MEDDOCS Open Access Publisher

ISSN: 2637-4501

Annals of Gastroenterology and the Digestive System

Open Access | Research Article

An Acute Gastroenteritis Outbreak Caused by Enteropathogenic Escherichia Coli (EPEC) in China

Peng Zhang[1]; Liping Chen[1]*; Wei Yan[1]; Zhiqiang Liang[2]; Lei Ji[1]

[1]Huzhou Center for Disease Control and Prevention, Huzhou 313000, China.

[2]Anji Center for Disease Control and Prevention, Huzhou, China.

***Corresponding Author(s): Liping Chen**

Huzhou Center for Disease Control and Prevention, 999 Changxing Road, Huzhou, Zhejiang 313000, China.

Email: lipingchen1106@hotmial.com

Received: Sep 05, 2023

Accepted: Sep 20, 2023

Published Online: Sep 27, 2023

Journal: Annals of Gastroenterology and the Digestive System

Publisher: MedDocs Publishers LLC

Online edition: http://meddocsonline.org/

Keywords: Enteropathogenic *Escherichia coli*; Foodborne disease; Outbreak; WGS.

Abstract

Background: Foodborne diseases or foodborne diarrhea are important reasons affecting the global population. Diarrheagenic *E. coli* is the most important pathogens, which causes diarrhea in humans. On May 27, 2022, Anji County Hospital of Chinese Medicine treated several patients with acute onset of gastroenteritis. It was found that this was an outbreak caused by two different EPECs.

Methods: According to the case definition, the local public health workers started the investigation. Stool samples collected from probable case patients and delicatessen owners were forwarded for *Salmonella* spp., *Shigella* spp., *V. parahaemolyticus*, and Diarrheagenic *E. coli* testing. Environment and food samples were tested for the same pathogens. All detections were carried out according to the ''National foodborne disease surveillance manual for 2022'' (China National Center for Food Safety Risk Assessment, 2022). The isolated strains were then subjected to PFGE analysis, antibiotic susceptibility tests, and Whole Genome Sequencing analysis.

Results: Six families had purchased and eaten the cold pork purchased from the delicatessen produced by the owner of the shop. 37 people had ate the cold pork, 20 of them were ill. All of them met the definition of possible cases. The incidence rate was 54.05% (20/37). 37 suspected cases, 20 probable cases and 6 laboratory-confirmed cases were determined in this outbreak. A total of 15 stool samples and 5 food samples were collected. Nine isolates (five cases, one food producer and three food samples) were confirmed as Enteropathogenic *E. coli*-positive. The results of PFGE were obviously clustered into two banding patterns, with an overall similarity of 58.92%. Four cases presented 100% similarity with the food producer. Another case and 3 cold pork formed a band pattern with a similarity of 100%. Two serotypes were observed among the nine isolates: Out: H4, O16:H4, and two STs (ST226, ST10) were found.

Conclusions: This study presented here a foodbrone outbreak event caused by eating cold pork contaminated by EPEC. The detected pathogenic bacteria were not homologous after analysis.

Cite this article: Zhang P, Chen L, Yan W, Liang Z, Ji L. An Acute Gastroenteritis Outbreak caused by Enteropathogenic Escherichia Coli (EPEC) in China. Ann Gastroenterol Dig Syst. Ann Gastroenterol Dig Syst. 2023: 6(2): 1079.

Introduction

Foodborne diarrhea is important reason affecting the global population [1-2]. Diarrheagenic *Escherichia coli* (Diarrheagenic *E. coli*) is one of the most common bacterial agents of foodborne diarrheal disease [3]. *E. coli* is a Gram-negative, facultative anaerobic and rod-shaped bacterium, which is a common symbiotic bacteria in mammalian large intestine [4]. However, some *E. coli* strains can cause serious infection [4].

Diarrheagenic *E. coli*, which causes humans diarrhea, can be divided into seven different pathotypes according to its specific virulence characteristics, distinct epidemiological and clinical features: Enterotoxigenic E. coli (ETEC), Enteroinvasive E. coli (EIEC), Enteroaggregative E. coli (EAEC), Diffuse-Adhering E. coli (DAEC), Cytolethal distending toxin-producing E. coli, Enteropathogenic E. coli (EPEC), and Enterohaemorrhagic E. coli (EHEC) [5].

Enteropathogenic *E. coli* (EPEC) is the uppermost pathogen infecting children in the worldwide, and can cause fatal diarrhea in infants in developing countries [6]. Previous studies demonstrated that in China, EPEC is one of the most common diarrheagenic *E. coli* [7-8] and were found in many food sources [9-10]. In this study, we investigated an outbreak of gastroenteritis caused by EPEC infection in China.

Materials and Methods

The outbreak

On May 27, 2022, Anji County Hospital of Chinese Medicine treated several patients with acute onset of gastroenteritis. The patients reported having eaten cold pork purchased from the same delicatessen before the onset of the illness. This suspected outbreak of foodborne diseases was subsequently reported to the market supervision department and the health administrative authority. An investigation was conducted by Anji CDC.

Case definition

A suspected case was defined as a person with one of the symptoms including abdominal pain, diarrhea or vomiting (diarrhea meant three or more episodes within 24 hours, or vomiting meant more than once within 24 hours) after having eaten cold pork purchased from the delicatessen since May 25, 2022. A probable case could be determined if two or more symptoms described above presented. A probable case could be defined as a laboratory-confirmed case, if Enteropathogenic *Escherichia coli* (EPEC) was detected in the vomit or diarrhea of the patient.

Epidemiologic investigation

According to the case definition, the local public health workers interviewed the delicatessen owners, physician-in-charge, and checked the outpatient and hospitalization records to determine the cases. At the same time, with the help of the foodborne disease monitoring and reporting system, the case search was carried out among people who had eaten the cold pork purchased from the delicatessen. Probable cases were further confirmed based on questionnaire investigation. Probable cases were analyzed by clinical symptoms and descriptive epidemiology. On May, 27, a detailed sanitary investigation of the delicatessen was carried out, and environment and food samples were obtained for laboratory testing.

Laboratory investigation

Stool samples collected from probable case patients and delicatessen owners were forwarded for *Salmonella* spp., *Shigella* spp., *V. parahaemolyticus*, and Diarrheagenic *E. coli* testing. Environment and food samples were tested for the same pathogens. All detections were carried out according to the ''National foodborne disease surveillance manual for 2022'' (China National Center for Food Safety Risk Assessment, 2022).

For Diarrheagenic *E. coli* testing, environment and food samples were enriched in Enterobacteriaceae Enrichment Broth (Hopebio, Qingdao, China) at 42^{0}C up to 18h, followed by plating on levine- eosin–methylene blue agar (Hopebio, Qingdao, China), and MacConkey agar (Hopebio, Qingdao, China), for incubation at 37^{0}C up to 24 h. The Enrichment procedure could be omitted when stool samples were processed. Presumptive colonies were identified by using Diarrheagenic *Escherichia coli* detection kit (real-time PCR method) (ABT, Beijing, China).

Pulsed field gel electrophoresis

PFGE (Pulsed field gel electrophoresis) typing for *E. coli* isolates was carried out according to the recommended protocol [11]. *Xba* I was selected as the restriction enzyme, and the digestion fragments were subjected to PFGE in a 1% Seakem Gold Agarose gel (Lonza Company, Swiss) in 0.5% Tris-boric acid-ethylenediaminetetraacetic acid (EDTA) buffer using a CHEF Mapper XA system (Bio-Rad Laboratories, Richmond, CA, USA). The electrophoresis time was 19 h. The *Xba* I digested DNA from Salmonella strain H9812 was used as a standard. BioNumerics software v. 7.6 (Applied Maths, Kortrijk, Belgium) was used for Gel images analysis.

Antibiotic susceptibility tests

The antimicrobial resistance patterns of the 9 isolates were determined by the broth microdilution method, following the standards of the Clinical and Laboratory Standards Institute [12]. The following 16 antibiotics were tested using the Sensititre™ CHNENF (Thermo scientific, American. B1481A): Chloramphenicol (CHL); Colistin (CT); Ertapenem (ETP); Meropenem (MEM); Cefotaxime (CTX); Ceftazidime(CAZ); Ceftazidime/avibactam (CZA); Tetracycline (TET); Tigecycline (TIG); Ciprofloxacin (CIP); Nalidixic (NAL); Azithromycin (AZM); Amikacin (AMI); Streptomycin (STR); Ampicillin (AMP); and Ampicillin/sulbactam (AMS). The breakpoints for resistance, intermediate and susceptible, were referred to CLSI [12].

Whole genome sequencing analysis

The total DNA from each strain was extracted from overnight cultures using the bacterial genomic DNA extraction kit (TIANGEN biotech co., Beijing, China), according to the manufacturer's instructions. The DNA concentration was determined using the Qubit 4 (Thermo Fisher Scientific, Waltham, MA, USA) and Qualified DNA was stored in −80^{0}C until use.

The WGS libraries were constructed with Metagenomic DNA library Kit (Cat No: MD001T-P1, Hangzhou Matridx Biotechnology Co.,Ltd) and then sequenced on the NextSeq 500/550 High Output Reagent Cartridge v2 300 cycles (Illumina, San Diego, CA 92122, USA). After sequencing, the low-quality reads were removed, and then all the original sequences belonging to E. coli were screened through BWA comparison; The genome was assembled with SPAdes v3.15.3 [13].

The serotype of each strain was determined using the genes deposited in the Center for Genomic Epidemiology (www.genomicepidemiology.org, accessed on 20 September 2022) for E. coli as part of their web-based serotyping tool (Serotype-

Finder 2.0, https://cge.food.dtu.dk/services/SerotypeFinder/), with a similarity of 85% and minimum length of 60%; the ST of each strain was analyzed using the MLST 2.0 Escherichia. coli#1 approach provided by the Center for Genomic Epidemiology (https://cge.food.dtu.dk/services/MLST/, accessed on 20 September 2022). The virulence factor of each strain were determined using the genes deposited in the Center for Genomic Epidemiology for E. coli as part of their web-based VirulenceFinder 2.0 tool (https://cge.food.dtu.dk/services/VirulenceFinder/, accessed on 20 September 2022), with the similarity of 90% and minimum length of 60%.

Statistical analysis

Descriptive analysis was performed with SPSS 23.0 (SPSS, Inc.). The chi-square test or Fisher's test was used to compare qualitative variables. The case-control odds ratio (OR) and 95% confidence intervals (95% CIs) were calculated to measure the association between exposure and outcome. Statistical significance was defined as $p < 0.05$.

Ethics

This study was approved by the Ethics committee of Huzhou Center for Disease Control and Prevention. Informed consent for the stool samples was obtained from the patients or their guardians.

Results

Epidemiological investigation

The delicatessen is located in the Chengnan Community of Lingfeng Street, Anji County. It sells bulk cooked meat and cold dishes all the year round. The customers are basically residents living in the community. The bulk cooked meat and cold dishes in the shop are produced by the owner and his wife in the shop. The processing place is about 15 square meters. Only one sink, a processing table of about 2 square meters, and two freezers are set up. There are no windows in the processing place, and the indoor ambient temperature is high. There is no disinfection facility on site.

Six families had purchased and eaten the cold pork purchased from the delicatessen produced by the owner of the shop. 37 people had ate the cold pork, 20 of them were ill. All of them met the definition of possible cases. According to the statistics of possible cases, the incidence rate was 54.05% (20/37). 37 suspected cases, 20 probable cases and 6 laboratory-confirmed cases were determined in this outbreak. The 20 probable cases with the main symptoms of diarrhea and vomiting were from six families. All the families had no history of eating together. 20 cases all the cold pork purchased from the shop.

Table 1: Symptoms of 20 cases.

Symptom	Number of cases	Percentage%
vomiting	18	90
abdominal	5	10
diarrhea	18	90

The first case, a male patient, aged 40, began to have nausea (six times) and diarrhea (five times) at 20:00 on May 26, without fever. The final case occurred at 00:00 on May 27. The incidence peak presented at 20:30 on May 26, and the time between the first case and the last case was about 4h. According to the epidemiological curve, this outbreak was a homologous exposure event. The suspicious meal was the dinner on May 26 (at about 18 o'clock). The suspicious food is the cold pork purchased on May 26. The 20 cases were mainly concentrated in 2 to 4 hours after dinner, and the peak appeared within 2.5 to 3 hours, with the longest incubation period of 6 hours, the shortest incubation period of 2 hours, and the average incubation period of 3 hours (Figure 1). The specific distribution of onset time is shown in Figure 1. Among the 20 possible cases, the youngest patient was 4 years old and the oldest was 44 years old. There were 14 males and 6 females. In all probable cases, the main clinical symptoms were abdominal pain, diarrhea and vomiting. Fever and other symptoms were rare (Table 1). All the 20 patients received emergency treatment in local hospitals. After giving symptomatic support treatment, including rehydration and antidiarrheal medication, they were all cured without any severe cases or deaths.

Laboratory results

A total of 15 stool samples were collected (including 13 cases, 1 for the owner of the shop and 1 for the owner's wife). Five food samples were collected (two cold pork left by sick households, one cold pork being sold in the shop, one other cold mixed vegetables, and one chili oil in the shop). Two kitchen environment samples were collected.

All the samples were all negative for *Salmonella* spp., *Shigella* spp., and *V. parahaemolyticus*. Nine isolates (five cases, one food producer and three cold pork samples) confirmed as Enteropathogenic *E. coli*-positive. Enteropathogenic *E. coli* isolates were further typed with PFGE (Figure 2). The results of PFGE were obviously clustered into two banding patterns, with an overall similarity of 58.92%. Four cases presented 100% similarity with the food producer. Another case and 3 cold pork formed a band pattern with a similarity of 100%. Strains from the three cases and the food producer had multiple drug resistance to NAL-AZM-AMP-AMS. Other strains had resistance to TET-NAL (Figure 2). All the isolates were resistant to NAL.

Regarding the 9 EPEC isolates, 2 serotypes were observed: Out: H4, O16:H4,, and 2 STs were found, including ST226, ST10. Serotype was highly correlated with ST (Table 2). The distribution of virulence genes was divided into two types. There were 12 virulence genes shared by 9 isolates. The strain from food source had 10 more other virulence genes, while the strain from food producer had 2 more other virulence genes.

Table 2 Serotype, ST, and virulence factor of the EPEC isolates in this study.

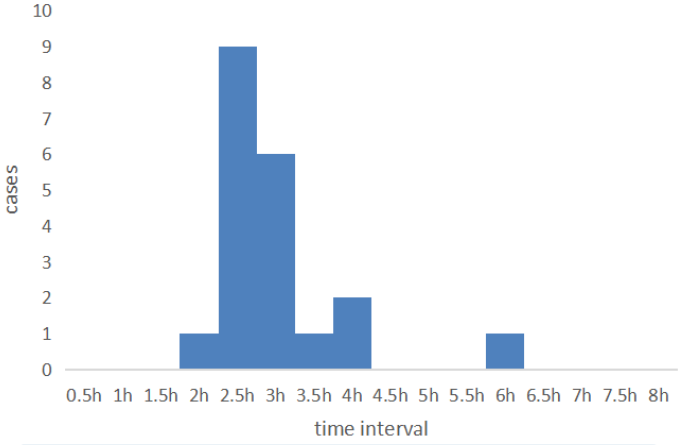

Figure 1: The onset time distribution of 20 probable cases.

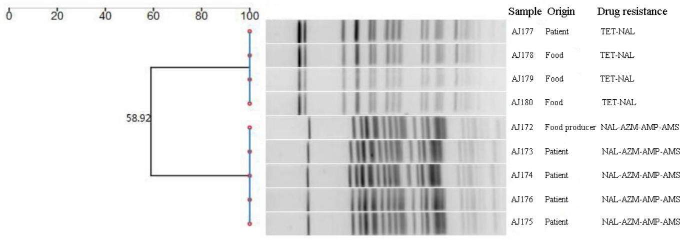

Figure 2: Analysis of PFGE and antibiotic sensitivity test

Strain	Origin	Serotype	ST	Virulence factor																									
				capU	eatA	AslA	air	csgA	fimH	gad	hha	hlyE	nlpI	terC	traT	yehA	yehB	yehC	yehD	fdeC	fyuA	irp2	iss	kpsE	kpsMII_K5	mchA	papA_feiA_F8	senB	sitA
AJ172	food producer	Out：H4	226	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
AJ173	patient	Out：H4	226	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
AJ174	patient	Out：H4	226	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
AJ175	patient	Out：H4	226	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
AJ176	patient	Out：H4	226	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
AJ177	patient	O16:H4	10	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
AJ178	food	O16:H4	10	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
AJ179	food	O16:H4	10	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
AJ180	food	O16:H4	10	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

Nucleotide Sequence Accession Numbers

The draft genome sequences of the E. coli strains used in this study are available in GenBank under the following accession numbers: JAOTPW000000000, JAOXFK000000000, JAOXFL000000000, JAOXFM000000000, JAOXFN000000000, JAOXFO000000000, JAOXFP000000000, JAOXFQ000000000, JAOXFR000000000.

Discussion

This study presented here a foodbrone outbreak event caused by eating cold pork contaminated by EPEC. We detected EPEC from patients, food producer and food. Specifically, we found that the detected pathogenic bacteria were not homologous after analysis, that is, this event was caused by two different EPECs. EPEC is characterized by releasing the attaching and effacing (A/E) lesions from enterocytes [14]. It attaches to the small intestinal cells through bundles of villi and penetrates the microvilli structure by inducing typical A/E lesions [14]. Foodbrone outbreak caused by diarrheagenic *E. coli* is second only to *V. parahaemolyticus* in Huzhou area [15-16]. The detection rate of diarrheagenic *E. coli* among surveillance cases of foodborne diseases has increased year by year. It is inconsistent with other areas in Zhejiang province, but consistent with the results of Hangzhou [15-16].

As an increasingly serious public health problem, foodborne disease is a major obstacle to the world's social and economic development. During 2021, A total of 5493 foodborne disease outbreaks (FBDOs) were reported in China, resulting in 32,334 cases, and 117 deaths. Among the identifed causes of FBDOs, the number of cases caused by bacteria were the largest, accounting for 11585 cases (53.05%, 11585/21839) [17]. Bacteria were also the main cause of FBDOs in Zhejiang Province [15].

One event may have multiple pathogens [18]. This makes it more difficult to trace the source and investigate the transmission chain. In our study, two types of EPEC were detected in patients. One type was homologous with the food, and the other was homologous with the food producer. The patients got infected with different bacteria after having the same food. The pathogens isolated from patients were the same as those detected in food. So the patients got sick because they ate the contaminated food. But we don't know the source where the food got contaminated. How the patients who infected with the strain homologous with the strain from the food producer got sick? One possibility was that two kinds of bacteria were actually contaminated in the food. Maybe the uneven distribution in food leaded to the different infection in people and different detection result. The food producer, as asymptomatic infected person, did not do a good job of self health monitoring and personal hygiene before making ready to eat food. He contaminated the food when processing. We supposed that the other bacteria may also come from the food producer, which means that the food producer was actually a co-infected person with multiple bacteria. Another possibility was that one bacteria came from the food, and another bacteria came from the contaminated container, or spices added to the food. Recently, novel outbreak-associated food vehicles emerged and some bacteria can survive for a long time [19]. Contamination of food can occur anywhere from farm to table, due to improper preparation, handling or storage [20].

The drug resistance of *E. coli* has become a global issue. It is worth noting that some multi-drug-resistant strains were found in this study. The drug resistance situation was basically consistent with other regions in China [21]. Drug resistant strains were constantly emerging and showing an upward trend in foodborne pathogenic bacteria [22-23]. More attention needs to be paid as the high resistance rate to commonly used antibiotics in clinical practice would bring difficulties to patients' clinical treatment. Previous studies have suggested that EPEC has certain dominant serotypes, which have been used as the basis for diagnosing EPEC [24]. The "Diagnostic Standards for Infectious Diarrhea" in China also lists the serum groups that EPEC should meet [25]. This method of determining EPEC based on serum groups is still widely used in China. But the serotype of the strains we detected was different from the serotypes in the standard. The research results of Gao et al. also indicate that the dominant serum group of EPEC may have changed, or there may be more serotypes of EPEC strains exist [26]. Therefore, simply using serum groups to diagnose EPEC may lead to missed or false detections. The virulence genes of EPEC are partially carried by bacteriophages, making them susceptible to horizontal transfer, transmission, or loss [27]. The isolates we detected have different virulence gene compositions, which may be related to horizontal transfer. But all the isolates we detected can cause diarrhea, indicating that there were many virulence genes associated with diarrhea.

There were some limitations of this study. Because our investigation was limited to delicatessens and the patients. We did not know the source of the bacteria in the food and the transmission route of the bacteria carried by the food producer.

In general, this event was caused by two different EPECs. We can't ignore multiple infection sources when conducting foodborne outbreaks investigation. Proper food preparation can prevent the occurence of most foodborne diseases. To reduce the outbreaks of bacterial foodborne diseases, food handlers should pay attention to food safety and follow the standard operating procedures. The government should adopt targeted prevention strategies according to the characteristics of different pathogens.

Declarations

Consent for publication: Not applicable

Availability of data and material: The readers interested in

using the data may contact the corresponding author

Competing interests: The authors declare that they have no competing interests

Funding: Not applicable

Acknowledgements

We thank the staff of Anji CDC for collecting the samples and isolating all the strains.

References

1. Lee H, Yoon Y. Etiological Agents Implicated in Foodborne Illness World Wide. Food Sci Anim Resour 2021; 41: 1-7.
2. Scallan E, Hoekstra RM, Angulo FJ, et al. Foodborne illness acquired in the United States-major pathogens. Emerg Infect Dis 2011;17: 7-15.
3. Wang J, Song F, Walia K, et al. Using convolutional neural networks to extract keywords and keyphrases: A case study for foodborne illnesses. In Proceedings of the 2019 18th IEEE International Conference on Machine Learning and Applications (ICMLA), Boca Raton, FL, USA. 2019; 1398–1403.
4. Alizade H, Hosseini Teshnizi S, Azad M, et al. An overview of diarrheagenic Escherichia coli in Iran: A systematic review and meta-analysis. J Res Med Sci 2019; 24: 23.
5. Bouzari S, Farhang E, Hosseini SM, et al. Prevalence and antimicrobial resistance of shiga toxin-producing Escherichia coli and enteropathogenic Escherichia coli isolated from patients with acute diarrhea. Iran J Microbiol. 2018; 10: 151-157.
6. Abba K, Sinfield R, Hart CA, et al. Pathogens associated with persistent diarrhoea in children in low and middle income countries: systematic review. BMC Infect Dis 2009; 9: 88.
7. Shen H, Zhang J, Li Y, et al. The 12 Gastrointestinal Pathogens Spectrum of Acute Infectious Diarrhea in a Sentinel Hospital, Shenzhen, China. Front Microbiol 2016; 7: 1926.
8. Zhou Y, Zhu X, Hou H, et al. Characteristics of diarrheagenic Escherichia coli among children under 5 years of age with acute diarrhea: a hospital based study. BMC Infect Dis 2018; 18: 63.
9. Zhang S, Wu Q, Zhang J, et al. Occurrence and Characterization of Enteropathogenic Escherichia coli (EPEC) in Retail Ready-to-Eat Foods in China. Foodborne Pathog Dis 2016; 13: 49-55.
10. Zhang S, Yang G, Huang Y, et al. Prevalence and Characterization of Atypical Enteropathogenic Escherichia coli Isolated from Retail Foods in China. J Food Prot 2018; 81: 1761-1767.
11. Ribot EM, Fair MA, Gautom R, et al. Standardization of pulsed-field gel electrophoresis protocols for the subtyping of Escherichia coli O157:H7, Salmonella, and Shigella for PulseNet. Foodborne Pathog Dis 2006; 3: 59-67.
12. Clinical and Laboratory Standards Institute (CLSI). Performance Standards for Antimicrobial Susceptibility Testing, 29th ed.; CLSI supplement M100; Clinical and Laboratory Standards Institute: Wayne, PA, USA. 2019.
13. Bankevich A, Nurk S, Antipov D, et al. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 2012; 19: 455-77.
14. Gambushe SM, Zishiri OT, El Zowalaty ME. Review of Escherichia coli O157:H7 Prevalence, Pathogenicity, Heavy Metal and Antimicrobial Resistance, African Perspective. Infect Drug Resist 2022; 15: 4645-4673.
15. Chen L, Sun L, Zhang R, et al. Surveillance for foodborne disease outbreaks in Zhejiang Province, China, 2015-2020. BMC Public Health 2022; 22: 135.
16. Chen L, Wang J, Zhang R, et al. An 11-Year Analysis of Bacterial Foodborne Disease Outbreaks in Zhejiang Province, China. Foods 2022; 11: 2382.
17. LI Hongqiu, JIA Huayun, ZHAO Shuai, et al. Analysis of foodborne disease outbreaks in Chinese Mainland in 2021. Chinese Journal of Food Hygiene. 2022; 34: 816-821.
18. Qiu Q, Dewey-Mattia D, Subramhanya S, et al. Food recalls associated with foodborne disease outbreaks, United States, 2006-2016. Epidemiol Infect 2021; 149: e190.
19. Whitham HK, Sundararaman P, Dewey-Mattia D, et al. Novel Outbreak-Associated Food Vehicles, United States. Emerg Infect Dis 2021; 27: 2554-2559.
20. National Institute for Public Health and the Environment (RIVM), The Netherlands; Iulietto MF, Evers EG. Modelling and magnitude estimation of cross-contamination in the kitchen for quantitative microbiological risk assessment (QMRA). EFSA J 2020; 18: e181106.
21. Tang Zhen, Shen Yun, Qin Si, et al. Analysis of the infection status and drug resistance of diarrhea causing Escherichia coli in foodborne diseases in Jiangsu Province in 2017. Journal of Nanjing Medical University. 2018; 38: 1371-1375.
22. Magiorakos AP, Srinivasan A, Carey RB, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: An international expert proposal for interim standard definitions for acquired resistance. Clin Microbiol Infect 2012; 18: 268-281.
23. Pan HJ, Zhang JM, Kuang D, et al. Molecular analysis and antimicrobial susceptibility of enterotoxigenic Escherich ia coli from diarrheal patients. Diag Microbiol Infect Dis 2015; 81: 126-131.
24. Nataro JP, Kaper JB. Diarrheagenic Escherichia coli. Clin Microbiol Rev. 1998; 11: 142-201.
25. The Ministry of Health. WS 271-2007 Diagnostic criteria of infectious diarrheaS. Beijing: The Ministry of Health of the People's Republic of China. 2007. (in Chinese)
26. Gao Xiang, Zhao Hongqing, Zhen Bojun, et al. Analysis of the characteristics of pathogenic Escherichia coli strains isolated from diarrhea patients in Beijing area. Disease Surveillance 2013; 28: 347-350
27. Werber D, Scheutz F. The importance of integrating genetic strain information for managing cases of Shiga toxin-producing E. coli infection. Epidemiol. Infect 2019, 147: e264.