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Review Paper

Antibiotic Resistance Looming in Whole Environment Due To Biomedical Waste

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ABSTRACT

Antibiotics are main sole of medical health-care facilities. After the antibiotic discovery health facilities become life saver. It is used in many diseases, infections and post operative cases. It is also used in agriculture and in animal husbandry. But biomedical waste (BMW) or any waste containing antibiotics create a lots of problems for upcoming future. BMW or any waste containing antibiotics provide a suitable site where many micro-organisms interact with these antibiotics and continuous exposure of micro-organisms with antibiotics lead to emergence of antibiotic resistance. When any germ defeats the designated drugs to kill them it is called Antibiotic resistance. BMW contained expired medicine and antibiotic or unused antibiotic that become a major cause of antibiotic resistance. In my study Total coliforms (TC), Fecal coliforms (FC), Fecal staphylococcus (FSc), Escherichia coli, Klebsiella pneumoniae, and Pseudomonas aeruginosa were found in biomedical waste sample, Escherichia coli, Klebsiella pneumoniae, Staphylococcus aureus, Pseudomonas aeruginosa, Salmonella typhi and Enterococcus faecalis, were found in the body samples, whereas Escherichia coli, and Pseudomonas aeruginosa were found in Daha River (Siwan, Bihar) samples. Among all these isolated bacterial stain Escherichia coli, and Pseudomonas aeruginosa were common in all three types of my study samples i.e., Biomedical waste samples, Daha River samples and body-fluid samples. Escherichia coli, Pseudomonas aeruginosa and Staphylococcus aureus were found to be multidrug resistant in which Pseudomonas aeruginosa and Staphylococcus aureus comes under serious threats of Antibiotic resistant according to the Centers for Disease Control and Prevention (CDC-2019). This also linked the microbiological findings and antibiotic-resistant organisms' emergence between waste water sample of HCF, body fluid and Daha River

INTRODUCTION

Anthropogenic activities are one of the major cause that accelerate the emergence of antibiotic-resistant micro-organism (bacteria/fungi). Most of

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the country does not differentiate between municipal waste and biomedical waste and release their biomedical waste along with the municipal waste and in this manner the whole waste becomes more problematic. Discharge of hospital waste, veterinaries, pharmaceutical plants (Obayiuwana et al.2018), dairies, animal excreta, domestics animal husbandry, municipal waste and poultry (Pruden et al.2013) are additionally posing the risk of antibiotic contamination.

Because BMW contain 15-25%bio-hazardous waste. It also contains expired medicine and antibiotics. The improper disposal of unwanted or expired medications, which are dumped in landfills or the sewage system, manufacturing waste effluents, or unintentional spills during production or distribution can also be regarded as significant points of contamination (Akici et al.2018). Hospital effluents contain the highest concentration of antibiotics (Mohit Kumar et al.2019). So, these waste becomes a major site for interaction between antibiotic and micro-organism. And continuous interaction leads to resistant micro-organism arise. Despite their short half-lives, antibiotics can cause microorganisms to develop resistance with repeated exposure (Tasho and Cho, 2016). It is a matter of serious concern that resistance is transferable, which means that if the resistant bacteria are allowed to spread in the environment, they would probably pass on the genotype to other bacteria of the same species or different ones. Antibiotic resistant bacteria/ micro-organism can be passed from person to person within community by many routes either by contaminated surface, equipment, hands of hospital staff, coughing or sneezing.

It is very important to prevent the exposure of antibiotic unnecessarily in environment because emergence of antibiotic resistance bacteria in India and other sites recently is in alarming issue for upcoming future. In addition to domestic and industrial effluents, the pharmaceutical industries considerably contribute to the total antibiotic concentration added to the influent of the sewage treatment facilities (Harrabi et al.2018).

MATERIAL AND METHODS

Study time period- 1 year.

Study Area- Different Government and Private Hospitals

Biomedical liquid waste samples were taken and cultured for bacteria isolation and then checked on MHA (Mueller–Hinton agar) Plate for Antibiotic Sensitive Test (AST).

We used antibiotic disc diffusion test with the help of sterile blank antibiotic discs that is paper disc of antibiotics for antibiotic sensitivity test.

RESULT AND DISCUSSION

Total coliforms (TC), Fecal coliforms (FC), Fecal staphylococcus (FSc), *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* were found in biomedical waste samples during my study period in my study area (Siwan, Bihar). *Escherichia coli*, *Pseudomonas aeruginosa* and *Staphylococcus aureus* were found to be multidrug resistant in which *Pseudomonas aeruginosa* and *Staphylococcus aureus* comes under serious threats of Antibiotic resistant according to the Centers for Disease Control and Prevention (CDC)-2019 (Table.1).



Table.1. Bacteria and Fungi Listed in the 2019 Antibiotic Resistance Threats Report

Urgent Threats	Serious Threats	Concerning Threats	Watch List
-Carbapenem-resistant <i>Acinetobacter</i> - <i>Candida auris</i> - <i>Clostridioides difficile</i> -Carbapenem-resistant Enterobacterales -Drug-resistant <i>Neisseria gonorrhoeae</i>	-Drug-resistant <i>Campylobacter</i> -Drug-resistant <i>Candida</i> -ESBL-producing Enterobacterales -Vancomycin-resistant Enterococci (VRE) -Multidrug-resistant <i>Pseudomonas aeruginosa</i> -Drug-resistant nontyphoidal <i>Salmonella</i> -Drug-resistant <i>Salmonella</i> serotype Typhi -Drug-resistant <i>Shigella</i> -Methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) -Drug-resistant <i>Streptococcus pneumoniae</i> -Drug-resistant Tuberculosis	-Erythromycin- Resistant Group A <i>Streptococcus</i> -Clindamycin- resistant Group B <i>Streptococcus</i>	-Azole-resistant <i>Aspergillus fumigatus</i> -Drug-resistant <i>Mycoplasma genitalium</i> -Drug-resistant <i>Bordetella pertussis</i>

Source: Centers for Disease Control and Prevention (CDC-2019)- Antibiotic Resistance Threats Report

My study coincides with result of Gajalakshmi P and Raja A (2019). These researchers found *Escherichia coli*, *Pseudomonas aeruginosa* and *Staphylococcus aureus* were to be multidrug resistant. Allen HK et al.2010 also reported that in health-care acquired and community infection, *Escherichia coli*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Staphylococcus aureus*, *Streptococcus pneumoniae*, *Enterococcus*, and *Mycobacterium tuberculosis* were most frequently found as multi drug resistance. *Escherichia coli*, and *Pseudomonas aeruginosa* being multidrug resistant bacteria are alarming issue. *Escherichia coli* responsible for diarrhoea, abdominal cramp, renal damage, pneumonia, UTI (urinary tract infection), bacteremia, neonatal meningitis while *Pseudomonas aeruginosa* responsible for many

diseases like severe urinary tract infection (UTI), Pneumonia, meningitis, septicemia, endocarditis, endophthalmitis, external otitis and etc. The antibiotic-resistant list of isolated bacterial strain from biomedical waste are given in the table.2. along with their mean value. The mean value of *Escherichia coli* was high. Again, the mean value of their antibiotic resistance shows the similarity with Gajalakshmi P and Raja A (2019) findings. Ampicillin (Amp), Ciprofloxacin (Cip), Amikacin (Ami), Tetracycline (Tet), Cefotaxime (Ctx), Ofloxacin (OfI), Gentamycin (Gen) all these antibiotics are most frequently use in medical treatment i.e., surgery, orthopedics, medicine, heart, gynaetrics and general ward, so related antibiotic-resistant bacteria are most likely to be found in these ward's waste. According to the A.M.A. Chowdhury (2013), in hospital waste samples ciprofloxacin resistance occurrence is very high than non-hospital samples. The excreta

disposal system or drainage of any hospital either it is government or private not in good working system. So, antibiotic resistance bacteria of these related antibiotics run from government and many

private hospitals through the town and reached to the Daha River along with domestic drainage system. And finally in this manner it enters into food chain and then into food web.

Table.2. Antibiotic Resistant list of Isolated Bacterial Strain from Biomedical Waste

Name of Isolates	Name of Resistant Antibiotics							Mean
	Amp	Cip	Ami	Tet	Ctx	OfI	Gen	
<i>Escherichia coli</i>	10	5	10	10	0	3	0	5.4
<i>Pseudomonas aeruginosa</i>	8	5	7	6	0	2	1	4.1
<i>Klebsiella pneumoniae</i>	6	3	6	5	1	2	0	3.3

Ampicillin (Amp), Ciprofloxacin (Cip), Amikacin (Ami), Tetracycline (Tet), Cefotaxime (Ctx), Ofloxacin (OfI), Gentamycin (Gen)

CONCLUSION

My study area (Siwan, Bihar) is a hub of medical facilities due to patient belt area. That's why it produces a lot of bio-medical waste in solid and liquid form both, but there is lack of proper and scientific treatment of these bio-medical waste here. Microbiological investigations of bio-medical waste samples indicate presence of Total coliforms (TC), Fecal coliforms (FC), Fecal staphylococcus (FSc), *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* during my study period in my study area (Siwan, Bihar), in which *Escherichia coli*, and *Pseudomonas aeruginosa* were found multidrug resistance according to the report of Centers for Disease Control and Prevention (CDC-2019). So, it is an alarming issue.

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