



Bacterial Dynamics in Antibiotic Wastewater Treatment – A Review

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ABSTRACT

Globally, significant amounts of antibiotic wastewaters are discharged into receiving waters daily directly or indirectly. Conventional wastewater treatment processes do not always adequately removed pharmaceuticals causing environmental dissemination of low levels of these compounds. Pharmaceutical compounds including antibiotics and other drugs have been observed in the aquatic environment. Antibiotic-resistant bacteria are a major threat to health care worldwide, and besides hospital and veterinary settings it has been suggested that non-clinical environments, such as wastewaters, may play a significant role in resistance development and dissemination. These compounds have been detected in surface water, ground water, sewage effluents and even in drinking water. Antibiotic resistance genes can be associated traits from one bacterium to another. Together with the pathogens that are present in the reclaimed water, antibiotic resistant bacteria can potentially exchange mobile genetic elements to create the perfect microbial storm. Recent studies has proven that tremendous usage of antibiotics is leading to antibiotic resistance in bacteria This paper is a review on bacterial dynamics in antibiotic wastewater treatment

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1. Introduction

Wastewater treatment systems consist of physical, chemical and biological processes. The biological mechanism makes use of living organisms (generally bacteria) enhancing their functions in the natural ecosystems, in a built environment. While most physical and chemical processes are widely employed and fully understood, the biological units in wastewater treatment have traditionally been based on empirical approaches, where the microbial communities are generally treated as uncertainties. Classical microbiology techniques have not been able to cope with the complexity of wastewater treatment biological processes for treating antibiotics in wastewater. For example, most bacterial species present in wastewater have not yet been cultivated in any laboratory. A

deeper examination of the different bacterial communities would increase the possibilities to succeed in understanding the failures and virtues of wastewater treatment under different conditions.

2. Background

Presence of antibiotics in wastewater is an alarming problem. Antibiotics are constantly released to the environment through wastewater treatment plant (WWTP) effluents (Marti et al., 2013). Antibiotic-resistance genes (ARGs) are considered as emerging environmental contaminants. Hospital and municipal sewage are the major sources of ARGs for the receiving freshwater bodies (Nadine et al., 2014). Antibiotic resistance represents a global health problem, requiring better understanding of the ecology of

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antibiotic resistance genes (ARGs), their selection and their spread in the environment.

Generally, drugs are absorbed by the organism after intake and are subject to metabolic reactions. However, a significant fraction of the original substances leave human or animal organisms un-metabolized via urine or feces being therefore emitted into raw sewage, sewage sludge or manure (Carballa et al., 2004). Every year, large quantities of human pharmaceutical products are consumed worldwide. Many drugs and their metabolites, referred to as pharmaceutically active compounds (PhACs), are not fully metabolized prior to household discharge resulting in their common occurrence in wastewater treatment plants (WWTPs) (Bound and Voulvoulis, 2005; Sedlak et al., 2000).

Wastewater treatment plants (WWTPs) are regarded as one of the most important sources of antibiotics in the environment (Zhou et al., 2013). Antibiotics have been measured in WWTP influents worldwide (Hirsch et al., 1999; Kümmerer, 2009; Tamtam et al., 2008). They are suspected to present an environmental risk, e.g., fostering bacterial resistance (Czekalski et al., 2010; Servais and Passerat, 2009). For this reason, antibiotics in urban systems and discharges have been subject to increased investigation in the last decade (Neu, 1992; Pruden et al., 2006; Verlicchi et al., 2012). Several studies have reported evidence of seasonal fluctuations in concentrations of various antibiotics in WWTPs and in natural waters (Conley et al., 2008; Göbel et al., 2005; Lissemore et al., 2006; Santos et al., 2009). The changing wastewater characteristics and imposition of stricter wastewater discharge regulations have led to a greater emphasis on WTP inlet fluxes (Tchobanoglous et al., 2003). Various antibiotics have been frequently detected in groundwater (Barnes et al., 2008; Batt et al., 2006a), drinking water (Focazio et al., 2008), surface water (Hirsch et al., 1999; Yang et al., 2011), sediment (Zhou et al., 2011) and agricultural lands (Hu et al., 2010; Karci and Balcioglu, 2009). Wide occurrence of antibiotics in the environment could affect aquatic and terrestrial organisms (Costanzo et al., 2005; Kotzerke et al., 2008; Liu et al., 2009), alter microbial activity and community composition (Underwood et al., 2011), and lead to prevalence of bacterial resistance to antibiotics (LaPara et al., 2011; Su et al., 2012; Tao et al., 2010). Overall removal refers to the loss of a parent compound due to various degradation and transformation mechanisms except its sorption to sludge, while aqueous removal means the loss of a parent compound from the aqueous phase in a treatment plant. Overall removal percentages and aqueous removal percentages were compared to analyze the fate of antibiotics during wastewater treatment (Zhou et al., 2013).

3. Review of Literature

Zhou et al., 2013 worked on municipal wastewater coming from two municipal wastewater treatment plants, plant A activated sludge with chlorination, and plant B oxidation ditch with UV and found the presence of sulfonamides, diaminopyrimidines, tetracyclines, fluoroquinolones, macrolides, polyether ionophores, polypeptides, lincosamides, chloramphenicol derivatives, and β -lactams in the wastewater. In the municipal wastewater treatment plants, sulfamethoxazole, trimethoprim, norfloxacin, ofloxacin and anhydro erythromycin were the predominant antibiotics in the effluents, while in the sludge oxytetracycline, tetracycline, ofloxacin and norfloxacin were dominant with much higher

concentrations than the others. The removals for the sulfonamides, macrolides, trimethoprim, lincomycin and chloramphenicol were mainly attributed to their biodegradation process, while the removals for the tetracyclines and fluoroquinolones were mainly due to their sorption onto sludge.

Varela et al., 2014 worked on hospital effluent and raw inflow and from the treated effluent wastewater treatment plant and detected the presence of various antibiotics in these wastewaters. Antimicrobials tetracycline, oxytetracycline, doxycycline, chlorotetracycline, penicillin G, penicillin V, sulfamethazine, sulfathiazole, sulfamethoxazole, ciprofloxacin and ofloxacin. Ciprofloxacin resistance was significantly more prevalent in hospital effluent than in raw inflow, for all the bacterial groups studied. In contrast, amoxicillin resistance prevalence was not significantly different in both sites. Ciprofloxacin and arsenic concentrations were positively correlated with ciprofloxacin resistance prevalence, mainly in hospital effluent samples. The bacterial populations correlated with the concentrations of sulfamethoxazole and tetracycline were different of those correlated with ciprofloxacin, ofloxacin and arsenic.

Novo et al., 2013 conducted experiments on raw and treated (municipal sewage and pre-treated industrial wastewaters mainly from food-industry and animal farming) municipal wastewater treatment plant and detected the presence of tetracycline, sulfamethoxazole, ciprofloxacin and amoxicillin. The bacterial community structure was distinct in raw and in treated wastewater and varied over time. Temperature and COD were correlated with the variation of the bacterial community structure of raw and treated wastewater, respectively. Temperature was positively correlated with the prevalence of sulfonamide resistant heterotrophs and enterobacteria in treated wastewater. Tetracycline concentration in the raw wastewater was positively correlated with the antibiotic resistance prevalence in treated wastewater, although not specifically with tetracycline resistance.

Qiu et al., 2013 worked on synthetic pharmaceutical wastewater. Wastewater upflow anaerobic sludge blanket (UASB) and membrane bioreactor (MBR) berberine are the treatment units used for treating synthetic pharmaceutical water. Combined UASB–MBR process was proposed for berberine removal from synthetic wastewater. Promising results indicated that combined UASB–MBR process is feasible and efficient in berberine reduction.

Nolvak et al., 2013 worked on activated sludge wastewater treatment domestic, municipal wastewater combined with the effluents from the dairy and meat industries from horizontal subsurface flow filter mesocosms. Tetracyclines, macrolides, sulfonamides, penicillins, and fluoroquinolones are the antibiotics found in the treatment unit. Seven targeted antibiotic resistance genes were detectable in the influent and effluent of the horizontal subsurface flow filter mesocosms within a pilot-scale hybrid constructed wetland for treating municipal wastewater. The horizontal subsurface flow filter mesocosms proved more efficient in reducing sulfonamide resistance encoding *sul1* concentrations compared to some traditional wastewater treatment options.

Schwartz et al., 2003 conducted experiments on wastewater, surface water, and drinking water biofilms (river water consists of water from

sewage treatment plant, hospital etc.). The *vanA* vancomycin-resistance gene from enterococci, the *mecA* methicillin-resistance gene from staphylococci and the *ampC* L-lactam-resistance gene from Enterobacteriaceae were amplified predominantly from hospital wastewater biofilms. *VanA* genes and *ampC* genes were also detected in all other wastewater and environmental biofilms. The *vanA* and *ampC* antibiotic-resistance genes were detected in drinking water biofilms, whereas enterococci and Enterobacteriaceae, which are said to carry these genes originally, were never found in these biofilms.

Coutu et al., 2013 found presence of trimethoprim, norfloxacin, ciprofloxacin, ofloxacin, clindamycin and metronidazole in wastewater treatment plant influent. In this study, dominant time scale in the mass flux variability of several antibiotics in sewage water reaching the Wastewater Treatment Plant have been assessed. Mass fluxes were observed to be higher in winter than in summer. This is particularly the case for ciprofloxacin, with the winter mass flux being up to 3–4 times that in summer. These data are consistent with the hypothesis that the measurements reflect the seasonal consumption of antibiotics, driven by associated seasonality in pathologies.

Drillia et al., 2005 conducted experiments on activated sludge mixed liquor from wastewater treatment plant. Sulfamethoxazole was the antibiotic present in the treatment unit. Sulfamethoxazole serves as a carbon and/or a nitrogen source for the enhanced culture of microorganisms that are able to degrade it. It seems that the enzymatic mechanism responsible for the compound degradation is not activated as long as there is a readily degradable carbon source available in excess of ammonium. However, if the conditions necessary for the activation of this mechanism prevail, then the enzymes are not inhibited in the case ammonium is afterwards present. These observations help understand the occasional presence of sulfamethoxazole in the wastewater treatment plant effluents. Sulfamethoxazole is expected to be detected in wastewater treatment plant effluents, whenever there are easily biodegradable carbon and nitrogen sources contained in wastewaters that would prevent the initiation of the pharmaceutical degradation. In the case, there is a depletion of easily biodegradable matter sulfamethoxazole degradation is more likely to take place, so that there will be no need to maintain a bioaugmentation reactor.

Masse et al., 2000 detected the presence of tylosin, lyncomycin, tetracycline, sulphamethazine, penicillin and carbadox in swine manure slurry. The individual or combined effects of carbadox, tylosin, penicillin, tetracycline, sulphamethazine and lyncomycin on psychrophilic anaerobic digestion of swine manure slurry in intermittently fed sequencing batch reactors were examined in this study. Only penicillin and tetracycline had an inhibitory effect on methane production when applied at the maximum allowable dose in feed.

Batt et al., 2006 detected sulfamethoxazole, trimethoprim, ciprofloxacin, tetracycline, and clindamycin from effluents from three wastewater treatment plants. The effluent from three local wastewater treatment plants revealed concentrations of six of the seven test compounds on three sampling occasions, indicating that a chronic exposure to low levels of antibiotics exists as the result of incomplete elimination by current wastewater treatment processes. Although all sampling took place during

the fall and winter seasons, it would be likely that some detection of these compounds would also take place during summer and spring conditions. Results from this study show that the sampled wastewater treatment plant processes are not effective in the complete removal of the target antibiotics. However, since only the effluent from each plant was sampled, it is not possible at this time to quantify the percent removal efficiency of antibiotics by the different processes employed in the plants. Benedek et al., 2010 found municipal wastewater from activated sludge treatment system and detected sulfamethoxazole, tetracycline and ciprofloxacin. This study presents a process model that predicts the removal of the antibiotic micropollutants, sulfamethoxazole (SMX), tetracycline (TCY), and ciprofloxacin (CIP), in an activated sludge treatment system. A novel method was developed to solve the inverse problem of inferring process rate, sorption, and correction factor parameter values from batch experimental results obtained under aerobic and anoxic conditions. Instead of spiking the batch reactors with reference substances, measurements were made using the xenobiotic organic micropollutant content of preclarified municipal sewage. Parent compound formation and removal were observed, and the model developed using the simulation software WEST showed limited efficiency to describe the selected micropollutants profiles, when growth substrate removal occurs. The model structure was optimized by accounting for competitive inhibition by readily biodegradable substrates.

Carballa et al., 2004 worked on municipal wastewater where industrial and hospital discharge is maximum. The eight compounds which were detected in raw wastewaters (galaxolide, tonalide, ibuprofen, naproxen, sulfamethoxazole, estrone, 17 β -estradiol and iopromide). The overall removal efficiencies of the STP ranged between 70% and 90% for the fragrances, 40–65% for the anti-inflammatories, around 60% for the antibiotic sulfamethoxazole and 65% for 17 β -estradiol. Two mechanisms can be used to explain this elimination: the degradation of the compound and the adsorption onto primary and secondary sludges. This implies that a complete management of the pollution associated with these particular compounds must necessarily take into consideration the treatment of the excess of sludges.

Ben et al., 2009 the removal of antibiotics by Fenton's reagent in the sequencing batch reactor (SBR) pretreated swine wastewater was investigated in this work. Fenton's reagent could effectively remove all the selected antibiotics, including five sulfonamides and one macrolide at an initial concentration of 1.0 mg/L, from the SBR pretreated swine wastewater.

Elmolla et al., 2012 detected amoxicillin and cloxacillin in antibiotic wastewater and domestic wastewater. Sequencing batch reactor (SBR) was used for treating these wastewaters. The optimum H₂O₂/COD and H₂O₂/Fe²⁺ molar ratios of Fenton pretreatment of an antibiotic wastewater containing amoxicillin and cloxacillin were 2.5 and 20, respectively. Under the optimum operating conditions, complete degradation of the antibiotics occurred in 1 min. The best operating conditions for treatment of the antibiotic wastewater by combined Fenton-SBR process were H₂O₂/COD molar ratio 2.5, H₂O₂/Fe²⁺ molar ratio 150, Fenton reaction time 120 min and HRT of 12 h. Combined Fenton-SBR is a feasible process for antibiotic wastewater treatment.

Joss et al., 2006 worked on detecting antibiotics present in sewage sludge present in conventional activated sludge treatment plant (CAS) and from a membrane bioreactor (MBR). Azithromycin, Clarithromycin, (Anhydro-) erythromycin, N4-acetyl-sulfamethoxazole and Roxithromycin were the antibiotics detected. For many compounds municipal wastewater treatment represents an obligatory and final treatment step prior to release into the environment. An overview of kbio values shows, that biological degradation in municipal wastewater treatment contributes only to a limited extent to the overall load reduction of pharmaceuticals.

Borjesson et al., 2009, methicillin was found in municipal wastewater from municipal wastewater treatment plant. Using molecular methods and cultivation, methicillin-resistant *S. aureus* was for the first time detected in a municipal activated sludge and trickling filter wastewater treatment plant. The wastewater treatment process reduces *mecA* gene concentrations, which can partly be explained by removal of biomass.

Fan et al., 2011, in this worked on treating synthetic wastewater in sequencing batch reactors. This study suggests that the presence of erythromycin or erythromycin-H₂O at concentrations as low as found in the environment can enhance establishment of antibiotic resistance, and will provide important information to substantiate correlation between resistance proliferation and antibiotics at sub-inhibitory concentrations.

Wang et al., 2011 did laboratory-scale wastewater (synthetic wastewater) treatment in sequencing batch reactors. The presence of PhACs did not significantly inhibit the performance of bioreactors or microbial community structure when PhACs were introduced individually. When introduced in mixtures, some PhAC combinations caused significant inhibition of ammonia removal as well as a decrease in ammonia-oxidizing bacteria diversity suggesting that PhAC mixture effects may play an important role in an overall treatment's nitrification potential.

Zhang et al., 2013 worked on treating mother liquor samples, non-antibiotic fermentation wastewater using sequential batch reactor and a two-stage submerged biological contact reactor and detected oxytetracycline. Despite the bacteriostatic effects of antibiotics, the microbial structures from two biological wastewater treatment systems treating antibiotic production wastewater were proven to be functionally diverse. The abundance of several fungal carbondegrading genes (e.g., *glx*, *lip*, *mnp*, *endochitinase*, *exoglucanase* genes) was significantly correlated with antibiotic concentrations.

Yang et al., 2014 collected influent and effluent samples, anaerobic digestion sludge and activated sludge samples from sewage treatment plant and detected Acridine, Acriflavine, Aminoglycoside, Bacitracin, Beta-lactam, Bicyclomycin, Chloramphenicol, Fosfomycin, Fosmidomycin, Polymyxin, Quinolone, Sulfonamide, Tetracycline, Trimethoprim, Vancomycin in the samples. High-throughput sequencing based metagenomic analysis revealed board profile of antibiotic resistance genes (ARGs) in sewage treatment plant (STP). Totally 271 ARGs subtypes belonging to 18 ARGs types were identified in influent, effluent, anaerobic digestion sludge and activated sludge samples. 78 of the subtypes persisted through sewage/sludge treatment process. Sewage treatment in STP was effective in removing ARGs from influent. The total removal efficiency of ARGs in influent was 99.82%.

Balcioğlu et al., 2003 treated synthetic pharmaceutical formulation wastewater containing two human antibiotics and a veterinary antibiotic in ozone reactor and detected ceftriaxone sodium, cephalosporine group; and penicillin VK, penicillin group. The results of the study have delineated that ozonation at natural pH values provides a promising technique for the treatment of antibiotic formulation wastewater. Results revealed that pH control was essential to obtain efficient COD and UV254 removal.

Akiyama et al., 2010 detected ofloxacin, trimethoprim, and sulfamethoxazole in municipal wastewater from municipal wastewater treatment plant. In this study, *E. coli* was used as indicator bacteria for fecal contamination and are part of the larger community of total coliforms. Results were not the same for the two target bacteria. For example, proportions of antibiotic resistance in *E. coli* in winter (December) were observed, while ampicillin-resistant coliform decreased.

Berglund et al., 2014 detected Azithromycin, Ciprofloxacin, Clarithromycin, Clindamycin, Doxycycline, Erythromycin, Norfloxacin, Oxytetracycline, Sulfamethoxazole, Tetracycline, Trimethoprim and Vancomycin in effluent wastewater from treatment plant samples. Surface-flow constructed wetlands was used for treatment. The average measured removal efficiency of antibiotics achieved implies that surface-flow constructed wetlands (CWs) could serve as a useful and cost effective alternative to conventional treatment methods in removing or reducing levels of antibiotics in wastewater. The results indicate that short-term exposure of low levels of antibiotics does not have an effect on resistance gene abundance in these CWs.

Cardona et al., 2014 collected samples from water and sediment from a river. River is impacted by both antibiotic production plant (APP) and urban wastewater treatment plant (WWTP) and detected the presence of penicillin, ampicillin, doxycycline, tetracycline, erythromycin, azithromycin and streptomycin. This study demonstrates that both APP and WWTP discharges increased antibiotic resistance in fecal bacteria located at the nearest sampling site downstream of the discharges. However, antibiotic resistance decreased as the distance to the effluents increased, probably because of the dilution effect on antibiotics and therefore their selective pressure. Multidrug-resistant bacteria were also detected, their percentages being related to the type of water treatment process.

Amin et al., 2006 a laboratory-scale anaerobic sequencing batch reactor was used to treat a model substrate mixture representing pharmaceutical wastewater at an organic loading rate of 2.9 g COD/(L d). After reaching stable operation the reactor was first exposed to low (1 mg/L) and, subsequently, to high (200 mg/L) concentrations of the antibiotic erythromycin. In batch tests evaluating the specific methanogenic activity, conversion of the model substrate mixture was only slightly affected by the presence of erythromycin.

Kim et al., 2005 worked on two lab-scale sequencing batch reactors (SBRs). One SBR was spiked with 250 µg/L tetracycline and other SBR was evaluated at tetracycline concentrations found in the influent of the wastewater treatment plant (WWTP) where the activated sludge. A study was conducted to examine the influence of hydraulic retention time (HRT) and solid retention time (SRT) on the removal of tetracycline in the

activated sludge processes. Two lab-scale sequencing batch reactors (SBRs) were operated to simulate the activated sludge process. One SBR was spiked with 250 µg/L tetracycline, while the other SBR was evaluated at tetracycline concentrations found in the influent of the wastewater treatment plant (WWTP) where the activated sludge was obtained. The concentrations of tetracyclines in the influent of the WWTP ranged from 0.1 to 0.6 µg/L. Three different operating conditions were applied during the study. Batch equilibrium experiments yielded an adsorption coefficient (K_{ads}) of 8400 ± 500 mL/g and a desorption coefficient (K_{des}) of 22 600 ± 2200 mL/g. No evidence of biodegradation for tetracycline was observed during the biodegradability test, and sorption was found to be the principal removal mechanism of tetracycline in activated sludge.

Mechanism involved in antibiotic resistance:

Excessive use of antibiotics is leading to antibiotic resistance bacteria. Antibiotic resistance is the ability of bacteria or other microbes to resist the effects of an antibiotic. Antibiotic resistance occurs when bacteria change in some way that reduces or eliminates the effectiveness of drugs, chemicals, or other agents designed to cure or prevent infections. The bacteria survive and continue to multiply, causing more harm. Development of resistance to an antibiotic depends on how much is being used and how often bacteria are exposed to the drug. It's related to the volume of use and the ability of bacteria to change their coat of armor. It can happen in months, it can happen in weeks, over a period of years. Bacteria become resistant through adaptations or acquisition and transmission of antibiotic resistance. Genes conferring resistance are most often found to occur on the same plasmids with the genes, which confer resistance to various therapeutically useful antibiotics.

Antibiotic resistance genes can be associated with mobile genetic elements, which in turn allow a promiscuous transfer of resistance traits from one bacterium to another. Together with the pathogens that are present in the reclaimed water, antibiotic resistant bacteria can potentially exchange mobile genetic elements to create the —perfect microbial storm. Given the significance of this issue, a deeper understanding of the occurrence of antibiotics in reclaimed water, and their potential influence on the selection of resistant microorganisms would be essential (Hong et al., 2013).

The combination of three major adaptation mechanisms may contribute to explain the spread and selection of antibiotic resistant populations: i) the occurrence of horizontal transfer of antibiotic resistance genes (Baquero, 2004; Walsh, 2006); ii) the preferential proliferation of resistant bacteria due to selective pressures imposed by antimicrobial residues or heavy metals (Graham et al., 2011; Tello et al., 2012; Hellweger, 2013) and iii) the bacterial community rearrangement to fit the occurrence of substances with antimicrobial activity, such as antimicrobial residues or heavy metals (Lawrence et al., 2008; Graham et al., 2011; Gillings, 2013; Huerta et al., 2013; Novo et al., 2013). Furthermore, besides of antibiotics themselves, antibiotic-resistant bacteria and genes is another concern to the environment, they could be considered to be “pollutants and superbugs” as their wide-spread dissemination is clearly undesirable (B.M. Kuehn et al., 2007; S. Xia et al., 2012).

Methodology adopted for detecting presence of antibiotics:

The bacterial communities present in wastewater and wastewater treatment systems have been traditionally studied from a classical microbiological perspective, i.e. based on the culture of microorganisms or isolation-based methods. By cultivating bacterial isolates, researchers were able to identify important groups of microorganisms providing valuable information on their metabolic role in wastewater treatment. However, culture-dependent techniques selected for fast-growing bacteria are easily adapted to laboratory conditions and thus can't be considered representative of the composition and diversity of the microbial communities inhabiting wastewater. In recent years, the application of culture-independent methods such as molecular biology techniques, has revealed more accurate information about biological wastewater treatment, the bacterial communities involved and the roles they play (Amann and Ludwig, 2000; Wagner and Loy, 2002; Sanz and Köchling, 2007; Gilbride et al., 2006). These techniques can be distinguished according to whether they make use of polymerase chain reaction (PCR) to amplify a targeted sequence or not (Dorigo et al., 2005).

4. Summary

From the above studies we can conclude that tremendous usage of antibiotics is leading to antibiotic resistance in bacteria. Various studies conducted on antibiotics in water and wastewater concluded that presence of antibiotics in municipal wastewater treatment plants, influent and effluent from wastewater treatment plants, hospital effluent, pharmaceutical wastewater, raw wastewater, rivers, surface water, and drinking water biofilm.

Many lab scale studies have been conducted for treating antibiotic wastewater using horizontal subsurface flow constructed wetland, up flow anaerobic sludge blanket, membrane bioreactor, trickling filter, anaerobic sequencing batch reactor and concluded that the antibiotics degradation in a treatment unit may depend on temperature, sorption, process rate, hydraulic retention time.

The study reflects the future impact of above-mentioned parameters, which is the path breaking study for environmental management for the sustainable development.

5. Conclusion

The horizontal transfer of antibiotic resistance genes, proliferation of resistant bacteria due to selective pressures imposed by antimicrobial residues and the bacterial community rearrangement to fit the occurrence of substances with antimicrobial activity may contribute to explain the spread and selection of antibiotic resistant populations

Antibiotics degradation and transformation mechanisms may refer to loss of a parent compound.

In most of the cases antibiotics are present in wastewater treatment systems so in biological treatment system, antibiotic treatment should also be adopted for antibiotic degradation.

The study of bacterial dynamics in wastewater is a crucial area for the study which has not been explored enough.

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