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## REVIEW

# An assessment of degradation of xenobiotic compounds by soil borne bacteria and their adaptation to organic xenobiotic compounds: A review

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Global environmental pollution caused by the complex mixture of xenobiotic drugs and toxic chemicals has become a major environmental problem worldwide. Many such type of xenobiotic compounds effect the environment due to their high toxicity, persistence and low biodegradability. Microbial-assisted degradation of xenobiotic compounds is considered the most efficient and effective method. Bacteria have significant catabolic potential for biodegradation processes and involve different catabolic genes, enzymes to various degradation pathways. Microorganisms can detoxify and use pollutants for their growth and metabolic activities. However, different microbial groups survive in highly polluted environments and have significant biodegradation capabilities that can break down and transform pollutants into less harmful chemicals so present study, specifically defined the effects of xenobiotic compounds in soil, water, plants, human health, environment and role of bacterial originated enzymes involved in degradation of these xenobiotic chemicals.

**Keywords:** Enzymes, biodegradation, microbial-assisted degradation, xenobiotic compounds.

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## INTRODUCTION

Xenobiotic compounds can be defined in a strict or broader sense. Consequently, “any compounds that are released in any compartment of the environment by the action of man and thereby occur in a concentration that is higher than natural” are included in a larger definition of xenobiotics. Heavy metals, polycyclic aromatic hydrocarbons (PAHs), and oil derivatives like toluene are also included in this broader category. We will only address bacterial adaptation to organic xenobiotics as described by Leisinger in this review, and we'll just call them xenobiotics or xenobiotic substances (Top and Springael, 2003). Environment is everything that is around us all the time and affects our daily life in the world. A safe and healthy environment is essential to survive in this world. However, a variety of human activities, including exposure to environmental xenobiotics, constitute the primary cause of pollution and harm in the era of industrialization and urbanisation. Xenobiotics are substances that

are not found or expected to be found in living organisms.

The term “xenobiotics” is often used in the context of environmental pollution and refers to synthetic substances widely produced for commercial, agricultural, and domestic use (Mishra and Srinivasan, 2001). There is increasing public concern about the intentional or unintentional introduction into the environment of various xenobiotics that pose high risks to humans and animals (Godheja *et al.* 2016). Environmental xenobiotics include pesticides, polycyclic aromatic hydrocarbons (PAHs), pharmaceutically active compounds (PhACs), personal care products (PCPs), phenolic resins, chlorinated compounds, and other chemicals.

Microbial communities can adapt to the presence of xenobiotics in the environment through various mechanisms or combinations. First, by inducing the necessary genes, the large population of bacteria that can tolerate and even degrade the compound will increase. Secondly, cells can be modified by a variety of changes, such as

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nucleotide changes or DNA rearrangements that lead to degradation of compounds and they can obtain background information of relevant individuals or different groups in society through horizontal gene transfer (HGT). Finally, single cells that can best maintain or reduce the xenobiotic will be selected and screened through the population until they form a greater proportion of the microbial community than before the removal of the xenobiotic. In response to environmental stress, microbes have evolved a variety of defence mechanisms, including mutation, DNA recombination, and horizontal gene transfer. Horizontal transfer of genes plays an important role in the transfer of catabolic genes and thus enables the transfer of organisms to polluted areas.

In many artificially produced chlorinated chemicals, the breaking of carbon-halogen bonds is catalysed by bacterial de-halogenases. This is a critical phase in the process of detoxifying common organic contaminants. Catabolic pathways to form new compounds some appear to have evolved through the accumulation of horizontally transmitted genes and subsequent mutations and genetic modifications. Recent studies have demonstrated the existence of novel exogenous catabolic mobile genetic elements, such as catabolic genomic islands, that integrate into the chromosome after mutation. The significance of the combination of horizontal gene transfer and patchwork is still unclear, but recent reports suggest that this process occurs in the infected area. Global pollution from exogenous compounds has become a matter of concern. Many xenobiotic compounds affect the environment due to their high toxicity, persistence and low biodegradability. Microbial-assisted degradation of xenobiotic compounds is considered as the most efficient and effective method. Significant catabolic potential exists in bacteria, and genes, enzymes, and degradation pathways are involved in biodegradation processes. Numerous microorganisms, including *Streptomyces*, *Rhodococcus*, *Kojima*, *Penicillium*, *Aeromonas*, *Alcaligenes*, *Microbacteria*, *Micrococci*, *Methanospirillum*, *Candida*, and *Chrysois* is involved in this process. Microorganisms can use exhaust gases as carbon or nitrogen to control their growth and

metabolic activity (Miglani *et al.*, 2022). Different microbial groups survive in highly polluted environments and have significant biodegradation capabilities that can break down and transform pollutants. However, investigating these xenobiotics diseases necessitates the use of an increasing number of techniques. To characterize hazardous bacteria, their metabolic processes, new proteins, and catabolic genes involved in the degradation process, diverse approaches such as metagenomics, proteomics, transcriptomics, and metabolomics are now applied. This method is effective for learning about organisms' genetic diversity and community structure.

Advanced molecular methods to characterize complex microbial communities can provide insight into their structure and function and help to resolve questions regarding the biodegradation potential of bacteria. This review article discusses the biodegradation potential of microorganisms and provides insight into recent advances and omics approaches for the unique characterization of xenobiotic biodegradative microorganisms in the environment. Microbial remediation of xenobiotic compounds is considered one of the most effective, efficient and economical methods that can consumes organic solvents such as oxygen, carbon or nitrogen added to control their growth (Embrandiri *et al.* 2016). There are diverse microbial communities that thrive in toxic and highly stressful environments, including soil, water, human intestines, hydrothermal vents, acid mine runoff, and oil reservoirs (Dhakal *et. al*, 2018). Due to their genetic and functional diversity, microbial populations have the potential to improve the environment (Baun *et al.* 2012). Therefore, examining the microbial species present in the contaminated environment provides important information about the specific microbial characteristics that increase the rate of degradation. However, the effective use of microbial purification strategies requires a technological process that leads to a deeper understanding of microbial activity and survival under environmental stress.

The development of molecular, biotechnological, bioinformatics and systems biology tools relevant to bioremediation problems has provided gene-

level mechanisms for bioremediation (Maurya, 2016). In addition, the direct study of infectious diseases, including all microbial diseases, presents new challenges to the scientific community in sharing information about the world without microbial diseases (Derby *et al.* 2021). The development of advanced molecular tools and a better understanding of microbial metabolism and genetic structure and function have accelerated the development of new technologies to enhance bioremediation to eliminate environmental pollution (Zhou *et al.* 2022). Soil is an ideal environment for a wide variety of microbial communities. It is estimated that one gram of soil contains approximately  $10^9$  bacteria, but only less than 1% of these can be sampled in the laboratory (Elekwachi *et al.* 2014). Culture-based identification of distinct microbial populations in different areas is a difficult task limited by the rapid growth of microbial diversity (Liu *et al.* 2019). Therefore, it is possible to uncover the diversity and functional dynamics of the microbial community in contaminated environments using contemporary culture-independent molecular approaches. Additionally, recent advances in molecular tools and technologies have provided new insights in the field of bioremediation and transformed traditional research (Bhandari *et al.*, 2021). Omics technology is the result of advanced molecular technology and directly characterizes microbial genome structure without the need for culture. Therefore, the use of modern technologies such as metagenomics, transcriptomics, and proteomics has produced important information about the gene and protein expression levels of all microbial communities in the environment in order to reveal the mechanisms of microbial degradation and bioremediation (Perelo, 2010). Omic method is efficient, fast and accurate molecular method. It investigates advanced microbial degradation processes, metabolic activities, genetic control and molecular biology aspects of xenobiotics (Azubuike *et al.* 2016).

The application of bacteria to remove exogenous substances from soil, water or sediments by conversion or mineralization into harmless products such as  $\text{CO}_2$  and  $\text{H}_2\text{O}$  is the main idea of bioremediation strategies (Stefnac *et al.* 2021). *Idium* and *Exophiala* have been reported to play

a role in the efficient biodegradation of xenobiotic compounds in soil/water environment due to their excellent bioremediation potential (Saraswat, 2014). The biodegradation ability of bacteria is generally affected by soil, salinity, temperature, carbon source, moisture content, pH, nitrogen source, amount of inoculum (Sikandar *et al.* 2013). Microorganisms have significant catabolic capacity, genes, enzymes and degradation pathways involved in the bioremediation process that may be responsible for the transformation of new properties and characteristics (Fent *et al.* 2006). Additionally, microbial plasmids are thought to be responsible for further amplification, transformation and delivery of new biodegradable genes or enzymes (Faroon and Ruiz, 2016). These new genes or enzymes, due to horizontal gene transfers, endow microorganisms with the biodegradation ability to remove or eliminate most environmental contaminants (Yadav, 2020). The treatment process for diseases can be further improved by the successful application of genome editing and biochemical technologies, which alter existing bacteria and lead to the development of genetically, modified organisms capable of degrading many xenobiotics simultaneously. Advances in genetic control techniques provide more accurate information and explore the future of xenobiotic bioremediation by intelligent organisms (Piers and Joshi, 2005). The most common type of xenobiotics are synthetic pesticides, particularly the organochlorine pesticides (OCPs), which have been used for a very long time in both agriculture and insect control programs all over the world. Due to their durability and bioaccumulative nature, a number of OCPs, including benzene hexachloride (BHC), dieldrin, aldrin, dichloro diphenyl trichloro ethane (DDT), and hexachlorocyclohexane, are extremely dangerous in the environment. One of the most toxic organochlorine xenobiotic compounds is lindane ( $\alpha$ -hexachlorocyclohexane), which has been thoroughly researched for its microbial biodegradation through physical interactions (soil structure, carbon and oxygen gradients, pH, and temperature) and chemical interactions (dechlorination, dehydroxylation, and dehydrogenation) (Moore, 2008). Increased lindane residues in the environment caused serious harm to humans and other organisms,

such as carcinogenesis, mutagenicity, endocrine disruption, and immune system disorders (Mishra *et al.* 2021).

Bacterial strain genera including Burkholderia, Bacillus, Pseudomonas, Kocuria, Archromobacter, Sphingomonas, and Chromohalobacter have all been shown to biodegrade lindane under both axenic and anoxic conditions. This process involves dehydrogenation, dehydrochlorination, and hydroxylation, and ultimately leads to complete degradation or mineralization. Pyrethroids are general insecticides used to control agricultural and domestic pests. Cypermethrin, cyhalothrin, deltamethrin, cyfluthrin and bifenthrin are examples of synthetic pyrethroids (Wang *et al.* 2022). These pesticides are toxic and persistent and can cause molecular toxicity, neurotoxicity, and reproductive toxicity (Sall *et al.* 2022). One of these pyrethroids, cypermethrin, can cross the blood-brain barrier and harm the body and immune system. The persistence of pesticides in the environment poses a threat to humans and other non-native species on land and in water (Juliano and Magrini, 2017). It has been reported that microbial species of the genera *Acinetobacter*, *Trichoderma*, *Luteiella*, *Pseudomonas*, *Cunninghamia*, and *Bacillus* can degrade common insecticides such as cypermethrin and other pyrethroid insecticides via pyrethroid hydrolases (Priyanka *et al.*, 2022).

### **Degradation method**

Nowadays, various methods, including metagenomics, proteomics, transcriptomics, and metabolomics, are used to characterize harmful bacteria, their metabolic processes, novel proteins, and catabolic genes involved in the degradation process. This technique is very effective in gaining information about the genetic diversity and community structure of organisms. Advanced molecular methods to characterize complex microbial communities can provide insight into their structure and function and helps to solve questions regarding the biodegradation potential of bacteria. Xenobiotics can be classified according to different criteria, including its properties, areas of use, physical properties and patho-physiological effects. The effects on people

and the environment cannot be ignored. Chronic exposure even to low levels can cause toxic, mutagenic or teratogenic effects. Wastewater treatment plant that cannot effectively reduce the release of xenobiotics are one of the main products of xenobiotics in the environment i.e., xenobiotics reach the environment and affect humans and animals. To reduce the negative impact, many laws and regulations have been implemented in the EU and around the world aimed at removing xenobiotics from industry, the environment and the social environment and preventing them from polluting the environment (Godheja *et al.* 2016).

### **Parameters influencing bioavailability and the rate of biodegradation**

The extent of biodegradation and the rate at which it occurs depend on the chemical structure and concentration of the compound being degraded, the type and number of microorganisms present, and the physicochemical properties of the environment. In laboratory as well as environmental systems, only the fraction of the xenobiotic pollutant that is dissolved in the aqueous phase is generally assumed to be available to the microorganisms for degradation. Bioavailability is controlled by parameters such as the physical state of the pollutant compound (solid, liquid, gaseous), its solubility in water, and its tendency to adsorb or bind to soil or sediment particles. In soil aggregates or other solids, microbes may be excluded from entering the smaller micropores. Xenobiotics present in the micropores are thus unavailable to the microorganisms and must diffuse through pore water to the grain surface in order to be degraded. However, diffusion in soil systems may be limited by adsorption. In fact, adsorption, immobilization and confinement of micropores are the main reasons for the persistence of many impurities. Aging, which is the contamination of soil or sediment by organisms over a long period of time, also affects bioavailability: pollutants can affect soil and sediment products, allowing bacteria to become active over time. Many xenobiotics, such as polycyclic aromatic hydrocarbons and polychlorinated biphenyls, poorly soluble in water and are mostly adsorbed and fixed by the soil matrix and sediments (Baun *et al.* 2012). As

mentioned above, the molecular structure of xenobiotics is characterized by “non-physical” changes and stable chemical properties that can hinder or prevent biodegradation. Unfavourable concentrations of the xenobiotic compound also affect biodegradation. In high concentrations, many xenobiotics are toxic to organisms, including the degradative bacteria. On the other hand, there may be a minimum concentration below which a compound is not degraded any more. Synthesis of catabolic enzymes may not occur when the concentration of a chemical is below a level that is effective for induction of the corresponding catabolic genes. Besides, the minimal threshold concentration depends mainly on the kinetic parameters of growth and metabolism, but also on the thermodynamics of the overall transformation reaction. In fact, constant substrate affinity is the most important factor for the biodegradation of pollutants to low concentrations (Godheja *et al.* 2016). In aerobic systems, minimum substrate concentrations can range from 0.1 to 1.0 mg L<sup>-1</sup>, but in environmental systems the final concentrations required are generally 1 µg L<sup>-1</sup> or less (Fetzner, 2002). Other factors that affect biodegradation include environmental factors such as temperature, pH, moisture content and salinity, the presence of interfering chemicals, the availability of energy and nutrients, and the presence of oxygen or other energy sources. For instance, the availability of oxygen in soil is often the limiting factor for aerobic biodegradation processes. Additionally, the presence of competing organisms or predators in the microbial community can also affect biodegradation (Derby *et al.* 2021). When determining the rate of biodegradation it is important to remember that the visible xenobiotic “disappears” from the body. The ecosystem does not necessarily mean that it is biodegraded, as bio-transformation, leaching or chemical change *viz.*, polymerization, modification, decomposition as part of the degradation can also cause loss. Monitoring a chemical’s environmental destiny requires keeping an eye on its byproducts as well as the parent compound’s disappearance (Zhou *et al.* 2022). The rates of xenobiotic biodegradation in the environment may range from days and weeks to years and decades. The organophosphate insecticide malathion disappears from soil within approximately one

week, and the herbicide 2, 4-D (2,4-dichlorophenoxyacetic acid) is degraded within four to six weeks in soil. Modern herbicides are designed to undergo biodegradation within one cropping season. On the other hand, there are recalcitrant xenobiotics that persist in the environment for many years. Simple structural changes of a molecule, such as the addition of a chlorine substituent, can convert a readily biodegradable compound such as 2,4-D into a more persistent substance such as 2,4,5-T (2,4,5-trichlorophenoxyacetic acid) (Elekwachi, 2014).

### **Effects of Xenobiotic compounds**

Microbial consortia have the potential to improve biodegradation processes in xenobiotic-contaminated soil/water environments. However, many of the important organisms involved in bioremediation are still unidentified because not all organisms in nature can be introduced *in-vitro* but exist in a viable but non-cultural (VBNC) environment. Therefore, there is a great need for new applications and modern technologies to understand the genetics and molecular biology of organisms to discover the hidden knowledge of these VBNC diseases. New molecular design techniques offer promising avenues for deep understanding of microbial communities, from molecules to genes. New Omics technologies such as metagenomics, transcriptomics, and proteomics provide information about nucleic acids, enzymes, catabolic genes, plasmids, and metabolic machinery and metabolites produced during the biodegradation process. The collaboration of many omics studies introduces the perspective of systems biology to provide a better understanding of the whole. The relationship between genes, proteins and the environment in the process of microbial degradation provides a gene therapy tool that enables the development of various new technologies such as genome editing and next-generation tools CRISPR-Cas9, TALEN and ZFN. It contains genes for specific degradation activities and provides unique insights into microbial remediation. Additionally, the success of omics technology is not possible without the use of bioinformatics tools. Bioinformatics has revolutionized the creation of genomic and

proteomic databases, facilitating information on the cellular and metabolic processes of environmental contaminants. The application of this technique in biological research paves the path for further investigation into the possibilities of microbial bioremediation and its capacity to eradicate external problems (Mishra and Srinivasan, 2001).

### **Effects of exogenous chemicals in the soil**

Exogenous chemicals such as dioxins, 1,1,1-trichloro-2,2-bis (4-chlorophenyl) ethane (DDT), polychlorinated bis Benzene (PCB), chlordane, polycyclic aromatic hydrocarbons (PAHs) and nitroaromatic compounds pose a major threat to soil ecosystems in developing countries. However, there are reports that some other compounds such as benzene, nitrobenzene, toluene, xylene, aniline, ethylbenzene, trinitrotoluene/dibenzofuran and chlorinated solvents may be xenobiotic, especially in the soil ecosystem (Godheja *et al.*, 2016). Due to one or more aromatic rings and azo linkages, cosmetics and personal care items also contribute as xenobiotic pollutants, particularly parabens in soil and air and azodyes in soil. The use of pesticides, fertilizers, military operations, industrial processes, fuel burning, and soil alterations in high-yield agricultural techniques are examples of anthropogenic activities that increase the concentration of these chemical compounds in soil and have negative consequences (Migliani *et al.* 2022). The chemical properties and locations of xenobiotics affect their bioavailability and distribution in soil; Soil organic matter (SOM) plays an important role. Pesticides (pesticides, insecticides, fungicides, algicides, fungicides, etc.) are chemicals used in plant protection and management and have been the most widely used chemicals in the environment in the past year. Millions of tons of pesticides are produced and distributed worldwide each year. Environmental factors such as temperature, soil pH and moisture affect the behavior of persistent pollutants (POPs) in soil. One possible strategy is to mix the material with soil organic matter (SOM). A lot of xenobiotics and their broken down derivatives are commonly employed in humification because they resemble humic precursors. It was suggested that this resulting process could be used to reduce

environmental pollution in soil. Inorganic minerals interact well with exogenous substances and play an important role in the transformation of exogenous substances (Embrandiri *et al.* 2016).

### **Impact of exogenous chemicals in water**

Diffuse contribution and point contribution of urban industrial development, transportation, construction and other human activities such as residential pollution to urban surface water and groundwater. The presence of chemicals and signs of human activity in urban sewers has been the subject of many studies. Certain popular xenobiotic sensors need to be treated with municipal wastewater at sewage treatment plants before they may be released into waterways. Various types of metals, xenobiotics and synthetic products such as polycyclic aromatic hydrocarbons, phthalates and pesticides are also found in different waters. Foreign substances can enter water from many sources include air emissions; water runoff from roads and land; renewable products from industry, sewage and fossil fuel products; incineration waste. Additionally, xenobiotics enter the water table through leaching, which compromises the ecological stability of aquatic ecosystems. The presence of exogenous pollutants can cause oxidative stress in aquatic organisms (Dhakal *et al.* 2018). A recent study found increased oxidative stress in fish in an artificial lake in Eleyele, Nigeria. Another study shows that exogenous compounds alter the homeostasis of fish and cause oxidative stress by increasing the amount of reactive oxygen species and inhibiting antioxidant systems.

### **Effects of exogenous substances on plants**

Xenobiotics have a variety of effects on the physiological and morphological traits of plants. For example, particulate matter from the automotive industry alters the proteins, cysteine concentrations, photosynthetic pigments, leaf area, and foliar surface of plants. Various xenobiotics with different structure and composition can cause changes in gene expression, regulation and signaling in higher plants. Xenobiotics, such as phytohormone analogs, interact with phytohormone receptors and signaling pathways. Metals that are necessary for plant growth, such Cu, Zn, Fe, and Mo, are

harmful at high concentrations; however, non-necessary metals, including Pb, Cd, Hg, and As, are harmful even at low concentrations in plant growth. The effects are negative. Concentrations are lower during plant growth. Xenobiotics can damage plant DNA due to the production of reactive oxygen species and oxidative stress. Due to the toxicity of xenobiotics in plants, signaling pathways are affected by interfering with various signaling receptors (such as G protein-coupled receptors and receptor tyrosine kinases) (Embrandiri *et al.* 2016).

### **Effects of Xenobiotics on human health**

Xenobiotics pollute the environment and therefore their assimilation by existing animals has increased significantly in recent years. The introduction of these chemicals into ecosystems will cause allergic reactions, death of biological organisms, genetic changes, and decline of ecosystem processes. Humans are exposed to a variety of xenobiotics (both medical and non-essential xenobiotics) throughout their lives through ingestion, inhalation, dermal or other systemic exposure, which may pose risks to human health. Xenobiotics can alter the human gut microbiota and cause dysbiosis, which is directly associated with many diseases. The continuous process of biotransformation always attempts to balance the metabolic activity of xenobiotics with the elimination of their mutagenic metabolites as they are transformed into the environment and remove invading substances from the body. When this balance is disrupted, chronic diseases and DNA damage occur in the body. The toxicity of xenobiotics varies greatly between individuals. These oscillations are caused by the body's sensitivity and intraspecific variation. There are many things that are foreign to the human body. These drugs directly and indirectly cause problems and irritation in many organs and systems of the human body.

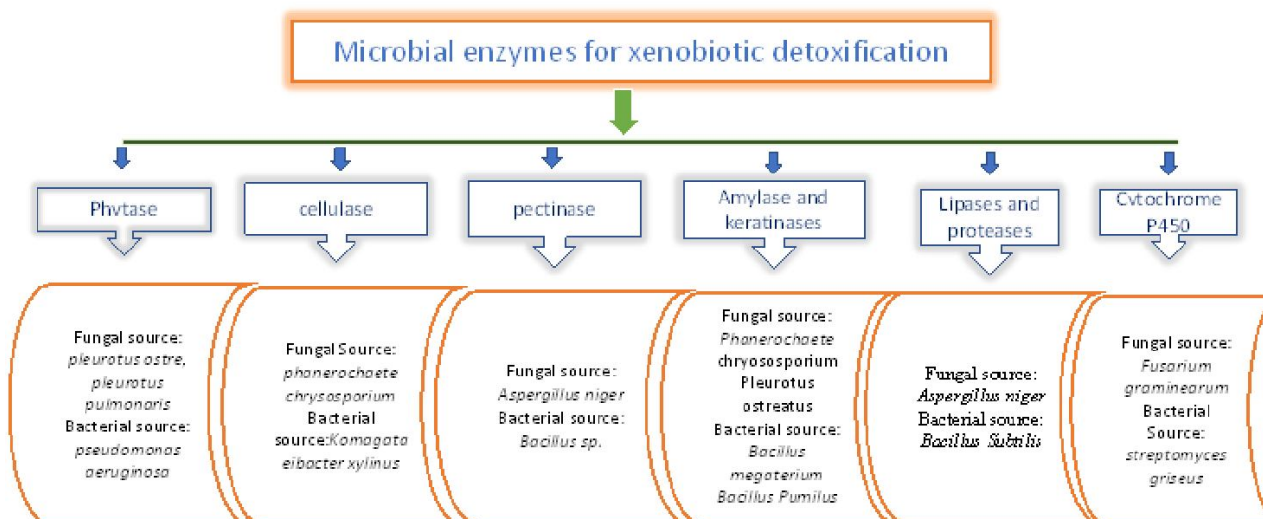
### **Xenobiotic degradative enzymes related to Bacteria**

Bacteria are known for their extraordinary ability to rapidly multiply, grow, and withstand harsh environments. Recent genome studies of

organisms that digest xenobiotics suggest that they evolved by incorporating genes that destroy xenobiotics. *Pseudomonas*, *Escherichia*, *Sphingobacterium*, *Pandora*, *Rhodococcus*, *Bacillus*, *Bacillus*, *Moraxella*, *Micrococcus* (aerobic bacteria), *Pelatomaculum*, *Desulfotomaculum*, *Syntropicobacter*, *Syntropus*, *Desulfovibrio*, *Methanopicilla* were isolated from soil and characterized for the biodegradation potential of xenobiotic compounds (DDT, lindane, PCB, TNT and crystal violet (Malla *et al.* 2018). The human gut microbiota has direct xenobiotic metabolic capacity, but also influences host metabolic gene expression and host enzyme activity (Miglani *et al.* 2022). Strain 1D of thermotolerant bacteria isolated from oil-contaminated soil at a refinery was identified as *Gordonia* species by the analysis of 16S rRNA and *gyrB* gene sequences. It was determined that aromatic compounds (xenobiotics) act as electron-free substrates in the absence of oxygen (anaerobic conditions), and bacteria grow by oxidizing substances in the presence of electron acceptors (Mishra and Srinivasan, 2001). The first step in enzymatic biodegradation is choosing an enzyme for a bioremediation application; this enzyme has to be able to break down the intended contaminants into less harmful compounds. Many types of bacteria can convert harmful foreign substances into toxic or non-toxic substances with the help of special enzymes contained within them. Due to structural changes at the molecular level in xenobiotic compounds, different enzymes are needed for the biodegradation of different hydrocarbon species. Degradation of aliphatic hydrocarbons occurs through mono-oxygenases (addition of oxygen molecule to the terminal methyl functionality) or di-oxygenases (addition of two oxygen atoms, resulting in peroxide formation and conversion to fatty acids). The oxidized fatty acid molecule forms intermediates in the TCA cycle, which subsequently metabolize to produce CO<sub>2</sub> and H<sub>2</sub>O. Aromatic hydrocarbons degrade slowly due to lack of solubility, formation of toxic metabolites, and metabolite inhibition. First, these compounds are converted to cis-dihydrodiols and degraded by dioxygenases via the ortho or meta-cleavage method. Cleavage of the aromatic ring then occurs between the hydroxyl group in the ortho cleavage pathway and the adjacent hydroxyl group

**Table 1:** Microorganisms and microbial communities using transcriptomic and meta transcriptomic approaches in biodegradation.

Microorganisms/ microbial communities	Isolation/ culture source	Xenobiotics/ pollutants	Comments/result
<i>Dehalococcoides mccartyi</i> (within trichloroethene-dechlorinating community)	Dechlorinated enrichment culture	Trichloro-ethane (TCE)	Transcriptomic approach identified genes encoding for rRNA, and reductive dehalogenases <i>tceA</i> and <i>vcrA</i> as the most expressed genes for TCE-dechlorinating community, while in <i>D. mccartyi</i> , hydrogenases <i>hup</i> and <i>vhu</i> were identified.
<i>Rhodococcus</i> sp. CS-1	Drinking-water treatment plant	Phenol	Transcriptomic analysis showed that <i>Rhodococcus</i> sp. CS-1 was capable of phenol degradation via ketoacid pathway.
<i>Rhodococcus erythropolis</i> D310-1	Activated-sludge sample	Chlorimuron-ethyl	RNA-seq results suggested that <i>cyt P450</i> carboxylesterase and glycosyltransferase genes are key genes expressing degradation of chlorimuron-ethyl.
<i>Burkholderia zhejiangensis</i> CEIB S4-3	Pesticide	Methyl parathion	Transcriptomic analysis of CEIB S4-3 strain showed transcriptional changes occurred in response to methyl parathion, and identified expressed genes related to its biodegradation.
<i>Sphingomonas haloaromaticamans</i> P3	Wastewater disposal site soil	Polyphenol	Transcriptomics analysis of strain P3 revealed expression patterns of catabolic genes of <i>ortho</i> -phenyl phenol degradation pathway
<i>Novos phingobium</i> sp. LH128	Contaminated soil	Phenanthrene	Transcriptomics analysis showed remarkably higher expression of phenanthrene degradation.

**Fig.1:** Microbial enzymes in xenobiotic management. The figure summarizes a few representative enzymes and their corresponding microbial sources involved in xenobiotic detoxification (Miglani *et al.* 2022).

in the Meta cleavage pathway, eventually forming the middle of the intermediate pathway (Miglani *et al.* 2022).

### Effects of xenobiotics on the Environment

Environmental pollution caused by xenobiotic is a worldwide problem resulting from human

activities such as urbanization and population growth. Many harmful compounds are released into the environment, causing pollution of the ecosystem. Soil, sediment, and water include notable materials such as pesticides, fertilizers, heavy metal ions, oil derivatives, and polycyclic aromatic hydrocarbons (PAHs). In a time of



change, science and technology has become the centre of human exploitation of resources, destroying many ecosystems (Liu *et al.* 2019). Unreasonable usage of pharmaceutical waste, human, and veterinary medications is another well-known source of environmental pollution. In contrast to other chemicals, medications may have an effect on aquatic life. However, it is thought that there is very little chance of acute environmental damage from medications. The situation may be different with long-term effects; However, evidence regarding its long-term effects and toxicity is insufficient. Additionally, although many aquatic organisms are exposed to toxicity throughout their lives, there is little or no evidence of effects across many generations of life (Bhandari *et al.* 2021). Major xenobiotics are harmful to the environment, plants, animals and humans.

## CONCLUSION

The omics approach is a good way to understand environmental toxicology and its remediation by using hybrid or combination methods to determine the various effects of xenobiotics and other pollutants on animals and plants, including various ecosystems. Advantages include a better understanding of catabolic genes, degradative enzymes, and other metabolic pathways. In soil/water ecosystems contaminated with xenobiotics, the microbial community appears to play an important role in the successful biodegradation process. Multi-molecular techniques have the capacity to perform in-depth analysis of microbial communities at all levels, from genes to molecules and from organisms to ecosystems. Many organisms with strong catabolic potential have been identified and described. Numerous enzymes, particularly those made by unculturable microorganisms, have been discovered due to the omics method. This new step led to the discovery of many organic biocatalysts suitable for commercial use. This review discusses several articles that used single isolated or mixed microbial organisms for the biotransformation of xenobiotics in diseased areas. Practical considerations must be made while evaluating resistant microbial technology, yet there is still debate on their field applicability. To achieve remarkable breakthroughs in

bioremediation, however, further research is needed to create innovative genetically engineered strains with strong catabolizing genes that can create ecosystems free of xenobiotics. Furthermore, to tackle xenobiotic contamination, careful consideration must be given to the combined strategy of green nanotechnology and microbe-mediated bioremediation.

## DECLARATIONS

Conflict of interest: Author declares no conflict of interest.

## REFERENCES

- Azubuiké, C.C., Chikere, C.B., Okpokwasili, G.C. 2016. Bioremediation techniques- classification based on site of application: Principle, advantages, limitations, and prospects. *World J. Microbiol. Biotechnol.* **32**:180.
- Baun, A., Sørensen, S.N., Rasmussen, R.F. 2012. Hartmann, N.B.; Koch, C.B. Toxicity and bioaccumulation of xenobiotic organic compounds in the presence of aqueous suspensions of aggregates of nano-C60. *Aquat. Toxicol.* **86**: 379–387.
- Bhandari, S., Poudel, D.K., Marahatha, R., Dawadi, S., Khadayat, K., Phuyal, S., Shrestha, S., Gaire, S., Basnet, K., Khadka, U. et al. 2021. Microbial Enzymes Used in Bioremediation. *J. Chem.* **8849512**: 1–17.
- Derby, A.P., Fuller, N.W., Huff Hartz, K.E., Segarra, A., Connon, R.E., Brander, S.M., Lydy, M.J. 2021. Trophic transfer, bioaccumulation and transcriptomic effects of permethrin in inland silversides, *Menidiaberyllina*, under future climate scenarios. *Environ. Pollut.* **275**: 116-5
- Dhakal, K., Gadupudi, G.S., Lehmler, H.J., Ludewig, G., Duffel, M.W., Robertson, L.W. 2018. Sources and toxicities of phenolic polychlorinated biphenyls (OH-PCBs). *Environ. Sci. Pollut. Res. Int.* **25**: 16277–16290.
- Elekwachi, O. 2014. Global use of bioremediation technologies for decontamination of ecosystems. *J. Bioremed. Biodegrad.* **5**: 1–30.
- Embrandiri, A., Kiyasudeen, S.K., Rupani, P.F., Ibrahim, M.H. 2016. Environmental xenobiotics and its effect on natural ecosystem. In *Plant Response to Xenobiotic* (Eds. A.Singh, S.M.Prasad, R.P.Singh) Springer: Singapore, pp. 1–18.
- Faroon, O., Ruiz, P. 2016. Polychlorinated biphenyls: New evidence from the last decade. *Toxicol. Ind. Health* **32**: 1825–1847.
- Fent, K., Weston, A.A., Caminada, D. 2006. Ecotoxicology of human pharmaceuticals. *Aquat. Toxicol.* **76**: 122–159.
- Fetzner, S. 2002. Biodegradation of xenobiotics. *Biotechnology*, **10**: 215-246.
- Godheja, J., Shekhar, S.K., Siddiqui, S.A., Modi, D.R. 2016. Xenobiotic compounds present in soil and water: A review on remediation strategies. *J. Environ. Anal. Toxicol.* **6**:21-61.
- Juliano, C., Magrini, G.A. 2017. Cosmetic ingredients as emerging pollutants of environmental and health concern. A Mini-Review. *Cosmetics* **4**: 11.
- Liu, L., Bilal, M., Duan, X.H., Iqbal, H.M.N., Iqbal, N. 2019. Mitigation of environmental pollution by genetically engineered bacteria- current challenges and future perspectives. *Sci. Total Environ.* **667**: 444–454.

- Malla, M.A., Dubey, A., Yadav, S., Kumar, A., Hashem, A., Abd-Allah, E.F. 2018. Understanding and designing the strategies for the microbe-mediated remediation of environmental contaminants using omics approaches. *Front. Microbiol.* **9**: 1132.
- Maurya, P.K. 2016. Bioaccumulation of xenobiotics compound of pesticides in riverine system and its control technique: A critical review. *J. Ind. Pollut. Control.* **32**: 580–594.
- Mishra, V., Lal, R., Srinivasan. 2001. Enzymes and operons mediating xenobiotic degradation in bacteria. *Critical reviews in microbiology*, **27**: 133-166.
- Mishra, S., Lin, Z., Pang, S., Zhang, W., Bhatt, P., Chen, S. 2021. Recent advanced technologies for the characterization of xenobiotic-degrading microorganisms and microbial communities. *Front. Bioengineering Biotechnol.* **9**: 632059.
- Moore, C.J. 2008. Synthetic polymers in the marine environment: A rapidly increasing, long-term threat. *Environ. Res.* **108**: 131–139.
- Miglani, R., Parveen, N., Kumar, A., Ansari, M. A., Khanna, S., Rawat, G., ... Ansari, M. N. 2022. Degradation of xenobiotic pollutants: an environmentally sustainable approach. *Metabolites*, **12**: 818.
- Perelo, L.W. 2010. *In situ* and Bioremediation of organic pollutants in aquatic sediments. *J. Hazard. Mater.* **177**: 81–89.
- Piers, M.D.F. and Joshi, M. 2005. The role of halocarbons in the climate change of the troposphere and stratosphere. *Clim. Chang.* **71**: 249–266.
- Priyanka, J.V., Rajalakshmi, S., Kumar, P.S., Krishnaswamy, V.G., Al Farraj, D.A., Elshikh, M.S., Gawwad, M.R.A. 2022. Bioremediation of soil contaminated with toxic mixed reactive azo dyes by co-cultured cells of *Enterobacter cloacae* and *Bacillus subtilis*. *Environ.Res.* **204**: 112–136.
- Sall, M.L., Diaw, A.K.D., Gningue-Sall, D., Efremova Aaron, S., Aaron, J.J. 2022. Toxic heavy metals: Impact on the environment and human health, and treatment with conducting organic polymers, a review. *Environ. Sci. Pollut. Res.* **27**: 29927–29942.
- Saraswat, S. 2014. Patent Analysis on Bioremediation of Environmental Pollutants. *J. Bioremed. Biodeg* **5**: 251.
- Sikandar, A., Shehzadi, K., Arshad, Q., Munir, K. 2013. Phytoremediation: An analytical technique for the assessment of biodegradation of organic xenobiotic pollutants: A review. *Int. J. Sci.* **4**:2250-2253
- Top, E. M., Springael, D. 2003. The role of mobile genetic elements in bacterial adaptation to xenobiotic organic compounds. *Curr. Opinion Biotechnol.* **14**: 262-269.
- Wang, X., Sial, M.U., Bashir, M.A., Bilal, M., Raza, Q.U.A., Ali Raza, H.M., Rehman, A., Geng, Y. 2022. Pesticides Xenobiotics in Soil Ecosystem and Their Remediation Approaches. *Sustainability* **14**:3353.
- Yadav, A. 2020. Potential impact of Polychlorinated biphenyls on plant and environmental health. *Int. J. Plant. Soil. Sci.* **32**:51-57
- Zhou, Y., Yao, L., Pan, L., Wang, H. 2022. Bioaccumulation and function analysis of glutathione S-transferase isoforms in *Manila clam (Ruditapes philippinarum)* exposed to different kinds of PAHs. *J. Environ. Sci.* **112**: 129–139.