

DOI: 10.21055/0370-1069-2023-4-84-90

УДК 616-022.14(597)

Le Thi Lan Anh¹, Ta Thi Loan¹, Dinh Thu Minh², Vu Thi Thuong¹, Pham Thi Ha Giang¹,
Bui Thi Thanh Nga¹, Pham Viet Hung¹, Nguyen Ngoc Tan¹, Trieu Phi Long³, Le Thi Van Anh⁴,
Hoang Dang Hieu¹

**Antibiotic Resistance Patterns in Shiga Toxin-Producing *Escherichia coli* (STEC),
Salmonella, *Shigella* and *Staphylococcus aureus* Isolated at Two Communal Kitchens
Located in Hanoi City, Vietnam**

¹Institute of Tropical Medicine, Joint Vietnam-Russia Tropical Science and Technology Research Center, Hanoi, Vietnam;

²Hanoi University of Science, Vietnam National University, Hanoi, Vietnam;

³Military Institute of Preventive Medicine, Hanoi, Vietnam;

⁴Publishing House for Science and Technology, Vietnam Academy of Science and Technology, Hanoi, Vietnam

Abstract. The aim of our study was to investigate the antibiotic resistance profiles of Shiga toxin-producing *Escherichia coli* (STEC), *Salmonella* spp., *Shigella* spp., and *Staphylococcus aureus* strains. **Materials and methods.** 660 samples were collected at two communal kitchens in Hanoi, Vietnam between 2021 and 2022. They included foodstuffs, environmental (food processing tools) and biological ones (swabs from the hands of personnel). The VITEK® 2 Compact system in combination with DNA sequencing was used to identify bacterial species. The antibiotic susceptibility test (AST) was performed according to Kirby-Bauer Disk Diffusion Susceptibility protocol following Clinical & Laboratory Standards Institute (CLSI) method (M100-Ed32). **Results and discussion.** In total, 53 pathogenic bacterial strains have been detected, including 11 STEC, 24 *Salmonella enterica*, 9 *Shigella sonnei*, *Shigella flexneri*, and 8 *S. aureus*. AST of STEC has showed the highest resistance rates to tetracycline and chloramphenicol (90.9 %); trimethoprim+sulfamethoxazole (81.8 %); ampicillin, gentamycin and piperacillin (63.6 %). The STEC isolates were susceptible to carbapenem group. Among the *Salmonella* strains, 50 % demonstrated resistance to ampicillin, followed by tetracycline and piperacillin (45.8 %). Additionally, 25 % were resistant to ticarcillin+clavulanic acid, 20.8 % – to trimethoprim+sulfamethoxazole, and 16.7 % – to chloramphenicol. All *Salmonella* strains exhibited susceptibility to gentamicin, cefoxitin, imipenem, meropenem, and ceftazidime. AST of *Shigella* strains revealed the highest resistance rate for tetracycline (30 %), followed by cefazolin and ceftazidime (20 %). However, all *Shigella* strains were susceptible to cefoxitin, carbapenem groups, and chloramphenicol. Among the *S. aureus* strains, 50 % exhibited resistance to erythromycin, azithromycin, clindamycin, penicillin, telithromycin, and gentamicin, followed by ciprofloxacin, moxifloxacin, levofloxacin, and chloramphenicol (25 %). All *S. aureus* strains were still susceptible to trimethoprim+sulfamethoxazole, daptomycin, linezolid, doxycycline, minocycline, and vancomycin. Our findings reflect the current situation on antibiotic resistance among pathogenic bacteria strains circulating at the study sites during food processing. They are an evidence of potential risk of food poisoning. There is a need to undertake the proper containment measures on the part of authorities or policy makers.

Key words: Shiga toxin-producing *E. coli* (STEC), *Salmonella*, *Shigella*, *Staphylococcus aureus*, antibiotic resistance pattern.

Conflict of interest: The authors declare no conflict of interest.

Funding: The authors declare no additional financial support for this study.

Bioethics: The study was approved by the Ethics Committee in Biomedical Research of the Vietnam-Russia Tropical Center No. 1536/CN-HĐĐĐ dated May 24, 2021.

Acknowledgements: We would like to thank the Molecular Biology Laboratory, Institute of Tropical Medicine, Joint Vietnam-Russia Tropical Science and Technology Research Center for supporting us in conducting this study.

Corresponding author: Le Thi Lan Anh, e-mail: leanhbio@gmail.com.

Citation: Le Thi Lan Anh, Ta Thi Loan, Dinh Thu Minh, Vu Thi Thuong, Pham Thi Ha Giang, Bui Thi Thanh Nga, Pham Viet Hung, Nguyen Ngoc Tan, Trieu Phi Long, Le Thi Van Anh, Hoang Dang Hieu. Antibiotic Resistance Patterns in Shiga Toxin-Producing *Escherichia coli* (STEC), *Salmonella*, *Shigella* and *Staphylococcus aureus* Isolated at Two Communal Kitchens Located in Hanoi City, Vietnam. *Problemy Osobo Opasnykh Infektsii [Problems of Particularly Dangerous Infections]*. 2023; 4:84–90. (In Russian). DOI: 10.21055/0370-1069-2023-4-84-90

Received 21.09.2023. Revised 05.10.2023. Accepted 24.10.2023.

Le Thi Lan Anh, ORCID: <https://orcid.org/0000-0002-5927-9857>
Ta Thi Loan, ORCID: <https://orcid.org/0000-0003-2586-0122>
Dinh Thu Minh, ORCID: <https://orcid.org/0009-0003-8410-3612>
Vu Thi Thuong, ORCID: <https://orcid.org/0009-0007-3664-080X>
Pham Thi Ha Giang, ORCID: <https://orcid.org/0009-0004-9309-6108>
Bui Thi Thanh Nga, ORCID: <https://orcid.org/0000-0002-4119-1339>

Pham Viet Hung, ORCID: <https://orcid.org/0000-0002-8622-9935>
Nguyen Ngoc Tan, ORCID: <https://orcid.org/0009-0003-3969-4361>
Trieu Phi Long, ORCID: <https://orcid.org/0000-0002-2472-6370>
Le Thi Van Anh, ORCID: <https://orcid.org/0000-0002-7413-2802>
Hoang Dang Hieu, ORCID: <https://orcid.org/0009-0007-6679-7381>

Le Thi Lan Anh¹, Ta Thi Loan¹, Dinh Thu Minh², Vu Thi Thuong¹, Pham Thi Ha Giang¹, Bui Thi Thanh Nga¹, Pham Viet Hung¹, Nguyen Ngoc Tan¹, Trieu Phi Long³, Le Thi Van Anh⁴, Hoang Dang Hieu¹

Профили антибиотикорезистентности у шига-токсин-продуцирующей *Escherichia coli* (STEC), *Salmonella*, *Shigella* и *Staphylococcus aureus*, выделенных на двух общественных кухнях, расположенных в городе Ханой, Вьетнам

¹Институт тропической медицины Совместного Вьетнамско-Российского тропического научно-исследовательского и технологического центра, Ханой, Вьетнам;

²Ханойский исследовательский университет, Вьетнамский национальный университет, Ханой, Вьетнам;

³Военный институт профилактической медицины, Ханой, Вьетнам;

⁴Издательство науки и технологий, Вьетнамская академия наук и технологий, Ханой, Вьетнам

Целью нашего исследования являлось изучение профилей устойчивости к антибиотикам штаммов шига-токсин-продуцирующих *Escherichia coli* (STEC), *Salmonella* spp., *Shigella* spp. и *Staphylococcus aureus*. **Материалы и методы.** В период с 2021 по 2022 г. на двух общественных кухнях в Ханое, Вьетнам, было собрано 660 образцов. Они включали в себя образцы пищевых продуктов, внешней среды (предметы для обработки пищи) и биологические образцы (смывы с рук персонала). Для идентификации видов бактерий использовали систему VITEK® 2 Compact, наряду с секвенированием ДНК. Тест на чувствительность к антибиотикам (AST) проводился в соответствии с протоколом Kirby-Bauer Disk Diffusion Susceptibility по методу Института клинических и лабораторных стандартов (CLSI) (M100-Ed32). **Результаты и обсуждение.** Всего выявлено 53 штамма патогенных бактерий, в том числе 11 STEC, 24 *Salmonella enterica*, 9 *Shigella sonnei*, *Shigella flexneri* и 8 *S. aureus*. AST STEC выявил наиболее высокий уровень резистентности к тетрациклину и хлорамфениколу (90,9 %); триметоприму+сульфаметоксазолу (81,8 %); ампициллину, гентамицину и пиперациллину (63,6 %). Изоляты STEC проявили чувствительность к группе карбапенемов. Среди штаммов сальмонелл 50 % устойчивы к ампициллину. Вторую позицию занимали тетрациклин и пиперациллин (45,8 %). При этом 25 % были устойчивы к тикарциллину+клавулановой кислоте, 20,8 % – к триметоприму+сульфаметоксазолу и 16,7 % – к левомицетину. Все штаммы сальмонелл проявляли чувствительность к гентамицину, цефокситину, имипенему, меропенему и цефтазидиму. AST штаммов *Shigella* spp. показал самый высокий уровень устойчивости к тетрациклину (30 %), цефазолину и цефтазидиму (20 %). Однако все штаммы шигелл были чувствительны к цефокситину, группам карбапенемов и хлорамфениколу. Среди штаммов *S. aureus* 50 % проявили устойчивость к эритромицину, азитромицину, клиндамицину, пенициллину, телитромицину и гентамицину, а 25 % – к ципрофлоксацину, моксифлоксацину, левофлоксацину и хлорамфениколу. Однако все штаммы *S. aureus* проявили чувствительность к триметоприму+сульфаметоксазолу, даптомицину, линезолиду, доксициклину, миноциклину и ванкомицину. Полученные нами результаты отражают текущее положение дел касательно устойчивости к антибиотикам среди штаммов патогенных бактерий, циркулирующих на объектах исследования при переработке пищевых продуктов. Они являются свидетельством потенциального риска пищевого отравления. Существует необходимость принятия надлежащих мер по контролю над патогенными агентами со стороны властей и руководящих органов.

Ключевые слова: шига-токсин-продуцирующие *E. coli* (STEC), *Salmonella*, *Shigella*, *Staphylococcus aureus*, профили антибиотикорезистентности.

Конфликт интересов. Авторы подтверждают отсутствие конфликта финансовых/нефинансовых интересов, связанных с написанием статьи.

Финансирование. Авторы заявляют об отсутствии дополнительного финансирования при проведении данного исследования.

Биоэтика. Исследование одобрено Комитетом по этике биомедицинских исследований Вьетнамско-Российского тропического центра № 1536/CN-HĐĐĐ от 24 мая 2021 г.

Благодарность. Мы бы хотели поблагодарить Лабораторию молекулярной биологии Института тропической медицины Объединенного Вьетнамско-Российского научно-исследовательского тропического центра науки и технологий за поддержку в проведении данного исследования.

Корреспондирующий автор: Le Thi Lan Anh, e-mail: leanhbio@gmail.com.

Для цитирования: Le Thi Lan Anh, Ta Thi Loan, Dinh Thu Minh, Vu Thi Thuong, Pham Thi Ha Giang, Bui Thi Thanh Nga, Pham Viet Hung, Nguyen Ngoc Tan, Trieu Phi Long, Le Thi Van Anh, Hoang Dang Hieu. Профили антибиотикорезистентности у шига-токсин-продуцирующей *Escherichia coli* (STEC), *Salmonella*, *Shigella* и *Staphylococcus aureus*, выделенных на двух общественных кухнях, расположенных в городе Ханой, Вьетнам. *Проблемы особо опасных инфекций*. 2023; 4:84–90. DOI: 10.21055/0370-1069-2023-4-84–90

Поступила 21.09.2023. Отправлена на доработку 05.10.2023. Принята к публ. 24.10.2023.

Gastroenteritis is widespread all over the world. The most common causes of it are bacteria, including STEC, *Salmonella*, *Shigella* and *Staphylococcus aureus* [1]. In Vietnam, children with gastroenteritis and other food poisoning conditions caused by *E. coli*, *Shigella*, *Salmonella* infections have been reported [2].

Shiga toxin producing *Escherichia coli* is a major factor of food-borne illnesses [3, 4]. Data from the World

Health Organization (WHO) show that STEC strains cause 2.5 million cases each year, of which 1.2 million are food-borne ones [5].

Salmonella spp. is accountable for nearly one-third of food-borne infection outbreaks in the European Union. In 2018, EU member states documented 5,146 food-borne illness outbreaks, affecting 48,365 people. Out of those, 1,581 outbreaks were attributed to *Salmonella*

spp. Annually, *Salmonella* bacteria cause approximately 68,000 deaths [6].

According to WHO, there are an estimated 80 million cases of shigellosis worldwide each year with approximately 700,000 deaths happening annually as a result of this infection [7]. Four species of *Shigella* have been identified: *S. flexneri*, *S. sonnei*, *S. boydii*, and *S. dysenteriae*. *S. sonnei* is widespread in Vietnam and Thailand, whereas *S. flexneri* is abundant in Indonesia and Cambodia [8].

Staphylococcus aureus also creates a burden of food-borne diseases, with approximately 241,000 cases estimated to occur annually in the United States. However, the actual number of cases caused by *S. aureus* may be significantly higher as sporadic cases of the disease are not reported in the United States [9].

Antibiotic resistance of *Salmonella*, *Shigella* and *S. aureus* strains isolated from the environment and biological samples such as foodstuffs, swabs from the surface of processing equipment, material from under fingernails, and stool samples has been reported globally. In particular, the rate of strains resistant to tetracycline, ampicillin, and chloramphenicol is increasingly common [10, 11].

Contamination with *Salmonella*, *Shigella*, *E. coli* and *S. aureus* of food from retail markets and canteens have been reported in Vietnam [12, 13]. Cases of food poisoning at the communal kitchens of industrial parks or at schools have become frequent in recent years. In this context, training in food safety control at communal kitchens, as well as surveillance studies on the prevalence of strains of food-borne infectious agents, including STEC, *Salmonella*, *Shigella* and *S. aureus* play an important role in minimizing poisoning incidents.

This work is devoted to the assessment of the antibiotic resistance in STEC, *Salmonella* spp., *Shigella* spp., and *S. aureus* strains collected at two communal kitchens in Hanoi city, Vietnam. The study describes the strains with multi-drug resistance.

Materials and methods

Study setting. In 2021 and 2022, we conducted surveillance at two communal kitchens, which process food for staff of two industrial companies located in Hanoi city, Vietnam. The survey was performed as part of routine food safety inspection.

Sample collection. A total of 660 samples, including food samples (501), swabs from the surface of pro-

cessing tools (100), surface of dining tables (25), swabs from the hands of food processors (34) were collected.

As regards food samples, we gathered 25 g of material (vegetables, meat and seafood) at the study site. Then, samples were placed in a sterile specialized plastic zip bag and stored at 4 °C to 10 °C in a designated sample transport box. Collected samples were transferred to the laboratory within 2 hours from the time of collection. Samples were individually labeled, recording time, location, and type.

Swabs were taken from surface of tables, knives, bowls, cutting boards, and hands of food processors. We used a sterile cotton swab dipped in 10 % peptone buffered water solution to wipe both sides of the tools and hands. After that, the cotton pad was put in a sterile test tube and store at 4 °C to 10 °C in an allocated sample transport box.

Culture isolation and identification of STEC, *Salmonella* spp., *Shigella* spp., and *S. aureus*. Isolation of STEC, *Salmonella*, and *Shigella* was performed according to the ISO 21567:2004 and ISO 6579-1:2017 with some modifications. MacConkey agar (Oxoid; UK) and CHROMagar STEC (CHROMagar™, France) were used for isolation of STEC [14], HE agar (Oxoid; UK) and CHROMagar™ *Salmonella* – for *Salmonella* spp. [15], and *Salmonella shigella* agar (SS agar) (Oxoid; UK) and HE agar – for *Shigella* spp. CHROMagar™ Staph was used for *S. aureus* [16]. The suspicious colonies were identified using the Vitek 2 compact automatic identification system.

All specified bacterial strains were seeded onto TSB medium (Oxoid; UK) for downflow DNA extracting using a genomic DNA isolation kit (QIAGEN, Germany) and PCR amplification of STEC, *Salmonella* spp., *Shigella* spp., and *S. aureus* genomic fragments. The primer sequences and PCR results are shown in the Table 1. PCR products were investigated with the help of electrophoresis in 1.5 % agarose gel. In order to confirm the identification of isolated strains, PCR products were sent to Macrogen Company (Korea) for DNA sequencing using Sanger method.

Antibiotic susceptibility testing. The antibiotic susceptibility test was performed using Kirby-Bauer methodology. For quality control, *E. coli* ATCC 25922, *Salmonella enterica typhi* ATCC 14028, *Shigella sonnei* (Levine) Weldin (ATCC® 25931™), *Staphylococcus aureus* ATCC 25923 were used according to QC standard for Disc Diffusion Antibigram of CLSI's document version 2022. The following an-

Table 1

List of oligonucleotide primers used in this study

| Target gene | Primer | Primer sequence (5'-3') | PCR product size (bp) | Annealing temperature/time (°C/s) | References |
|-------------|--------|-------------------------|-----------------------|-----------------------------------|------------|
| Gyrase B | F1 | gaagtcacatgaccgttctgca | 1200 | 60/15 | [17] |
| | R1 | gcagggtacggatgtcgagcc | | | |
| 16s rRNA | F2 | agagtttgatcctggctcag | 1250 | 49/15 | [18] |
| | R2 | ggttacctgtttacgactt | | | |

tibiotics (Oxoid, Basingstoke, Hampshire, England) were applied for STEC, *Shigella* spp. and *Salmonella* spp.: Ampicillin (AMP 10 µg), Cefazolin (CZ 30 µg), Gentamicin (CN 10 µg), Tobramycin (TOB 10 µg), Amikacin (AK 30 µg), Amoxicillin+Acid clavulanic (AMC 30 µg), Ampicillin+Sulbactam (SAM 20 µg), Piperacillin+Tazobactam (TZP 110 µg), Ticarcillin+Clavulanic (TIM 85 µg), Cefuroxime (CXM 30 µg), Cefepime (FEP 30 µg), Cefoxitin (FOX 30 µg), Ciprofloxacin (CIP 5 µg), Levofloxacin except *Salmonella* spp. (LEV 5 µg), Ertapenem (ETP 10 µg), Imipenem (IPM 10 µg), Meropenem (MEM 10 µg), Piperacillin (PRL 100 µg), Trimethoprim+Sulfamethoxazole (SXT 25 µg), Aztreonam (ATM 30 µg), Ceftazidime (CAZ 30 µg), Chloramphenicol (C 30 µg). The antibiotics used for *S. aureus* isolates were Erythromycin (E 15 µg), Azithromycin (AZM 15 µg), Clindamycin (DA 2 µg), Cefoxitin (FOX 30 µg), Penicillin (P 10 µg), Trimethoprim+Sulfamethoxazole (SXT 25 µg), Linezolid (LZD 30 µg), Telithromycin (TEL 15 µg), Doxycycline (DO 30 µg), Minocycline (MH 30 µg), Tetracycline (TE 30 µg), Chloramphenicol (C 30 µg), Ciprofloxacin (CIP 5 µg), Moxifloxacin (MXF 5 µg), Gentamicin (CN 10 µg), Levofloxacin (LEV 5 µg). The strains were designated sensitive (S), moderately sensitive (M), or resistant (R) in compliance with CLSI guidelines (M100-Ed32).

Results and discussion

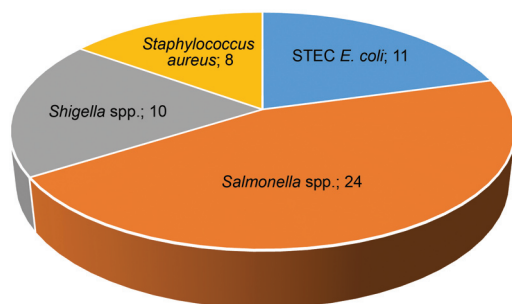
Identification of STEC, *Salmonella*, *Shigella* and *S. aureus*. In this study, we detected 53 pathogenic bacterial strains, including 11 STEC, 24 *Salmonella* spp., 10 *Shigella* spp., and 8 strains of *S. aureus*, using conventional microbiology method. The gyrase B gene-based sequencing showed that 24 *Salmonella* spp. strains belonged to *Salmonella enterica*. Out of 10 *Shigella* spp. strains, nine were identified as *Shigella sonnei* and one was *Shigella flexneri* according to DNA sequencing (Figure).

Antibiotic susceptibility testing of isolated strains. The results of AST of STEC, *Salmonella* spp., and *Shigella* spp. strains are described in detail in Table 2. We have established that 11 STEC isolates exhibited susceptibility to cefoxitin, ertapenem, imipenem, and meropenem antibiotics. Conversely, those strains displayed the highest resistance to tetracycline and chloramphenicol – 90.9 %

(10 out of 11 strains). Trimethoprim+sulfamethoxazole occupied the second place, with 9 out of 11 strains exhibiting resistance (81.8 %). Resistance to ampicillin, gentamicin, and piperacillin was 63.6 % (7 out of 11 strains), 45.5 % for cefazolin (5 out of 11), 36.4 % for cefuroxime, cefepime, cefotaxime, and aztreonam (4 out of 11), and 27.3 % for ciprofloxacin and tobramycin (3 out of 11). Importantly, 81.8 and 54.5 % of STEC strains showed moderate susceptibility to amikacin and ticarcillin+clavulanic, respectively. Additionally, 10 out of 11 STEC strains showed multidrug resistance to 9–13 different antibiotics, while only one strain was sensitive to 23 out of 24 tested antimicrobials and moderately sensitive to 1 antibiotic. Regarding the test results for 24 isolates of *Salmonella* spp., it was found that all of them were sensitive to gentamicin, cefoxitin, imipenem, meropenem, and ceftazidime. The highest resistance rate of 50 % (12 strains) was in the response to ampicillin, followed by tetracycline and piperacillin in 11 out of 24 strains (45.8 %), ticarcillin+clavulanic acid in 6 out of 24 strains (25 %), trimethoprim+sulfamethoxazole in 5 out of 24 strains (20.8 %), chloramphenicol in 4 out of 24 strains (16.7 %). Resistance levels were lower for piperacillin+tazobactam in 2 out of 24 strains (8.3 %), cefazolin, ampicillin+sulbactam, cefoxitin, ciprofloxacin, ertapenem, and aztreonam in 1 out of 24 strains (4.2 %). 7.5 % of *Salmonella* strains were moderately susceptible to cefazolin. Among them, 12 out of 24 strains exhibited multidrug resistance to 3–8 different antibiotics. Moreover, our findings indicate that all 10 isolated *Shigella* strains were sensitive to antibiotics including cefoxitin, ertapenem, imipenem, meropenem, and chloramphenicol. The *Shigella* strains demonstrated the highest resistance to tetracycline (30 %), followed by cefazolin, ceftazidime at 20 %, and cefuroxime, cefepime, ampicillin, gentamicin, ticarcillin+clavulanic acid, trimethoprim+sulfamethoxazole, and aztreonam in one out of 10 strains (10 %). 40 % of *Shigella* isolates were moderately susceptible to piperacillin+tazobactam. Only one *Shigella* strain showed multidrug resistance to 10 different antibiotics. It is of interest that STEC, *Salmonella* spp. and *Shigella* spp. were susceptible to 3 out of 24 tested antibiotics (cefepime, imipenem and meropenem).

Regarding *S. aureus* strains, the AST revealed the highest resistance to erythromycin, azithromycin, clindamycin, penicillin, telithromycin, and gentamicin in 4 out of 8 strains (50 %). The second position is occupied by ciprofloxacin, moxifloxacin, levofloxacin, and chloramphenicol – 2 out of 8 strains (25 %) (Table 3). All 8 isolated *S. aureus* strains were sensitive to 5 out of 18 tested antibiotics including daptomycin, doxycycline, minocycline, linezolid, vancomycin, and trimethoprim+sulfamethoxazole. Additionally, out of 8 isolated strains of *S. aureus*, 5 strains exhibited multidrug resistance, ranging from 2 to 5 different types of antibiotics.

Contamination with STEC, *Salmonella*, *Shigella* and *S. aureus* is one of the main causes of food poisoning. Therefore, food safety control and regular monitoring of



Proportion of isolated bacterial strains

Table 2

Antibiotic resistance patterns of isolated bacteria

| Antibiotics | STEC | | | <i>Salmonella</i> spp. | | | <i>Shigella</i> spp. | | |
|-----------------------------|-------------|-------------|------------|------------------------|------|------------|----------------------|-------------|------------|
| | R, % | M, % | S, % | R, % | M, % | S, % | R, % | M, % | S, % |
| Ampicillin | 63.6 | 0.0 | 36.4 | 50.0 | 0.0 | 50.0 | 10.0 | 0.0 | 90.0 |
| Piperacillin | 63.6 | 9.1 | 27.3 | 45.8 | 4.2 | 50.0 | 10.0 | 10.0 | 80.0 |
| Aztreonam | 36.4 | 9.1 | 54.5 | 4.2 | 0.0 | 95.8 | 10.0 | 0.0 | 90.0 |
| Amikacin | 9.1 | 81.8 | 9.1 | 0.0 | 4.2 | 95.8 | 0.0 | 10.0 | 90.0 |
| Gentamicin | 63.6 | 0.0 | 36.4 | 0.0 | 0.0 | 100 | 10.0 | 0.0 | 90.0 |
| Tobramycin | 27.3 | 18.2 | 54.5 | 0.0 | 8.3 | 91.7 | 0.0 | 10.0 | 90.0 |
| Cefazolin | 45.5 | 9.1 | 45.5 | 4.2 | 37.5 | 58.3 | 20.0 | 20.0 | 60.0 |
| Cefuroxime | 36.4 | 0.0 | 63.6 | 0.0 | 12.5 | 87.5 | 10.0 | 0.0 | 90.0 |
| Cefepime | 36.4 | 0.0 | 63.6 | 0.0 | 8.3 | 91.7 | 10.0 | 0.0 | 90.0 |
| Ceftazidime | 18.2 | 9.1 | 72.7 | 0.0 | 0.0 | 100 | 20.0 | 0.0 | 80.0 |
| Chloramphenicol | 90.9 | 0.0 | 9.1 | 16.7 | 0.0 | 83.3 | 0.0 | 0.0 | 100 |
| Cefoxitin | 0.0 | 0.0 | 100 | 0.0 | 0.0 | 100 | 0.0 | 0.0 | 100 |
| Cefotaxime | 36.4 | 9.1 | 54.5 | 4.2 | 8.3 | 87.5 | 10.0 | 10.0 | 80.0 |
| Ciprofloxacin | 27.3 | 27.3 | 45.5 | 4.2 | 29.2 | 66.7 | 0.0 | 20.0 | 80.0 |
| Levofloxacin | 18.2 | 9.1 | 72.7 | 0.0 | 0.0 | 0.0 | 0.0 | 20.0 | 80.0 |
| Ertapenem | 0.0 | 0.0 | 100 | 4.2 | 0.0 | 95.8 | 0.0 | 0.0 | 100 |
| Imipenem | 0.0 | 0.0 | 100 | 0.0 | 0.0 | 100 | 0.0 | 0.0 | 100 |
| Meropenem | 0.0 | 0.0 | 100 | 0.0 | 0.0 | 100 | 0.0 | 0.0 | 100 |
| Tetracyclin | 90.9 | 0.0 | 9.1 | 45.8 | 0.0 | 54.2 | 30.0 | 0.0 | 70.0 |
| Amoxicillin+Acid clavulanic | 0.0 | 18.2 | 81.8 | 0.0 | 8.3 | 91.7 | 0.0 | 10.0 | 90.0 |
| Ampicillin+Sulbactam | 18.2 | 9.1 | 72.7 | 4.2 | 16.7 | 79.2 | 0.0 | 10.0 | 90.0 |
| Piperacillin+Tazobactam | 0.0 | 18.2 | 81.8 | 8.3 | 29.2 | 62.5 | 0.0 | 40.0 | 60.0 |
| Ticarcillin+Clavulanic | 0.0 | 54.5 | 45.5 | 25.0 | 0.0 | 75.0 | 10.0 | 0.0 | 90.0 |
| Trimethoprim+Sulfamethazole | 81.8 | 0.0 | 18.2 | 20.8 | 0.0 | 79.2 | 10.0 | 0.0 | 90.0 |

Note: R – resistant, S – susceptible, M – moderately susceptible.

Table 3

Antibiotic resistance patterns of *Staphylococcus aureus* isolates

| Antibiotics | R, % | M, % | S, % |
|-----------------------------|-------------|------|------------|
| Azithromycin | 50.0 | 0.0 | 50.0 |
| Erythromycin | 50.0 | 0.0 | 50.0 |
| Clindamycin | 50.0 | 0.0 | 50.0 |
| Cefoxitin | 0.0 | 12.5 | 87.5 |
| Chloramphenicol | 25.0 | 0.0 | 75.0 |
| Ciprofloxacin | 25.0 | 0.0 | 75.0 |
| Levofloxacin | 25.0 | 0.0 | 75.0 |
| Moxifloxacin | 25.0 | 0.0 | 75.0 |
| Daptomycin | 0.0 | 0.0 | 100 |
| Doxycycline | 0.0 | 0.0 | 100 |
| Minocycline | 0.0 | 0.0 | 100 |
| Tetracyclin | 0.0 | 25 | 75.0 |
| Gentamicin | 50.0 | 0.0 | 50.0 |
| Linezolid | 0.0 | 0.0 | 100 |
| Telithromycin | 50.0 | 0.0 | 50.0 |
| Penicillin | 50.0 | 0.0 | 50.0 |
| Vancomycin | 0.0 | 0.0 | 100 |
| Trimethoprim+Sulfamethazole | 0.0 | 0.0 | 100 |

Note: R – resistant, S – susceptible, M – moderately susceptible.

hygiene and proper processing conditions play a significant role in containment of the infection. Currently, studies on the prevalence of pathogens (STEC, *Salmonella*, *Shigella*, *S. aureus*) are mainly conducted at retail markets and animal slaughter sites, but there is insufficient monitoring at communal kitchens. Over the past 5 years, reports of food poisoning caused by microorganisms in collective kitchens in industrial parks or at schools in Vietnam have been increasing. However, testing for the presence of microbial agents is only performed after a registered case of poisoning.

In this study, a total of 53 bacterial strains were collected at two communal kitchens located in Hanoi City, Vietnam. The majority of the isolates (24 strains) were identified as *Salmonella*. Next in the list were STEC strains (11), followed by *Shigella* (10 strains), and *Staphylococcus aureus* (8 strains). These findings suggest that *Salmonella* spp. are the most common agents at the two public kitchens in Hanoi. It is generally known that human infection with *Salmonella* mainly occurs through direct or indirect contact with infected animals and contaminated food products, including meat, poultry, raw milk, eggs, and water. Previously, it was reported that average rate of chicken meat contamination

with *Salmonella* in six regions of Vietnam was 45.9 %. In Hanoi City, it reached 51.1 % [12].

Transmission of pathogenic microorganisms and toxigenic agents through food has been recognized as a significant risk for many decades. The widespread resistance of bacteria to antibiotics is a major threat that leads to hundreds of thousands of deaths annually. One of the most alarming issues is the increasing number of bacteria that are resistant to commonly used antibiotics, including those considered as last-resort treatments. This concern was officially acknowledged by WHO in 2014 as a major global health challenge.

In our study, STEC demonstrated the highest resistance to currently used antibiotics. In comparison to a study by Tran Thi Le Trieu *et al.* on 24 surveyed *E. coli* strains, the highest resistance was observed to ampicillin (79.17 %), followed by streptomycin (62.50 %), and amoxicillin/clavulanic acid (54.17 %) [19]. Another study by B. González-Santamarina *et al.* on 23 *Salmonella* strains isolated from pig slaughterhouses and pork markets revealed the highest resistance to ampicillin (73.9 %) and piperacillin and moxifloxacin (both 69.6 %), followed by trimethoprim and trimethoprim with sulfamethoxazole (both 56.5 %) [20]. Research on *Salmonella* strains isolated from chickens and chicken farm environments in three households in Vinh Long province, Vietnam by Ho Xuan Yen *et al.*, showed the high rate of resistance to such antibiotics as ampicillin (100 %), chloramphenicol (95 %), cefuroxime, streptomycin, and tetracycline (90 %), and moderate resistance to doxycycline (85 %). They exhibited lower resistance to trimethoprim/sulfamethoxazole (60 %) and had minimal resistance to colistin (25 %) [21].

The study of C.S. Toro *et al.* on 349 strains of *Shigella* revealed some interesting evidence: 100 % of the strains were found to be sensitive to ciprofloxacin. On the other hand, those strains demonstrated high level of resistance to other antibiotics. The resistance rates were as follows: streptomycin (305 strains, 87.4 %), trimethoprim (264 strains, 75.6 %), ampicillin (257 strains, 73.6 %), tetracycline (257 strains, 73.6 %), sulfamethoxazole/trimethoprim (256 strains, 73.3 %), and chloramphenicol (195 strains, 55.9 %) [22]. Resistance to tetracycline was observed in both *S. sonnei* and *S. flexneri* [23]. Furthermore, the study of S. Khaghani *et al.* indicated that at least 25 % of *S. flexneri* strains isolated from Abuzar Children's Hospital in Ahvaz, southwestern Iran exhibited resistance to three commonly prescribed antibiotics: ampicillin, trimethoprim-sulfamethoxazole and nalidixic acid [24].

A recent study conducted by V. Velasco *et al.* on 55 strains of *Staphylococcus aureus* in Chile uncovered the fact that a significant number of the isolated strains showed resistance to penicillin (83.6 %). Moreover, a considerable proportion of the isolates, approximately 38.2 %, displayed resistance to multiple types of antibiotics [25].

Our research has demonstrated that the detected STEC, *Salmonella* spp., *Shigella* spp., and *S. aureus*

strains exhibited significant resistance rate to several antibiotics such as tetracycline, ampicillin, penicillin. This result is consistent with other listed above studies that were previously carried out. However, it is noteworthy that certain antibiotics, such as cefoxitin, remain effective against all four groups of isolated bacteria. Additionally, all collected bacterial strains in this study were still sensitive to carbapenem such as imipenem, and meropenem. Furthermore, the combination of multiple antibiotics increased effectiveness of neutralization, as observed with combinations such as amoxicillin+clavulanic acid or trimethoprim+sulfamethoxazole, which increase sensitivity of bacterial strains. These findings highlight the potential benefits of utilizing appropriate antibiotic combinations to combat infections caused by indicated bacterial groups.

Summing up the above, we isolated a total of 53 strains from four different bacterial groups, STEC, *Salmonella* spp., *Shigella* spp., and *Staphylococcus aureus*, collected at two communal kitchens in Hanoi city, Vietnam. Among these groups, *Salmonella* spp. was the predominant bacterial species, accounting for 24 strains. However, it is of note that STEC raises the highest level of concern as it exhibited resistance to certain antibiotics such as tetracycline and chloramphenicol, as high as 90.1 %. Additionally, out of the 11 STEC strains analyzed, 10 strains showed resistance to multiple antibiotics, indicating a multidrug-resistant phenotype. Thus, the design of kitchens and the training of personnel on food safety and hygiene practices play a pivotal role in mitigating the risk of transmission of pathogenic bacteria and preventing food-borne diseases.

Our findings reflect the current situation on antibiotic resistance in circulating pathogenic bacteria found at the study sites in the course of food processing. They evidence a potential risk of food poisoning and the need to take appropriate sanitary measures on the part of authorities or policy makers.

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Authors:

Le Thi Lan Anh, Ta Thi Loan, Vu Thi Thuong, Pham Thi Ha Giang, Bui Thi Thanh Nga, Pham Viet Hung, Nguyen Ngoc Tan, Hoang Dang Hieu. Institute of Tropical Medicine, Joint Vietnam-Russia Tropical Science and Technology Research Center. 63, Nguyen Van Huyen Street, Hanoi, Vietnam. E-mail: tropcenterhanoi@mail.com.

Dinh Thu Minh. Hanoi University of Science, Vietnam National University. Hanoi, Vietnam.

Trieu Phi Long. Military Institute of Preventive Medicine. Hanoi, Vietnam.

Le Thi Van Anh. Publishing House for Science and Technology, Vietnam Academy of Science and Technology. Hanoi, Vietnam.

Об авторах:

Le Thi Lan Anh, Ta Thi Loan, Vu Thi Thuong, Pham Thi Ha Giang, Bui Thi Thanh Nga, Pham Viet Hung, Nguyen Ngoc Tan, Hoang Dang Hieu. Институт тропической медицины Совместного Вьетнамско-Российского тропического научно-исследовательского и технологического центра. 63, Nguyen Van Huyen Street, Hanoi, Vietnam. E-mail: tropcenterhanoi@mail.com.

Dinh Thu Minh. Ханойский исследовательский университет, Вьетнамский национальный университет. Вьетнам, Ханой.

Trieu Phi Long. Военный институт профилактической медицины. Вьетнам, Ханой.

Le Thi Van Anh. Издательство науки и технологий, Вьетнамская академия наук и технологий. Вьетнам, Ханой.