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Profiling of meropenem-resistant bacteria in a river receiving wastewater effluent from a pharmaceutical industrial unit

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The aim of the present study was to understand the seasonal occurrence and diversity of species of meropenem-resistant bacteria in the Gumuncheon river receiving effluents from a pharmaceutical industry in Seoul, Korea. Water samples were collected from the Gumuncheon river in Kyoung-gi province during winter (January), spring (April), summer (August), and fall (November) of 2018. Water samples were plated in triplicate on tryptic soy agar plates containing 16 mg/L meropenem. Meropenem-resistant bacteria were isolated and genetically identified using 16S rRNA analysis. The predominant bacterial genera identified were *Elizabethkingia*, *Pseudomonas*, *Chryseobacterium* and *Stenotrophomonas*. Among these; *Pseudomonas* species *Pseudomonas chengduensis* and *Pseudomonas taiwanesis* showed resistance against 15 antibiotics. To prevent the occurrence and spread of meropenem-resistant bacteria in rivers, it is necessary to implement methods that can simultaneously kill multi-drug resistant bacteria and remove antibiotics from pharmaceutical industry effluent discharge. Further, to stop the spread of meropenem-resistant bacteria in environment, effluent discharge water should be stringently assessed for their risk of being an environmental hazard.

Key words: Carbapenem, Meropenem, Multi-drug resistant, *Elizabethkingia*, *Pseudomonas*, *Chryseobacterium*, *Stenotrophomonas*.

INTRODUCTION

Carbapenem antibiotics, such as meropenem, imipenem, and doripenem, are the last-line of antibiotics used on bacteria resistant to β -lactam antibiotics. *In vitro* experiments have shown that carbapenem antibiotics have broader antibacterial activities than combinations of

penicillin, cephalosporin, and β -lactam/ β -lactamase inhibitors (Bassetti et al., 2009). Generally, imipenem, panipenem, and doripenem are effective antibiotics against Gram-positive bacteria (GPB), whereas carbapenem antibiotics, such as meropenem, biapenem,

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and ertapenem, are more effective against Gram-negative bacteria (GNB) (Bassetti et al., 2009).

Carbapenem antibiotics enter GNB through outer membrane proteins (OMPs) known as porins (Martinez-Marinez, 2008). Carbapenem antibiotics pass through the periplasmic space and subsequently inhibit peptide cross-linking by permanent acylation of penicillin-binding proteins (PBPs). PBPs facilitate the synthesis of peptidoglycans present in the bacterial cell wall (Hashizume et al., 1984). Cell wall synthesis is a dynamic three-dimensional process with synthesis and autolysis occurring simultaneously. As a result, inhibition of PBPs causes weakening of peptidoglycans, thereby resulting in cell rupture due to osmotic pressure (Van Dam et al., 2009).

Carbapenem resistance has been reported in many bacteria. For example, Enterobacteriaceae including *Escherichia coli*, *Klebsiella* spp., *Klebsiella pneumoniae*, and *Enterobacter* spp., and GPB, including *Stenotrophomonas* spp., *Streptococcus* spp., *Staphylococcus* spp., *Bacillus magisterium*, and *Bacillus licheniformis* show gradual resistance to carbapenem antibiotics often used in clinical practice (Papp-Wallace et al., 2011; Go et al., 2017; Hwang and Kim, 2018). In particular, carbapenem-resistant Enterobacteriaceae (CRE) are becoming important public health risks (Gupta et al., 2011).

The pharmaceutical industry produces effluent discharge which carries various types of antibiotics that are not degraded during the wastewater treatment process. Antibiotics that are discharged without being completely degraded can cause disturbances in aquatic ecosystems and will be hazardous for human life (Kim and Kim, 2016). Pharmaceutical industry wastewater treatment plants may also discharge wastewater directly into rivers if they satisfy the effluent standards for general metrics such as biochemical oxygen demand (BOD), chemical oxygen demand (COD), suspended solids (SS), total nitrogen (T-N), and total phosphorus (T-P), similar to non-pharmaceutical wastewater treatment plants (Hwang and Kim, 2018).

The purpose of this study was to identify the seasonal frequency of occurrence, species variety, and antibiotic resistance spectrum of meropenem-resistant bacteria in rivers receiving wastewater discharged from a pharmaceutical industrial park.

MATERIALS AND METHODS

Collection area and methods

Gumuncheon river; from where the study samples were collected, is a tributary of the Balancheon river. The Hyangnam Pharmaceutical Industrial Park, located in Hwaseong-si (Gyeonggi Province, South Korea), houses 10 pharmaceutical companies that discharge

wastewater into the Gumuncheon river. We sampled 1L of river water at 37.097598N and 126.902025 E in January, April, August, and November of 2018. Samples were collected in sterile collection bottles and refrigerated during transportation to the laboratory (Hwang et al., 2018).

Water temperature, dissolved oxygen (DO), and the pH of the river water were measured using a DO/pH meter (DH-32P, Toa, Japan). Prior to analyzing T-N, T-P, and total organic carbon (TOC), a 0.45 µm pore filter (Advnatec, Japan) was used to remove any suspended solids and temperature, DO, and pH were measured at the sampling point. T-N and T-P were measured using Integral Futura continuous flow analyzer (Alliance, USA), while TOC was measured using TOC-L (Shimadzu, Japan). BOD and COD were analyzed in accordance with the water pollution standard method (NIER, 2018).

Isolation of heterotrophic bacteria

To measure the heterotrophic bacterial count within each sample, the samples were diluted 100-fold using sterilized saline solution and 1.0 ml from each dilution each was spread 3 times on 3 agar plates (pour plate agar, Difco, USA) and incubated at 35°C for 48 h.

Identification of meropenem-resistant bacteria and antibiotic resistance test

To identify the meropenem-resistant bacteria, samples were diluted by 10-fold using sterilized saline solution and 0.1 ml each was spread on three tryptic soy (TS) agar plates (Difco, USA) containing 16 mg/L of meropenem (Daewoong Pharmaceutical, Korea) and cultured at 35°C for 48 h. Meropenem-resistant bacteria were subjected to 16S rRNA analysis for species identification. Colony polymerase chain reaction (PCR) was used to amplify the 16S rRNA gene of resistant bacteria from pure colonies (Kim and Kim, 2016). To determine the antibiotic sensitivities of the identified bacteria, disk diffusion assays were performed with ampicillin, ceftizoxime, vancomycin, imipenem, clindamycin, gentamicin, erythromycin, ciprofloxacin, nitrofurans, rifampin, ampicillin/sulbactam, aztreonam, spectinomycin, trimethoprim, tetracycline, and chloramphenicol. The diameter of the inhibition zone was measured in mm and interpreted according to the Clinical Laboratory Standards Institute (CLSI) guidelines (CLSI, 2013; Hwang et al., 2018).

RESULTS

The general quality metrics of the river samples are shown in Table 1. Temperature (7.5-28.5°C), pH (7.15-7.45), DO (6.1-11.0 mg/L), BOD (2.7-5.8mg/L), COD (8.2-15.1 mg/L), T-P 0.103-0.182 mg/L), T-N (8.056-12.566 mg/L), and TOC (5.3-9.2 mg/L) were measured.

The numbers of heterotrophic and meropenem-resistant bacteria identified are shown in Table 2. The counts of heterotrophic bacteria in the winter, spring, summer, and fall seasons were 3.4, 4.0, 5.6 and 5.1 ($\times 10^4$ CFU/ml) respectively, while the numbers of meropenem-resistant bacteria were 14.0, 8.3, 1.2 and 9.0 ($\times 10^2$ CFU/ml) respectively.

The prevalence of each strain by season is shown in

Table 1. Quality of water sampled from the river receiving pharmaceutical industry discharge water.

Indicators	Sampling months in 2018			
	January	April	August	November
Temperature(°C)	7.5	20.1	28.5	18.2
pH	7.42	7.15	7.34	7.45
DO (mg/L)	11.0	10.0	6.1	8.4
BOD (mg/L)	5.8	4.0	2.7	4.3
COD (mg/L)	15.1	10.7	9.7	8.2
Total phosphorus (mg/L)	0.145	0.127	0.182	0.103
Total nitrogen (mg/L)	12.566	8.305	9.644	8.056
TOC (mg/L)	9.2	5.6	5.3	5.8

DO: dissolved oxygen, BOD: biological oxygen demand, COD: chemical oxygen demand, TOC: total organic carbon.

Table 2. Season-wise distribution of culturable bacteria and meropenem resistant bacteria.

Indicators	Sampling months in 2018			
	January	April	August	November
Heterotrophic bacteria(CFU/ml)	$3.4 \times 10^4 \pm 1.3 \times 10^3$	$4.8 \times 10^4 \pm 2.6 \times 10^3$	$5.6 \times 10^4 \pm 1.5 \times 10^3$	$5.1 \times 10^4 \pm 2.8 \times 10^3$
Meropenem resistant Bacteria (CFU/ml)	$4.0 \times 10^2 \pm 2.0 \times 10^2$	$8.3 \times 10^2 \pm 2.1 \times 10^2$	$1.2 \times 10^3 \pm 4.0 \times 10^2$	$9.0 \times 10^2 \pm 1.2 \times 10^2$
Meropenem resistant bacteria (%)	1.18	1.73	2.14	1.82

Table 3. The *Elizabethkingia* genus was the dominant genus in the winter season, and was also partially identified in the spring and fall when the water temperature was low; however, it was not identified in summer. The *Pseudomonas* genus was not identified in the winter and summer but was identified during the spring and the fall. The *Chryseobacterium* genus was identified as the dominant genus in the spring, summer, and winter; the *Stenotrophomonas* genus was also identified in the same periods. The *Cupriavidus*, *Acinetobacter*, and *Pandoraea* genera were identified in the summer season only.

The results of the antibiotic resistance tests of the isolated meropenem-resistant bacteria are shown in Tables 4, 5, and 6. The *Elizabethkingia* genus commonly showed resistance to eight antibiotics (ampicillin, ceftizoxime, vancomycin, imipenem, meropenem, nitrofurantoin, aztreonam, and trimethoprim), while the *Pseudomonas* genus showed resistance to thirteen antibiotics (ampicillin, ceftizoxime, vancomycin, imipenem, meropenem, clindamycin, erythromycin, nitrofurantoin, rifampin, ampicillin/sulbactam, trimethoprim, tetracycline, and chloramphenicol). The *Chryseobacterium* genus, which was the dominant genus in the spring, summer, and fall, showed resistance to five antibiotics (colistin, ampicillin, ceftizoxime, ampicillin/sulbactam, and

aztreonam). The *S. maltophilia*, which appeared in the spring, summer, and fall, showed resistance to ten antibiotics (ampicillin, ceftizoxime, vancomycin, imipenem, meropenem, clindamycin, ampicillin/sulbactam, spectinomycin, aztreonam, and trimethoprim). Among bacteria that appeared only in the summer season, *C. plantarum* showed resistance to seven antibiotics (ampicillin, vancomycin, imipenem, meropenem, clindamycin, gentamicin, and aztreonam), *A. junii* showed resistance to nine antibiotics (ampicillin, ceftizoxime, vancomycin, imipenem, meropenem, clindamycin, nitrofurantoin, rifampin, and trimethoprim), and *P. promouosa* showed resistance to eleven antibiotics (colistin, ampicillin, vancomycin, meropenem, clindamycin, gentamicin, erythromycin, nitrofurantoin, rifampin, spectinomycin, and aztreonam).

DISCUSSION

We evaluated the occurrence and season-wise prevalence of meropenem-resistant bacteria in Gumuncheon river receiving wastewater effluents from a pharmaceutical industrial unit. The average water temperature during the winter was 7.5°C, which was lower than the temperature of other sessions for the river.

Table 3. Number of meropenem-resistant bacteria detected by season.

Species	Sampling months in 2018				Total
	January	April	August	November	
<i>Elizabethkingia amiricola</i>	11	-	-	3	14
<i>Elizabethkingia ameningoseptica</i>	1	-	-	-	1
<i>Elizabethkingia anophelis</i>		1	-	-	1
<i>Pseudomonas taiwanesis</i>	-	3	-	-	3
<i>Chryseobacterium indologenes</i>	-	17	-	-	17
<i>Pseudomonas chengduensis</i>	-	2	-	2	4
<i>Stenotrophomonas maltophilia</i>	-	2	5	4	11
<i>Chryseobacterium cucumeris</i>	-	-	22	15	37
<i>Cupriavidus plantarum</i>	-	-	3	-	3
<i>Acinetobacter junii</i>	-	-	3	-	3
<i>Pandoraea pnomenusa</i>	-	-	3	-	3
<i>Pseudomonas pseudoalcaligenes</i>	-	-	-	3	3
Total	12	25	36	27	100

Table 4. Antibiotic resistance spectrum of meropenem-resistant *Elizabethkingia miricola*, *Elizabethkingia meningoseptica*, *Elizabethkingia anophelis*, and *Pseudomonas taiwanesis*.

Spectrum	Species			
	<i>E.miricola</i>	<i>E. meningoseptica</i>	<i>E. anophelis</i>	<i>P. tawnensis</i>
	(n=14) R%	(n=1) R%	(n=1) R%	(n=3) R%
Ampicillin	100	100	100	100
Ceftizoxime	100	100	100	100
Vancomycin	21	100	100	100
Imipenem	100	100	100	100
Meropenem	100	100	100	100
Clindamycin	57	0	0	100
Gentamicin	100	0	100	33
Erythromycin	79	0	100	100
Ciprofloxacin	57	0	100	100
Nitrofurantoin	100	100	100	100
Rifampin	0	0	0	100
Ampicillin/Sulbactam	100	0	100	100
Aztreonam	100	100	100	100
Spectinomycin	43	0	100	100
Trimethoprim	57	100	100	100
Tetracycline	0	0	0	100
Chloramphenicol	0	0	0	100

The increase in water temperature was assumed to be the result of an inflow of effluents from the sewage treatment plant. The concentration of T-P, a limiting nutrient for microbial growth on water surface, was found to be 0.103-0.182 mg/L, which was exceedingly higher than the concentration needed for microbial growth (100

µg T-P/L). It showed that the sampled river water satisfied the conditions for growth of antibiotic resistant bacteria (Correll, 1999). Our results clearly show that the present allowed limit of T-P concentration (4 mg/L) for pharmaceutical industrial wastewater treatment plant effluents should be lowered, considering the additional

Table 5. Antibiotic resistance spectrum of meropenem-resistant *Chryseobacterium indologenes*, *Pseudomonas chengduensis*, *S. maltophilia* and *Chryseobacterium cucumeris*.

Spectrum	Species			
	<i>C. indologenes</i>	<i>P. chengduensis</i>	<i>S. maltophilia</i>	<i>C. cucumeris</i>
	(n=17) R%	(n=4) R%	(n=11) R%	(n=37) R%
Ampicillin	100	100	100	100
Ceftizoxime	100	100	100	100
Vancomycin	100	100	100	46
Imipenem	6	100	100	0
Meropenem	100	100	100	100
Clindamycin	0	100	100	0
Gentamicin	94	100	55	100
Erythromycin	0	100	73	0
Ciprofloxacin	0	100	0	0
Nitrofurantoin	77	100	82	19
Rifampin	0	100	82	0
Ampicillin/Sulbactam	100	100	100	100
Aztreonam	100	0	100	100
Spectinomycin	0	100	100	0
Trimethoprim	0	100	100	0
Tetracycline	0	100	0	0
Chloramphenicol	0	100	9	0

Table 6. Antibiotic resistance spectrum of meropenem-resistant *Chryseobacterium plantarum*, *A. junii*, *Pseudomonas pnomenusa*, and *Pseudomonas pseudoalcaligenes*.

Spectrum	Species			
	<i>C. plantarum</i>	<i>A. junii</i>	<i>P. pnomenusa</i>	<i>P. pseudoalcaligenes</i>
	(n=3) R%	(n=3) R%	(n=3) R%	(n=3) R%
Ampicillin	100	100	100	100
Ceftizoxime	0	100	0	100
Vancomycin	100	100	100	100
Imipenem	100	100	0	100
Meropenem	100	100	100	100
Clindamycin	100	100	100	100
Gentamicin	100	0	100	0
Erythromycin	0	0	100	100
Ciprofloxacin	0	0	0	0
Nitrofurantoin	33	100	100	100
Rifampin	33	100	100	67
Ampicillin/Sulbactam	0	0	0	100
Aztreonam	100	0	100	100
Spectinomycin	67	0	100	0
Trimethoprim	0	100	33	100
Tetracycline	0	0	0	0
Chloramphenicol	0	33	0	100

amount of T-P that could be introduced into the river from nearby farmland or domestic sewage (Hwang and Kim, 2018).

The percentage of meropenem-resistant bacteria among the heterotrophic bacteria identified in the river samples was 1.18-2.14%, which was higher than the percentage measured in a similar river which did not receive the wastewater effluents (Kim and Kim, 2015). It is known that as the number of non-pathogenic bacteria increases, the number of antibiotic-resistant bacteria could also increase through gene transfer from pathogenic to non-pathogenic bacteria (Levy and Marshall, 2004).

The *Elizabethkingia* genus contains Gram-negative, obligate aerobic bacillus species, and is an emerging healthcare threat as it has been reported to be associated with various life-threatening infections including sepsis, neonatal meningitis, and nosocomial pneumonia. Moreover, improperly processed animal-derived food and companion animals are known reservoirs for this antibiotic resistant bacterial pathogen. *Elizabethkingia anophelis* isolated in clinical practice (Figueroa Castro et al., 2017; Lee et al., 2021) and *E. anophelis* isolated from horses (Johnson et al., 2018) were reportedly susceptible to ciprofloxacin; however, the *E. anophelis* isolated in the present study was ciprofloxacin-resistant. Further studies are required to determine whether this difference was due to mutation of one or more genes involved in bacterial DNA separation (Drlica and Zhao, 1997). Similarly, *E. meningoseptica* isolated from clinical samples has shown resistance to various β -lactams and colistin, but is reported to be susceptible to vancomycin (Ratnamani and Rao, 2013). However, the *E. meningoseptica* isolated in the present study was resistant to not only ampicillin, imipenem, meropenem, and the β -lactam/ β -lactamase inhibitor ampicillin/Sulbactam, but also to colistin and vancomycin. On the other hand, the *E. meningoseptica* isolated in the present study showed greater susceptibility to tetracycline, clindamycin, erythromycin, and gentamicin than *E. meningoseptica* from hospital effluents described previously. Thus, more in-depth studies are required to determine whether this difference could be attributed to the difference in their source (NIER, 2013; Gullberg et al., 2011). *E. miricola*, which is an opportunistic oral pathogen, has exhibited resistance to many antibiotics, including imipenem, meropenem, carbapenem, colistin, and gentamicin (Zdziarski et al., 2017; Howard et al., 2020); the *E. miricola* isolated in the present study also showed resistance to those antibiotics.

There have been no reports of *Pseudomonas taiwanensis*, a known pathogen of soil microorganisms (Wang et al., 2010) and insects (Chen et al., 2014), acting as a clinical pathogen. However, the *P. taiwanensis* isolated in the present study showed resistance to

sixteen antibiotics (ampicillin, ceftizoxime, vancomycin, imipenem, meropenem, clindamycin, erythromycin, ciprofloxacin, nitrofurantoin, rifampin, ampicillin/sulbactam, spectinomycin, aztreonam, trimethoprim, tetracycline, and chloramphenicol). Similarly, *Pseudomonas chengduensis* has been reported in landfill leachate (Tao et al., 2014), but has not been identified in clinical samples. The *P. chengduensis* isolated in the present study showed resistance to ampicillin, ceftizoxime, vancomycin, imipenem, meropenem, clindamycin, gentamicin, erythromycin, ciprofloxacin, nitrofurantoin, rifampin, ampicillin/sulbactam, spectinomycin, trimethoprim, tetracycline, and chloramphenicol. *Pseudomonas pseudoalcaligenes*, another member of the *Pseudomonas* genus, showed resistance to six antibiotics (ampicillin, ceftizoxime, vancomycin, clindamycin, erythromycin, and chloramphenicol), similar to *P. pseudoalcaligenes* strains isolated from hospital effluents.

Chryseobacterium, which was the dominant genus identified in sampled water during spring, summer, and fall, is a Gram-negative bacillus commonly found in environment. *Chryseobacterium indologenes* is an opportunistic pathogen that causes sepsis (McKew, 2014; Izaguirre-Anariba and Sivapalan, 2020). *C. indologenes* isolated from patients has been reported to be resistant to ampicillin, amoxicillin-clavulanate, cefepime, meropenem, gentamicin, and nitrofurantoin, however the *C. indologenes* isolated in the present study showed resistance to colistin, ampicillin, ampicillin-sulbactam, ceftizoxime, vancomycin, meropenem, gentamicin, and aztreonam. *Chryseobacterium cucumeris*, another member of the *Chryseobacterium* genus, was resistant to colistin, ampicillin, ampicillin-sulbactam, ceftizoxime, meropenem, gentamicin, and aztreonam.

Stenotrophomonas maltophilia, isolated in the spring, summer, and fall, is strongly associated with human respiratory infection. It is a multi-drug resistant bacterium commonly found in environment. Due to its low permeability, it is known to be resistant to cephem antibiotics, such as cefepime and ceftazidime, as well as to β -lactams. Moreover, presence of genes encoding β -lactamases, multi-drug resistant efflux pumps, and antibiotic-modifying enzymes confers it with resistance to various antibiotics (Brook, 2012; Adegoka et al., 2017). Similarly, the *S. maltophilia* isolated in the present study showed resistance to not only β -lactam and cephem antibiotics, such as ampicillin and ceftizoxime, but also to vancomycin, imipenem, meropenem, clindamycin, ampicillin/sulbactam, spectinomycin, aztreonam, and trimethoprim.

Cupriavidus plantarum has been isolated from the plant rhizosphere (Estrada-de Los Santos et al., 2014), but there are no known reports of this bacteria in clinical samples. The *C. plantarum* identified in the present study

showed resistance to ampicillin, vancomycin, imipenem, meropenem, clindamycin, gentamicin, and aztreonam.

Acinetobacter junii is an opportunistic pathogen that has been reported to show resistance to ampicillin and ciprofloxacin (Cayô et al., 2011); in the present study, the *A. junii* showed resistance to a greater number of antibiotics (ampicillin, ceftizoxime, vancomycin, imipenem, meropenem, clindamycin, nitrofurantoin, rifampin, and trimethoprim). Similarly, *Pandoraea pnomenusa* isolated from patients with cystic fibrosis has been reported to show resistance to cephem antibiotics such as ceftizoxime and β -lactam/ β -lactamase inhibitors (Ambrose et al., 2016); however, the *P. pnomenusa* identified in the present study was resistant to colistin, ampicillin, vancomycin, meropenem, clindamycin, gentamicin, erythromycin, nitrofurantoin, rifampin, spectinomycin, and aztreonam, but not to cephem antibiotics or β -lactam/ β -lactamase inhibitors.

Resistance to carbapenem antibiotics is known to result from mutations that affect the production of β -lactamase and the functional expression of efflux pumps, porins, and PBPs (Drlica and Zhao, 1997; Giske et al., 2008; Hashizume et al., 1984). There is an imminent need to study the underlying mechanism of antimicrobial resistance observed in meropenem-resistant *Acinetobacter junii*, *C. cucumeris*, *C. indologenes*, *Cupriavidus plantarum*, *E. anopheles*, *Elizabethkingi ameningoseptica*, *Elizabethkingi amiricola*, *Pandoraea pnomenusa*, *Pseudomonas pseudoalcali genes*, *Pseudomonas chengduensis*, *Pseudomonas tawnensis*, and *Stenotrophomonas maltophilia*, isolated in the present study.

Biofilms, sewage effluent sediments, wastewater treatment plant effluents, sewage sludge, pharmaceutical manufacturing plants, liquid manure tanks, and manure-fertilized soil are known to act as hot spots for the occurrence and spread of antibiotic resistance (Berkner et al., 2014). In South Korea, the industrial effluents are generally checked for total coliforms and ecotoxicity according to the classification of effluent discharge zones. Our results show that there is a need to perform toxicity tests and environmental hazard assessments on effluents containing antibiotics or antimicrobial substances, such as pharmaceutical industry discharge water, to prevent the occurrence and spread of antibiotic resistance (Hernando et al., 2006; Escher et al., 2011). In Korea, the ecotoxicity testing is performed by using water fleas (Hwang and Kim, 2018). It is believed that the toxicity testing of the effluents that include trace amounts of antimicrobial substances, too should be performed using microorganisms. The pharmaceutical industrial park that discharges wastewater into the river sampled in the present study has a wastewater treatment facility; however, there is a high probability of occurrence of antibiotic resistance due to an inflow of processed water

containing various clinical disinfectants and discharge from antibiotic-manufacturing pharmaceutical factories. In general, the concentrations of antibiotics present in pharmaceutical effluents are significantly lower than the ones used in clinical practice (NIER, 2013). These concentrations, though not high enough to kill bacteria, are sufficient to exert selective pressure on bacteria to develop antimicrobial resistance (Gullberg et al., 2011). Therefore, it is necessary to implement proper treatment methods, including membrane filtration, ozonation, and UV disinfection, to completely remove the antibiotics and antibiotic-resistant bacteria present in pharmaceutical effluents to reduce their flow into the environment (Pruden et al., 2013).

Conclusion

The present study identified the species, contamination level, seasonal distribution, and antibiotic-resistance spectrum of meropenem-resistant bacteria in a river receiving pharmaceutical industry discharge. Our study showed that the presence of multi-drug resistant bacteria in the river water poses a threat to human health due to wider reach and use of river water. The outcomes of our study highlight the need to implement methods that can simultaneously disinfect multi-drug resistant bacteria and remove antibiotics from effluent containing discharge water from pharmaceutical and industrial units.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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