. Typhimurium</i> (2)	3	1,9	0,6–5,6
<i>S. Muenchen</i> (2)	2	1,3	0,3–4,6
<i>S. Bareilly</i> (1)	2	1,3	0,3–4,6
<i>S. Infantis</i> (1)	1	0,7	0,1–3,6
<i>S. Stanley</i> (1)	1	0,7	0,1–3,6
<i>S. Braenderup</i> (1)	1	0,7	0,1–3,6
Всего Total	153	100	
Sporadic cases of <i>Salmonella</i> strains isolation			
Sporadic incidence (<i>n</i> = 270)			
<i>S. Enteritidis</i>	55	20,4	16,0–25,6
<i>S. Muenchen</i>	34	12,6	9,2–17,1
<i>S. Typhimurium</i>	17	6,3	4,0–9,9
Другие серотипы Other serotypes	164	60,7	54,8–66,4
Food (<i>n</i> = 239)			
<i>S. Infantis</i>	95	39,7	33,8–46,1
<i>S. Enteritidis</i>	39	16,3	12,2–21,5
<i>S. Typhimurium</i>	11	4,6	2,6–8,1
Другие серотипы Other serotypes	94	39,3	33,4–45,6
Environment (<i>n</i> = 90)			
<i>S. Infantis</i>	13	14,4	8,6–23,2
<i>S. Typhimurium</i>	11	12,2	7,0–20,6
<i>S. Bovismorbificans</i>	10	11,1	6,1–19,3
Другие серотипы Other serotypes	56	62,2	51,9–71,5
Total	599		

tary file in online version on the journal's website, DOI: <https://doi.org/10.36233/0372-9311-451-1>.

The percentage of resistant strains of the entire collection of studied *Salmonella* to certain AMA classes was characterized by the following distribution: 61.3% (95% CI 57.8–64.7) of the studied strains showed phenotypic resistance to quinolones, 28.1% (95% CI 25.0–31.4) — to tetracyclines, 19.1% (95% CI 16.5–22.1) — to penicillins, 18.6% (95% CI 16.0–21.6) — to β -lactam combination agents, 16.5% (95% CI 14.0–19.3) — to folate pathway antagonists, 10.1% (95% CI 8.2–12.5) — to phenicols, 5.6% (95% CI 4.2–7.5) — to aminoglycosides, 4.7% (95% CI 3.5–6.6) — to cepheids, 4.4% (95% CI 3.1–6.1) — to monobactams, 3.9% (95% CI 2.8–5.6) — to lipopeptides. No penem-resistant strains have been identified.

Strains ($n = 153$) from 113 loci of outbreak incidence of salmonellosis were distributed as follows: in 2019 — 53; in 2020 — 15; in 2021 — 17; in 2022 — 28. 77 (68.1%) outbreaks were characterized by only 1 representative strain. In other cases, 2–4 representative strains were found in the outbreak. The leading serotype in outbreaks was *S. Enteritidis* ($n = 138$). In turn, serotypes *S. Typhimurium*, *S. Infantis*, *S. Muenchen*, *S. Abony*, *S. Stanley*, *S. Braenderup*, and *S. Bareilly* were

related to single cases. The largest proportion (67.3%; 95% CI 59.5–74.2) of strains showed resistance to 1–2 AMA classes (Fig. 1). Strains susceptible to all tested AMAs accounted for 28.1% (95% CI 21.6–35.7), while the proportion of MDR strains was only 4.6% (95% CI 2.2–9.1)

Isolates obtained from humans as well as from other sources, not associated with cases of outbreak incidence of salmonellosis according to epidemiological data, were represented by 599 strains. Each isolation source had its own dominant serotypes. Among sporadic cases, *S. Enteritidis* was predominant (20.4%; 95% CI 16.0–25.6), for food and environment — *S. Infantis* (39.7%; 95% CI 33.8–46.1 and 14.4%; 95% CI 8.6–23.2). At the same time, *S. Typhimurium* was also among the frequently occurring serotypes (Table 1).

It should be noted that among the strains with sporadic incidence and those isolated from the environment, there were approximately equal proportions of those susceptible to AMAs (35.2%; 95% CI 29.7–41.1 and 40%; 95% CI 30.5–50.3), resistant to 1–2 AMA classes (38.1%; 95% CI 32.6–44.1 and 34.4%; 95% CI 25.4–44.7) and strains with an MDR profile (26.7%; 95% CI 21.7–32.2 and 25.6%; 95% CI 17.7–35.4). *Salmonella* isolated from food had the highest proportion of MDR

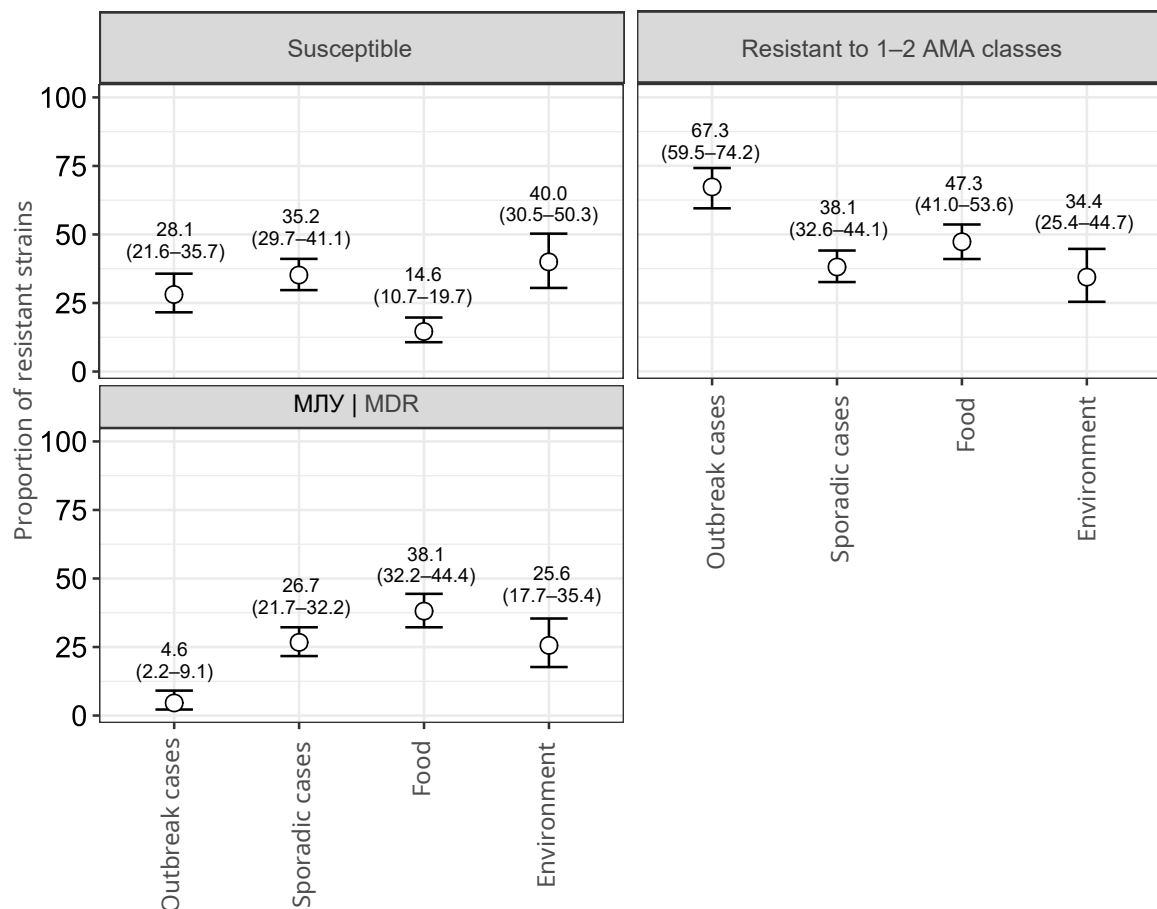


Fig. 1. The proportion of resistant *Salmonella* strains (indicating 95% CI), isolated from various sources and susceptible to all AMAs, resistant to 1–2 AMA classes, resistant to 3 or more AMA classes (MDR).

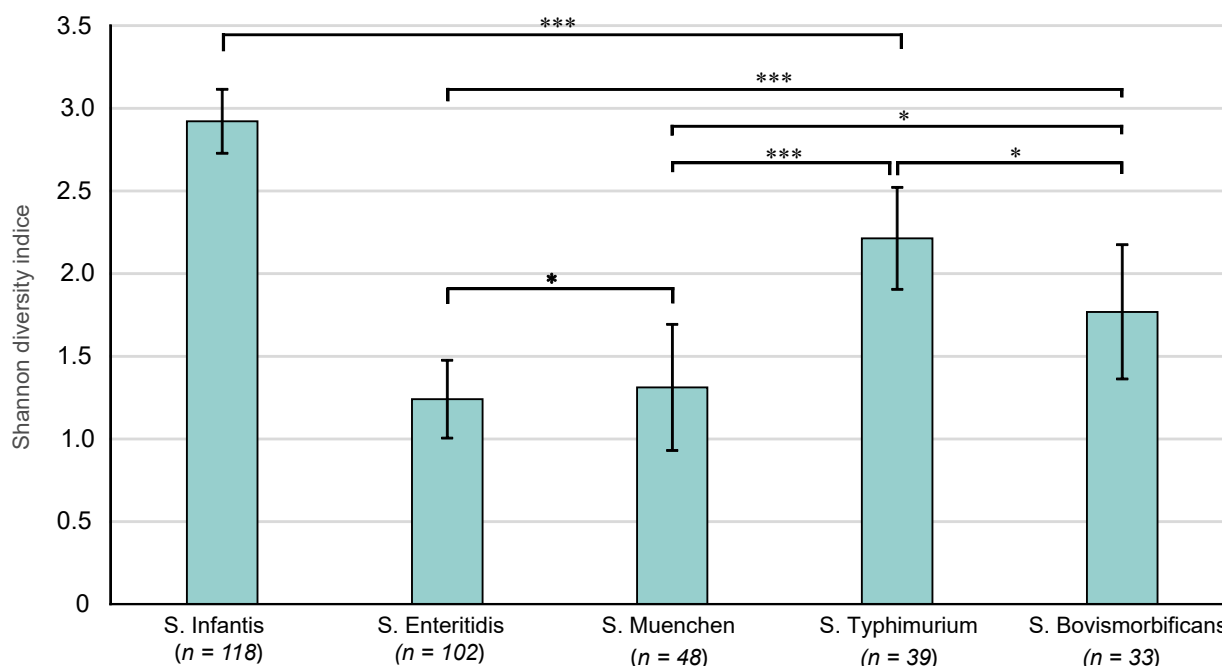


Fig. 2. Distribution of Shannon diversity indices (indicating 95% CI) for *Salmonella* serotypes not associated with outbreaks and with the largest number of resistance profiles.

* — slightly different in diversity ($p > 0.05$); *** — significant difference ($p < 0.05$).

phenotypes (38.1%; 95% CI 32.6–44.1) and the lowest proportion (14.6%; 95% CI 10.7–19.7) of susceptible strains in comparison with other sources (Fig. 1). In addition, strains not associated with outbreak incidence were characterized by a high diversity of antibiotic resistance profiles. We identified 85 different profiles. Frequently occurring serotypes had the largest number of profiles: *S. Enteritidis* ($n = 11$), *S. Infantis* ($n = 31$), *S. Muenchen* ($n = 10$), *S. Typhimurium* ($n = 14$), and *S. Bovismorbificans* ($n = 11$).

Comparison of Shannon diversity indices (H) based on antibiotic resistance profiles of frequently occurring *Salmonella* serotypes not related to outbreak incidence, and evaluation of the significance of differences showed that the diversity in *S. Infantis* strains was significantly higher than in *S. Typhimurium* strains ($p < 0.05$; **Fig. 2**). At the same time, *S. Typhimurium* did not differ from *S. Bovismorbificans* in the diversity of resistance profiles ($p > 0.05$), but had a significantly ($p < 0.05$) higher diversity than *S. Muenchen*. The diversity for *S. Bovismorbificans* showed a slight difference from *S. Muenchen* ($p > 0.05$), but was significantly ($p < 0.05$) higher compared to the diversity of *S. Enteritidis*. However, *S. Muenchen* and *S. Enteritidis* did not differ by diversity ($p > 0.05$). Thus, *S. Infantis* had the highest diversity of antibiotic resistance profiles ($H = 2.89$; 95% CI 2.70–3.08) compared with other serotypes. However, *S. Enteritidis* had the lowest diversity ($H = 1.24$; 95% CI 1.01–1.46), despite ranking 2nd by the number of strains isolated from sporadic cases, along with *S. Muenchen*.

Comparative evaluation of phenotypic resistance of *Salmonella* strains to AMA classes, isolated from various sources

Strains from all sources were characterized by low resistance to aminoglycosides, lipopeptides, and phenicols, while a significant proportion of strains were characterized by high rates of resistance to quinolones (**Fig. 3**).

Analyzing the frequency of identified resistant strains among various isolation sources relative to certain AMA classes, it can be seen that the proportion of strains resistant to penicillins, β -lactam combination agents, cepheids, monobactams, folate pathway antagonists, and tetracyclines was significantly higher or, in case of cepheids and monobactams, was found only in the group of sources: “sporadic cases”, “food”, “environment” in comparison with strains from outbreak cases (Fig. 3).

The highest rate of resistance to tetracyclines (49.0%; 95% CI 42.7–55.3) was associated with strains isolated from food products.

The proportion of strains resistant to quinolones and associated with outbreak incidence (68.0%; 95% CI 60.2–74.8) and food products (73.6%; 95% CI 67.7–78.8) was higher compared to other sources.

Comparative evaluation of phenotypic resistance to AMA classes and serotype diversity of *Salmonella*

Analysis of resistance to AMA classes of strains belonging to the most common *Salmonella* serotypes revealed the prevalence of resistant strains among the *S. Typhimurium* and *S. Bovismorbificans* serotypes. In

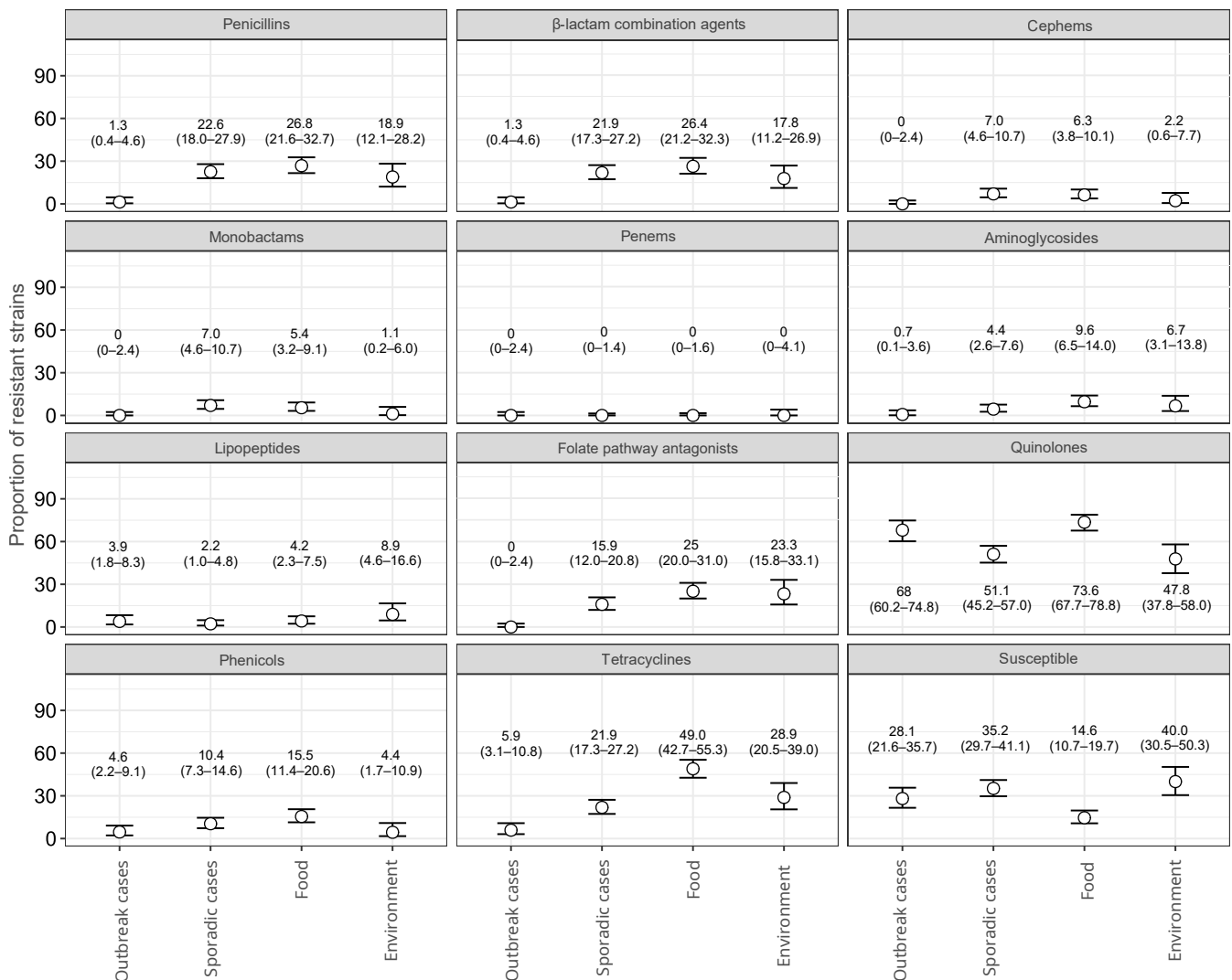


Fig. 3. Proportion of resistant *Salmonella* strains (indicating 95% CI) to different classes of antimicrobial agents from different isolation sources.

particular, the proportion of strains resistant to penicillins was 57.1 and 93.9%, and to β-lactam combination agents — 57.1 and 87.9%, respectively. At the same time, the proportion of strains resistant to folate pathway antagonists and tetracyclines in *S. Bovismorbificans* was at a high level (90.9%; 95% CI 76.4–96.9), and significantly exceeded similar indicators compared to *S. Typhimurium* (9.5%; 95% CI 3.8–22.1 and 47.6%; 95% CI 33.4–62.3, respectively; **Fig. 4**).

S. Infantis strains differed from other serotypes by their high resistance to quinolones (92.4%; 95% CI 86.2–96.0) and phenicolcs (24.4%; 95% CI 17.5–32.8), and also showed increased resistance to folate pathway antagonists (45.4%; 95% CI 36.7–54.3) and tetracyclines (76.5%; 95% CI 68.1–83.2).

It should be noted that a significant proportion of strains of all serotypes showed resistance to quinolones and were divided into 3 groups according to the degree of resistance to this AMA class. The first group with the highest proportion of resistant strains included *S. Infan-*

tis. The second group included *S. Enteritidis* (70.0%; 95% CI 63.9–75.4) and *S. Muenchen* (78.0%; 95% CI 64.8–87.2), among which the proportion of resistant strains was significantly higher than for the third group, which included *S. Typhimurium* (38.1%; 95% CI 25.0–53.2), *S. Bovismorbificans* (33.3%; 95% CI 19.8–50.4), and other serotypes (43.7%; 95% CI 37.8–49.6).

The resistance of strains of all analyzed serotypes to cepheims, monobactams, and lipopeptides did not exceed 10%. The proportion of strains resistant to aminoglycosides also remained low, less than 10%, and only for *S. Infantis* (16.8%; 95% CI 11.2–24.5) and *S. Bovismorbificans* (12.1%; 95% CI 4.8–27.3) this indicator was higher.

Comparison of the diversity of resistance profiles of S. Enteritidis strains isolated from outbreaks and from clinical specimens of sporadic cases

The number of resistance profiles for *S. Enteritidis* strains isolated from outbreaks ($n = 7$) was slight-

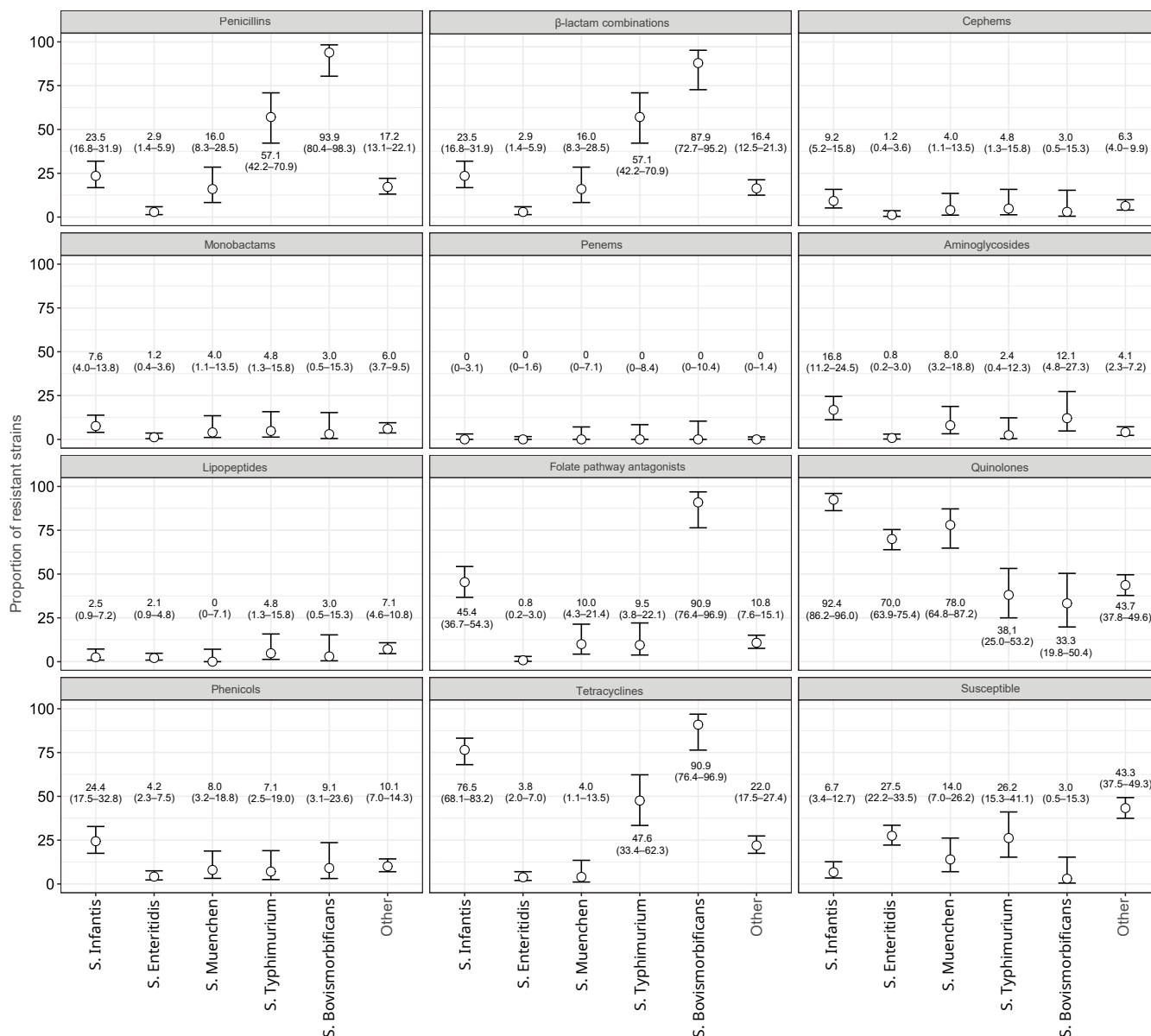


Fig. 4. Proportion of resistant strains of the most common *Salmonella* serotypes (indicating 95% CI) to AMA classes.

ly lower than for sporadic incidence ($n = 9$; Fig. 5). Moreover, all *S. Enteritidis* strains were characterized by high resistance to quinolones (70.0%; 95% CI 63.9–75.4) and resistance to other AMA classes at a level below 5% (Fig. 4). Only 27.5% (95% CI 22.2–33.5) were sensitive to all antibiotics tested. Comparison of Shannon diversity indices between groups of *S. Enteritidis* strains isolated from outbreaks ($H = 0.98$; 95% CI 0.81–1.15) and in sporadic incidence ($H = 1.33$; 95% CI 1.03–1.62), showed a significant difference ($p < 0.05$) and a predominance of resistance profiles in the diversity in the case of sporadic incidence (Table 2).

Discussion

Monitoring of phenotypic antibiotic bacterial resistance is an important tool for epidemiological sur-

veillance in the fight against the increase in bacterial resistance to AMAs throughout the world, which is aimed at obtaining information about the dynamics of changes in the phenotypic characteristics of socially significant pathogens and developing comprehensive measures to address this issue. Based on an extensive collection of strains, we attempted to characterize in the presented studies the resistance of non-typhoidal *Salmonella* circulating in Russia in recent years.

It is necessary to pay attention to the fact that, in order to create a collection of strains for evaluating antibiotic bacterial resistance, we formed a collection of representative *Salmonella* strains, which, in contrast to a study based on all strains allows us to avoid misconceptions about the detection frequency of a particular resistance profile and obtain objective data. Similar approaches were used before in other studies [17, 18].

Table 2. The number of *Salmonella* strains of a certain AMA resistance profile for the compared groups

Resistance profile	Number of strains
Outbreak cases	
Susceptible	35
Ciprofloxacin	90
Ampicillin, ampicillin/sulbactam, ciprofloxacin, chloramphenicol	1
Ciprofloxacin, chloramphenicol, tetracycline	5
Chloramphenicol, tetracycline	2
Colistin, ciprofloxacin	4
Tobramycin, ciprofloxacin	1
Total	138
Sporadic cases	
Susceptible	20
Ciprofloxacin	26
Ampicillin, ampicillin/sulbactam, piperacillin, cefotaxime, ceftazidime, cefepime, aztreonam, ciprofloxacin	2
Ampicillin, ampicillin/sulbactam, piperacillin, cefotaxime, ceftazidime, cefepime, aztreonam	1
Ampicillin, ampicillin/sulbactam, piperacillin, trimethoprim/sulfamethoxazole, ciprofloxacin, tetracycline	1
Ampicillin, ampicillin/sulbactam, piperacillin, trimethoprim/sulfamethoxazole	1
Ciprofloxacin, chloramphenicol	2
Chloramphenicol, tetracycline	1
Tobramycin, ciprofloxacin	1
Total	55

An assessment of the serotype diversity of *Salmonella* and phenotypic resistance to AMA classes showed that the dominant position in terms of isolation frequency was occupied by serotypes *S. Enteritidis*, *S. Infantis*, *S. Muenchen*, *S. Typhimurium*, *S. Bovismorbificans*, which accounted for 64.4% of the studied strains. *S. Enteritidis* strains predominated in the sporadic incidence, and *S. Infantis* — in food products and environment. In the meantime, *S. Typhimurium* ranked 3rd by detection frequency in various sources.

The comparison of the levels of resistance to the main AMA classes of the entire collection of strains in our study with the results of previous studies showed

a similar picture. According to S.A. Egorova et al., in St. Petersburg and the Leningrad region in 2014–2018 the percentage of resistant strains of non-typhoidal *Salmonella* averaged 78.6%, and that of strains resistant to quinolones was 63.3% [10], which correlates with the results of our study (72.2 and 61.3%, respectively). At the same time, the proportion of strains resistant to cepheims was almost 2 times lower: 1.6% versus 4.7%. Interestingly, the proportion of identified strains with an MDR phenotype was also 2 times lower — 13.0% versus 25.7% in our study, which may be due to differences in the sample of strains relative to the isolation sources. The detection frequency of *Salmonella* strains with the MDR phenotype in the European Union (28.6%) is close to our average data for the entire collection of strains [19]. According to the report of the National Antimicrobial Resistance Monitoring System for Enteric Bacteria (NARMS),⁸ the proportion of clinical strains with the MDR phenotype among non-typhoidal *Salmonella* in the United States was 9.3% in 2018, which is 2 times higher compared to the proportion of strains with MDR, which belonged to outbreak incidence (4.6%) in our study, but is almost 3 times lower when compared with strains found in sporadic incidence (26.7%). The proportion of clinically resistant strains to certain AMA classes, such as quinolones and cepheims, identified in the USA was 8.5 and 3.5%, respectively; in our study, these figures corresponded to 68.0 and 0.0% for strains with outbreak incidence, and 51.1 and 7.0% for sporadic cases of disease. The significant discrepancy in quinolone resistance is explained, among other things, by differences in the interpretation criteria of CLSI and EUCAST.

The comparative analysis of *Salmonella* strains from different sources made it possible to identify a number of patterns. Resistance levels to many AMA classes (penicillins, β -lactam combination agents, folate pathway antagonists, and tetracyclines) were higher in strains not associated with outbreak incidence. This observation is consistent with earlier studies showing that the acquisition of resistance, particularly through horizontal genes transfer, can reduce the adaptiveness and competitiveness of the microorganisms (fitness of bacteria) having a detrimental effect on the vital physiological processes of the bacterium [20, 21]. Based on our data, this may manifest in a decrease in the virulent properties of *Salmonella* and, as a consequence, a decrease in the epidemic potential.

The highest percentage of tetracycline-resistant strains was found in food products, and environmental strains had the highest frequency of lipopeptide resistance. The only AMA class to which resistance manifested at a high level across different sources were

⁸ Centers for Disease Control and Prevention. National Antimicrobial Resistance Monitoring System for Enteric Bacteria (NARMS): human isolates final report, 2019. Atlanta; 2023.

quinolones. The high frequency of quinolone-resistant *Salmonella* strains among various sources can be explained by the widespread use of this group of AMAs in animal husbandry. The chemical stability of this group of antibiotics and their ability to accumulate in various environmental objects in low concentrations leads to the emergence and selection of antibiotic-resistant forms of bacteria most effectively [22, 23]. Moreover, chromosomal mutations associated with intermediate-level quinolone resistance in *S. Enteritidis* do not affect the adaptiveness level of the microorganism [24].

In our study, the percentages of susceptible and resistant strains from sporadic incidence and environmental sources (samples from water bodies and wastewater) were similar, but these isolation sources differed significantly in the diversity of dominant serotypes. According to data published earlier [25, 26], despite the leading position of *S. Enteritidis* among clinical isolates, this serotype was rarely found in wastewater specimens, while *S. Infantis* was the dominant serotype in terms of isolation frequency. The data obtained may indicate poor survival rate of *S. Enteritidis* strains in the environment compared to other serotypes. If we consider the ratio of strains resistant to AMA classes for these isolation sources, we can see that resistance to quinolones, penicillins, β -lactam combination agents and tetracyclines remained at approximately the same level. However, strains isolated from the environment were more resistant to lipopeptides and folate pathway antagonists.

It is noteworthy that the highest percentage of resistant *Salmonella* strains, including MDR, are associated with food. A significant contribution to the resistance to AMAs for this source was made by *S. Infantis* strains with their dominant resistance to quinolones (92.4%), tetracyclines (76.5%), folate pathway antagonists (45.4%), phenicols (24.4 %), penicillins (23.5%) and β -lactam combination agents (23.5%). In addition, this serotype had the highest percentage of strains resistant to third-generation cephalosporins (9.2%), which may indicate the production of β -lactamases. The spread of *S. Infantis* clones with the MDR phenotype is recorded throughout the world [27–29]. According to NARMS, between 2018 and 2019, the number of MDR *Salmonella* isolates obtained from chicken meat product samples increased from 22% to 29%, while the percentage of MDR isolates from retail chicken meat increased from 20% to 32%⁹. A significant contribution to the increase in the spectrum of resistance was made by an increase in the number of detected isolates of *S. Infantis* with the MDR phenotype, which may be a consequence of the use of AMAs

such as ampicillin, co-trimoxazole, chloramphenicol, and tetracycline in human and veterinary medicine [11, 30, 31]. The resistance of *Salmonella* strains isolated from food products to penicillins and tetracyclines in our study (26.8 and 49.0%, respectively) correlates with the data from the European Food Safety Authority (EFSA) [32], in which the resistance of *Salmonella* strains isolated from broiler and turkey carcasses to ampicillin and tetracycline reached 18.8–19.1 and 48.1–50.3%, respectively.

The analysis of the data obtained allowed identifying the resistance features of clinical strains of *Salmonella*, which were detected in different epidemiological situations: outbreak and sporadic incidence in people. Thus, outbreaks of salmonellosis were characterized by the highest percentage of strains resistant to 1–2 AMA classes (67.3%) and the lowest percentage of MDR strains (4.6%). On the contrary, the proportion of MDR strains isolated in sporadic incidence was 5.8 times higher than for outbreak incidence, which is explained by the significant contribution of *S. Typhimurium* strains and other serotypes to the total resistance. Like outbreak strains, sporadic strains were more often resistant to quinolones, which is confirmed by the dominant resistance of the *S. Enteritidis* (70.0%) and *S. Muenchen* (78.0%) serotypes to this AMA class. Resistance to penicillins (22.6%), β -lactam combination agents (21.9%), and tetracyclines (21.9%) was significantly influenced by the presence of *S. Typhimurium* strains, which were more often resistant to these AMA classes. Similar data were published in a joint report by EFSA and the European Center for Disease Prevention and Control in 2022 [32], which stated that a high percentage of MDR *Salmonella* strains (25.4%) isolated from humans in 2019–2020 was justified by the significant contribution of *S. Typhimurium* and *S. Kentucky* resistant strains. High levels of resistance to ampicillin (29.8%), sulfonamides (30.1%), and tetracyclines (31.2%) varied by serotype from low for *S. Enteritidis* to extremely high for *S. Typhimurium* and *S. Kentucky*.

Over the period of many years of monitoring, *S. Enteritidis* remains the main serotype causing outbreak incidence of salmonellosis [33]. Our data demonstrate that both among outbreak and sporadic cases of salmonellosis, the dominant serotype was *S. Enteritidis*. In addition, this serotype occupied the second ranking position (16.3%) when isolated from food products. Comparison of *S. Enteritidis* strains from outbreak and sporadic cases showed a slight difference in the number of resistance profiles and a low level of resistance to many AMA classes, except for quinolones. However, despite the higher number of strains from outbreaks (2.5 times higher than sporadic ones), the diversity of resistance profiles was significantly lower. Another feature of *S. Enteritidis* is the high rate of occurrence of strains with resistance to quinolones, which amounted to 70.0%, which is consistent with the data from studies

⁹ Centers for Disease Control and Prevention. National Antimicrobial Resistance Monitoring System for Enteric Bacteria (NARMS): human isolates final report, 2019. Atlanta; 2023. URL: <https://www.fda.gov/animal-veterinary/national-antimicrobial-resistance-monitoring-system/2019-narms-update-integrated-report-summary> (дата обращения 07.09.2023)

conducted in St. Petersburg [10], where the resistance of *S. Enteritidis* strains isolated from humans was 71.0%. According to the NARMS surveillance system¹⁰, *S. Enteritidis* strains were the most common serotype among isolates with reduced ciprofloxacin susceptibility in 2019, accounting for 45% of *Salmonella* isolated from humans. It is known that resistance to quinolones in *Salmonella* can be caused by the presence of horizontally (plasmids, transposons, integrons) and vertically (chromosomal mutations) inherited genetic traits [34]. It was shown that the contribution of chromosomal mutations to quinolone resistance for *S. Enteritidis* was significantly higher [35]. The percentage of *Salmonella* strains resistant to quinolones due to single nucleotide substitutions in the region of the DNA gyrase and topoisomerase IV genes reached 97.54%, while the presence of plasmid-mediated resistance was detected only for 1.1% of strains [36].

The second rank by the number of strains isolated from humans was occupied by the *S. Muenchen* serotype (12.6%). It was also the etiological agent in two outbreaks of salmonellosis during the four-year observation period. An increase in the incidence of this serotype is recorded both in individual regions of Russia [37, 38] and in other countries [39]. According to the *Salmonella* Monitoring Reference Center¹¹ for 2021, *S. Muenchen* occupied the 5th ranking position in terms of frequency of isolation from humans and food products and the 6th position — from the environment. It is interesting

to note that in our study, *S. Enteritidis* and *S. Muenchen* had the least diversity of resistance profiles and did not differ significantly from each other.

Conclusion

In the presented study, we have described the phenotypic resistance of *Salmonella* and compared the diversity of resistance profiles of the most common serotypes in Russia, based on a sample of representative strains of non-typhoidal *Salmonella*. A significant contribution to the population of resistant *Salmonella* is made by strains that are not related to the outbreak incidence. Almost half (57.6%) of the studied strains were resistant to at least one AMA class, among which the most frequently detected resistance was to quinolones, tetracyclines, penicillins, and folate pathway antagonists, which have been applied for a long time or are currently used in human and veterinary medicine. In addition, non-typhoidal *Salmonella* isolated from various sources had a wide variety of resistance profiles. Among them, the largest number of strains characterized by resistance were found among serotypes *S. Infantis*, *S. Typhimurium*, and *S. Bovismorbificans*.

Continuous monitoring of antibiotic resistance and tracking of MDR in *Salmonella* strains plays a key role in addressing the issue of antibiotic resistance and provides valuable information for epidemiological surveillance in order to develop prevention strategies.

¹⁰ Centers for Disease Control and Prevention. National Antimicrobial Resistance Monitoring System for Enteric Bacteria (NARMS): human isolates final report, 2019. Atlanta; 2023.

¹¹ Rozhnova S.Sh., Podkolzin A.T., Kuleshov K.V. et al. Information Bulletin of *Salmonella* Monitoring Reference Center No. 34. Moscow; 2022.

СПИСОК ИСТОЧНИКОВ | REFERENCES

1. Majowicz S.E., Musto J., Scallan E., et al. The global burden of nontyphoidal *Salmonella gastroenteritis*. *Clin. Infect. Dis.* 2010;50(6):882–9.
DOI: <https://doi.org/https://doi.org/10.1086/650733>
2. Scallan E., Hoekstra R.M., Angulo F.J., et al. Foodborne illness acquired in the United States — major pathogens. *Emerg. Infect. Dis.* 2011;17(1):7–15.
DOI: <https://doi.org/10.3201/eid1701.P11101>
3. Chen H.M., Wang Y., Su L.H., Chiu C.H. Nontyphoid *Salmonella* infection: microbiology, clinical features, and antimicrobial therapy. *Pediatr. Neonatol.* 2013;54(3):147–52.
DOI: <https://doi.org/10.1016/j.pedneo.2013.01.010>
4. Иванов А.С. Современные представления об антибиотикорезистентности и антибактериальной терапии сальмонеллезов. *Клиническая микробиология антимикробная химиотерапия*. 2009;11(4):305–26. Ivanov A.S. Antimicrobial resistance and therapy of salmonella infections. *Clinical Microbiology and Antimicrobial Chemotherapy*. 2009;11(4):305–26.
EDN: <https://elibrary.ru/kyiwwn>
5. Тапальский Д.В., Осипов В.А., Жаворонок С.В. и др. Проблемы устойчивости сальмонелл к клинически значимым антибактериальным препаратам. *Проблемы здоровья и экологии*. 2005;(1):103–10. Tapal'skiy D.V., Osipov V.A., Zhavoronok S.V., et al. The problems of resistance of salmonellas to clinically significant antibiotics. *Health and Ecology Issues*. 2005;(1):103–10.
DOI: <https://doi.org/10.51523/2708-6011.2005-2-1-20>
EDN: <https://elibrary.ru/yufosd>
6. Van T.T., Nguyen H.N., Smooker P.M., Coloe P.J. The antibiotic resistance characteristics of non-typhoidal *Salmonella enterica* isolated from food-producing animals, retail meat and humans in South East Asia. *Int. J. Food Microbiol.* 2012;154(3):98–106.
DOI: <https://doi.org/10.1016/j.ijfoodmicro.2011.12.032>
7. Mała L., Popowska M. Antimicrobial resistance of *Salmonella* spp. isolated from food. *Rocz. Panstw. Zakł. Hig.* 2016;67(4):343–58.
8. Павлова А.С., Егорова А.Е., Крутова Н.Е. и др. Распространенность и характеристика БЛРС-продуцирующих штаммов *Salmonella enterica*, циркулирующих на территории России (2016–2020 гг.). *Клиническая микробиология антимикробная химиотерапия*. 2022;24(3):236–47. Pavlova A.S., Egorova A.E., Krutova N.E., et al. The prevalence and characterization of ESBL-producing strains of *Salmonella enterica* circulating in the territory of the Russian Federation (2016–2020). *Clinical Microbiology and Antimicrobial Chemotherapy*. 2022;24(3):236–47. DOI: <https://doi.org/10.36488/cmacc.2022.3.236-247>
EDN: <https://elibrary.ru/nukwkwf>
9. Zinsstag J., Schelling E., Waltner-Toews D., Tanner M. From "one medicine" to "one health" and systemic approaches to health and well-being. *Prev. Vet. Med.* 2011;101(3-4):148–56.
DOI: <https://doi.org/10.1016/j.prevetmed.2010.07.003>
10. Егорова С.А., Кафтырева Л.А., Сужаева Л.В. и др. Устойчивость к антимикробным препаратам и клинически значимые механизмы резистентности штаммов *Salmonella*, выделенных в 2014–2018 гг. в Санкт-Петербурге, Россия. *Клиническая лабораторная диагностика*. 2019;64(10):620–6. Egorova S.A., Kaftyreva L.A., Suzhaeva L.V., et al. Antimicrobial resistance and clinical significant resistance mechanisms of *Salmonella* isolated in 2014–2018 in St. Petersburg, Russia. *Russian Clinical Laboratory Diagnostics*. 2019;64(10):620–6.
DOI: <https://doi.org/10.18821/0869-2084-2019-64-10-620-626>
EDN: <https://elibrary.ru/wnxhri>
11. Решетнева И.Т., Перьянова О.В., Дмитриева Г.М., Остапова Т.С. Антибиотикорезистентность сальмонелл, выделенных на территории Красноярского края. *Гигиена и санитария*. 2015; 94(2):35–8. Reshetneva I.T., Per'yanova O.V., Dmitrieva G.M., Ostapova T.S. Antibiotic resistance of *Salmonella* spp. isolated in the territory of the Krasnoyarsk region. *Hygiene & Sanitation*. 2015;94(2):35–8.
EDN: <https://elibrary.ru/tphjlx>
12. Кузнецова Н.А., Соловьева А.С., Раков А.В. Чувствительность к антибиотикам у штаммов *Salmonella*. *Здоровье. Медицинская экология. Наука*. 2018;(3):50–8. Kuznetsova N.A., Solov'eva A.S., Rakov A.V. Antibiotic resistance of *Salmonella*. *Health. Medical Ecology. Science*. 2018;(3):50–8. DOI: <https://doi.org/10.5281/zenodo.1488030>
EDN: <https://elibrary.ru/ytdulb>
13. Евмененкова И.Г., Мурач Л.В. Анализ резистентности штаммов *Salmonella* spp. к антибиотикам в Смоленском регионе за 2012–2017 гг. *Смоленский медицинский альманах*. 2018;(1):93–6. Evmenenkova I.G., Murach L.V. Analysis of resistance of strains of *Salmonella* spp. to antibiotics in the Smolensk region for 2012–2017. *Smolensk Medical Almanac*. 2018;(1):93–6. EDN: <https://elibrary.ru/xtfirl>
14. Шитова О.И., Казьянин А.В., Захарова Ю.А. Эпидемиологические особенности, биологическая характеристика и чувствительность к антимикробным препаратам сальмонелл, циркулирующих в Пермском крае. *Сибирский медицинский журнал (г. Томск)*. 2011;26(2-2):116–20. Shitova O.I., Kaz'yanin A.V., Zakharova Yu.A. Epidemiological aspects, biological characteristics and sensitivity to antimicrobial agents of salmonellas circulating in Perm region. *The Siberian Medical Journal*. 2011;26(2-2):116–20.
EDN: <https://elibrary.ru/nupzpv>
15. Peters T.M. Pulsed-field gel electrophoresis for molecular epidemiology of food pathogens. *Methods Mol. Biol.* 2009;551:59–70. DOI: https://doi.org/10.1007/978-1-60327-999-4_6
16. Hutcheson K. A test for comparing diversities based on the Shannon formula. *J. Theor. Biol.* 1970;29(1):151–4.
DOI: [https://doi.org/10.1016/0022-5193\(70\)90124-4](https://doi.org/10.1016/0022-5193(70)90124-4)
17. San Martín B., Lapiere L., Toro C., et al. Isolation and molecular characterization of quinolone resistant *Salmonella* spp. from poultry farms. *Vet. Microbiol.* 2005;110(3-4):239–44.
DOI: <https://doi.org/10.1016/j.vetmic.2005.07.005>
18. Edelstein M., Pimkin M., Dmitrachenko T., et al. Multiple outbreaks of nosocomial salmonellosis in Russia and Belarus caused by a single clone of *Salmonella enterica* serovar *Typhimurium* producing an extended-spectrum beta-lactamase. *Antimicrob. Agents Chemother.* 2004;48(8):2808–15.
DOI: <https://doi.org/10.1128/AAC.48.8.2808-2815.2004>
19. European Food Safety Authority and European Centre for Disease Prevention and Control (EFSA and ECDC). The European Union summary report on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in 2017. *EFSA J.* 2018;16(12):e05500.
DOI: <https://doi.org/10.2903/j.efsa.2018.5500>
20. Gillespie S.H. Antibiotic resistance in the absence of selective pressure. *Int. J. Antimicrob. Agents*. 2001;17(3):171–6.
DOI: [https://doi.org/10.1016/s0924-8579\(00\)00340-x](https://doi.org/10.1016/s0924-8579(00)00340-x)
21. Zhang Q., Sahin O., McDermott P.F., Payot S. Fitness of antimicrobial-resistant *Campylobacter* and *Salmonella*. *Microbes Infect.* 2006;8(7):1972–8.
DOI: <https://doi.org/10.1016/j.micinf.2005.12.031>
22. Janecko N., Pokludova L., Blahova J., et al. Implications of fluoroquinolone contamination for the aquatic environment — a review. *Environ. Toxicol. Chem.* 2016;35(11):2647–56.
DOI: <https://doi.org/10.1002/etc.3552>
23. Kümmerer K. *Pharmaceuticals in the Environment: Sources, Fate, Effects and Risks*. Heidelberg: Springer Verlag; 2008.
DOI: <https://doi.org/10.1007/978-3-540-74664-5>
24. O'Regan E., Quinn T., Frye J.G., et al. Fitness costs and stability of a high-level ciprofloxacin resistance phenotype in *Salmonella enterica* serotype enteritidis: reduced infectivity associated with decreased expression of *Salmonella* pathogenicity island 1 genes. *Antimicrob. Agents Chemother.* 2010;54(1):367–74.
DOI: <https://doi.org/10.1128/AAC.00801-09>

25. Masarikova M., Manga I., Cizek A., et al. *Salmonella enterica* resistant to antimicrobials in wastewater effluents and black-headed gulls in the Czech Republic, 2012. *Sci. Total Environ.* 2016;542(Pt. A):102–7. DOI: <https://doi.org/10.1016/j.scitotenv.2015.10.069>
26. Koivunen J., Siitonen A., Heinonen-Tanski H. Elimination of enteric bacteria in biological-chemical wastewater treatment and tertiary filtration units. *Water Res.* 2003;37(3):690–8. DOI: [https://doi.org/10.1016/s0043-1354\(02\)00305-6](https://doi.org/10.1016/s0043-1354(02)00305-6)
27. Proietti P.C., Stefanetti V., Musa L., et al. Genetic profiles and antimicrobial resistance patterns of *Salmonella infantis* strains isolated in Italy in the food chain of broiler meat production. *Antibiotics (Basel)*. 2020;9(11):814. DOI: <https://doi.org/10.3390/antibiotics9110814>
28. Bertani A.M.J., Cunha M.P.V., de Carvalho E., et al. Genomic characterization of a multi-drug resistant, CTX-M-65-producing clinical isolate of *Salmonella infantis* isolated in Brazil. *Microbes Infect.* 2022;24(5):104972. DOI: <https://doi.org/10.1016/j.micinf.2022.104972>
29. Burnett E., Ishida M., de Janon S., et al. Whole-genome sequencing reveals the presence of the bla_{CTX-M-65} gene in extended-spectrum β-lactamase-producing and multi-drug-resistant clones of *Salmonella* serovar Infantis isolated from broiler chicken environments in the Galapagos islands. *Antibiotics (Basel)*. 2021; 10(3):267. DOI: <https://doi.org/10.3390/antibiotics10030267>
30. Шадрова Н.Б., Прунтова О.В., Корчагина Е.А. Антибиотикорезистентность изолятов сальмонелл, выделенных из продуктов животного происхождения. *Ветеринария сегодня*. 2022;11(1):27–34. Shadrova N.B., Pruntova O.V., Korchagina E.A. Antimicrobial resistance of *Salmonella* isolates recovered from animal products. *Veterinary Science Today*. 2022;11(1):27–34. DOI: <https://doi.org/10.29326/2304-196X-2022-11-1-27-34> EDN: <https://elibrary.ru/oioussq>
31. Сердюченко И.В., Пестунова С.А., Калмыков З.Т. и др. Использование химического препарата энрофлоксацина в пчеловодстве. *Ветеринарная патология*. 2020;(2):84–90. Serdyuchenko I.V., Pestunova S.A., Kalmykov Z.T., et al. Use of the enrofloxacin in beekeeping. *Veterinary Pathology*. 2020;(2):84–90. DOI: <https://doi.org/10.25690/VETPAT.2020.72.2.011> EDN: <https://elibrary.ru/hveuxe>
32. European Food Safety Authority; European Centre for Disease Prevention and Control. The European Union Summary Report on Antimicrobial Resistance in zoonotic and indicator bacteria from humans, animals and food in 2019–2020. *EFSA J.* 2022;20(3):e07209. DOI: <https://doi.org/10.2903/j.efsa.2022.7209>
33. Кулешов К.В., Павлова А.С., Егорова А.Е. и др. Филогенетический анализ изолятов *Salmonella enterica* subsp. *enterica* серовар *Enteritidis*, ассоциированных со спорадической и групповой заболеваемостью в России. *Эпидемиология и инфекционные болезни. Актуальные вопросы*. 2023;13(2): 76–82. Kuleshov K.V., Pavlova A.S., Egorova A.E., et al. The phylogenomic analysis of *Salmonella enterica* subsp. *enterica* serovar *Enteritidis* isolates associated with sporadic and group morbidity in Russia. *Epidemiology and Infectious Diseases*. 2023;13(2):76–82. DOI: <https://doi.org/10.18565/epidem.2023.13.2.76-82>
34. Wasyl D., Hoszowski A., Zajac M. Prevalence and characterisation of quinolone resistance mechanisms in *Salmonella* spp. *Vet. Microbiol.* 2014;171(3-4):307–14. DOI: <https://doi.org/10.1016/j.vetmic.2014.01.040>
35. Lunn A.D., Fábrega A., Sánchez-Céspedes J., Vila J. Prevalence of mechanisms decreasing quinolone-susceptibility among *Salmonella* spp. clinical isolates. *Int. Microbiol.* 2010;13(1):15–20. DOI: <https://doi.org/10.2436/20.1501.01.107>
36. Wang Y., Liu Y., Lyu N., et al. The temporal dynamics of antimicrobial-resistant *Salmonella enterica* and predominant serovars in China. *Natl Sci. Rev.* 2022;10(3):nwac269. DOI: <https://doi.org/10.1093/nsr/nwac269>
37. Амплеева Н.П., Павелкина В.Ф., Маркина Е.С. Этиологическая структура сальмонеллеза и чувствительность микроорганизмов к антибактериальным препаратам. *Вестник Северо-Восточного федерального университета имени М.К. Аммосова. Серия: Медицинские науки*. 2023;(1): 5–11. Ampleeva N.P., Pavelkina V.F., Markina E.S. Etiological structure of salmonellosis and sensitivity of microorganisms to antibacterial drugs. *Vestnik of North-Eastern Federal University. Medical Sciences*. 2023;(1):5–11. DOI: <https://doi.org/10.25587/SVFU.2023.30.1.011> EDN: <https://elibrary.ru/ulhbwbk>
38. Тарасенко Т.Т., Косенок Е.В., Семейкина Л.М., Шевердина Ф.Н. О заболеваемости сальмонеллезом в Приморском крае. *Здоровье. Медицинская экология. Наука*. 2016;(3):134–9. Tarasenko T.T., Kosenok E.V., Semykina L.M., Sheverдина F.N. On the incidence of salmonellosis in the Primorsky region of Russia. *Health. Medical Ecology. Science*. 2016;(3):134–9. DOI: <https://doi.org/10.18411/hmes.d-2016-128> EDN: <https://elibrary.ru/wmmsuf>
39. Bassal R., Davidovich-Cohen M., Yakunin E., et al. Trends in the epidemiology of non-typhoidal salmonellosis in Israel between 2010 and 2021. *Int. J. Environ. Res. Public Health*. 2023;20(9):5626. DOI: <https://doi.org/10.3390/ijerph20095626>

Information about the authors

Anastasia S. Pavlova[✉] — researcher, Laboratory of molecular diagnostics and epidemiology of enteric infections, Central Research Institute of Epidemiology, Moscow, Russia, a.pavlova@cmd.su, <https://orcid.org/0000-0003-4619-9337>

Konstantin V. Kuleshov — Cand. Sci. (Biol.), Head, Laboratory of molecular diagnostics and epidemiology of enteric infections, Central Research Institute of Epidemiology, Moscow, Russia, <https://orcid.org/0000-0002-5238-7900>

Natalia E. Krutova — junior researcher, Laboratory of molecular diagnostics and epidemiology of enteric infections, Central Research Institute of Epidemiology, Moscow, Russia, <https://orcid.org/0000-0003-2925-5376>

Anna N. Guseva — junior researcher, Laboratory of molecular diagnostics and epidemiology of enteric infections, Central Research Institute of Epidemiology, Moscow, Russia, <https://orcid.org/0000-0001-7028-0253>

Alexandr T. Podkolzin — D. Sci. (Med.), Deputy director for epidemiology, Central Research Institute of Epidemiology, Moscow, Russia, <https://orcid.org/0000-0002-0044-3341>

Author contribution. All authors confirm that they meet the International Committee of Medical Journal Editors criteria for authorship, made a substantial contribution to the conception of the work, acquisition, analysis, interpretation of data for the work, drafting and revising the work, final approval of the version to be published.

The article was submitted 16.07.2023;
accepted for publication 10.10.2023;
published 28.10.2023

Информация об авторах

Павлова Анастасия Сергеевна[✉] — н.с. лаб. молекулярной диагностики и эпидемиологии кишечных инфекций, ЦНИИ Эпидемиологии Роспотребнадзора, Москва, Россия, a.pavlova@cmd.su, <https://orcid.org/0000-0003-4619-9337>

Кулешов Константин Валерьевич — к.б.н., зав. лаб. молекулярной диагностики и эпидемиологии кишечных инфекций ЦНИИ Эпидемиологии Роспотребнадзора, Москва, Россия, <https://orcid.org/0000-0002-5238-7900>

Крутова Наталья Евгеньевна — м.н.с. лаб. молекулярной диагностики и эпидемиологии кишечных инфекций ЦНИИ Эпидемиологии Роспотребнадзора, Москва, Россия, <https://orcid.org/0000-0003-2925-5376>

Гусева Анна Николаевна — м.н.с. лаб. молекулярной диагностики и эпидемиологии кишечных инфекций ЦНИИ Эпидемиологии Роспотребнадзора, Москва, Россия, <https://orcid.org/0000-0001-7028-0253>

Подколзин Александр Тихонович — д.м.н., зам. директора по эпидемиологии, ЦНИИ Эпидемиологии Роспотребнадзора, Москва, Россия, <https://orcid.org/0000-0002-0044-3341>

Участие авторов. Все авторы подтверждают соответствие своего авторства критериям ИСМЖЕ, внесли существенный вклад в проведение поисково-аналитической работы и подготовку статьи, прочли и одобрили финальную версию до публикации.

Статья поступила в редакцию 16.07.2023;
принята к публикации 10.10.2023;
опубликована 28.10.2023