SEROLOGICAL PATTERN AND ANTIMICROBIAL SUSCEPTIBILITY OF *SALMONELLA* ISOLATED FROM PEOPLE AND FOOD ITEMS IN SOUTHERN PROVINCES OF VIETNAM

Egorova S.A.[1],
Truong Quang Nguyen[2],
Kaftyreva L.A.[1,3],
Kozhukhova E.A.[4],
Makarova M.A.[1,3],
Cuong Quoc Hoang[2],
Vu Hoang Nguyen[2],
Huong Thuy Dang[2],
Thi Quynh Lan Tran[5],
Tram Khac Vo[6],
Long Thanh Nguyen[6],
Diep Thi Ngoc Nguyen[6],
Tu Le Kha Bui[6],
Thu Le Kieu Nguyen[6]

[1] Saint Petersburg Pasteur Institute, Saint Petersburg, Russia

[2] Department of Microbiology and Immunology, Pasteur Institute in Ho Chi Minh City, Vietnam

[3] State Institution of Higher Professional Education 'I. I. Mechnikov North-Western State Medical University', Russian Ministry of Health

[4] State Institution of Higher Professional Education 'Pavlov University in Saint Petersburg', Russian Ministry of Health

[5] Faculty of Animal Science and Veterinary Medicine, University of Agriculture and Forestry (Nong Lam University, Ho Chi Minh city), Vietnam.

[6] Department of Animal Husbandry and Veterinary Medicine of Ho Chi Minh City, Vietnam

СЕРОЛОГИЧЕСКАЯ СТРУКТУРА И ЧУВСТВИТЕЛЬНОСТЬ К АНТИБИОТИКАМ ШТАММОВ *SALMONELLA*, ВЫДЕЛЕННЫХ ОТ ЛЮДЕЙ И ИЗ ПИЩЕВЫХ ПРОДУКТОВ В ЮЖНЫХ ПРОВИНЦИЯХ ВЬЕТНАМА

Егорова С. А.[1]
Truong Quang Nguyen[2]
Кафтырева Л. А.[1,3]
Кожухова Е. А.[4]
Макарова М. А.[1,3]
Cuong Quoc Hoang[2]
Nguyen Hoang Vu[2]
Huong Thuy Dang[2]
Thi Quynh Lan Tran[5]
Tram Khac Vo[6]
Long Thanh Nguyen[6]
Diep Thi Ngoc Nguyen[6]
Tu Le Kha Bui[6]
Thu Le Kieu Nguyen[6]

[1] Лаборатория кишечных инфекций, Федеральное бюджетное учреждение науки «Санкт-Петербургский научно-исследовательский институт эпидемиологии и микробиологии им.Пастера» Федеральной службы по надзору в сфере защиты прав потребителей и благополучия населения.
[2] Институт Пастера в г. Хо Ши Мин, Социалистическая Республика Вьетнам
[3] Федеральное государственное бюджетное образовательное учреждение

высшего образования "Северо-Западный государственный медицинский университет им. И.И. Мечникова" Министерства здравоохранения Российской Федерации.

[4] Федеральное государственное бюджетное образовательное учреждение высшего образования «Первый Санкт-Петербургский государственный медицинский университет им. акад. И.П. Павлова».

[5] Факультет животноводства и ветеринарии, Университет сельского и лесного хозяйства, г. Хо Ши Мин, Социалистическая Республика Вьетнам.

[6]Департамент животноводства и ветеринарии г. Хо Ши Мин, Социалистическая Республика Вьетнам

Резюме

В статье представлены современные данные о серогрупповой структуре и чувствительности к антибиотикам штаммов *Salmonella,* выделенных в южных провинциях Социалистической Республики Вьетнам. Всего исследовано 189 штаммов из коллекции Института Пастера в г. Хошимин: выделенных от людей - 86 и из свинины - 103 штамма. Штаммы идентифицировали до серовара с использованием реакции агглютинации на стекле с О- и Н-сыворотками и мультиплексных ПЦР для выявления Н 1- и 2 фазы. Чувствительность к антибиотикам определяли диско-диффузионным методом согласно рекомендациям EUCAST (2019 г.). Штаммы, выделенные от людей, преимущественно принадлежали серогруппе О4 (69,8%), доля штаммов других серогрупп колебалась от 1,2% (редкая группа О16) до 11,6% (О9). Около половины штаммов (44,7%), выделенных из свинины, относились к серогруппе О3,10 (от людей – только 7,0% штаммов); штаммы серогрупп О7, О4 и О8 выделяли значительно реже (22,3%, 14,6% и 13,6%); к группам О9, О13 и О18 принадлежали единичные штаммы. Вне зависимости от источника выделения около 80,0% штаммов *Salmonella* были устойчивы к антибиотикам различных групп (исключая карбапенемы): 70,0% – к тетрациклинам, около половины (54,0, 47,1 и 46,6%) – к пефлоксацину, аминопенициллинам и хлорамфениколу, почти 40% – к триметоприм/сульфаметоксазолу и налидиксовой кислоте. Доля устойчивых к цефтриаксону и гентамицину была значительно выше у штаммов, выделенных от людей, чем из свинины: 12,8 и 1,0%, 30,2 и 1,9%, соответственно. Множественной резистентностью (к 3 и более группам антибиотиков) обладали 62,8% штаммов, выделенных от людей и 43,7% - из свинины. Следует отметить, что резистентность к 6 группам антибиотиков чаще выявляли у штаммов, выделенных от людей, чем из свинины (15,1% и 1,0%, соответственно). Множественную резистентность отмечали у штаммов различных сероваров, но преимущественно у S. Typhimurium (36,4%).

Наиболее часто встречали фенотип множественной устойчивости AMP,TE,QN,C,SXT (30,3%), выявленный у штаммов сероваров S. Typhimurium, S. Bredeney, S. Corvallis, S. Give, S. London, S. Rissen, S. Meleagridis.

Таким образом, у штаммов *Salmonella,* выделенных в южных провинциях Вьетнама, выявлена устойчивость к современным препаратам выбора (фторхинолонам и цефалоспоринам), что, наряду с потерей чувствительности к «традиционным» антибиотикам (ампициллин, хлорамфеникол, триметоприм/ сульфаметоксазол), существенно сокращает арсенал антимикробных (этиотропных) препаратов, потенциально эффективных для терапии осложненных форм сальмонеллеза.

Ключевые слова: *Salmonella*, устойчивость к антибиотикам, множественная резистентность, Вьетнам, серовар.

Abstract

This article presents current relevant data on the serogroup pattern and antibiotic susceptibility of *Salmonella* strains isolated in the southern provinces of the Socialist Republic of Vietnam. There were examined 189 *Salmonella* strains isolated from: human feces in acute diarrhea (86 strains); and pork samples (103 strains). Serological O-group identification was performed by slide agglutination with O- and H- antisera and multiplex PCR to detect H phase-1 and phase-2. Antimicrobial susceptibility testing was performed by using the disk-diffusion method according to the EUCAST (version 2019) recommendations. Strains isolated from humans predominantly belonged to O4 group (69.8%). The percentage of other serogroups varied from 1.2% (rare group O16) to 11.6% (O9). About a half of strains (44.7%) isolated from pork samples turned out to belong to the O3,10 serogroup (versus 7.0% of strains from humans). Serogroups O7, O4 and

O8 were less frequent (22.3%, 14.6% and 13.6%, respectively). Single strains belonged to serogroups O9, O13, and O18.

Regardless of the isolation source, about 80% of *Salmonella* strains were resistant to antibiotics from different antimicrobial groups (besides carbapenems): 67.0% were resistant to tetracycline; about half were resistant to pefloxacin, ampicillin and chloramphenicol (54.0%, 47.1%, 46.6%); and up to 40% were resistant to trimethoprim/sulfamethoxazole and nalidixic acid. The proportion of strains resistant to ceftriaxone and gentamycin was markedly higher in those of human vs. pork origin: 12.8% vs. 1.0% and 30.2 vs 1.9%, respectively. Moreover, 62.8% and 43.7% strains of human and pork origin, respectively, showed multidrug resistance (to 3 and more antimicrobial groups). In addition, simultaneous resistance to 6 antimicrobial groups was detected much more frequently in *Salmonella* strains isolated from humans vs. pork samples (15.1% vs. 1.0%, respectively). Multidrug resistance (MDR) was observed in strains of different serovars, predominantly S. Typhimurium (36.4%). The predominant MDR (30.3%) phenotype (AMP, TE, QN, C, SXT) was revealed in serovars of S. typhimurium, S. bredeney, S. corvallis, S. give, S. london, S. rissen, and S. meleagridis. Thus, *Salmonella* strains isolated in the southern Vietnamese provinces featured resistance to fluoroquinolones and cephalosporins. Taking into account simultaneous loss of susceptibility to 'old' antimicrobials (ampicillin, chloramphenicol, trimethoprim/sulfamethoxazole), it crucially restricts the list of effective medicines to treat complicated salmonellosis cases.

Keywords: *Salmonella*, antimicrobial resistance, multidrug resistance, Vietnam, serovar

Introduction. According to WHO data, from 1 to 1.7 billion cases of acute diarrhea are registered annually. Thus, they are the leading infectious illness, followed only by acute respiratory infection. Globally, acute diarrhea accounts for more than 500,000 deaths in children, occupying second place in mortality in those younger than 5 years old (https://www.who.int/news-room/fact-sheets/detail/diarrhoeal-disease). In Russia as well as in European countries, the causative agents in up to 70% of acute diarrheal cases (especially food-borne outbreaks) are Rotavirus and Norwalk viruses. The most widespread bacterial agents of acute diarrhea cases are *Salmonella* and *Campylobacter* [8, 12]. Salmonellosis is known to have different clinical patterns, predominantly resulting from digestive tract effects, with potential to spread beyond it with development of toxic and dehydration syndromes of various severity. *Salmonella* has potential to cause food-born infection with small and large outbreaks [12].

In Vietnam, the prevalence of acute diarrhea in infants is 271 per 1000 children. In more than 70% of cases, there were detected such viruses as Rotavirus (50.0% of samples) and Norwalk (24.0%). Among bacterial agents, *Campylobacter* (20.0%), *Salmonella* (18.0%), and *Shigella* (16.0%) were found [9,15]. In 2009 – 2010 in Ho Chi Minh City, non-typhoid *Salmonella* were detected in 5.4% of acute diarrhea cases in children under 5 years old [24]. Compared to Russia, where serovar S. Enteritidis accounts for more than 80.0% of cases and has dominated for many years, in Vietnam the serogroup spectrum of *Salmonella* isolated both from humans and food is more diverse. For example, an examination of adult hospitalized cases in 2008-2013 revealed S. Enteritidis and S. Typhimurium in 48.0% and 26.0% of cases, respectively [20]. *Salmonella* isolated from healthy food workers in different years belonged to different serogroups and serovars. For example, *Salmonella* isolates in 2011 were as follows: serogroup E (32.7%); serovar S. Paratyphi B (29.1%); and serogroups C and B (18.2% and 10.9%, respectively). Strains isolated in 2012 belonged to: S. Enteritidis (30.0%); serogroup B (17.5%); serogroups C and D (except S. Enteritidis) (12.5%); and serogroups A and E (10.0%). In 2013, strains

from serogroups B, E, and C dominated (55.6%, 22.2% and 16.7%, respectively) [23].

In Vietnam, there have been many examinations of samples taken from food-producing animals, poultry, prawns, fish, and food items as potential sources and vehicles of *Salmonella* transmission to humans. High levels of contamination with *Salmonella* (belonging to 28 - 53 serogroups) have been described [16, 17, 19, 22, 25, 26, 27].

Examination of pigs and chickens revealed that contaminated samples were found in 50.0% of poultry farms and in 70.0% of pig breeding farms. The isolates belonged to 28 serovars, with leading of: *S.* Weltevreden (up to 20.0%); S. Typhimurium (12.0%); and *Salmonella* 4:12: i:- (11%) [17, 25]. *S.* Weltevreden was detected in every forth shrimp farm in the Mekong delta covering three Vietnamese provinces [19]. Some studies (2004 - 2016 in provinces of Southern Vietnam) showed that the prevalence of *Salmonella* isolated from pigs increased significantly from 5.2% to 64.4% of samples. In Vinh Long, *Salmonella* was isolated from sick and healthy pigs (61.5% and 8.8%, respectively). In Dong Thap, the percentage of *Salmonella* contaminated samples was 64.7% in chickens and 91.3% in pigs [16,27].

Antimicrobial therapy is usually prescribed: to patients with systemic (invasive) salmonellosis; middle or severe course (e.g., fever longer than 48 hours); age less than 6 months or more than 50 years; with immune deficiency; or with severe concurrent diseases. Empiric therapy suggests prescribing fluoroquinolones, extended spectrum cephalosporins, or trimethoprim/sulfamethoxazole [1,6,10,21]. However, *Salmonella* isolated from humans, animals, and food items is displaying increasing antimicrobial resistance in many countries [13]. In Russia, the percentage of such *Salmonella* strains (isolated from humans, animals, and food items) is up to 50-70.0% [2,3,4,5,7].

Most *Salmonella* strains (about 60.0%) examined by different researchers in 2004-2017 in Vietnam were resistant to such antibiotics as: ampicillin (more than 40.0% of strains); tetracycline (more than 50.0%); trimethoprim/sulfamethoxazole

(up to 60.0%); chloramphenicol (up to 50.0%); and ciprofloxacin (more than 30.0% of strains) [16-19,22,23,25-28]. According to different research data, from 17 to 52.2% of strains had multidrug resistance (MDR). S. Kentucky ST198 was considered the most frequent MDR serovar, with high levels of resistance to β-lactams and quinolones.

Notably, there was one strain (from pork) exhibiting colistin resistance. It is the first colistin-resistant *Salmonella* found in meat in Vietnam [18,28]. Some data indicate that the percentage of *Salmonella* strains producing ESBL (TEM and CTX genetic families) is equal to 5.3%. Strains predominantly belonged to serogroup B, with S. Paratyphi B included [23]. This study's objective was to characterize the serogroup structure and to evaluate antimicrobial susceptibility of *Salmonella* isolated from humans and food samples in South Vietnam.

Materials and methods. The study was performed within a framework of scientific cooperation between the Saint Petersburg Pasteur Institute and the Pasteur Institute in Ho Chi Minh City. The samples studied were 189 *Salmonella* strains isolated in South Vietnam: 86 strains from feces of humans with acute diarrhea; and 103 from pork samples.

Salmonella serological identification to O-group was first determined by slide agglutination with O-group antisera (Saint Petersburg Scientific Research Institute of Vaccine and Serum, Russia). Phase-1 and phase-2 were then detected by multiplex PCR [11,14], with subsequent confirmation by slide agglutination with phase-1 and phase-2 antisera.

Antimicrobial susceptibility testing was done according EUCAST recommendations (version 2019, https://www.eucast.org/ast_of_bacteria/) by the disk-diffusion method with Mueller-Hinton agar and antibiotic disks (Oxoid). The tested antimicrobials belonged to different antibiotic classes: β-lactams (ampicillin, ceftazidime, ceftriaxone, meropenem); quinolones (nalidixic acid, pefloxacin); tetracycline; phenicols (chloramphenicol); trimethoprim/sulfamethoxazole;

polymyxins (colistin); and aminoglycosides (gentamycin, amikacin). Results were interpreted according EUCAST criteria, version 2019 (https://www.eucast.org/fileadmin/ src/media/PDFs/EUCAST_files/Breakpoint_tables/v_9.0_Breakpoint_Tables.pdf). For the category 'resistant to fluoroquinolones', the following breakpoints (zone of inhibition) were used: pefloxacin < 24 mm; and nalidixic acid < 16 mm.

Results. *Salmonella* strains belonged to several O-groups (Table 1): O4 (B) – 75 strains (39.7%); O3,10 (E) – 52 strains (27.5%); O7 (C_1) – 30 (15.9%); O8 (C_2) – 16 (8.5%); O9 (D) – 12 (6.3%); and to rare groups – 4 strains (2.1%). Some differences in serogroup spectrum were revealed in strains isolated from humans versus those from pork items as presented in Figure 1.

Strains isolated from humans predominantly belonged to group O4 (69.8%). The percentages of other serogroups varied from 1.2% (rare groups) to 11.6% (O9). About half of strains isolated from pork (44.7%) belonged to serogroup O3,10 (versus 7.0% in strains from humans). Serogroups O7, O4, and O8 were less frequent (22.3%, 14.6% and 13.6%, respectively). Single strains from pork belonged to serogroups O9, O13, and O18. It is worth mentioning the obvious difference in proportions of serogroup O4 and O9 in strains isolated from pork (14.6% and 1.9%, respectively) versus those from humans (69.7% and 11.6%, respectively).

The studied *Salmonella* strains were resistant (about 80%) to antibiotics from different antimicrobial groups. More than half of strains (52.4%) had MDR to 3 or more antimicrobial groups (Table 2). For the majority of antimicrobials tested, there was no significant difference in the proportion of resistant strains (resistant/overall) in terms of sample source (humans, pork).

Up to 70.0% of strains were resistant to tetracycline. About half of strains were resistant to pefloxacin, ampicillin, and chloramphenicol. About 40% were resistant to trimethoprim/sulfamethoxazole and nalidixic acid. However, it’s worth mentioning that in pork strains none featured resistance to amoxicillin/clavulanic

acid, ceftazidime and amikacin. The proportion of strains resistant to ceftriaxone and gentamycin, in those from humans versus those from pork, were significantly different: 12.8% vs.1.0%; and 30.2 vs 1.9%, respectively (Table 2). Noteworthy is the fact that 16.4% of *Salmonella* strains were resistant to pefloxacin, but susceptible to nalidixic acid. This indicates transferable resistance mechanisms to fluoroquinolones. All tested *Salmonella* strains were susceptible to carbapenems.

Multidrug resistant *Salmonella* strains were identified in samples both from humans and pork (62.8% and 43.7%, respectively) (Table 3). However, simultaneous resistance to 6 antimicrobials was detected much more frequently in *Salmonella* strains isolated from humans than in those isolated from pork (15.1% vs. 1.0%, respectively).

In general, MDR was detected in 52.4% (n=99) of *Salmonella* belonging to different serovars, but serovar S. Typhimurium represented the biggest proportion of MDR strains (36.4%, n=36). The predominant MDR phenotype (AMP, TE, QN, C, SXT) was detected in 30.3% of MDR strains belonging to serovars S. Typhimurium, S. Bredeney, S. Corvallis, S. Give, S. London, S. Rissen, and S. Meleagridis. Most of these strains were isolated from pork samples.

Discussion. Our research results suggest that in southern provinces of Vietnam, *Salmonella* strains isolated from people predominantly belonged to serogroup O4 (about 70.0%). The proportion of strains belonging to other serogroups (13-15 serovars) was much lower, varying from 1.2% to 11.6%. The spectrum of *Salmonella* strains isolated in Vietnam differs significantly from that in Russia, where more than 70.0% of strains isolated from humans belong to serogroup O9 (*S. Enteritidis*) [8]. The difference likely results from the Vietnamese tradition of consuming sea food, which is frequently contaminated by *Salmonella* strains of a broad spectrum serovars (such as *S.* Weltevreden, S. Senftenberg, *S.* Rissen, *S.* Lexington, *S.* Saintpaul, *S.* Newport, *S.* Albany, *S.* Anatum, and others). About a half

of strains isolated from pork belonged to serogroup O3,10, whereas 35 *Salmonella* serovars were isolated in total.

Our data are consistent with results of other studies. Analysis of raw meat samples, taken in markets and supermarkets in different cities and provinces of Vietnam, revealed a high level of *Salmonella* contamination: 58.3% of beef samples; up to 70.0% of pork; up to 65.0% of chicken meat; up to 50.0% of cultured shrimp; and 37.0% of cultured fish. The serovar spectrum varied from 14 to 53: S. Weltevreden, S. Rissen, S. Anatum, S. London, S. Derby, S. Infantis, S. Typhimurium, S. Reading, S. Agona, S. Dabou, S. Albany, S. Emek, and S. Corvallis [22,26].

The difference in serogroup spectrum of strains isolated in Vietnam from human and pork samples can likely also be explained by gastronomic (food cooking) traditions in Vietnamese society where seafood, poultry meat, and eggs are considered the main factor in transmission of *Salmonella* to humans.

Our research results suggest that more than 70.0% of *Salmonella* strains (isolated both from human and pork samples in Vietnam) were resistant to antimicrobials. Moreover, every second strain carried an MDR phenotype. The research revealed quite a high percentage of strains resistant to tetracycline (67.2%), fluoroquinolones (54.0%), ampicillin (47.1%), trimethoprim/sulfamethoxazole (42.3%), and chloramphenicol (46.6%). Strains resistant to 3rd/4th generation cephalosporins were seen (6.4%). Our results don’t contradict earlier published research carried out in Vietnam [16-19,22,23,25-28]. Similar research carried out in Russia has suggested that: more than 60% of local *Salmonella* strains are resistant to quinolones; not more than 10.0% are resistant to 'old' antimicrobials (tetracycline, chloramphenicol, ampicillin); and less than 2.0% are resistant to 3rd/4th generation cephalosporins. The percentage of MDR strains was much lower (about 15.0%) versus that in Vietnamese strains [4].

In February 2017, the WHO published a list of antibiotic-resistant 'priority pathogens' listing 12 bacterial species as the most threatening to human health [29].

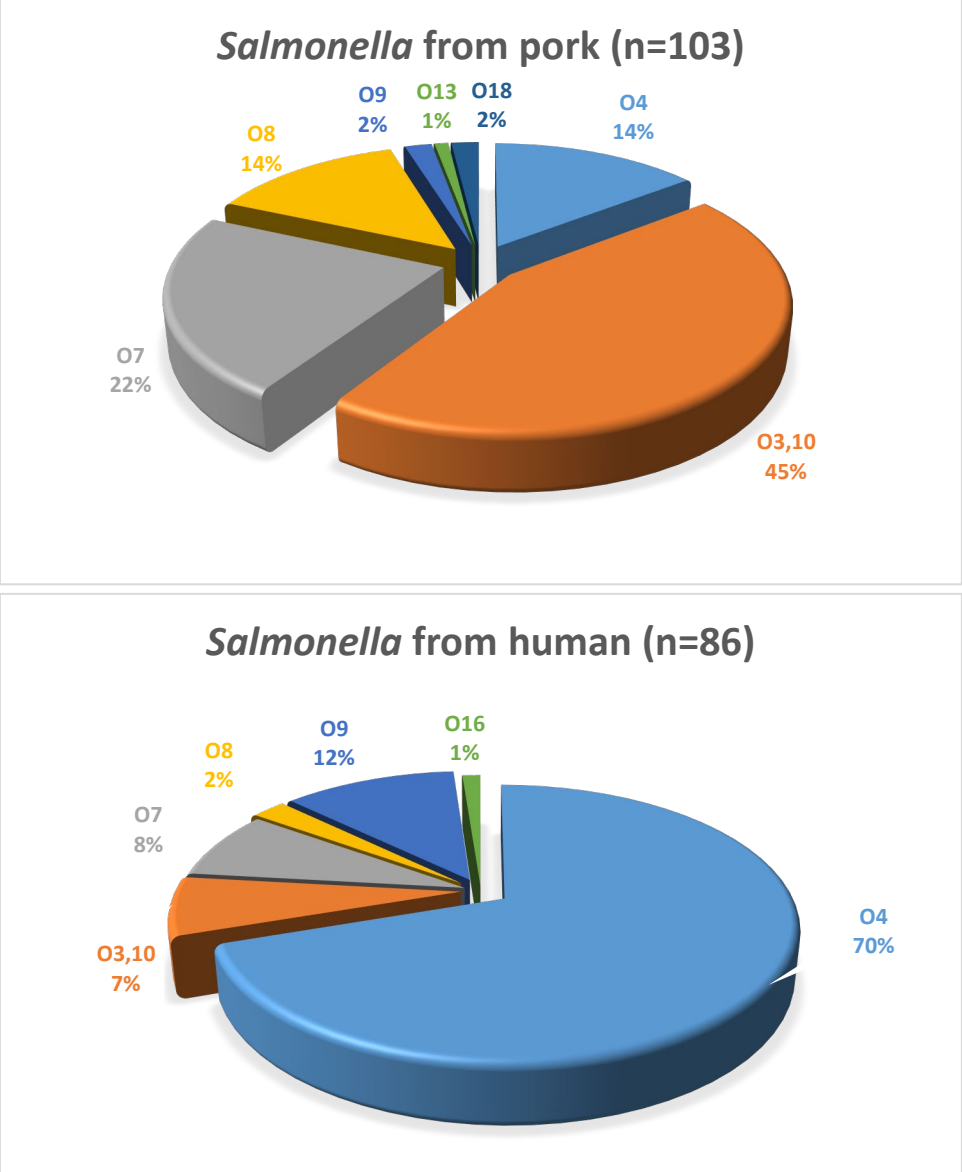
Salmonella resistant to fluoroquinolones (until recently having been considered first line medicines for salmonellosis treatment) are now in a highly prioritized group together with such agents as *Enterococcus* spp., *Staphylococcus aureus*, *Neisseria gonorrhoeae*, *Helicobacter pylori*, and *Campylobacter* spp. In our study, half of the isolated *Salmonella* belonged to this highly prioritized group of resistant bacteria.

The appearance of *Salmonella* producing extended spectrum ß-lactamase (ESBL) makes the empiric usage of extended spectrum cephalosporins (ESC) restricted for salmonellosis treatment. In conformity with published data in Russia, the percentage of such strains (in serovars *S.* Virchow, *S.* Enteritidis, *S.* Typhimurium, *S.* Newport) is 0.2–10.0%. There have been detected ESBL belonging to such genetic groups as CTX-M and AmpC cephalosporinases [4,5]. In our study, cephalosporin-resistant strains (6.4%) were mainly isolated from humans. They belonged to S. Typhimurium (group O4), with some strains of group O3,10.

The resistance to fluoroquinolones and cephalosporins observed, simultaneous with the loss of *Salmonella* susceptibility to 'old' antimicrobials (ampicillin, chloramphenicol, trimethoprim/sulfamethoxazole), crucially restrict the list of medicines potent to treat complicated salmonellosis. Antimicrobial usage in raising of farm livestock may account for the appearance of resistant *Salmonella* strains and their spread to humans. As such, resistance restriction requires prevention of resistance formation in strains circulating in farm livestock.

FIGURES

Figure 1. Serogroup pattern of *Salmonella* spp. isolated from humans and pork in southern provinces of Vietnam.



ISSN 2220-7619 (Print)
ISSN 2313-7398 (Online)

TABLES

Table 1. *Salmonella* serovars isolated from humans and pork in southern provinces of Vietnam (number of strains, proportion, 95% confidence interval).

O-group	Serovar	Number of strains isolated from		
		human	pork	Total
4	S. Typhimurium	40	5	45
	S. Stanley	12	0	12
	S. Southampton	2	1	3
	S. Saintpaul	2	0	2
	S. Remo	1	0	1
	S. Heidelberg	1	0	1
	S. Derby	0	1	1
	S. Vuadens	0	1	1
	S. Bredeney	0	3	3
	not identified	2	4	6
	Total O4	**60** **69.8%*** 95% CI 58.9-79.2	**15** **14.6%*** 95% CI 8.4-22.9	**75** **39.7%** 95% CI 32.7-47.0
3,10	S. Weltevreden	1	1	2
	S. Anatum	0	8	8
	S. Give	0	13	13
	S. Bloomsbury	0	4	4
	S. Epicrates	0	1	1
	S. Lexington	0	5	5
	S. London	0	4	4
	S. Meleagridis	0	1	1
	not identified	5	9	14
	Total O3,10	**6** **7.0%*** 95% CI 2.6-14.6	**46** **44.7%*** 95% CI 34.9-54.8	**52** **27.5%** 95% CI 21.3-34.5
7	S. Choleraesuis	2	0	2
	S. Rissen	1	4	5
	S. Larochelle	1	0	1
	S. Eingedi	0	1	1
	S. Gatow	0	1	1
	S. Bonn	0	2	2
	S. Afula	0	2	2

	S. Lockleaze	0	1	1
	S. Djugu	0	3	3
	S. Virchow	0	1	1
	S. Nola	0	1	1
	not identified	3	7	10
	Total O7	**7** **8.1%** 95% CI 3.3-16.0	**23** **22.3%** 95% CI 14.7-31.6	**30** **15.8%** 95% CI 11.0-21.9
8	S. Newport	1	1	2
	S. Corvalis	0	7	7
	S. Pakistan	0	1	1
	S. Bellevue	0	1	1
	not identified	1	4	5
	Total O8	**2** **2.3%** 95% CI 0.3-8.2	**14** **13.6%** 95% CI 7.6-21.7	**16** **8.5%** 95% CI 4.9-13.4
9	S. Enteritidis	8	0	8
	S. Wangata	0	1	1
	not identified	2	1	3
	Total O9	**10** **11.6%** 95% CI 5.7-20.4	**2** **1.9%** 95% CI 0.2-6.8	**12** **6.4%** 95% CI 3.3-10.8
13	S. Myrria	0	1	1
16	S. Hvittingfoss	1	0	1
18	S. Cotia	0	1	1
	Salmonella II	0	1	1
	Total other groups	**1** **1.2%** 95% CI 0.03-6.3	**3** **2.9%** 95% CI 0.6-8.3	**4** **2.1%** 95% CI 0.6-5.3
TOTAL		**86**	**103**	**189**

* differences are statistically significant

Table 2. Antimicrobial susceptibility and resistance of *Salmonella* spp. isolated from different sources in southern provinces of Vietnam.

Resistance phenotype	Isolated from						Total (n=189)		
	human (n=86)			pork (n=103)					
	n	%	95% CI	n	%	95% CI	n	%	95% CI
Susceptible	13	15.1	8.3-24.5	28	27.2	18.9-36.8	41	21.7	16.0-28.3
Resistant to 1 or more antibiotics	73	84.9	75.5-91.7	75	72.8	63.2-81.1	148	78.3	71.7-84.0
Resistant to:									
- ampicillin	50	58.1	47.0-68.7	39	37.9	28.5-48.0	89	47.1	39.8-54.5
- amoxicillin/clavulanic acid	2	2.3	0.3-8.2	0	0.0	0-2.9	2	1.1	0.1-3.8
- ceftriaxone	11	**12.8****	6.6-21.7	1	**1.0****	0.02-5.3	12	6.4	3.3-10.8
- ceftazidime	4	4.7	1.3-11.5	0	0.0	0-2.9	4	2.1	0.6-5.3
- pefloxacin	48	55.8	44.7-66.5	54	52.4	42.4-62.4	102	54.0	46.6-61.2
- nalidixic acid	35	40.7	30.2-51.8	36	35.0	25.8-45.0	71	37.6	30.6-44.9
- trimethoprim/ sulfamethoxazole	38	44.2	33.5-55.3	42	40.8	31.2-50.9	80	42.3	35.2-49.7
- chloramphenicol	49	57.0	45.9-67.6	39	37.9	28.5-48.0	88	46.6	39.3-53.9
- tetracycline	58	67.4	56.5-77.2	69	67.0	57.0-75.9	127	67.2	60.0-73.8
- gentamycin	26	**30.2****	20.8-41.1	2	**1.9****	0.2-6.8	28	14.8	10.1-20.7
- amikacin	1	1.2	0.03-6.3	0	0.0	0-2.9	1	0.5	0.01-2.9
Resistant to 3 and more groups (MDR*):	54	62.8	51.7-73.0	45	43.7	33.9-53.8	99	52.4	45.0-59.7
- 3 groups	7	8.1	3.3-16.1	5	4.9	1.6-11.0	12	6.3	3.3-10.8
- 4 groups	13	15.1	8.3-24.5	17	16.5	9.9-25.1	30	15.9	11.0-21.9

- 5 groups	18	20.9	12.9-31.1	22	21.4	13.9-30.5	40	21.2	15.6-27.7
- 6 groups	13	**15.1****	8.3-24.5	1	**1.0****	0.02-5.3	14	7.4	4.1-12.1
- 7 groups	3	3.5	0.7-9.9	0	0.0	0-2.9	3	1.6	0.3-4.6

*MDR – multidrug resistant

** differences are statistically significant

Table 3. MDR phenotypes of *Salmonella* isolated from different sources in southern provinces of Vietnam.

Resistance phenotypes (antibiotic groups[1])	Strains isolated from				Total
	human		pork		
	n	serovars	n	serovars	n
Resistant to 3 groups	**7**		**5**		**12**
TE, QN, SXT	0	-	2	Nhóm O:7 S. Djugu	2
TE, QN, C	1	S. Typhimurium	0	-	1
TE, C, SXT	0	-	1	S. Anatum	1
TE, AMG, QN	1	S. Stanley	0	-	1
AMP, TE, SXT	0	-	1	S. Rissen	1
AMP, TE, QN	5	group O:3,10 group O:8 S. Typhimurium	1	Nhóm O:9	6
Resistant to 4 groups	**13**		**17**		**30**
TE, QN, C, SXT	4	S. Newport S. Saintpaul S. Stanley S. Typhimurium	6	Nhóm O:4 Nhóm O:7 S. Anatum	10
TE, AMG, QN, C	1	S. Typhimurium	0	-	1
AMP, TE, QN, SXT	0	-	3	group O:4 S. Bonn	3
AMP, TE, QN, C	1	S. Typhimurium	2	S. Derby S. Gatow	3
AMP, TE, C, SXT	3	group O:7 S. Stanley	4	group O:3,10 S. Eingedi S. Epicrates S. Myrria	7
AMP, TE, AMG, C	1	S. Typhimurium	0	-	1
AMP, QN, C, SXT	2	S. Saintpaul S. Typhimurium	1	group O:3,10	3
AMP, C3-4, QN, C	1	group O:3,10	0	-	1
AMP, AMG, QN, C	0	-	1	S. Typhimurium	1
Resistant to 5 groups	**18**		**22**		**40**
TE, AMG, QN, C, SXT	2	S. Typhimurium	0	-	2
AMP, TE, QN, C, SXT	8	group O:3,10	22	group O:7	30

		S. Heidelberg S. Rissen S. Stanley S. Typhimurium		S. Bredeney S. Corvalis S. Give S. London S. Meleagridis S. Rissen S. Typhimurium	
AMP, TE, AMG, QN, C	1	S. Typhimurium	0	-	1
AMP, TE, AMG, C, SXT	2	S. Typhimurium	0	-	2
AMP, C3-4, TE, QN, C	4	S. Choleraesuis S. Typhimurium	0	-	4
AMP, AMG, QN, C, SXT	1	group O:7	0	-	1
Resistant to 6 groups	**13**		**1**		**14**
AMP, TE, AMG, QN, C, SXT	12	S. Enteritidis S. Larochelle S. Typhimurium	1	S. Give	13
AMP, C3-4, TE, AMG, QN, C	1	S. Typhimurium	0	-	1
Resistant to 7 groups	**3**		0		**3**
AMP, C3-4, QN, TE, C, AMG, SXT	3	group O:9 S. Typhimurium	0	-	3
TOTAL MDR strains	**54**		**45**	-	**99**

MDR – multidrug resistant. [1] Antibiotic groups: AMP – aminopenicillins (ampicillin); C3-4 – cephalosporins of 3-4 generations (ceftriaxone, ceftazidime); CARB – carbapenems (meropenem); QN – quinolones (nalidixic acid, pefloxacin); AMG – aminoglycosides (gentamycin, amikacin); TE – tetracyclines (tetracycline); C – phenicols (chloramphenicol); SXT – trimethoprim/sulfamethoxazole.

МЕТАДАННЫЕ

Ответственный автор:

Егорова Светлана Александровна, доктор медицинских наук, старший научный сотрудник лаборатории кишечных инфекций.

Egorova Svetlana Aleksandrovna, PhD (Medicine), Doctor of Science (Medicine); Senior Researcher, Laboratory of Enteric Infections

Федеральное бюджетное учреждение науки «Санкт-Петербургский научно-исследовательский институт эпидемиологии и микробиологии им. Пастера»

Федеральной службы по надзору в сфере защиты прав потребителей и благополучия населения
Saint Petersburg Pasteur Institute

197101, Россия, Санкт-Петербург, улица Мира, 14
Телефон: +7 812 2324883; факс: +7 812 2329217
E-mail egorova72@mail.ru
14 Ulitsa Mira, Saint Petersburg 197101, Russia
Telephone: +7 812 2324883; Fax: +7 812 2329217
E-mail egorova72@mail.ru

Авторы:
Truong Quang Nguyen, исследователь, Лаборатория кишечных инфекций, Отдел микробиологии и иммунологии; Институт Пастера в г. Хо Ши Мин, Социалистическая Республика Вьетнам.

Кафтырева Л.А., доктор медицинских наук, заведующая лабораторией кишечных инфекций; Федеральное бюджетное учреждение науки «Санкт-Петербургский научно-исследовательский институт эпидемиологии и микробиологии им.Пастера» Федеральной службы по надзору в сфере защиты прав потребителей и благополучия населения;
профессор кафедры медицинской микробиологии Федерального государственного бюджетного образовательного учреждения высшего образования "Северо-Западный государственный медицинский университет им. И.И. Мечникова" Министерства здравоохранения Российской Федерации.

Кожухова Е.А., кандидат медицинских наук, старший научный сотрудник; Федеральное государственное бюджетное образовательное учреждение

высшего образования «Первый Санкт-Петербургский государственный медицинский университет им. акад. И.П. Павлова».

Макарова М.А., доктор медицинских наук, старший научный сотрудник лаборатории кишечных инфекций; Федеральное бюджетное учреждение науки «Санкт-Петербургский научно-исследовательский институт эпидемиологии и микробиологии им.Пастера» Федеральной службы по надзору в сфере защиты прав потребителей и благополучия населения;
доцент кафедры медицинской микробиологии Федерального государственного бюджетного образовательного учреждения высшего образования "Северо-Западный государственный медицинский университет им. И.И. Мечникова" Министерства здравоохранения Российской Федерации.

Cuong Quoc Hoang, PhD (медицина), заместитель директора Института Пастера в г. Хо Ши Мин, Социалистическая Республика Вьетнам.

Vu Hoang Nguyen, заведующий Лаборатории кишечных инфекций, Отдел микробиологии и иммунологии; Институт Пастера в г. Хо Ши Мин, Социалистическая Республика Вьетнам.

Huong Thuy Dang, исследователь, Лаборатория кишечных инфекций, Отдел микробиологии и иммунологии; Институт Пастера в г. Хо Ши Мин, Социалистическая Республика Вьетнам.

Thi Quynh Lan Tran, PhD, заведующий Отделом ветеринарных наук; Факультет животноводства и ветеринарии, Университет сельского и лесного хозяйства, г. Хо Ши Мин, Социалистическая Республика Вьетнам.

Tram Khac Vo, заведующий Лабораторией здоровья животных и Терапевтического отдела; Департамент животноводства и ветеринарии г. Хо Ши Мин, Социалистическая Республика Вьетнам.

Long Thanh Nguyen, сотрудник Департамента животноводства и ветеринарии г. Хо Ши Мин, Социалистическая Республика Вьетнам.

Diep Thi Ngoc Nguyen, сотрудник Департамента животноводства и ветеринарии г. Хо Ши Мин, Социалистическая Республика Вьетнам.

Tu Le Kha Bui, сотрудник Лаборатории здоровья животных и Терапевтического отдела; Департамент животноводства и ветеринарии г. Хо Ши Мин, Социалистическая Республика Вьетнам.

Thu Le Kieu Nguyen, сотрудник Лаборатории здоровья животных и Терапевтического отдела; Департамент животноводства и ветеринарии г. Хо Ши Мин, Социалистическая Республика Вьетнам.

Serological structure and antimicrobial susceptibility of *Salmonella* isolated from humans and food items in southern provinces of Vietnam

Серологическая структура и чувствительность к антибиотикам штаммов *Salmonella*, выделенных от людей и из пищевых продуктов в южных провинциях Вьетнама

8 стр., 1 рисунок, 3 таблицы
Раздел журнала: Оригинальная статья
Дата отправления статьи: 25.05.2022

ТИТУЛЬНЫЙ ЛИСТ

Серологическая структура и чувствительность к антибиотикам штаммов *Salmonella*, выделенных от людей и из пищевых продуктов в южных провинциях Вьетнама

Serological structure and antimicrobial susceptibility of *Salmonella* isolated from humans and food items in southern provinces of Vietnam

1. Егорова Светлана Александровна[1], доктор медицинских наук, старший научный сотрудник лаборатории кишечных инфекций.
Egorova Svetlana A.[a], PhD (Medicine), Doctor of Science (Medicine); Senior Researcher of the Laboratory of Enteric Infections

2. Truong Quang Nguyen[2], исследователь, Лаборатория кишечных инфекций, Отдел микробиологии и иммунологии
Truong Quang Nguyen[b], MSc (Biotechnology); Researcher, Laboratory of Enteric Infections, Microbiology and Immunology Department

3. Кафтырева Лидия Алексеевна[1,3], доктор медицинских наук, заведующая лабораторией[1];
профессор кафедры медицинской микробиологии[3].
Kaftyreva Lidia A.[a,c], PhD (Medicine), Doctor of Science (Medicine); Laboratory Head[a]; Professor, Medical Microbiology Faculty[c].

4. Кожухова Елена Алексеевна[4], кандидат медицинских наук, старший научный сотрудник.
Kozhukhova Elena A.[d], PhD (Medicine); Senior Researcher

5. Макарова Мария Александровна[1,3], доктор медицинских наук, старший научный сотрудник;
доцент кафедры медицинской микробиологии[3].
Makarova Mariia A.[a,c], PhD (Medicine), Doctor of Science (Medicine); Senior Researcher[a]; Associate Professor, Medical Microbiology Faculty[c]

6. Cuong Quoc Hoang[2], PhD (медицина), заместитель директора
Cuong Quoc Hoang[b], PhD (Medicine); Deputy Director

7. Nguyen Hoang Vu[2], заведующий Лаборатории кишечных инфекций, Отдел микробиологии и иммунологии
Nguyen Hoang Vu[b], MSc (Biology); Head of the Laboratory of Enteric Infections, Department of Microbiology and Immunology

8. Huong Thuy Dang[2], исследователь, Лаборатория кишечных инфекций, Отдел микробиологии и иммунологии
Huong Thuy Dang[b], BSc (Biotechnology); Researcher, Laboratory of Enteric Infections, Department of Microbiology and Immunology

9. Thi Quynh Lan Tran[5,] PhD, заведующий отделом ветеринарных наук
Thi Quynh Lan Tran[e], PhD, MSc, D.V.M; Head and Lecturer, Department of Veterinary Biosciences.

10. Tram Khac Vo[6], заведующий Лабораторией здоровья животных и Терапевтического отдела
Tram Khac Vo[f], MSc, Dr (Medicine); Head, Animal Health Laboratory and Treatment Division

11. Long Thanh Nguyen[6], сотрудник Департамента животноводства и ветеринарии г. Хо Ши Мин
Long Thanh Nguyen[f], MSc (Biotechnology); Department of Animal Husbandry and Veterinary Medicine of Ho Chi Minh City

12. Diep Thi Ngoc Nguyen[6], сотрудник Департамента животноводства и ветеринарии г. Хо Ши Мин
Diep Thi Ngoc Nguyen[f], MSc, Dr (Veterinarian); Department of Animal Husbandry and Veterinary Medicine of Ho Chi Minh City

13. Tu Le Kha Bui[6], сотрудник Лаборатории здоровья животных и Терапевтического отдела
Tu Le Kha Bui[f], Dr (Veterinarian); Animal Health Laboratory and Treatment Division

14. Thu Le Kieu Nguyen[6], сотрудник Лаборатории здоровья животных и Терапевтического отдела
Thu Le Kieu Nguyen[f], Dr (Veterinarian); Animal Health Laboratory and Treatment Division

[1] Лаборатория кишечных инфекций, Федеральное бюджетное учреждение науки «Санкт-Петербургский научно-исследовательский институт эпидемиологии и микробиологии им.Пастера» Федеральной службы по надзору в сфере защиты прав потребителей и благополучия населения.
[a] Laboratory of Enteric Infections, Saint Petersburg Pasteur Institute, Federal Service for Surveillance on Consumer Rights Protection and Human Wellbeing

[2] Институт Пастера в г. Хо Ши Мин, Социалистическая Республика Вьетнам
[b] Pasteur Institute in Ho Chi Minh City, Vietnam.

[3] Федеральное государственное бюджетное образовательное учреждение высшего образования "Северо-Западный государственный медицинский университет им. И.И. Мечникова" Министерства здравоохранения Российской Федерации.
[c] State Institution of Higher Professional Education 'I. I. Mechnikov North-Western State Medical University', Russian Ministry of Health

[4] Федеральное государственное бюджетное образовательное учреждение высшего образования «Первый Санкт-Петербургский государственный медицинский университет им. акад. И.П. Павлова».
[d] State Institution of Higher Professional Education 'Pavlov University in Saint Petersburg', Russia

[5] Факультет животноводства и ветеринарии, Университет сельского и лесного хозяйства, г. Хо Ши Мин, Социалистическая Республика Вьетнам.
[e] Faculty of Animal Science and Veterinary Medicine, University of Agriculture and Forestry (Nong Lam University - Ho Chi Minh city), Vietnam.

[6]Департамент животноводства и ветеринарии г. Хо Ши Мин, Социалистическая Республика Вьетнам
[f] Department of Animal Husbandry and Veterinary Medicine of Ho Chi Minh City, Vietnam

Сокращенное название статьи для верхнего колонтитула:

Характеристика *Salmonella*, выделенных во Вьетнаме

Salmonella isolated in Vietnam

Ключевые слова: *Salmonella*, устойчивость к антибиотикам, множественная резистентность, Вьетнам, серовар.
Keywords: *Salmonella*, antimicrobial resistance, multidrug resistance, Vietnam, serovar

Адрес для переписки:
197101, Санкт-Петербург, улица Мира, 14
Телефон: +7 812 2324883; факс: +7 812 2329217
E-mail egorova72@mail.ru

Corresponding address:
14 Ulitsa Mira, Saint Petersburg 197101, Russia
Telephone: +7 812 2324883; Fax: +7 812 2329217
E-mail egorova72@mail.ru

REFERENCES

Порядковый номер ссылки	Авторы, название публикации и источника, где она опубликована, выходные данные	ФИО, название публикации и источника на английском	Полный интернет-адрес (URL) цитируемой статьи и/или
1.	Андреева И.В., Стецюк О.У. Отпуск без проблем: современные подходы к профилактике и лечению диареи путешественников // Клиническая микробиология и антимикробная химиотерапия. 2018. Т. 20, № 3. С. 172-180.	Andreeva I.V., Stetsiouk O.U. Current approaches to prophylaxis and treatment of travelers' diarrhea. Clinical Microbiology and Antimicrobial Chemotherapy, 2018, vol. 20, no.3, pp.172-180	https://cmac-journal.ru/en/publication/2018/3/cmac-2018-t20-n3-p172/cmac-2018-t20-n3-p172.pdf doi: 10.36488/cmac.2018.3.172-180
2.	Гончар Н.В., Лазарева И.В., Рычкова С.В., Кветная А.С., Альшаник Л.П., Фомичева Ю.В., Ныркова О.И., Кириленко Л.А. Заболеваемость детей сальмонеллезом и уровень резистентности клинических штаммов сальмонелл к	Gonchar N.V., Lazareva I.V., Rychkova S.V., Kvetnaja A.S., Al'shanik L.P., Fomicheva J.V., Nyrkova O.I., Kirilenko L.A. Child morbidity of salmonellosis and the level of resistance of clinical isolates	https://journal.niidi.ru/jofin/article/view/379/375 doi: 10.22625/2072-6732-2015-7-1-80-86

	антибактериальным препаратам в Санкт-Петербурге // Журнал инфектологии. 2015. Т. 7, № 1. С.80-86.	of salmonella to antibacterial preparations in saint Petersburg. Journal Infectology. 2015, vol. 7, no. 1, pp. 80-86.	
3.	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. С. 93-96.	Evmenenko I.G., Murach L.V. Analysis of resistance of strains of salmonella spp. to antibiotics in the Smolensk gerion for 2012-2017. Smolensk medical almanac, 2018, № 1, pp. 93-96.	https://www.elibrary.ru/item.asp?id=35256733
4.	Егорова С.А., Кафтырева Л.А., Сужаева Л.В., Забровская А.В., Войтенкова Е.В., Матвеева З.Н., Останкова Ю.В., Лихачев И.В., Сатосова Н.В., Кицбабашвили Р.В., Смирнова Е.В., Семченкова Л.И., Быстрая Т.Е., Сокольник С.Е., Уткина Н.П., Сихандо Л.Ю. Устойчивость к	Egorova S.A., Kaftyreva L.A., Suzhaeva L.V., Zabrovskaia A.V., Voitenkova E.V., Matveeva Z.N., Ostankova Y.V., Likhachev I.V., Satosova N.V., Kitsbabashvili R.V., Smirnova E.V., Semchenkova L.I., Bystraya T.E., Sokol’nik S.E., Utkina	http://dx.doi.org/10.18821/0869-2084-2019-64-10-620-626

	антимикробным препаратам и клинически значимые механизмы резистентности штаммов Salmonella, выделенных в 2014-2018 гг. в Санкт-Петербурге, Россия // Клиническая лабораторная диагностика. 2019. Т. 64, № 10. С. 620-626.	N.P., Sikhando L.Y. Antimicrobial resistance and clinical significant resistance mechanisms of Salmonella isolated in 2014-2018 in Saint Petersburg, Russia. Russian Clinical Laboratory Diagnostics, 2019, vol. 64, no. 10, pp. 620-626.	
5.	Забровская А.В., Егорова С.А., Антипова Н.А., Смирнова Е.В., Семченкова Л.И., Быстрая Т.Е., Сокольник С.Е., Уткина Н.П., Сихандо Л.Ю., Сатосова Н.В. Чувствительность к антибиотикам сальмонелл-доминирующих сероваров, выделенных в Северо-Западном федеральном округе РФ в 2004–2018 гг. из различных источников. Журнал	Zabrovskaia A.V., Egorova S.A., Antipova N.A., Smirnova E.V., Semchenkova L.I., Bystraya T.E., Sokolnik S.E., Utkina N.P., Sikhando L.Y., Satosova N.V. Antimicrobial susceptibility of dominant Salmonella serovars, isolated in North-West federal district in 2004–2018 from different sourses. Journal	https://doi.org/10.22625/2072-6732-2022-14-1-131-139 doi: 10.22625/2072-6732-2022-14-1-131-139

	инфектологии. 2022. Т. 14, № 1. С. 131-139.	Infectology, 2022, vol. 14, no. 1, pp. 131-139.	
6.	Козлов С.Н., Козлов Р.С. Современная антимикробная химиотерапия: руководство для врачей. Москва: ООО «Медицинское информационное агентство», 2017, 400 с.	Kozlov S.N., Kozlov R.S. Modern antimicrobial chemotherapy: a guidelines for doctors. Moscow: LLC "Medical Information Agency", 2017, 400 pp.	https://www.elibrary.ru/item.asp?id=32785761
7.	Кузнецова Н.А., Соловьева А.С., Раков А.В. Чувствительность к антибиотикам у штаммов Salmonella Enteritidis, циркулирующих на территории Сибири и Дальнего Востока, по данным многолетнего мониторинга // Здоровье. Медицинская экология. Наука. 2018. Т. 3. С. 50-58.	Kuznetsova N.A., Solovyeva A.C., Rakov A.V. Antibiotic resistance of Salmonella Enteritidis strains, circulated in territory of the siberia and far east, at multi-year monitoring. Health. Medical ecology. Science, 2018, no. 3, pp. 50–58	https://www.elibrary.ru/download/elibrary_36737763_67123086.pdf doi: 10.5281/zenodo.1488030

8.	О состоянии санитарно-эпидемиологического благополучия населения в Российской Федерации в 2020 году: Государственный доклад. М.: Федеральная служба по надзору в сфере защиты прав потребителей и благополучия человека. 2021. 256 с.	On the state of sanitary and epidemiological well-being of the population in Russia in 2020: State Report. Moscow: Federal Service on Customers' Rights Protection and Human Well-being Surveillance, 2021, 256 p.	https://www.rospotrebnadzor.ru/upload/iblock/5fa/gd-seb_02.06-_s-podpisyu_.pdf
9.	Anders K.L., Thompson C.N., Thuy N.T., Nguyet N.M., Tu le T.P., Dung T.T., Phat V.V., Van N.T., Hieu N.T., Tham N.T., Ha P.T., Lien le B., Chau N.V., Baker S., Simmons C.P. The epidemiology and aetiology of diarrhoeal disease in infancy in southern Vietnam: a birth cohort study. Int J Infect Dis., 2015, vol 35, pp. 3-10.	-	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4508461/ doi: 10.1016/j.ijid.2015.03.013.

10.	Centers for Disease Control and Prevention. Yellow Book, 2020. Chapter 2. Travelers' Diarrhea.		https://wwwnc.cdc.gov/travel/yellowbook/2020/preparing-international-travelers/travelers-diarrhea
11.	Echeita M.A., Herrera S., Garaizar J., Usera M.A. Multiplex PCR-based detection and identification of the most common Salmonella second-phase flagellar antigens. Res Microbiol., 2002, vol. 153, no. 2, pp. 107-113.	-	https://www.sciencedirect.com/science/article/abs/pii/S0923250801012955?via%3Dihub doi: 10.1016/s0923-2508(01)01295-5.
12.	EFSA and ECDC (European Food Safety Authority and European Centre for Disease Prevention and Control), 2018. The European Union summary report on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in 2017. EFSA	-	https://doi.org/10.2903/j.efsa.2018.5500 doi: 10.2903/j.efsa.2018.5500

	Journal, 2018, vol. 16, no. 12, e05500, pp. 262.		
13.	EFSA (European Food Safety Authority) and ECDC (European Centre for Disease Prevention and Control), 2022. The European Union Summary Report on Antimicrobial Resistance in zoonotic and indicator bacteria from humans, animals and food in 2019–2020. EFSA Journal, 2022, vol. 20, no. 3, e07209, pp 197.	-	https://doi.org/10.2903/j.efsa.2022.7209 doi: 10.2903/j.efsa.2022.7209
14.	Herrera-León S., McQuiston J.R., Usera M.A., Fields P.I., Garaizar J., Echeita M.A. Multiplex PCR for distinguishing the most common phase-1 flagellar antigens of Salmonella spp. Journal of clinical microbiology, 2004, vol. 42, no. 6, pp. 2581–2586.	-	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC427890/ doi: 10.1128/JCM.42.6.2581-2586.2004

15.	Huyen D.T.T., Hong D.T., Trung N.T., Hoa T.T.N., Oanh N.K., Thang H.V., Thao N.T.T., Hung D.M., Iijima M., Fox K., Grabovac V., Heffelfinger J., Batmunkh N., Anh D.D. Epidemiology of acute diarrhea caused by rotavirus in sentinel surveillance sites of Vietnam, 2012-2015. Vaccine, 2018, vol. 36, no. 51, pp. 7894-7900.	-	https://www.sciencedirect.com/science/article/pii/S0264410X18306133?via%3Dihub doi: 10.1016/j.vaccine.2018.05.008
16.	An H.T.T., Khai L.T.L. The prevalence and antibiotic resistance of Salmonella spp. isolated from pigs and farm environments in vinh long province. Can Tho University Journal of Science, 2018, vol. 54, Special issue: Agriculture (2018), pp. 26-33.	-	doi: 10.22144/CTU.JSI.2018.091
17.	Lettini A.A., Vo Than T., Marafin E., Longo A., Antonello K., Zavagnin P., Barco L., Mancin M., Cibin V., Morini M., Dang Thi	-	https://onlinelibrary.wiley.com/doi/abs/10.1111/zph.12265 doi:10.1111/zph.12265

	Sao M., Nguyen Thi T., Pham Trung H., Le L., Nguyen Duc T., Ricci A. Distribution of Salmonella Serovars and Antimicrobial Susceptibility from Poultry and Swine Farms in Central Vietnam. Zoonoses Public Health, 2016, vol. 63, pp.569-576.		
18.	Nhung N.T., Van N., Cuong N.V., Duong T., Nha, T.T., Hang T., Nhi N., Kiet B.T., Hien V.B., Ngoc P.T., Campbell J., Thwaites G., Carrique-Mas J. Antimicrobial residues and resistance against critically important antimicrobials in non-typhoidal Salmonella from meat sold at wet markets and supermarkets in Vietnam. International journal of food microbiology, 2018, vol. 266, pp. 301–309.	-	https://www.sciencedirect.com/science/article/pii/S0168160517305378?via%3Dihub doi: 10.1016/j.ijfoodmicro.2017.12.015

19.	Noor Uddin G.M., Larsen M.H., Barco L., Minh Phu T., Dalsgaard A. Clonal Occurrence of Salmonella Weltevreden in Cultured Shrimp in the Mekong Delta, Vietnam. PloS one, 2015, vol. 10, no. 7, e0134252.	-	https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0134252 doi:10.1371/journal.pone.0134252
20.	Phu Huong Lan N., Le Thi Phuong T., Nguyen Huu H., Thuy L., Mather A.E., Park S.E., Marks F., Thwaites G.E., Van Vinh Chau N., Thompson C.N., Baker S. Invasive Non-typhoidal Salmonella Infections in Asia: Clinical Observations, Disease Outcome and Dominant Serovars from an Infectious Disease Hospital in Vietnam. PLoS Negl Trop Dis., 2016, vol. 10. no. 8, e0004857.	-	https://journals.plos.org/plosntds/article?id=10.1371/journal.pntd.0004857 doi:10.1371/journal.pntd.0004857

21.	Riddle M.S., DuPont H.L., Bradley A., Connor B.A. ACG Clinical Guideline: Diagnosis, Treatment, and Prevention of Acute Diarrheal Infections in Adults. American J Gastroenterology, 2016, vol. 111, no. 5, pp. 602–622.	-	https://journals.lww.com/ajg/Fulltext/2016/05000/ACG_Clinical_Guideline__Diagnosis,_Treatment,_and.14.aspx doi: 10.1038/ajg.2016.126
22.	Ta Y.T., Nguyen T.T., To P.B., Pham da X., Le H.T., Thi G.N., Alali W.Q., Walls I., Doyle M.P. Quantification, serovars, and antibiotic resistance of salmonella isolated from retail raw chicken meat in Vietnam. J Food Prot., 2014, vol. 77, no. 1, pp. 57-66.	-	https://meridian.allenpress.com/jfp/article/77/1/57/173741/Quantification-Serovars-and-Antibiotic-Resistance doi: 10.4315/0362-028X.JFP-13-221.
23.	Tai DT. Circulation of extended-spectrum β-lactamase producing Salmonella isolated from food handler in Lam Dong provinces.	-	https://www.walshmedicalmedia.com/proceedings/circulation-of-extendedspectrum-946lactamase-

	2nd International Conference on Clinical Microbiology & Microbial Genomics, September 16-17, 2013, Hampton Inn Tropicana, Las Vegas, NV, USA		producing-salmonella-isolated-from-food-handler-in-lam-dong-provinces-1582.html
24.	Thompson C.N., Phan V.T., Le T.P., Pham T.N., Hoang L.P., Ha V., Nguyen V.M., Pham V.M., Nguyen T.V., Cao T.T., Tran T.T., Nguyen T.T., Dao M.T., Campbell J.I., Nguyen T.C., Tang C.T., Ha M.T., Farrar J., Baker S. Epidemiological features and risk factors of Salmonella gastroenteritis in children resident in Ho Chi Minh City, Vietnam. Epidemiol Infect., 2013, vol. 141, no. 8, pp.1604-13.	-	https://www.cambridge.org/core/journals/epidemiology-and-infection/article/epidemiological-features-and-risk-factors-of-salmonella-gastroenteritis-in-children-resident-in-ho-chi-minh-city-vietnam/765945ED1694C735070A11CD3769ECBF doi:10.1017/S0950268812002014
25.	Trung N.V., Carrique-Mas J.J., Nghia N.H., Tu L.T., Mai H.H., Tuyen H.T., Campbell J.,	-	https://onlinelibrary.wiley.com/doi/full/10.1111/zph.12270

	Nhung N.T., Nhung H.N., Minh P.V., Chieu T.T., Hieu T.Q., Mai N.T., Baker S., Wagenaar J.A., Hoa N.T., Schultsz C. Non-Typhoidal Salmonella Colonization in Chickens and Humans in the Mekong Delta of Vietnam. Zoonoses Public Health, 2017, vol. 64, no. 2, pp.94-99.		doi: 10.1111/zph.12270
26.	Thai T.H., Hirai T., Lan N.T., Yamaguchi R. Antibiotic resistance profiles of Salmonella serovars isolated from retail pork and chicken meat in North Vietnam. Int J Food Microbiol., 2012, vol. 156, no. 2, pp. 147-51.	-	https://doi.org/10.1016/j.ijfoodmicro.2012.03.016. doi: 10.1016/j.ijfoodmicro.2012.03.016.
27.	Tu L.T., Hoang N.V., Cuong N.V., Campbell J., Bryant J.E., Hoa N.T., Kiet B.T., Thompson C., Duy D.T., Phat V.V., Hien V.B., Thwaites G., Baker S., Carrique-Mas	-	https://doi.org/10.1017/S0950268815000102 doi: 10.1017/S0950268815000102

	J.J. High levels of contamination and antimicrobial-resistant non-typhoidal Salmonella serovars on pig and poultry farms in the Mekong Delta of Vietnam. Epidemiology and infection, 2015, vol. 143, no.14,pp. 3074–3086.		
28.	Van T.T., Moutafis G., Tran L.T., Coloe P.J. Antibiotic resistance in food-borne bacterial contaminants in Vietnam. Applied and environmental microbiology, 2007, vol. 73, no. 24, pp. 7906–7911.	-	https://journals.asm.org/doi/10.1128/AEM.00973-07?url_ver=Z39.88-2003&rfr_id=ori:rid:crossref.org&rfr_dat=cr_pub%20%200pubmed doi: 10.1128/AEM.00973-07
29.	WHO publishes list of bacteria for which new antibiotics are urgently needed. News Release 27.02.2017	-	http://www.who.int/ru/news-room/detail/27-02-2017-who-publishes-list-of-bacteria-for-which-new-antibiotics-are-urgently-needed