World Journal of
Biological and Pharmaceutical Research

Journal homepage: https://zealjournals.com/wjbpr/

ISSN: 2799-0338 (Online)

(RESEARCH ARTICLE)

A multidrug- resistance pattern of an *Escherichia coli* strain isolated from diarrheal stools at the China-Guinea Friendship Hospital of Kipé in Conakry

Abdoulaye Makanéra [1, 2, *], Mariam Condé [1], Taliby Dos Camara [3], Mamadou Alpha Diallo [1], Mariama Condé [1], Daouda Camara [1], Alpha Oumar Barry [1], Tiguidanké Diakité [1] and Oumar Souaré [1]

[1] Biomedical Laboratory of the China-Guinea Friendship Hospital, Kipé, Cité des Médecins, Commune Ratoma 30 BP: 710 Conakry, Republic of Guinea.
[2] Department of Medicine, Faculty of Health Sciences and Techniques, Chair of Fundamental Sciences, Gamal Abdel Nasser University of Conakry, PO Box: 1147 Republic of Guinea.
[3] Microbiology Laboratory, Department of Biology, Faculty of Sciences, and Gamal Abdel Nasser University of Conakry BP: 1147 Republic of Guinea.

World Journal of Biological and Pharmaceutical Research, 2022, 03(02), 018–023

Publication history: Received on 22 October 2022; revised on 29 November 2022; accepted on 02 December 2022

Article DOI: https://doi.org/10.53346/wjbpr.2022.3.2.0043

Abstract

Introduction: Diarrheal infections associated to multidrug resistant bacteria are a public health problem, particularly in the tropics.

Objective: The aim of this study was to describe a Multidrug resistant strain of *Escherichia coli* (*E. coli*) isolated from diarrheal stools.

Patients and methods: A sample of diarrheal stools from a 30 years old housekeeper patient was analysed at China-Guinea Friendship Hospital of Kipé/Conakry. Parasitological examination by optical microscopy, followed by bacteriological analysis were done. Cultures were carried out on different agar media. Bacterial identification, antibiograms and minimum inhibitory concentrations (MIC) were performed using the Vitek 2 System.

Results: The isolated *E. coli* strain was sensitive only to 4 of 29 antibiotics tested including imipenem, ertapenem, amikacin and nitrofurantoin. Intermediate sensitivity was detected towards minocycline. In contrast, this strain was resistant to piperacillin, cefuroxime, cefuroxime axetil, cefixime, ceftriaxone, cefepime, aztreonam, meropenem, levofloxacin, ofloxacin, tetracycline, tigecycline, chloramphenicol, trimethoprim, ampicillin, amoxicillin/clavulanic acid, ticarcillin, piperacillin/tazobactam, cephalothin, cefotaxime, ceftazidime, gentamicin, tobramycin, nalidixic acid, ciprofloxacin, ofloxacin and trimethoprim/sulfamethoxazole with high MICs.

Conclusion: The treatment of this multidrug-resistant *Escherichia coli* diarrheal infection requires appropriate antibiotic therapy, based on the results of an accurate antibiogram to be performed with rapid means for better patient care.

Keywords: *Escherichia coli*; Diarrheal stools; Multidrug-resistance; Antibiotics; Kipé/Conakry

* Corresponding author: Abdoulaye Makanéra
Biomedical Laboratory of the China-Guinea Friendship Hospital, Kipé, Cité des Médecins, Commune Ratoma 30 BP: 710 Conakry, Republic of Guinea.

1. Introduction

Escherichia coli is a Gram-negative bacterium belonging to the family of *Enterobacteriaceae*. It is a bacterial species often associated with various infections in humans including diarrhea. *E. coli* is a commensal bacterium of the digestive tract in humans and animals. However, some strains are pathogens associated with diarrhea but also with many infections in humans particularly in developing countries [1-3].

The treatment of diarrheal diseases caused by *Escherichia coli* often requires antibiotic therapy. Today, many strains of *Escherichia coli* have become multi-resistant to antibiotics. The acquisition in *Escherichia coli* of multi-drug-resistance genes to antibiotics is generally at the origin of therapeutic failures worldwide but particularly in developing countries. Indeed, in the developing countries the means of bacteriological diagnosis are limited with regard to the identification and carrying out antibiograms.

In many developing countries, antibiotic therapy is carried out in an anarchic manner with an undetermined frequency of cases of self-medication. Then development of antimicrobial resistance in *Escherichia coli* is a major concern worldwide.

Multidrug-resistant *Escherichia coli* has become a major public health problem in Guinea as elsewhere in the world, often leading to treatment failures with an enormous health burden [4-6].

Numerous data from the literature show that diarrhea is one of the ten main causes of death in the world and the second in low-income countries in children under 5 years of age [7-8].

The aim of this present study was to describe a strain of Multidrug-resistant *Escherichia coli* to antibiotics isolated from diarrheal stools in a 30-year-old woman at the China-Guinea Friendship Hospital of Kipé.

2. Material and methods

A sample of diarrheal stools from a 30-year-old female patient of a household profession was received on June 28, 2019 at the Biomedical Laboratory of the China-Guinea Friendship Hospital in Kipé/Conakry for coprological examinations. The interrogation showed that the patient had had more than six episodes of diarrhea in less than 24 hours.

The sample was subjected to parasitological examination by optical microscopy, followed by bacteriological analysis. Bacterial culture was carried out on agar media: MacConkey (MC) agar, *Salmonella-Shigella* (SS) agar (bioMérieux, France). The bacterial colonies isolated on MacConkey agar were subjected to identification and antibiograms using the Vitek 2 Compact 15 automaton (bioMérieux, France). Vitek 2 GN cards were used for bacterial identification and Vitek 2 AST N233 and Vitek 2 AST XN05 cards were used for antibiogram and determination of Minimum Inhibitory Concentrations (MIC).

3. Results

The parasitological examination of the diarrheal stools analyzed was negative, whereas the bacteriological analysis of these diarrheal stools allowed the isolation of the bacterial colonies on the nutrient agar and MacConkey agar media, whereas the culture on the SS medium was sterile. Bacterial identification on the Vitek 2 Compact 15 automaton using the Vitek 2 GN identification card revealed the presence of an *Escherichia coli* strain (Table 1). The antibiogram performed using Vitek 2 AST N233 Compact 15 cards showed resistance to the majority of antibiotics tested with high MICs (Table 1). The antibiogram carried out with the Vitek 2 AST XN05 cards showed multi-resistance to almost all the molecules tested with the exception of minocycline to which the strain of *Escherichia coli* had intermediate resistance (Table 1).

Table 1 Susceptibility profile of the strain of *Escherichia coli* isolated from diarrheal stools

Vitek 2 AST N233		Vitek 2 AST XN05	
Antibiotics	**Susceptibility (MIC : µg/l)**	**Antibiotics**	**Susceptibility (MIC : µg/l)**
Ampicillin	R≥32	Piperacillin	R>64
Amoxicillin/Clavulanic acid	R≥32	Cefuroxime	R >32
Ticarcillin	R ≥128	Cefuroxime axetil	R>32
Piperacillin/Tazobactam	R ≥ 128	Cefixime	R>2
Cephalothin	R ≥ 64	Ceftriaxone	R>32
Cefoxitin	R ≥ 64	Cefepime	R>32
Cefotaxime	R ≥ 64	Aztreonam	R>32
Ceftazidime	R ≥ 64	Meropenem	R>8
Ertapenem	S ≤ 0,25	Levofloxacin	R>4
Imipenem	S ≤ 0,25	Moxifloxacin	R>4
Amikacin	S ≤ 2	Minocycline	I=8
Gentamicin	R ≥16	Tetracycline	R>8
Tobramycin	R ≥ 16	Tigecycline	R>4
Nalidixic acid	R ≥32	Chloramphenicol	R>32
Ciprofloxacin	R ≥ 4	Trimethoprim	R>8
Ofloxacin	R ≥ 8		
Nitrofurantoin	S < 16		
Trimethoprim/Sulfamethoxazole	R≥320		

4. Discussion

The uncontrolled use of antibiotics is one of the main factors for the emergence and spread of antimicrobial resistance genes around the world, thus constituting a threat to global health [9].

The development of multi-resistance in *Escherichia coli* is a major concern worldwide. Multi-resistant *Escherichia coli* from diarrheal stools could be the cause of therapeutic failure with antibacterial molecules, reducing the possibilities of treatment with available molecules. This situation would be even more frequently dramatic in developing countries where the means of diagnosis are weak and the possibility of acquiring certain molecules such as carbapenems. The spread of bacterial multidrug-resistant strains in the environment can lead to many cases of morbidity and mortality in humans and animals.

Visitors to emerging economies stay in conditions with weak hygiene infrastructure. Their most common health problem is travelers' diarrhea [6].

In this study, the patient presented more than six episodes of diarrheal stool in daily. This is in line with the World Health Organization definition of diarrhea. Indeed, diarrhea was defined by the WHO criteria as passage of three or more loose or liquid stools per day, or more frequently than is normal for the individual [9].

Travellers' diarrhoea (TD) is the most frequent illness experienced by international travellers to lower-income countries with bacterial agents considered to account for 80–90% of cases [10].

Then, antibiotic resistance genes are subject to local, regional, national and international transmission. Indeed, multidrug-resistant bacteria are often carried around the world by international travelers. Different species of

Enterobacteriaceae producing extended-spectrum beta-lactamases, including *Escherichia coli*, are particularly implicated, particularly in cases of diarrhea in tropical countries. Some authors reported that the antimicrobial resistance (AMR) is being transported worldwide by international travelers [11-14]. Indeed 20–70% of visitors to low- and middle-income countries carry multidrug-resistant bacteria (MDR), particularly extended spectrum bêta-lactamase-producing *Enterobacteriaceae*, to their home country and may spread them further [11].

In this study, parasitological examination of diarrheal stools of the young woman did not make it possible to observe intestinal parasites. On the other hand, the bacteriological analyzes made it possible to identify a strain of *Escherichia coli*, thus suggesting that this diarrhea would be of bacterial origin. Treatment for this *Escherichia coli* associated diarrhea would require adequate antibiotic treatment. This means guided antibiotic therapy, therefore based on the results of an antibiogram.

The results of antibiotic susceptibility tests showed multi-resistance of the strain to the majority of the antibiotics tested with often high MICs (Table 1). This strain of *Escherichia coli* was resistant to all beta-lactams except carbapenems including ertapenem and imipenem. The susceptibility profile of this strain of Escherichia coli to carbapenem is comparable to the susceptibility profiles of uropathogenic *Escherichia coli* strains described in 2021 by Makanéra et al., [4]. However, the sensitivity profile of this present strains to other beta-lactams is different from the overall sensitivity profile of uropathogenic *Escherichia coli* strains described by the latter.

However, among the carbapenem molecules tested, this strain was only shown resistance to meropenem. This strain was thus a producer of extended-spectrum beta-lactamases (ESBL). These data are partly close to those reported in 2022 in Finland by Kantele et al, who described *Escherichia coli* strain with a frequency of 15% of ESBL-producing strains isolated from diarrheal stools in travelers from different countries [11]. On the other hand, these authors did not encounter any strains of Escherichia coli resistant to ertapenem (carbapenem) in their study. Similarly, our results are also similar in part to those found by Rodrigues et al., in 2022 who reported in their study an 8% (47/623) frequency of *Escherichia coli* collected from stools in Rio de Janeiro, Brazil [15]. In addition, Ljungquist et al, 2020, reported a 57% frequency of Escherichia coli strains isolated from diarrheal stools and producing ESBL [16].

The strain susceptibility test against aminoglycosides showed that the *Escherichia coli* strain was sensitive only to amikacin. On the other hand, this strain was resistant to gentamicin and to tobramycin with high MICs (Table 1). These results are partly comparable to those reported in Brazilia by de Pinho Rodriguez et al., in 2022 [15]. Indeed, these results showed a higher resistance frequencies of Escherichia coli strains isolated from diarrheal stools to gentamicin than to amikacin [15]. However, these authors did not test the sensitivity of their strains to tobramycin. However, these results are partly different from those reported previously in Guinea in 2021 on uropathogenic *Escherichia coli* trains. Indeed, these uropathogenic Escherichia coli were sensitive not only to amikacin, but also to tobramycin and gentamicin [4].

Quinolone sensitivity tests showed resistance to all molecules of this family which were tested with high MICs. Thus, the strain of *Escherichia coli* tested was resistant to ciprofloxacin, ofloxacin, nalidixic acid, levofloxacin, moxifloxacin (Table 1). These data are similar to those reported in 2022 by Kantel et al., [11]. Indeed, these authors reported a high frequency of resistance of their strains to ciprofloxacin which was the only quinolone molecule tested in their study [11]. On the other hand, this resistance profile of this strain of *Escherichia coli* to quinolones is rather comparable to that of uropathogenic strains of *Escherichia coli*, reported in Conakry in 2021 [4].

In Guinea, the multi-resistance of *Escherichia coli* strains to quinolones could partly be explained by the fact that quinolones have been widely used in this country for a very long time in an anarchic manner, particularly in cases of profuse diarrhea. The therapeutic use of quinolones during diarrhea was generally done without medical prescription by health professionals for fear in particular of cases of cholera or typhoid fever.

The results of the antibiogram also showed resistance to tetracycline, tigecycline and intermediate sensitivity to minocycline (Table 1). Susceptibility tests to sulfonamides of the *Escherichia coli* strain studied showed resistance to various molecules tested, including trimethoprim and the trimethoprim/sulfamethoxazole combination. These data are partly similar to those reported by Kantele et al., in 2022 who founded a high frequency of strain resistance to the trimethoprim/ sulfamethoxazole combination [11]. The strain of *Escherichia coli* studied in the present study was resistant to chloramphenicol.

The chloramphenicol is an antibiotic, which is no longer used therapeutically in Guinea, has in the past experienced the misuse of this molecule in cases of diarrheal diseases. This molecule is still in sensitivity tests for scientific reasons to

understand certain mechanisms used by bacteria in their antibiotic resistance strategies. Salleh et al reported in 2022, 21,9% of diarrheagenic *Escherichia coli* in Asia [17]

Finally, concerning furans, the results of the antibiogram showed that the strain of *Escherichia coli* studied was sensitive to nitrofurantoin (Table 1). These results are similar to those found by Kantele et al in 2022 who described a very low frequency of resistance to nitrofurantoin and therefore a high frequency of sensitivity of their strains to this molecule. These results are also comparable to those reported in Guinea on uropathogenic strains of *Escherichia coli*. Indeed, this molecule was very active on the majority of the strains studied strains [4]. Other studies concerning *Escherichia coli* resistance to nitrofurantoin were done around the world. Indeed, in 2019, Kot reported that the resistance *Escherichia coli* to nitrofurantoin is very low, favoring its use as a first-line antibacterial agent [18]. Studies conducted by Sanchez et al. (2016) showed that in the United States nitrofurantoin retains a high level of antibiotic activity against *Escherichia coli* isolated from urinary tract infections [19]. A comparison of the reports from the period of 2003 to 2012 revealed that resistance of *Escherichia coli* isolates from adults to nitrofurantoin only slightly increased (from 0.7% to 0.9%). Kresken et al., (2016) reported that studies carried out in Germany, Belgium and Spain showed that *Escherichia coli* is usually susceptible to nitrofurantoin [20]. Indeed, the rates of uropathogenic *Escherichia coli* resistance in these countries in the period 2013–2014 were below 1.5% [18,20].

5. Conclusion

All of these results show that the strain of *Escherichia coli* isolated from diarrheal stools shows multi-resistance to most of the antibiotic molecules tested. This multiresistance concerned all families of antibiotics tested except nitrofurans. Thus, the antibiotics active in this strain were nitrofurantoin, amikacin, ertapenem and imipenem. These data thus suggest the need for bacteriological diagnosis allowing bacterial identification as well as antibiogram for the purpose of appropriate antibiotic therapy in order to avoid the spread of multi-resistant bacteria to antibiotics.

Carbapenems (Imipenem and ertapenem), nitrofurantoin and aminoglycosides (amikacin, gentamicin and tobramycin) as well as some cephalosporins (piperacillin / tazobactam combination,) seem to be the antibiotics of choice of first line in the treatment of urogenital infections with *Escherichia coli.*

Compliance with ethical standards

Acknowledgments

This work was financed by grants from The Health Department of Republic of Guinea and The Popular Republic of China.

Disclosure of conflict of interest

The authors declare that they have no conflicts of interest.

Statement of informed consent

The informed consent of the patient to participate in the study was acquired and confidentiality was observed throughout the data collection process. The results were used for strictly scientific purposes.

References

[1] Sarba EJ, Kelbesa KA Bayu MD, Gebremedhin EZ, Borena BM, Teshale A. Identification and antimicrobial susceptibility profile of Escherichia coli isolated873 from backyard chicken in and around ambo, Central Ethiopia. BMC Vet. Res. 2019 ; 15(1), 85.

[2] Alizade H, Hosseini Teshnizi S, Azad M, Shojae S, Gouklani H, Davoodian P, Ghanbarpour R. An overview of diarrheagenic Escherichia coli in Iran: A systematic review and meta-analysis. J Res Med Sci. 2019, 25;24:23. doi: 10.4103/jrms.JRMS_256_18. PMID: 31007693; PMCID: PMC6450139.

[3] Darbandi A, Owlia P, Bouzari S, Saderi H. Diarrheagenic Escherichia coli pathotypes 28491244; PMCID: PMC5420388.

[4] Makanéra A, Camara T, Diallo AS, Chamassi R, Condé M, Diallo MA et al. Antibiotic sensitivity profile of uropathogenic Escherichia coli strains at the China-Guinea Friendship Hospital of Kipé in Conakry (Guinea). WJARR, 2021, 09(01), 075–085. Article DOI: 10.30574/wjarr.2021.9.1.0492

[5] Ibrahim ME, Bilal NE, Hamid ME. Increased multi-drug resistant Escherichia coli from hospitals in Khartoum state, Sudan. Afr Health Sci. 2012 Sep;12(3):368-75. doi: 10.4314/ahs.v12i3.19. PMID: 23382754; PMCID: PMC3557680

[6] Turunen KA, Kantele A. Revisiting travellers' diarrhoea justifying antibiotic treatment: prospective study. Journal of Travel Medicine, 2021, 1–10 doi: 10.1093/jtm/taaa237

[7] Khairy RMM, Fathy ZA, Mahrous DM, Mohamed ES, Abdelrahim SS. Prevalence, phylogeny, and antimicrobial resistance of Escherichia coli pathotypes isolated from children less than 5 years old with community acquired-diarrhea in Upper Egypt. BMC Infect Dis. 2020 1;20(1):908. doi: 10.1186/s12879-020-05664-6. PMID: 33256619; PMCID: PMC7708180.

[8] Canizalez-Roman A, Flores-Villaseñor HM, Gonzalez-Nuñez E, Velazquez-Roman J, Vidal JE, Muro-Amador S. Surveillance of Diarrheagenic Escherichia coli Strains Isolated from Diarrhea Cases from Children, Adults and Elderly at Northwest of Mexico. Front Microbiol. 2016 Nov 30;7:1924. doi: 10.3389/fmicb.2016.01924. PMID: 27965648; PMCID: PMC5127799.

[9] World Health Organization. Diarrhoea. Geneva: World Health Organization, 2020. http://www.who.int/topics/diarrhoea/en/ (accessed September 8, 2020).

[10] Rogelio Lopez-Velez R, Lebens M, Bundy L , Barriga J , Steffen R. Bacterial travellers' diarrhoea: A narrative review of literature published over the past 10 years. Travel Medicine and Infectious Disease 47 (2022) 102293. https://doi.org/10.1016/j.tmaid.2022.102293

[11] Kantele A, Lääveri T, Extended-spectrum bêta-lactamase-producing strains among diarrhoeagenic Escherichia coli—prospective traveller study with literature review, Journal of Travel Medicine, Volume 29, Issue 1, January 2022, taab042, https://doi.org/10.1093/jtm/taab042

[12] [12] Paltansing S, Vlot JA, Kraakman ME, Mesman R, Bruijning ML, Bernards AT, Visser LG, Veldkamp KE. Extended-spectrum β-lactamase-producing enterobacteriaceae among travelers from the Netherlands. Emerg Infect Dis. 2013 Aug;19(8):1206-13. doi: 10.3201/eid.1908.130257. PMID: 23885972; PMCID: PMC3739527.

[13] Kantele A, Lääveri T, Mero S, Vilkman K, Pakkanen SH, Ollgren J, Antikainen J, Kirveskari J. Antimicrobials increase travelers' risk of colonization by extended-spectrum betalactamase-producing Enterobacteriaceae. Clin Infect Dis. 2015 Mar 15;60(6):837-46. doi: 10.1093/cid/ciu957. Epub 2015 Jan 21. PMID: 25613287; PMCID: PMC4345818.

[14] Park JJ, Seo YB, Lee J. Antimicrobial Susceptibilities of Enterobacteriaceae in Community-Acquired Urinary Tract Infections during a 5-year Period: A Single Hospital Study in Korea. Infect Chemother. 2017 Sep;49(3):184-193. doi: 10.3947/ic.2017.49.3.184. PMID: 29027385; PMCID: PMC5620385.

[15] de Pinho Rodrigues, K.M., de Rezende, D.F., Pinto, M.P. et al. High levels of gut carriage of antimicrobial-resistant Escherichia coli in community settings in Rio de Janeiro, Brazil. Braz J Microbiol 53, 205–212 (2022). https://doi.org/10.1007/s42770-021-00673-2

[16] Ljungquist O, Kampmann C, Resman F, Riesbeck K, Tham J. Probiotics for intestinal decolonization of ESBL-producing Enterobacteriaceae: a randomized, placebo-controlled clinical trial, Clinical Microbiology and Infection, 2020 ; 26 (4): 456-462.

[17] Salleh, MZ, Nik Zuraina, NMN, Hajissa K, Ilias MI, Deris ZZ. Prevalence of Multidrug-Resistant Diarrheagenic Escherichia coli in Asia: A Systematic Review and Meta-Analysis. Antibiotics 2022, 11, 1333. https://doi.org/10.3390/antibiotics11101333

[18] Kot B, Wicha J, Grużewska A, Piechota M, Wolska K, Obrębska M. Virulence factors, biofilm-forming ability, and antimicrobial resistance of urinary Escherichia coli strains isolated from hospitalized patients. Turk J Med Sci. 2016; 46(6): 1908–1914

[19] Sanchez GV, Babiker A, Master RN, Luu T, Mathur A, Bordon J. Antibiotic resistance among urinary isolates from female outpatients in the United States in 2003 and 2012. Antimicrob Agents Chemother. 2016; 60(5): 2680–2683.

[20] Kresken M, Körber-Irrgang B, Biedenbach DJ, Batista N, Besard V, Cantón R, García-Castillo M, Kalka-Moll W, Pascual A, Schwarz R, et al. Comparative in vitro activity of oral antimicrobial agents against Enterobacteriaceae from patients with community-acquired urinary tract infections in three European countries. Clin Microbiol Infect. Jan 2016; 22(1): 63.e1–63.e5.

[21] Ibrahim ME. High antimicrobial resistant rates among Gram-negative pathogens in intensive care units. A retrospective study at a tertiary care hospital in Southwest Saudi Arabia. Saudi Med J. 2018 Oct;39(10):1035-1043. doi: 10.15537/smj.2018.10.22944. PMID: 30284588; PMCID: PMC6201019.