

Prevalence and antimicrobial resistance of *Shigella* species isolated from diarrheal patients in Ahvaz, southwest Iran

Ahmad Farajzadeh Sheikh^{1,2}
Mojtaba Moosavian^{1,2}
Mahtab Abdi²
Mohsen Heidary^{3,4}
Fatemeh Shahi²
Nabi Jomehzadeh⁵
Sakineh Seyed-Mohammadi^{1,2,6}
Morteza Saki^{1,2,6}
Saeed Khoshnood^{1,2,6}

¹Infectious and Tropical Diseases Research Center, Health Research Institute, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran;

²Department of Microbiology, Faculty of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran; ³Department of Microbiology, Faculty of Medicine, Iran University of Medical Sciences, Tehran, Iran; ⁴Student Research Committee, School of Allied Medical Sciences, Tehran, Iran; ⁵Abadan School of Medical Sciences, Abadan, Iran; ⁶Student Research Committee, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran

Correspondence: Saeed Khoshnood
Department of Microbiology, Faculty of Medicine, Ahvaz Jundishapur University of Medical Sciences, Golestan Street, PO Box 159, Ahvaz, Khozestan 61357-15794, Iran
Tel +98 91 6757 1873
Fax +98 61 3333 2036
Email Saeed.Khoshnood22@gmail.com

Introduction: Shigellosis is a significant global human health problem, and *Shigella* is in charge of almost 165 million cases of this disease annually, of whom 163 million cases are in developing countries and 1.5 million cases are in developed countries. The main aims of the current survey were to identify *Shigella* spp. isolated from diarrheal patients by conventional biochemical tests, determine the antimicrobial susceptibility profiles by disk diffusion method, and detect the *ipaH* gene using the PCR assay.

Methods: The bacterial isolates were identified as *Shigella* spp. by microbiological tests and were serogrouped by the slide agglutination test. Antimicrobial susceptibility testing was performed using the disk diffusion method. PCR was performed to detect the *ipaH* gene.

Results: The *Shigella* strains were isolated from 522 patients with various diarrhea, including bloody diarrhea (3%), mucoid plus bloody diarrhea (1.9%), mucoid diarrhea (3.2%), and watery diarrhea (3.2%). Overall, 69 (13.2%) isolates were positive for *Shigella* spp., of which 34 (49.3%) serotypes were identified as *Shigella flexneri*, 22 (31.9%) serotypes were identified as *Shigella sonnei*, 9 (13%) serotypes were identified as *Shigella boydii*, and 4 (5.8%) serotypes were identified as *Shigella dysenteriae*. Antibiotic susceptibility tests revealed that the highest resistance percentage was related to ampicillin (82%) and trimethoprim-sulfamethoxazole (77%), and ciprofloxacin and ceftriaxone were the best antibiotics against *Shigella* isolates.

Conclusion: We concluded that *Shigella* spp. can be considered as an etiological agent of diarrhea in southwest Iran. Since the drug resistance pattern of *Shigella* differs geographically and over time within a country, continuous and regular surveillance program is necessary.

Keywords: *Shigella*, diarrhea, resistance, Iran

Introduction

The *Shigella* species are facultative intracellular gram-negative pathogens that cause shigellosis, which remains a significant public health concern. *Shigella* spp. was adopted as a genus of the family Enterobacteriaceae in the 1950s and serogrouped into the following four species: subgroup A (*Shigella dysenteriae*), subgroup B (*Shigella flexneri*), subgroup C (*Shigella boydii*), and subgroup D (*Shigella sonnei*).^{1,2}

These enteric bacteria are in charge of almost 165 million cases of diarrhea annually, of whom 163 million cases are in developing countries and 1.5 million cases are in developed countries.^{3,4} The most common symptoms of shigellosis are light watery diarrhea, vomiting, fever, tenesmus, headache, and abdominal pain.

The illness is generally self-limiting but may become life threatening in patients with compromised immune systems or in the absence of adequate health care.⁵ Due

to the low infectious dose of *Shigella* spp. (10–100 organisms) compared with other enteric pathogens, shigellosis is a serious public health threat.² Lack of proper access to food sources and poor health care contribute to a high risk of morbidity and mortality in many developing countries. A variety of raw vegetables, salads, meat, milk, and other dairy products can serve as vehicles for the transmission of *Shigella* spp. Therefore, the most common causes of contamination are unsanitary practices of food handlers and fecally contaminated water.³

All age groups are affected by *Shigella*, but the age group under 5 years is most susceptible, because of low personal cleanliness and partially developed immunity and absence of past exposures.⁶ The proper and effective treatment for the disease leads to reduce the shedding of the bacteria and prevent lethal outcomes.

However, because of the antibiotic resistance development over the past half-century, the options for antimicrobial therapy in shigellosis are limited to a small number of drugs.⁷ Over time, the antimicrobial resistance patterns of *Shigella* spp. have changed according to geographical locations and the treatment process became more complicated.⁸

The main aims of this study were to identify *Shigella* spp. isolated from diarrheal patients by conventional biochemical tests, determine the antimicrobial susceptibility profiles by disk diffusion method, and detect the *ipaH* gene using the PCR assay.

Methods

Ethics statement

This study was approved by the ethics committee of Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran (No. IR.AJUMS.REC.1396.568). As a part of the Ahvaz Jundishapur University of Medical Sciences policy, written informed consent was obtained from all of the children's parents or legal guardian of any patient under the age of 18 years. The study was conducted in accordance with the Declaration of Helsinki.

Study area and specimen collection

This cross-sectional study was performed in cooperation with Golestan teaching hospital at the Jundishapur University belonging to the Iranian health system in Ahvaz, Iran, during November 2016 to October 2017. Golestan hospital is the second largest university-affiliated hospital located in Ahvaz city (the capital of Khuzestan state). Ahvaz city is located 820 km southwest of Tehran, the capital city of Iran. Stool samples were obtained from 522 patients aged 2–65 years

who were distinguished as suffering from diarrhea by the clinical physician.

Diarrhea means watery or loose stools, usually at least three times in 24 hours. Mucus or blood can appear in the stools with some infections. The patients undergoing antibiotic therapy at the time of sample collection and those with persistence diarrhea were not included. The specimens were collected in sterile plastic containers and immediately transported to the Department of Microbiology of the Ahvaz Jundishapur University of Medical Sciences for processing.

Biochemical test

The fecal specimens were cultivated on selective and differential media, including MacConkey agar, xylose lysine desoxycholate (XLD) agar, and *Salmonella–Shigella* (SS) agar (EMD Millipore, Billerica, MA, USA), and then were incubated at 37°C for 24 hours. Identification of *Shigella* was carried out by subjecting presumptive colonies onto triple sugar iron (TSI) agar, methyl red (MR) broth, Voges–Proskauer (VP) broth, lysine iron agar (LIA), urea broth, indole test, sulfide indole motility (SIM) test, and citrate utilization tests, and incubated for 24–48 hours at 37°C.^{9,10}

Serotyping

The bacterial isolates that were identified as *Shigella* by their morphological and biochemical features were emulsified in normal saline and mixed with an equal volume of specific *Shigella* antiserum (Baharafshan, Tehran, Iran). A macroscopic agglutination was considered as a positive reaction.¹¹

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method according to Clinical and Laboratory Standards Institute (CLSI) recommendations.¹² The susceptibilities of all isolates to different antibiotics were determined using ceftriaxone (CRO, 30 µg), erythromycin (ERY; 15 µg), ampicillin (AMP, 10 µg), chloramphenicol (CAM, 30 µg), nalidixic acid (NA, 30 µg), trimethoprim-sulfamethoxazole (SXT, 25 µg), ceftazidime (CAZ, 30 µg), ciprofloxacin (CIP, 5 µg), cefixime (CFM, 5 µg), and gentamicin, (GEN, 10 µg) (Mast Diagnostics Ltd., Merseyside, UK). *Escherichia coli* ATCC 25922 was used as quality control.

DNA extraction and PCR assay

DNA was extracted from *Shigella* colonies grown overnight on nutrient agar (EMD Millipore) by the boiling method. Briefly, bacteria were cultured in 5 mL of trypticase soy broth (EMD Millipore) and incubated for 24 hours at 37°C.

Then, 200 μ L of broth culture was mixed with 800 μ L of sterile distilled water and the suspension was heated at 95°C for 10 minutes.

Then, the solution was centrifuged at 12,000 \times g for 5 minutes to remove any cell debris. Finally, 200 μ L of the supernatant was stored at -20°C and used as the template for subsequent amplification. PCR amplification was performed to detect the *ipaH* gene in *Shigella* isolates.¹³ Amplification of the *ipaH* gene was carried out using a thermal gradient cycler (Eppendorf Co., Hamburg, Germany) with the following protocol^{14,15}: the PCR mixture contained 2.5 mL of 10 \times buffer (10 mM Tris-HCl and 50 mM KCl), 1.5 mM MgCl₂, 3 μ L of DNA template, 200 μ M each dNTPs, 0.4 μ M of each forward and reverse *ipaH* primer, 0.75 U of Taq polymerase, and sterilized distilled water to complete the reaction volume (25 μ L).

The expected sizes of PCR amplicons were revealed by electrophoresis on 1.5% horizontal agarose gel in Tris-borate-EDTA (TBE) buffer and stained with ethidium bromide (0.5 μ g/mL) (SinaClon, Tehran, Iran). Primer sequences, PCR conditions, and the PCR product size are shown in Table 1.¹⁶

Data analysis

The data were entered and analyzed using the SPSS software, Version 22.0 (IBM Corporation, Armonk, NY, USA) and Microsoft Excel 2016 (Microsoft Corporation, Redmond, WA, USA) statistical software.

Results

Stool samples were obtained from 522 diarrheal patients, and the mean age of patients was 30 \pm 1 years, with a range of 2–65 years. According to stool observation and clinical finding, 16 (3%) patients had bloody diarrhea, 26 (4.9%) patients had mucoid as well as bloody diarrhea, 10 (1.9%) patients had mucoid diarrhea, and 17 (3.2%) patients had watery diarrhea. Various age groups were \leq 6 years (55%), 7–10 years (21.6%), 11–20 years (14.5%), and \geq 21 years (8.8%). Three hundred and eighteen (60.9%) patients were male, and 204 (39.1%) patients were female (Table 2).

The patients have had various clinical symptoms, including headache (N=322, 61.7%), vomiting (N=141, 27%), fever (N=384, 73.5%), and abdominal pain (N=412, 78.9%). All the isolates were recognized by culture and serological tests, and then confirmed by the PCR method. In this study, 24 people were excluded from the study due to the use of antibiotics and 13 people were diagnosed with persistent diarrhea.

Overall, 69 (13.2%) isolates were confirmed as *Shigella* spp., of which 34 (49.2%) serotypes were identified as *S. flexneri*, 22 (31.9%) serotypes were identified as *S. sonnei*, 9 (13%) serotypes were identified as *S. boydii*, and 4 (5.8%) serotypes were identified as *S. dysenteriae*. All 69 isolates produced PCR amplicons of the *ipaH* gene of 500 bp.

Antibiotic susceptibility tests using the Kirby–Bauer method revealed that the highest resistance percentage was related to AMP (57, 82%), and SXT, 53 (77%), followed by NA (48, 69%), and ERY (47, 68.1%). In addition, *Shigella* spp. were resistant to the cephalosporins, of which 38 (55%) isolates were resistant to CFM and 33 (48%) isolates were resistant to CAZ.

The results showed that CIP and CRO were the best antibiotics against *Shigella* isolates, while more than 50% of *S. dysenteriae* strains were susceptible to NA, GEN, CRO, and CIP. Among the *S. boydii* strains, 55.5% were resistant to AMP, CFM, CAZ, and SXT. All *S. dysenteriae* strains were resistant to AMP, erythromycin, and SXT. Antibiotic resistance patterns of the four *Shigella* stereotypes are detailed in Table 3.

Table 2 Description of groups of patients with positive result for *Shigella* culture in this study

Age group	Number (%) of male	Number (%) of female	Number (%) of <i>Shigella</i> -positive culture result
\leq 6 years	187 (35.8)	100 (19.1)	48 (16.7)
7–10 years	60 (11.4)	53 (10.1)	13 (11.5)
11–20 years	45 (8.6)	31 (5.9)	6 (7.8)
\geq 21 years	26 (4.9)	20 (3.8)	2 (4.3)
Total	318 (60.9)	204 (39.1)	69 (13.2)

Table 1 Primers and PCR conditions for the amplification of *ipaH* gene

Gene	Primer sequence	Size of amplicon (bp)	PCR conditions	Reference
<i>ipaH-F</i>	5'-GTT CCT TGA CCG CCT TTC CGA TA-3'	500	5 minutes at 94°C; 35 cycles of 60 seconds at 94°C, 90 seconds at 60°C, 60 seconds at 72°C, and 10 minutes at 72°C	16
<i>ipaH-R</i>	5'-GCC GGT CAG CCA CCC TA-3'			

Table 3 Antibiotic resistance patterns of the *Shigella* spp.

Antibiotics	<i>S. flexneri</i> resistant, n (%)	<i>S. sonnei</i> resistant, n (%)	<i>S. boydii</i> resistant, n (%)	<i>S. dysenteriae</i> resistant, n (%)	Total resistance, n (%)
Ampicillin	28 (82.3)	20 (90.9)	5 (55.5)	4 (100)	57 (82.6)
Trimethoprim-sulfamethoxazole	26 (76.4)	18 (81.8)	5 (55.5)	4 (100)	53 (76.8)
Chloramphenicol	22 (64.7)	15 (68.1)	6 (66.6)	3 (75)	46 (66.6)
Nalidixic acid	25 (73.5)	17 (77.2)	4 (44.4)	2 (50)	48 (69.5)
Gentamicin	14 (41.1)	16 (72.7)	6 (66.6)	2 (50)	38 (55)
Erythromycin	22 (64.7)	17 (77.2)	4 (44.4)	4 (100)	47 (68.1)
Cefixime	18 (53)	12 (54.5)	5 (55.5)	3 (75)	38 (55)
Ceftazidime	15 (44.1)	10 (45.4)	5 (55.5)	3 (75)	33 (47.8)
Ceftriaxone	14 (41.1)	11 (50)	3 (33.3)	2 (50)	30 (43.4)
Ciprofloxacin	5 (14.7)	7 (31.8)	2 (22.2)	1 (25)	15 (21.7)

Abbreviations: *S. boydii*, *Shigella boydii*; *S. dysenteriae*, *Shigella dysenteriae*; *S. flexneri*, *Shigella flexneri*; *S. sonnei*, *Shigella sonnei*.

Discussion

Shigellosis is a significant global human health problem, and a more common serious condition in developing countries.^{3,4} Antibiotic therapy decreases the severity and duration of the infection and the fecal elimination of the organism, which in turn would prevent its further spread.¹⁷

The current study provides results of molecular characterization and antimicrobial resistance of *Shigella* spp. isolated from diarrheal patients in Iran. In this study, shigellosis was seen in all age groups and patients under the age of 10 years were the highest, because children in this age are most sensitive to shigellosis primarily due to the higher exposure to the contaminated environment, poor sanitation, and personal hygiene and less effective immune responses to *Shigella* spp.¹⁸

Identification of *Shigella* spp. as enteric pathogens with a universal impact has increased during recent years. In our study, *Shigella* spp. were isolated from 13.2% of diarrheal patients using cultural and biochemical methods, and the amplification of the *ipaH* gene has confirmed this isolation rate. This rate of isolation of *Shigella* was similar to studies in Iran (14%) and Brazil (10%) and, however, was different from studies in India (4%) and Ethiopia (4%).^{19–22} Furthermore, in our study, male and female children were equally affected, which is similar to the previous studies.^{20,23}

This investigation showed that most of the *Shigella* isolates were resistant to AMP, SXT, and NA (up to 60%). In addition, *Shigella* spp. were resistant to the CFM (59.5%), CAZ (55%), and CRO (43.6%). Among antibiotics tested for the susceptibility of *Shigella* spp. isolates, CIP was the best with 76.6% sensitivity followed by CRO with 44% sensitivity.

In a study performed by Jafari et al,²⁴ more than 90% of *Shigella* isolates were susceptible to CRO, CAZ, CFM, and

CIP. In another study conducted by Mostafavi et al,²⁵ *Shigella* serotypes have a very high level resistance to SXT and AMP and high level resistance to third-generation cephalosporins (>90% and 50% respectively).

All investigations performed in Iran during the last 20 years revealed a high level of resistance to SXT and AMP. Less than 30% of the *Shigella* isolates were sensitive to either of these two agents in Zahedan, Mashhad, and Zanjan provinces.^{6,25,26} The most common serotype isolated in our study was *S. Flexneri*, which was similar to Jomezadeh et al's report in Iran. According to their report, *S. flexneri* (52.7%) was the most common serogroup and the most resistance was seen regarding the SXT (80.5%) and AMP (63.8%).⁸

Overall, the low resistance rate to CIP in our study showed that fluoroquinolones are still ideal drugs for treating the shigellosis in our region. Due to the limitation of fluoroquinolones' prescription in children because of their side effects, the third-generation cephalosporins are used as a substitute treatment of shigellosis.²⁵

Conclusion

We conclude that *Shigella* spp. can be considered as an etiological agent of diarrhea with a high level of antibiotic resistance in Ahvaz, Iran. Also, since the drug resistance pattern of *Shigella* differs in geographical regions and over time within a country, continuous and regular surveillance programs are necessary.

Acknowledgments

We would like to thank the Department of Microbiology, Faculty of Medicine, Ahvaz Jundishapur University of Medical Sciences, for their cooperation. Our appreciation goes to the Vice Chancellor for Research affairs, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran,

and Tropical and Infectious Diseases Research Center of the University for their financial (Grant No. OG-96125) and executive support.

Disclosure

The authors report no conflicts of interest in this work.

References

1. Yang F, Yang J, Zhang X, et al. Genome dynamics and diversity of *Shigella* species, the etiologic agents of bacillary dysentery. *Nucleic Acids Res*. 2005;33(19):6445–6458.
2. Grimont F, Lejay-Collin M, Talukder KA, et al. Identification of a group of *Shigella*-like isolates as *Shigella boydii* 20. *J Med Microbiol*. 2007;56(Pt 6):749–754.
3. Alipour M, Talebjannat M, Nabiuni M. Polymerase chain reaction method for the rapid detection of virulent *Shigella* spp. *Int J Mol Clin Microbiol*. 2012;2(1):134–137.
4. Humphries RM, Linscott AJ. Laboratory diagnosis of bacterial gastroenteritis. *Clin Microbiol Rev*. 2015;28(1):3–31.
5. Schroeder GN, Hilbi H. Molecular pathogenesis of *Shigella* spp.: controlling host cell signaling, invasion, and death by type III secretion. *Clin Microbiol Rev*. 2008;21(1):134–156.
6. Gebrekidan A, Dejene TA, Kahsay G, Wasihun AG. Prevalence and antimicrobial susceptibility patterns of *Shigella* among acute diarrheal outpatients in Mekelle hospital, Northern Ethiopia. *BMC Res Notes*. 2015;8(1):611.
7. Walker JC, Verma NK. Identification of a putative pathogenicity island in *Shigella flexneri* using subtractive hybridisation of the *S. flexneri* and *Escherichia coli* genomes. *FEMS Microbiol Lett*. 2002;213(2):257–264.
8. Jomezadeh N, Babamoradi S, Kalantar E, Javaherizadeh H. Isolation and antibiotic susceptibility of *Shigella* species from stool samples among hospitalized children in Abadan, Iran. *Gastroenterol Hepatol Bed Bench*. 2014;7(4):218.
9. Taneja N, Mewara A, Kumar A, Verma G, Sharma M. Cephalosporin-resistant *Shigella flexneri* over 9 years (2001–09) in India. *J Antimicrob Chemother*. 2012;67(6):1347–1353.
10. Heidary M, Bahramian A, Hashemi A, et al. Detection of *acrA*, *acrB*, *aac(6′)-Ib-cr*, and *qepA* genes among clinical isolates of *Escherichia coli* and *Klebsiella pneumoniae*. *Acta Microbiol Immunol Hung*. 2017;64(1):63–69.
11. Van der Ploeg CA, Viñas MR, Terragno R, Bruno SB, Binsztein N. *Laboratory Protocol: Serotyping of Shigella spp.* Geneva: WHO Global Foodborne Infections Network; 2010.
12. Wayne P. *Clinical and Laboratory Standards Institute (CLSI) Performance Standards for Antimicrobial Disk Diffusion Susceptibility Tests 19th ed. Approved Standard*; CLSI document M100-S19; 2009.
13. Sedighi M, Halajzadeh M, Ramazanzadeh R, Amirzafarani N, Heidary M, Pirouzi S. Molecular detection of β -lactamase and integron genes in clinical strains of *Klebsiella pneumoniae* by multiplex polymerase chain reaction. *Rev Soc Bras Med Trop*. 2017;50(3):321–328.
14. Heidary M, Salimi Chirani A, Khoshnood S, et al. Molecular detection of aminoglycoside-modifying enzyme genes in *Acinetobacter baumannii* clinical isolates. *Acta Microbiol Immunol Hung*. 2017;64(2):143–150.
15. Khoshnood S, Eslami G, Hashemi A. Distribution of aminoglycoside resistance genes among *Acinetobacter baumannii* strains isolated from burn patients in Tehran, Iran. *Arch Pediatr Infect Dis*. 2017;5(3):e57263.
16. Na-Ubol M, Samosornsuk S, von Seidlein L, et al. Molecular characteristics of *Shigella* spp. isolated from patients with diarrhoea in a new industrialized area of Thailand. *Epidemiol Infect*. 2006;134(5):997–1003.
17. Talebreza A, Memariani M, Memariani H, Shirazi MH, Shamsabad PE, Bakhtiari M. Prevalence and antibiotic susceptibility of *Shigella* species isolated from pediatric patients in Tehran. *Arch Pediatr Infect Dis*. 2016;4(1):e32395.
18. Orrett FA. Prevalence of *Shigella* serogroups and their antimicrobial resistance patterns in southern Trinidad. *J Health Popul Nutr*. 2008;26(4):456–462.
19. Nunes MR, Magalhães PP, Penna FJ, Nunes JM, Mendes EN. Diarrhea associated with *Shigella* in children and susceptibility to antimicrobials. *J Pediatr*. 2012;88(2):125–128.
20. Demissie TA, Wubie T, Yehuala FM, Fetene M, Gudeta A. Prevalence and antimicrobial susceptibility patterns of *Shigella* and *Salmonella* species among patients with diarrhea attending Gondar Town Health Institutions, Northwest Ethiopia. *Sci J Pub Health*. 2014;2(5):469–475.
21. Savadkoochi RB, Ahmadpour-Kacho M. Prevalence of *Shigella* species and their antimicrobial resistance patterns at Amirkola children hospital, North of Iran. *Iran J Pediatr*. 2007;17(2):118–122.
22. Hosseini Nave H, Mansouri S, Sadeghi A, Moradi M. Molecular diagnosis and anti-microbial resistance patterns among *Shigella* spp. isolated from patients with diarrhea. *Gastroenterol Hepatol Bed Bench*. 2016;9(3):205.
23. Dallal MMS, Eghbal M, Sharafianpour A, Zolfaghari MR, Yazdi MKS. Prevalence and multiple drug resistance of *Shigella sonnei* isolated from diarrheal stool of children. *J Med Bacteriol*. 2015;4(3–4):24–29.
24. Jafari F, Hamidian M, Salmanzadeh-Ahrabi S. Molecular diagnosis and antimicrobial resistance pattern of *Shigella* spp. isolated from patients with acute diarrhea in Tehran, Iran. *Gastroenterol Hepatol Bed Bench*. 2009;1(1):11–17.
25. Mostafavi N, Bighamian M, Mobasherizade S, Kelishadi R. Resistance of *Shigella* strains to extended-spectrum cephalosporins in Isfahan province. *Med J Islam Repub Iran*. 2016;30:428.
26. Jamshidi A, Matbooei A. *Shigella* spp frequency, serotyping and antibiotic resistance pattern in acute diarrheic patients in Zanjan Shahid Beheshti Hospital, during 2003–2007. *Zums J*. 2008;16(62):77–84.

Infection and Drug Resistance

Publish your work in this journal

Infection and Drug Resistance is an international, peer-reviewed open-access journal that focuses on the optimal treatment of infection (bacterial, fungal and viral) and the development and institution of preventive strategies to minimize the development and spread of resistance. The journal is specifically concerned with the epidemiology of antibiotic

resistance and the mechanisms of resistance development and diffusion in both hospitals and the community. The manuscript management system is completely online and includes a very quick and fair peer-review system, which is all easy to use. Visit <http://www.dovepress.com/testimonials.php> to read real quotes from published authors.

Submit your manuscript here: <https://www.dovepress.com/infection-and-drug-resistance-journal>

Dovepress