

Special Article - Antibiotic Resistance

Prevalence of Antibiotic Resistance among Bacterial Isolates from Hospital Environments and Effluents

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Received: September 19, 2018; Accepted: October 10, 2018; Published: October 17, 2018

Abstract

Intensive use of antibiotics in hospitals provides an environment for antibiotic resistant organisms to flourish, largely unburdened by competition from susceptible organisms. As a result, hospital effluents contribute to the high rate of drug resistant bacteria discharged in the natural environment than domestic wastewater. Understanding the bacterial diversity in hospital wastewater is crucial as hospital acquired infections are an increasing problem. This review presents the microbial population in hospital environments and the identification of antimicrobial resistance strains using non-culture dependent methods reported earlier. In conclusion, the need to assess diversity of microbial population in hospital environment and effluent is required to control the load of antimicrobial drug resistant strains, which would ultimately enter into the environment as biological contaminants.

Keywords: Hospital Waste Water; Antibiotic Resistance; Multidrug Resistant Strains

Introduction

Antibiotic resistance is an increasing health problem as bacterial infections became lasting longer than ever. Due to the high magnitude of impact caused by antibiotic resistance, significant attention from medical community and researchers is happening over the years. Attention to the effects associated with the spread of resistance while treating the disease is necessary to address the prevalence of antibiotic resistance. Hospital wastewater is a hotspot of diversified bacteria and provides an environment for multi drug resistance due to antibiotics, disinfectants, metabolized drugs from patients' fluids [1-3] and contributes to the high rate of drug resistant bacteria discharged in the natural environment than domestic wastewater [4-6]. Hospital effluent contains antibiotic residues that are enough to kill susceptible bacteria and at the same time increases the number of resistant bacteria [7-9]. The intensive use of antibiotics in hospitals provides an environment for antibiotic resistant organisms to flourish, largely unburdened by competition from susceptible organisms. Some studies have shown that certain disinfectants and over exposure of hospital bacteria to disinfectants lead to increased antibiotic resistance [10,11]. Antibiotic resistant organisms are capable of causing life threatening infections that are difficult to control due to the limited treatment options. Characterization of bacteria from hospital environments would provide prevalence of antibiotic resistance among them [12,13] and reduces the further development of resistance to common antibiotics.

The levels of antibiotic resistance in hospital wastewater are higher than in urban wastewater due to antibiotic application patterns in hospitals. Understanding the bacterial diversity in hospital wastewater is crucial as hospital acquired infections are an increasing problem. Surveillance of microbiological analysis of hospital wastewater would control antibiotic resistance and nosocomial infections.

Methodology

A systematic search was carried out in Pub Med, Scopus and Web of Sciences using a combination of Boolean operators. Peer reviewed papers in English on the antibiotic resistance and hospital effluents were retrieved and evaluated based on titles and abstracts. The retrieved papers were managed using Mendeley and the data were consolidated.

Adverse effects of antibiotic resistance

Due to the higher antibiotic consumption in hospitals, the discharge of antimicrobial residues and resistant bacteria in the environment has strong impact on spread of antibiotic resistance. Antibiotic resistance is mediated by diverse resistance genes and it is evident that antibiotic resistance genes can transfer within bacterial communities [14]. These antibiotic resistance genes may either be intrinsic or acquired. Intrinsic resistance is caused in an organism whose innate chromosomal makeup predictable specifies resistance whereas acquired resistance is due to the mutation in its genetic composition. Genes mediating antimicrobial resistance may be found on plasmids, transposons or integrons. The adverse outcomes caused by antibiotic resistant strains mediated infections are higher than the infections caused by susceptible strains [15]. Patients infected with resistant strains require surgical procedures to cure the illness. Extended-spectrum β -lactamase producing strains are associated with higher rates of mortality in patients [16]. High prevalence of antibiotic resistance *Neisseria gonorrhoeae* strain infection leading to treatment failures and subsequent reproductive tract diseases [17]. The antibiotic resistance in community pathogens has led to increased use of other agents in patients admitted with other infection, introducing additional selection pressure for resistance and adding to hospital costs. The other effects include length of stay in hospitals, morbidity and mortality [18].

Table 1: Major bacterial isolates/phyla from hospital environment and effluents.

Bacterial Isolates	References
<i>Aeromonas</i> spp, <i>Kluyvera</i> spp	[41]
Carbapenem-resistant <i>Enterobacteriaceae</i>	[27]
Ciprofloxacin-resistant bacteria	[3]
<i>Citrobacter freundii</i> , <i>Enterobacter cloacae</i> , <i>Klebsiella oxytoca</i>	[56]
Coliforms and faecal Enterococci	[9]
<i>Enterobacter cloacae</i>	[5]
<i>Enterococcus</i> sp	[20]
<i>Escherichia coli</i>	[33,30,23]
<i>Escherichia coli</i> , <i>Acinetobacter</i>	[55]
<i>Escherichia coli</i> , <i>Citrobacter freundii</i>	[25]
Extended spectrum beta lactamase producing bacteria	[53,40]
<i>Faecalibacterium</i> , <i>Aeromonas</i> , <i>Prevotella</i>	[51]
<i>Gamma proteobacteria</i>	[39]
<i>Klebsiella</i> spp, <i>Pseudomonas</i> spp	[38]
Methicillin-resistant <i>S. aureus</i>	[34]
Proteobacteria, Bacteroidetes, Firmicutes and Actinobacteria.	[47]
<i>Pseudomonas aeruginosa</i>	[22,32,37,52]
<i>Pseudomonas aeruginosa</i> , <i>Enterobacter cloacae</i> , <i>Klebsiella pneumoniae</i>	[54]
<i>Pseudomonas</i> spp	[19,46]
<i>Salmonella</i> sp	[48]
<i>Salmonella</i> , <i>Shigella</i> , <i>Staphylococcus aureus</i> , <i>E.coli</i>	[13]
<i>Sphingomonas ursincola</i>	[14]
Vancomycin resistant <i>Enterococci</i>	[6,50]

Culture independent approaches

Had examined the bacterial communities using quantitative PCR and 16srRNA gene based pyrosequencing method [19,20]. qPCR was used to determine the presence of microbial contaminants from untreated hospital wastewaters [21,22]. Metagenomics combined with Search Engine for Antimicrobial Resistance (SEAR) is other technique to determine the full length antibiotic resistance genes from aquatic samples [23,24]. Meta transcriptomics can be used to identify the transcripts of antibiotic resistance genes in various samples [25]. Molecular epidemiological investigations involving Antimicrobial Resistance Determinant Microarray was used to determine the antimicrobial resistance in clinically relevant bacterial pathogens [26].

Antibiotic Resistance Strains in Hospital Environments

A large number of resistant bacteria have been found in the area of hospital wastewater discharge (Table 1) [13,27-55]. Hospital water bacteria seem to play an important role in the dissemination of resistance to antibiotics and the resistance genes are over expressed which is possibly related to the level of antibiotic usage in hospitals [56].

Conclusion

Antibiotic resistant bacteria are more prevalent in hospitals and are released in to the sewage systems and water bodies where

transfer of resistant genes occurs. There is a need to assess diversity of microbial population in hospital environment and wastewater to control the load of antimicrobial drug resistant strains, which would ultimately enter into the environment as biological contaminants.

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