Russian Journal of Infection and Immunity = Infektsiya i immunitet
2022, vol. 12, no. 6, pp. 1081–1090

Инфекция и иммунитет
2022, Т. 12, № 6, с. 1081–1090

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

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Abstract. This article presents current relevant data on the serogroups and antimicrobial 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 (vs 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 fluoro-

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Для цитирования:
Егорова С.А., Чуонг К.Н., Кафтырева Л.А., Кожухова Е.А., Макарова М.А., Куонг К.Х., Ву Х.Н., Хуонг Т.З., Лан Т.К.Ч., Чам К.В., Лонг Т.Н., Диеп Т.Н.Н., Ту Л.К.Б., Тху Л.К.Н. Серологическая структура и чувствительность к антибиотикам штаммов Salmonella, выделенных от людей и из пищевых продуктов в южных провинциях Вьетнама // Инфекция и иммунитет. 2022. Т. 12, № 6. С. 1081–1090. doi: 10.15789/2220-7619-SPA-1954

Citation:
Egorova S.A., Truong Q.N., Kaftyreva L.A., Kozhukhova E.A., Makarova M.A., Cuong Q.H., Vu H.N., Huong T.D., Lan T.Q.T., Tram K.V., Long T.N., Diep T.N.N., Tu L.K.B., Thu L.K.N. Serogroups and antimicrobial susceptibility of Salmonella isolated from people and food items in southern provinces of Vietnam // Russian Journal of Infection and Immunity = Infektsiya i immunitet, 2022, vol. 12, no. 6, pp. 1081–1090. doi: 10.15789/2220-7619-SPA-1954

DOI: http://dx.doi.org/10.15789/2220-7619-SPA-1954

quinolones 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.

Key words: *Salmonella, antimicrobial resistance, multidrug resistance, serovar.*

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

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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, серовар.*

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, 17, 18, 19, 22, 23, 25, 26, 27, 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 St. 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 (St. 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/

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

O-group	Serovar	Number of strains isolated from		
		human	pork	Total
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**

Note. *Differences are statistically significant.

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 Fig.

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

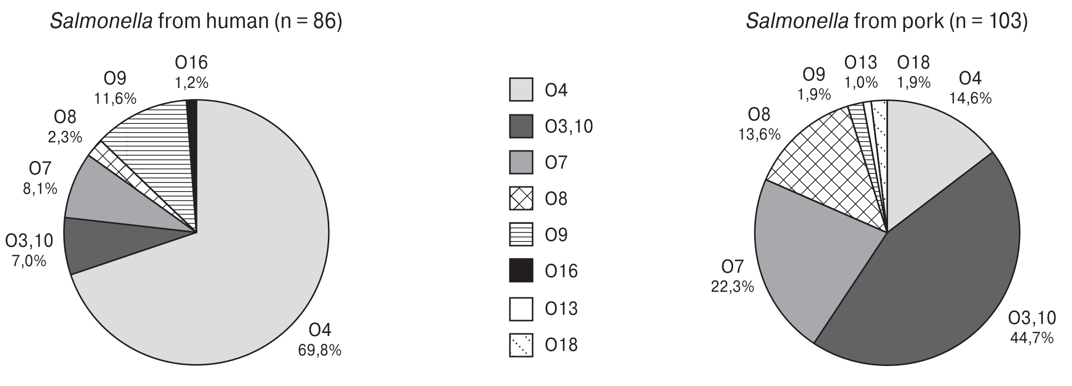

Figure. Serogroup pattern of *Salmonella* spp. isolated from humans and pork in southern provinces of Vietnam

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

Note. *MDR — multidrug resistant; **differences are statistically significant.

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.

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

Resistance phenotypes (antibiotic groups1)	Strains isolated from				Total
	human		pork		
	n	serovars	n	serovars	n
Resistant to 3 groups	7		5		12
TE, QN, SXT	0	–	2	group 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	group O:9	6
Resistant to 4 groups	13		17		30
TE, QN, C, SXT	4	*S.* Newport *S.* Saintpaul *S.* Stanley *S.* Typhimurium	6	group O:4 group 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 *S.* Heidelberg *S.* Rissen *S.* Stanley *S.* Typhimurium	22	group O:7 *S.* Bredeney *S.* Corvalis *S.* Give *S.* London *S.* Meleagridis *S.* Rissen *S.* Typhimurium	30
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

Note. 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.

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, 17, 18, 19, 22, 23, 25, 26, 27, 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 β-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.

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Поступила в редакцию 25.05.2022
Принята к печати 23.08.2022

Received 25.05.2022
Accepted 23.08.2022