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The Environmentally Sustainable Approach Of Xenobiotics Through The Utilisation Of Microbes And Their Byproduct: A Review

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Abstract

A xenobiotic is a synthetic foreign substance present in a living being that is not commonly created or exhibits within the body as chemical concoctions that are unfamiliar to the biosphere. Natural compounds can be converted intoxenobioticswhenthey are taken up by another life form. Xenobiotic would be made in a way that they would not be dismissed by the safe system.Due to continuous accumulation of recalcitrant xenobiotic compounds into the ecosystem released from various sources caused a serious global concern. Xenobiotics compounds are carcinogenic, mutagenic causing teratogenic effect and persist over a long period of time in the environment. Microorganisms exhibit promising capability to degrade xenobiotics compounds by their metabolic pathways. Specific catabolic genes are found in a microorganism which are helping in horizontal gene transfer facilitated the rapid microbial transformation of xenobiotic compounds. Molecularbiology-based techniques including DNA fingerprinting, microarrays and metagenomics are used for monitoring and identification of novel bacteria involved in this degradation process. This review provides an overview of microbial degradation process of xenobiotic compounds with the modern day technology.

Keywords: Biodegradation, Bioremediation, DNA, Enzymes, Metagenomics, Xenobiotics

1. Introduction

Chemically developed organic substances, the majority of which are not found in nature, are known as xenobiotics (Schlegel, 1986 and Steinberg, C. E. 2014). Compounds that are external factor to a live organism are referred to as xenobiotics. These substances build up in soil and water when they are not readily identified by the degradative enzymes currently in use (Esteve-NenezA*et al.*, 2001 and Mathew, B *et al*., 2017). Fungicides, insecticides, herbicides, nematicides, and so forth are examples of xenobiotics (Ashwath, P *et al*., 2023). The majority of which are phenyl carbonates, substituted hydrocarbons, and related substances.Some of these ingredients, which are applied in large amounts to soil and crops, are highly resistant and either degrade extremely slowly or not at all.Consequently, it would be highly desirable to find a novel catabolic pathway that would allow the contaminant to fully mineralize. Even though they are safe, synthetic fibres like polyethylene and polypropylene essentially never decompose. While the textiles' plastizers and softeners progressively oxidise, the polymer skeleton holds firm (Schlegel, 1986). Polyaromatic, chlorinated, and nitro-aromatic chemicals are among the xenobiotics that have been shown to be harmful, mutagenic, and carcinogenic to living things (Marghade, D. T *et al*., 2021).

However, of all living things, microbes are the finest candidates to introduce xenobiotic chemicals into natural biogeochemical cycles due to their diversity and adaptability to xenobiotics (Eyers, L *et al*., 2004). Certain xenobiotics have been demonstrated to be exceptionally resistant, despite the fact that more microbes are being identified as having the ability to break down these anthropogenic compounds (Esteve-Nunez *et al*., 2001). Finding new catabolic pathways that result in the mineralization of this pollutant would be more advantageous and provide a greater understanding of the variety of catabolic pathways involved in the breakdown of xenobiotics. It would also provide important information for bioremediation procedures because most earthly microorganisms cannot be isolated and grown on suitable conditions, they remain mostly uncharacterized.

Despite advancements in cultivation methods, scientific understanding of their natural growing conditions includes chemistry of the original environment, life in complex communities, obligate interactions with other organismsis yet insufficient to grow the majority of these microbes (Leadbetter, 2003 and Barton, L. L *et al*., 2011). Numerous molecular techniques that do not require cultivation have been created to investigate the variety of microbes in their natural habitat, whether or not they are cultivable (Bouchez, T*et al*., 2016).The majority of these

techniques (clone libraries, restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), denaturing gradient gel electrophoresis (DGGE, etc.) are based on PCR amplification and the subsequent sequencing and fingerprint analysis of bacterial rRNA genes. Our understanding of microbial diversity and the evolutionary tree of life has drastically changed as a result of the identification of numerous new bacterial lineages and their reassignment to the most ecologically significant group when employing these techniques (Castelle, C. J *et al.*, 2018).

2. Factors affecting xenobiotic degradation

They are so common, microorganisms can adapt to xenobiotic substances and use them as new growth and energy substrates.Synthetic organic compound pollution of the environment is now a problem for public health (Adeola, F. O *et al.*, 2020).Halogenated aromatics (such as benzenes, biphenyls, and anilines), halogenated aliphatic compounds, and a number of insecticides are among the several dangerous synthetic organic molecules that are slowly degradable that have been discovered (Spain JC, 1983; Leung, K. T *et al.*, 2019 and Miglani, R *et al.*, 2022). Many factors, including substrate type, microorganism species, and environmental conditions, may be responsible for the delayed biodegradation of these chemicals in their natural habitat (Figure1). These variables could include the presence of alternative nutrients, the accessibility of the substrates, predation, or unfavourable physiochemical conditions such as temperature, pH, redox potential, salinity, and oxygen concentration (Goldstein RM, 1985) (Table 1).

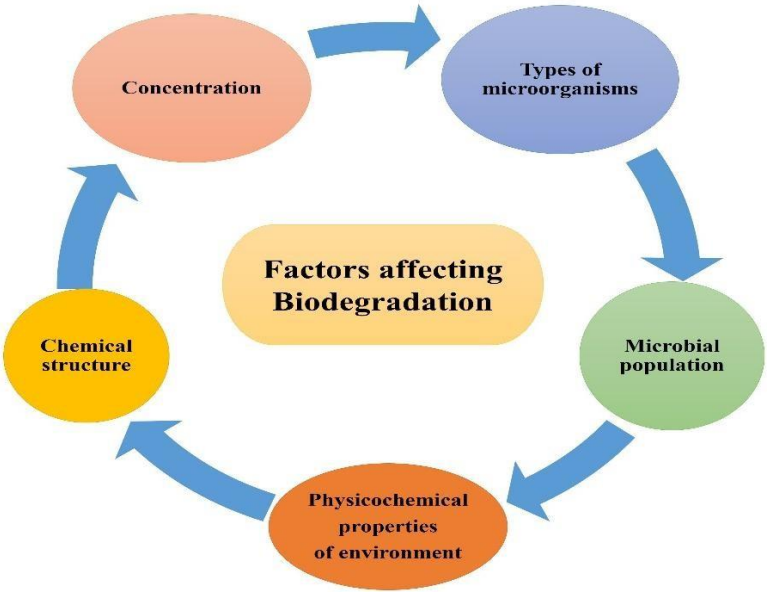

Figure 1: Factors affecting Biodegradation

In the absence of genetic information coding for the proper catabolic enzymes or proteins in the native microbiota, slow biodegradation of xenobiotics may also proceed. But after being exposed to unusual synthetic organic substances for an extended length of time, microbial populations frequently fully metabolise them (Reiger PG, 2002 and Ojo, O. A, 2007). Despite the fact that bacteria have been shown to acquire adaptive degradative capacities for specific organic compounds and to develop resistance to heavy metals over extended periods of acclimation in laboratory-simulated ecosystems (Pande, V *et al*., 2022).

	Substrate	**Microorganisam**	**Environment factors**
Factors affecting Biodegradation	Nature of pollutants	Population density	Temperature
	Physiochemical properties	Composition	pH
	Concentration	Intra/Inter specific interaction	Oxygen availability
	Biodegradability	Enzyme activity	Nutrient sources
	Toxicity	Turn over number	Salinity
	Chemical nature	Adaptation	
	Volatility		
	Polarity		

Table 1: Factors affecting Biodegradation

Acclimation to xenobiotics may be due toparticular enzymes being introduced into the microbial community, increasing the population's overall potential for degradation (Khan, A *et al*., 2019). Creation of a particular microbial community subpopulation that is capable of co-metabolizing with the main microbial population. Also, The selection of mutants that developed new metabolic activities or changed enzyme specificities but were absent when the community first encountered the foreign substances may also be the cause of adaptation (Barkay T, 1988).

This kind of selection process induction, growth, and mutation may be in charge of the adaptation seen in the mineralization of resistant foreign substances (Haigler*et al*., 1988). Evaluated of these genetic adaptation processes of xenobiotics, such as genetic recombination, transposition, mutational drift, and gene transfer, critically.These genetic tactics hasten the

bacterial catabolism pathway's evolutionary processes. Sequence data analysis revealed the diversification of microorganisms isolated from globally dispersed regions yet carrying xenobiotic catabolism genes (Haigler BE, 1988 and Timmis KN, 1999)suggested that the mineralization of resistant halogenated aromatics is caused by a genetically driven selection process (Haigler BE, 1988; Timmis KN, 1999;Nojiri, H *et al*., 2007;Nagata, Y *et al*., 2019 and Tourova, T*et al*., 2020).

3. Genes and degradation of aromatics

The recalcitrance of aromatic compounds with replacements makes them a unique class of xenobiotics. The natural environment does contain anaerobic mechanisms of biodegradation, however the aerobic processes of mineralization are more frequently described (Shweta, N*et al*., 2021 and Cabrera, M. Á*et al*., 2022). Several enzymes mediate the first biotransformation steps, which lead to the production of a restricted number of core intermediates such protocatechuates and substituted cathecols, according to a broad comparison of the main routes for the catabolism of aromatic compounds in bacteria (Reineke W, 1984, Díaz, E*et al*., 2001, Shweta, N *et al*., 2021 and Cabrera, M. Á *et al*., 2022). These intermediates that have undergone di-hydroxylation are directed towards a route known as "meta cleavage or ortho cleavage"Haigler BE, 1988.The breakdown of catechol and protocatechuate is mediated by the ortho cleavage pathways (Doten RC, 1987 ,Yadav, M*et al*., 2021). Furthermore, the enzymes responsible for the mineralization of chlorocathecols, or substituted catechols, are more appropriately referred to as the modified ortho cleavage pathway due to their broader substrate specificities.

S.No	Chemical compounds	Microorganisam
1	Hydrocarbons	*Pseudomonas, Nocardia, Arthrobacter, Mycobacterium*
2	PCBS	*Pseudomonas, Candida, Alcaligens*
3	Phenolics	*Pseudomonas, Flavobacterium, Trichosporum, Bacillus, Aspergillus*
4	Poly cyclic aromatic compounds	*Arthrobacter, Nocardia, Alcaligens*

Table 2: Microorganisam used in biodegradation process

This same mechanism has been identified in numerous different bacteria that metabolise chlorinated benzenes, including *Pseudomonas sp. Strain* B13 and

*Alcaligeneseutrophus*JMP134(Arora, P. K *et al*., 2014) (Table 2).The Modified ortho cleavage pathway genes for three bacteria species were extensively studied which includes (i) Theclc ABD operon of Pseudomonas putida (pAC27) (Ghosal D, 1989). (ii) The tfdCDEF operon of *A. eutrophus* JMP134 (Pjp4) (Don et al., 1985). (iii) The tcbCDEF operon of *Pseudomonas* sp. strain P51 (pP51 (Van der Meer JR, 1991) (Table 2). These and numerous other research' findings supported the notion that the genes for altered ortho cleavage pathways are typically found on catabolic plasmids, and that their arrangement into operon structures differs from that of the chromosomally encoded cat and pca genes (Guevara, G *et al*., 2019). The ortho cleavage pathway enzymes are encoded by the cat and pca genes, which are found on chromosomes (Kahlon, R. S *et al*., 1997).

4. Role of microbes in biodegradation

According to Gupta, A (2017), half of the biomass on our planet is made up of microbes. Because of human activities, the environment is disturbed and xenobiotic substances are introduced into the biosphere.Microorganisms may break down xenobiotics through their metabolic processes, which could be used as new carbon sources for the detoxification of harmful substances (Miglani, R *et al*., 2022). Microbes exhibit environmentally beneficial behaviour to combat pollution in the environment and aid in the biodegradation of xenobiotic substances (Kumar, M *et al*., 2017) (Table 2).

Microorganisms apply two modes of action for degradation of xenobiotics compound such as aerobic biodegradation and anaerobicbiodegradation. Since biofouling in subsurface remediation applications necessitates continual O2 supply (Sobti, R. C *et al*., 2022), aerobic biodegradation methods require excess O2 delivery systems. Additionally, the application of bioreactors results in significant energy expenditures and sludge formation (Zhang, M *et al*., 2020). Anaerobic bacteria are capable of effectively transforming or mineralizing a variety of xenobiotic compounds, such as tetrachloro ethylene, polychlorinated biphenyls (PCBs), and nitro-substituted aromatics, as well as anaerobic habitats such as sludge digesters, groundwater, sediments, water-laden soils, gastrointestinal contents, feedlot wastes, and landfill sites (Zhang, 2005, Agrawal, N *et al*., 2015) (Figure2).

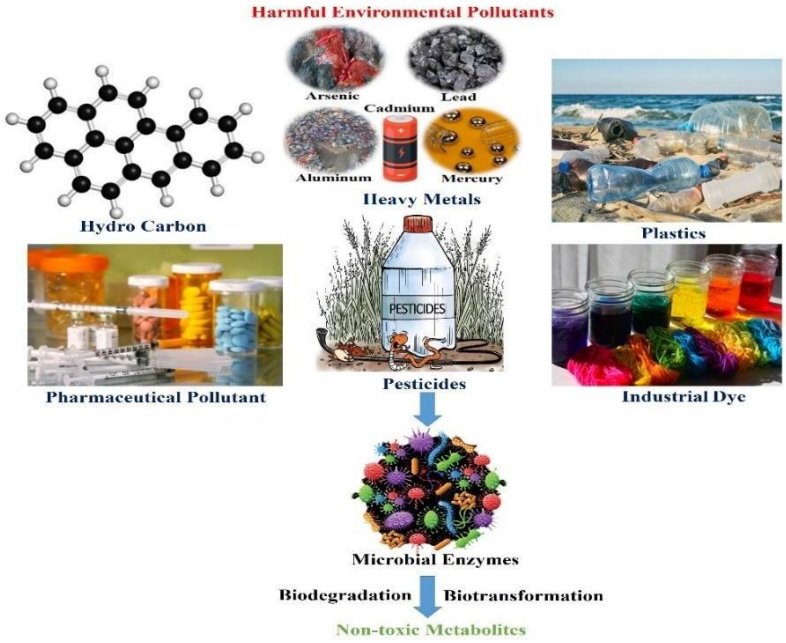

Figure2: Microbial enzymes in biodegradation of harmful environmental pollutants

In accordance with Chowdhury (2008) and Varsha (2011), the following are examples of anaerobic and aerobic xenobiotic degradative bacteria: *Pelatomaculum, Desulphovibrio, Methanospirillum, MethanosaetaDesulfotomaculum, Syntrophobacter*, and *Syntrophus.* Aerobic xenobiotic degradative bacteria include *Pseudomonas, Gordonia, Bacillus, Moraxella, Micrococcus, Escherichia, Sphingobium, Pandoraea,* and*Rhodococcus.*Since they are so good at breaking down a variety of polycyclic aromatic chemicals, including benzo pyrene and benzene, *Pseudomonas* species have been the subject of the most research (Cao, 2009). *Pseudomonas desmolyticum*NCIM 2112 has a remarkable capacity for xenobiotic chemical biodegradation (Rokade, 2013).

Microbes that employ xenobiotics as substrates thrive on and degrade them, which is particularly beneficial for bioremediation (Iyovo, 2010). A group of beneficial microorganisms that release organic acids and enzymes for the uptake and breakdown of xenobiotic substances is known as an effective microorganism (EM) (Monica, 2011). Microbes that are highly resistant to higher concentrations of xenobionts are gathered from contaminated locations such as residual sites, waste water, and distillery sludges (Narasimhulu, 2010). Tolerant bacteria can break down heavy metals and toxic organic pollutants that show tolerance to specific microorganisms (Tripathi, 2011). Activated sludges and aerated lagoons are the richest sources of microbiological resources and are utilised for the treatment of solid waste effluent (Priya, 2011).

The most effective usage of pseudomonas sp. is in the breakdown of xenobiotics, such as the aromatic and aliphatic hydrocarbons found in oils. *Pseudomonas* fluorescens SM1 strain is a viable option for remediation of some heavy metals and phenolics in extensively polluted environments (Wasi*et al*., 2011).*Brevibaccillusborstelensis* and *Rhodococcusruber* are said to be the degraders of polyethylenes, which are used to make plastics (Hadad, 2005).In an effort to better understand bacterial communities and their reactions to xenobiotic contaminants, scientists have isolated putative degraders and identified the genes involved in biodegradation processes (Greene, 2000).

Two major areas can be distinguished from a careful investigation of microbial diversity in an environment: research both independent of and depending on culture (Juck, 2000). Culture-independent methods can identify a broad variety of unknown pollutant-degrading microorganisms that may be present in contaminated environments (Margesin, R *et al*., 2003). The ability of microbial strains to proliferate in a given environment is necessary for conventional characterisation of the strains (Bakonyi, 2003). The last twenty years have seen the development of molecular technologies, such as 16S rRNA analysis, which have made studying wild microbial communities easier (Kubicek, 2003).

5. Biodegradation pathway of xenobiotics compound

Compounds in biodegradation processes can be either electron donors or electron acceptors, depending on the pollutant's level of oxidation. When bacteria breathe, oxygen serves as their primary electron acceptor.Numerous studies have been conducted on the aerobic decomposition of aromatic compounds; however, some polluted habitats, such as aquifers, aquatic sediments, and submerged soils, are frequently stressed and require alternate electron acceptors, such as nitrate, Fe (III), and sulphate (Chakraborty, 2004).

Biodegradation pathway

Aerobic degradation can break down several xenobiotics quickly and possibly, including petroleum hydrocarbons, chlorinated aliphatics, benzene, toluene, phenol, naphthalene, fluorine, and dichlorobenzenes. Several bacterial consortia that can thrive on these substances are generating enzymes that convert harmful substances into non-toxic ones. The two types of degradation process are listed in Table 3.

Aerobic biodegradation	Xenobiotic compound + $O_2 \rightarrow CO_2$ + H_2O + biomass + residue(s)	(Shimao, 2001)
Anaerobic biodegradation	Xenobiotic compound $\rightarrow CO_2$ + CH_4 + H_2O + biomass + residue(s)	(Jayasekara, 2005)

Table 3: Theaerobic and anaerobic degradation process

Carbon dioxide is created during the aerobic breakdown process. Anaerobic breakdown takes place in the absence of oxygen, producing methane rather than carbon dioxide (Adekunle, K et al., 2015). Mineralization is the process by which biodegradable materials are transformed into gases such as carbon dioxide, methane, and nitrogen molecules. When all of the carbon is transformed into carbon dioxide and all of the biodegradable biomass has been consumed, the mineralization process is finished (Kyrikou, 2007). Long carbon chains and straight structures in alkanes are thought to make them more susceptible to aerobic biodegradation. The process of alkane degradation through aerobic degradation involves oxidising the terminal methyl group into a carboxylic acid via an alcohol intermediate, which is followed by β-oxidation to complete mineralization (Cappelletti, M*et al*., 2019).

Aromatic compounds undergo aerobic breakdown by molecular oxygen oxidation, which results in intermediates. These intermediates subsequently enter major metabolic pathways, such as the Krebs cycle and β-oxidation (Phale, P. S *et al*., 2020). Microorganisms employ oxygen during aerobic respiration to hydroxylate the benzene ring, which causes the ring to fission later on. Mono- and di-oxygenase enzymes, which add one or two oxygen atoms to the ring, respectively, are the enzymes engaged in these activities (Philp, J. C *et al*., 2005 and Dyes, A, 2023).

6. Microbial enzymes involved in biodegradation

The enzymatic process of biodegradation, which is dependent on microorganisms, transforms contaminants into harmless byproducts (Table 4).

S.no	Enzyme	Role in bioremediation	Industrial use
1	**Oxygenases**	Increase the solubility of organic compounds in water, divide the structure of aromatic compounds, and carry out the dehalogenation reaction of polyhalogenated compounds to degrade them.	Biosensors, organic sytesis and biofuel
2	**Monooxygenases**	Degrade hydrocarbons such as aromatic	Involved in

		heterocyclic hydrocarbons, substituted methanes, alkanes, cycloalkanes, alkenes, and haloalkenes.	biodesulfurization, dehalogenation, denitrification, and hydroxylation of compounds
3	**Dioxygenases**	Degrade aromatic compounds into aliphatic products	
4	**Laccase**	Depolymerization of lignin to an array of phenols and degradation of bisphenol A	Cleaning agents for certain water purification system.
5	**Esterases**	To degrade man made pollutant includes plastics, polyurethane and polyesters	Used in cosmatics, paper, pulp, feed processing, detergent,synthesis of carbohydrate derivatives, food additives.
6	**Lipases**	To degrade cooking and pollutant water	Food industry, detergents, pharmaceuticals, leather, textiles, cosmetics and paper industries
7	**Cellulases**	Convert waste cellulosic material into food	Textile industry, paper and pulp industry and detergents factories.

Table 4: The microbial enzymes involved in biodegradation

Microbial Oxidoreductases

These enzymes break down chemical bonds to move electrons from a reduced organic substrate (donor) to an acceptor, which is a different chemical molecule. These oxidation-reduction processes convert pollutants into innocuous molecules (Karigar, 2011). By polymerizing, copolymerizing with other substrates, or binding to humic molecules, oxidoreductases detoxify harmful xenobiotics such as phenolic or anilinic chemicals (Park, 2006). Azole dyes have been decolorized and broken down using microbial enzymes (Husain, 2006). Microbial oxygenases are enzymes that belong to the oxidoreductase group (E.C. Class 1) of enzymes (Karigar, 2011). The primary enzymatic reaction of aerobic biodegradation is the oxidation reaction, which oxygenasescatalyse. By taking in oxygen from molecular oxygen (O2) and using FAD/NADH/NADPH as a co-substrate, oxygenasesoxidise their substrates. Organic substances are metabolised by oxygenases, which also split the aromatic ring, make them more

reactive, and make them soluble in water (Arora, 2009). Oxygenases can be further classified into two groups based on how many oxygen atoms are used for oxidation. First, monooxygenases 2. Dioxygenases.

Monooxygenases:

Monoxygenases allow an organic substance to absorb one molecular oxygen atom (Arora, 2009). Based on the existence of a cofactor, monooxygenases can be divided into two subclasses namely Flavin-dependent monooxygenases and P450 monooxygenases. The prosthetic group flavin and the coenzyme NADP or NADPH are found in flavin-dependent monooxygenases. Both eukaryotes and prokaryotes continue to produce P450 monooxygenases, which are oxygenases that include heme. Because of their strong region and stereo selectivity on a variety of substrates, monooxygenases function as biocatalysts in synthetic chemistry and bioremediation processes (Cirino, 2022). Numerous aromatic and aliphatic chemical processes, including desulfurization, dehalogenation, denitrification, ammonification, hydroxylation, biotransformation, and biodegradation, are catalysed by monooxygenases (Arora, 2009).

Dioxygenases:

The biodegradation phenomena can be divided into two categories based on the intricacy of the degradation pathways: Dioxygenases are multicomponent enzyme systems that add molecular oxygen to the convergent and divergent deterioration mode. Structurally diverse aromatic compounds are transformed into aromatic ring cleavage substrates, such as catechol, gentsate, protocatechuate, and their derivatives, in the convergent manner (Pandey A *et al*., 2023). One of the two potential pathways—the ortho-cleavage pathway or the meta-cleavage pathway—forms dihydroxylated intermediates when a metal-dependent dioxygenase channel is operating in divergent mode (Kumar v *et al*., 2017).

Extradiol and intradiol dioxygenases are two classes of intradiol dioxygenases (Harayama, 1989). In contrast to intradiol dioxygenases, which have nonheme iron (III) in their active site and catalyse ring cleavage at the C-C bond between the vicinal hydroxyl groups (ortho-cleavage), extradiol dioxygenases contain nonheme iron (II) in their active site and catalyse ring cleavage of the carbon-carbon (C-C) bond adjacent to the vicinal hydroxyl groups (meta-cleavage).

Microbial Dehalogenases:

According to Copley S. (1998), dehalogenase is crucial to the breakdown of chlorinated pollutants. By using halogenated substances as terminal electron acceptors, certain anaerobic microbes take use of dehalorespiration (Wohlfarth, 1997). The conversion of PCE (perchloroethylene) to either dichloroethylene (DCE) (Scholz-Muramatsu, 1995), ethylene, or ethane depending on the circumstances is an illustration of this process.Two reductive dehalogenases from Dehalococcoidesethenogenes strain 195 were partially purified and reported by Magnuson (1998); both enzymes are membrane proteins. PCE is reduced to TCE by the first enzyme, PCE-reductive dehalogenase, whereas vinyl chloride, trans-DCE, cis-DCE, and TCE are all reduced by the second enzyme, TCE-reductive dehalogenase.Phosphotriesterases, or PTEs, are microbially isolated enzymes that hydrolyze and remove phosphate-based pesticides (OPs) from the environment. This lessens the toxicity of OPs and their capacity to inactivate AchE (Ghanem, 2005). These enzymes mostly break down phosphoester bonds, such as P–O, P–F, P–NC, and P–S. One of the mechanisms involved in this hydrolysis is the presence of a water molecule in the phosphorus centre (Ortega-Gonzalez, D.K *et al*., 2013).

7. Catabolic gene organization involve in xenobiotic degradation.

A clustered organisation of genes is typically responsible for the reliable degradation of xenobiotics. These genes include those that encode catabolic enzymes, transport genes that encode proteins involved in the active uptake of compounds, and regulatory genes that control the expression of both catabolic and transport genes (Cao, B *et al.*, 2009). Widada (2002) states that two distinct methods can be used to examine the variety of catabolic genes in bacteria from environmental samples such as culture-dependent methods, and culture-independent methods.

Culture-dependent methods

Isolated bacterial cultures are used to harvest nucleic acid from environmental sources. More than 300 catabolic genes involved in the catabolism of aromatic chemicals have been identified and cloned from cultured bacteria. There are several methods, including shotgun cloning with indigo formation, clearing zone formation, meta-cleavage activity use as screening methods for cloning; applying proteomics (two dimensional gel electrophoresis analysis) of xenobioticinducible proteins to achieve genetic information, transposon mutagenesisto obtain a defective mutant, transposon mutagenesis using a transposon-fused reporter gene, applying a degenerate primer to generate a probe, and Using a brief homologous gene probe, it has been possible to identify the catabolic genes of different bacteria.

Culture-independent methods

Nucleic acid is directly extracted from environmental samples (Okuta, A *et al*., 1998). The amplification of DNA or cDNA from RNA isolated from environmental samples by PCR amplification using a degenerate primer set that is created by consensus or unique DNA sequence is required for the study of catabolic gene diversity utilising culture-independent molecular biological approaches. Cloning or gel electrophoresis are the methods used to separate the resulting PCR products (Watanabe, K *et al*., 2002). Whether the PCR-amplified gene is correct or not, the product must be sequenced in order to use the information that is produced to show the diversity of the associated gene.Khomenkov (2008) and Sinha (2009), states that plasmids function as mobile genetic elements and chromosomes as insertion elements, and that catabolic gene clusters encoded in both plasmids and chromosomes assist horizontal gene transfer.

8. Conclusion

Every year, the number of xenobiotic chemicals increases. These compounds have a significant effect on humans since neither the human body produces them nor does it incorporate them into regular meals. Instead, they resemble natural products that are perceived as natural by both humans and animals. As so, they are upsetting the latent generations as well as the environment as a whole. A major worldwide worry was raised as a result of the persistent buildup of resistant xenobiotic substances discharged from diverse sources into the ecosystem.Xenobiotics are substances that cause cancer, mutagenesis, teratogenic effects, and long-term environmental persistence. Microorganisms can break down xenobiotics through their metabolic processes. A microorganism has specific catabolic genes that aid in horizontal gene transfer and speed up the microbial transformation of xenobiotic substances. Metagenomics, DNA fingerprinting, and microarrays are examples of molecular biology-based approaches that are used to identify and track new microorganisms that are involved in the breakdown of xenobiotics.

9. References:

Adekunle, K. F., &Okolie, J. A. (2015). A review of biochemical process of anaerobic digestion. Advances in Bioscience and Biotechnology, 6(03), 205.

Adeola, F. O. (2020). Global impact of chemicals and toxic substances on human health and the environment. Handbook of Global Health, 1-30.

Agrawal, N., & Shahi, S. K. (2015). An environmental cleanup strategy-microbial transformation of xenobiotic compounds. International Journal of Current Microbiology and Applied Sciences, 4(4), 429-461.

Arora, P. K., & Bae, H. (2014). Bacterial degradation of chlorophenols and their derivatives. Microbial Cell Factories, 13, 1-17.

Arora, P. K., Kumar, M., Chauhan, A., Raghava, G. P., & Jain, R. K. (2009). OxDBase: a database of oxygenases involved in biodegradation. BMC research notes, 2, 1-8.

Ashwath, P., Manjunatha, K. G., Aksahy, S. D., Rao, R., Reddy, D., &Vittal, R. (2023). Pesticide and Xenobiotic Metabolism in Aquatic Organisms. In Xenobiotics in Aquatic Animals (pp. 1-66). Springer, Singapore.

Bakonyi, T., Derakhshifar, I., Grabensteiner, E., &Nowotny, N. (2003). Development and evaluation of PCR assays for the detection of Paenibacillus larvae in honey samples: comparison with isolation and biochemical characterization. Applied and Environmental Microbiology, 69(3), 1504-1510.

Barkay, T., & Pritchard, H. (1988). Adaptation of aquatic microbial communities to pollutant stress. Microbiological sciences, 5(6), 165-169.

Barton, L. L., & Northup, D. E. (2011). Microbial ecology. John Wiley & Sons.

Bouchez, T., Blieux, A. L., Dequiedt, S., Domaizon, I., Dufresne, A., Ferreira, S., ...&Ranjard, L. (2016). Molecular microbiology methods for environmental diagnosis. Environmental Chemistry Letters, 14, 423-441

Cabrera, M. Á., Márquez, S. L., & Pérez-Donoso, J. M. (2022). Comparative genomic analysis of Antarctic Pseudomonas isolates with 2, 4, 6-trinitrotoluene transformation capabilities reveals their unique features for xenobiotics degradation. Genes, 13(8), 1354.

Cao, B., Nagarajan, K., &Loh, K. C. (2009). Biodegradation of aromatic compounds: current status and opportunities for biomolecular approaches. Applied microbiology and biotechnology, 85, 207-228.

Cappelletti, M., Fedi, S., &Zannoni, D. (2019). Degradation of alkanes in Rhodococcus. Biology of Rhodococcus, 137-171.

Castelle, C. J., & Banfield, J. F. (2018). Major new microbial groups expand diversity and alter our understanding of the tree of life. Cell, 172(6), 1181-1197.

Chakraborty, R., & Coates, J. D. (2004). Anaerobic degradation of monoaromatic hydrocarbons. Applied microbiology and biotechnology, 64, 437-446.

Chowdhury, S., Mishra, M., Adarsh, V. K., Mukherjee, A., Thakur, A. R., & Chaudhuri, S. R. (2008). Novel metal accumulator and protease secretor microbes from East Calcutta Wetland. Am J BiochemBiotechnol, 4(3), 255-264.

Cirino, P. C., & Arnold, F. H. (2002). Protein engineering of oxygenases for biocatalysis. Current Opinion in Chemical Biology, 6(2), 130-135.

Copley, S. D. (1998). Microbial dehalogenases: enzymes recruited to convert xenobiotic substrates. Current opinion in chemical biology, 2(5), 613-617.

Don, R. H., Weightman, A. J., Knackmuss, H. J., &Timmis, K. N. (1985). Transposon mutagenesis and cloning analysis of the pathways for degradation of 2, 4-dichlorophenoxyacetic acid and 3-chlorobenzoate in Alcaligeneseutrophus JMP134 (pJP4). Journal of Bacteriology, 161(1), 85-90.

Doten, R. C., Ngai, K. L., Mitchell, D. J., &Ornston, L. N. (1987). Cloning and genetic organization of the pca gene cluster from Acinetobacter calcoaceticus. Journal of bacteriology, 169(7), 3168-3174.

Dyes, A. (2023). Microbial degradation of pollutants. Environmental Microbiology, Springer, Germany, 161-285.

Esteve-Núñez, A., Caballero, A., & Ramos, J. L. (2001). Biological degradation of 2, 4, 6-trinitrotoluene. Microbiology and molecular biology reviews, 65(3), 335-352.

Eyers, L., George, I., Schuler, L., Stenuit, B., Agathos, S. N., & El Fantroussi, S. (2004). Environmental genomics: exploring the unmined richness of microbes to degrade xenobiotics. Applied microbiology and biotechnology, 66, 123-130.

Ghanem, E., &Raushel, F. M. (2005). Detoxification of organophosphate nerve agents by bacterial phosphotriesterase. Toxicology and applied pharmacology, 207(2), 459-470.

Ghosal, D., & In-Soon, Y. (1989). Operon structure and nucleotide homology of the chlorocatechol oxidation genes of plasmids pJP4 and pAC27. Gene, 83(2), 225-232.

Goldstein, R. M., Mallory, L. M., & Alexander, M. (1985). Reasons for possible failure of inoculation to enhance biodegradation. Applied and environmental microbiology, 50(4), 977-983.

Greene, E. A., Kay, J. G., Jaber, K., Stehmeier, L. G., &Voordouw, G. (2000). Composition of soil microbial communities enriched on a mixture of aromatic hydrocarbons. Applied and Environmental Microbiology, 66(12), 5282-5289.

Guevara, G., Castillo Lopez, M., Alonso, S., Perera, J., & Navarro-Llorens, J. M. (2019). New insights into the genome of Rhodococcusruber strain Chol-4. BMC genomics, 20, 1-17.

Gupta, A., Gupta, R., & Singh, R. L. (2017). Microbes and environment. Principles and applications of environmental biotechnology for a sustainable future, 43-84.

Hadad, D., Geresh, S., & Sivan, A. (2005). Biodegradation of polyethylene by the thermophilic bacterium Brevibacillusborstelensis. Journal of applied microbiology, 98(5), 1093-1100.

Haigler, B. E., Nishino, S. F., & Spain, J. (1988). Degradation of 1, 2-dichlorobenzene by a Pseudomonas sp. Applied and Environmental Microbiology, 54(2), 294-301.

Harayama, S., & Rekik, M. (1989). Bacterial aromatic ring-cleavage enzymes are classified into two different gene families. Journal of Biological Chemistry, 264(26), 15328-15333.

Husain, Q. (2006). Potential applications of the oxidoreductive enzymes in the decolorization and detoxification of textile and other synthetic dyes from polluted water: a review. Critical reviews in biotechnology, 26(4), 201-221.

Iyovo, G. D., Du, G., & Chen, J. (2010). Sustainable bioenergy bioprocessing: biomethane production, digestate as biofertilizer and as supplemental feed in algae cultivation to promote algae biofuel commercialization. J MicrobBiochem Technol, 2(4), 100-106.

Jayasekara, R., Harding, I., Bowater, I., & Lonergan, G. (2005). Biodegradability of a selected range of polymers and polymer blends and standard methods for assessment of biodegradation. Journal of Polymers and the Environment, 13, 231-251.

Juck, D., Charles, T., Whyte, L. G., & Greer, C. W. (2000). Polyphasic microbial community analysis of petroleum hydrocarbon-contaminated soils from two northern Canadian communities. FEMS microbiology ecology, 33(3), 241-249.

Kahlon, R. S., Johl, P. P., & Singh, G. (1997). Protection of Environment: Microbial Degradation of Chemical Pollutants. Recent Advances in Ecobiological Research, 2, 71.

Karigar, C. S., & Rao, S. S. (2011). Role of microbial enzymes in the bioremediation of pollutants: a review. Enzyme research, 2011.

Khan, A., & Rao, T. S. (2019). Molecular evolution of xenobiotic degrading genes and mobile DNA elements in soil bacteria. In Microbial diversity in the genomic era (pp. 657-678). Academic Press.

Khomenkov, V. G., Shevelev, A. B., Zhukov, V. G., Zagustina, N. A., Bezborodov, A. M., & Popov, V. O. (2008). Organization of metabolic pathways and molecular-genetic mechanisms of xenobiotic degradation in microorganisms: A review. Applied Biochemistry and Microbiology, 44, 117-135.

Kubicek, C. P., Bissett, J., Druzhinina, I., Kullnig-Gradinger, C., &Szakacs, G. (2003). Genetic and metabolic diversity of Trichoderma: a case study on South-East Asian isolates. Fungal genetics and biology, 38(3), 310-319.

Kumar, M., Prasad, R., Goyal, P., Teotia, P., Tuteja, N., Varma, A., & Kumar, V. (2017). Environmental biodegradation of xenobiotics: role of potential microflora. Xenobiotics in the soil environment: monitoring, toxicity and management, 319-334.

Kyrikou, I., &Briassoulis, D. (2007). Biodegradation of agricultural plastic films: a critical review. Journal of Polymers and the Environment, 15, 125-150.

Leadbetter, J. R. (2003). Cultivation of recalcitrant microbes: cells are alive, well and revealing their secrets in the 21st century laboratory. Current opinion in microbiology, 6(3), 274-281.

Leung, K. T., Jiang, Z. H., Almzene, N., Nandakumar, K., Sreekumari, K., &Trevors, J. T. (2019). Biodegradation and bioremediation of organic pollutants in soil. Modern Soil Microbiology, Third Edition, 381-402.

Magnuson, J. K., Stern, R. V., Gossett, J. M., Zinder, S. H., & Burris, D. R. (1998). Reductive dechlorination of tetrachloroethene to ethene by a two-component enzyme pathway. Applied and Environmental Microbiology, 64(4), 1270-1275.

Margesin, R., Labbe, D., Schinner, F., Greer, C. W., & Whyte, L. G. (2003). Characterization of hydrocarbon-degrading microbial populations in contaminated and pristine alpine soils. Applied and environmental microbiology, 69(6), 3085-3092.

Marghade, D. T., Chahande, A. D., Tiwari, M. S., & Patil, P. D. (2021). Microbial degradation of xenobiotic compounds. Recent Advances in Microbial Degradation, 173-217.

Mathew, B. B., Singh, H., Biju, V. G., & Krishnamurthy, N. B. (2017). Classification, source, and effect of environmental pollutants and their biodegradation. Journal of Environmental Pathology, Toxicology and Oncology, 36(1).

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(9), 818.

Monica, S., Karthik, L., Mythili, S., &Sathiavelu, A. (2011). Formulation of effective microbial consortia and its application for sewage treatment. J Microbial Biochem Technol, 3, 051-055.

Nagata, Y., Kato, H., Ohtsubo, Y., & Tsuda, M. (2019). Mobile genetic elements involved in the evolution of bacteria that degrade recalcitrant xenobiotic compounds. DNA Traffic in the Environment, 215-244.

Narasimhulu, K. R. (2010). Isolation and Identification of Bacterial Strains and Study of their Resistance to Heavy Metals and Antibiotics. Journal of Microbial and Biochemical Technology, 2: 74-76.

Nojiri, H., Shintani, M., & Omori, T. (2004). Divergence of mobile genetic elements involved in the distribution of xenobiotic-catabolic capacity. Applied microbiology and biotechnology, 64, 154-174.

Ojo, O. A. (2007). Molecular strategies of microbial adaptation to xenobiotics in natural environment. Biotechnol Mol Biol Rev, 2(1), 001-013.

Okuta, A., Ohnishi, K., &Harayama, S. (1998). PCR isolation of catechol 2, 3-dioxygenase gene fragments from environmental samples and their assembly into functional genes. Gene, 212(2), 221-228.

Ortega-González, D. K., Zaragoza, D., Aguirre-Garrido, J., Ramírez-Saad, H., Hernández-Rodríguez, C., & Jan-Roblero, J. (2013). Degradation of benzene, toluene, and xylene isomers by a bacterial consortium obtained from rhizosphere soil of Cyperus sp. grown in a petroleum-contaminated area. Folia Microbiologica, 58, 569-577.

Pande, V., Pandey, S. C., Sati, D., Bhatt, P., &Samant, M. (2022). Microbial interventions in bioremediation of heavy metal contaminants in agroecosystem. Frontiers in microbiology, 13, 824084.

Pandey, A., Kumar, S., Kumar, S., Rajput, M., Singh, M., Pandey, C., & Bhardwaj, N. (2023). Role of microbial enzymes in bioremediation: Emerging opportunities and limitations. In Microbial Inoculants (pp. 277-300). Academic Press.

Park, J. W., Park, B. K., & Kim, J. E. (2006). Remediation of soil contaminated with 2, 4-dichlorophenol by treatment of minced shepherd's purse roots. Archives of environmental contamination and toxicology, 50, 191-195.

Phale, P. S., Malhotra, H., & Shah, B. A. (2020). Degradation strategies and associated regulatory mechanisms/features for aromatic compound metabolism in bacteria. Advances in Applied Microbiology, 112, 1-65.

Philp, J. C., Bamforth, S. M., Singleton, I., & Atlas, R. M. (2005). Environmental pollution and restoration: a role for bioremediation. Bioremediation: Applied Microbial Solutions for Real- World Environmental Cleanup, 1-48.

Priya, P. G., Ramamurthi, V., & Anand, P. (2011). Degradation studies of tannery effluents using electro flotation technique. J. of Chemical Engineering & Process Technology, 2(1), 1-4.

Rieger, P. G., Meier, H. M., Gerle, M., Vogt, U., Groth, T., &Knackmuss, H. J. (2002). Xenobiotics in the environment: present and future strategies to obviate the problem of biological persistence. Journal of Biotechnology, 94(1), 101-123.

Rokade, K. B., & Mali, G. V. (2013). Biodegradation of chlorpyrifos by Pseudomonas desmolyticum NCIM 2112. Int J Pharm Bio Sci, 4(2), 609-616.

Schlegel, H. G. (1986). Xenobiotics In. General Microbiology, 433.

Scholz-Muramatsu, H., Neumann, A., Meßmer, M., Moore, E., &Diekert, G. (1995). Isolation and characterization of Dehalospirillummultivorans gen. nov., sp. nov., a tetrachloroethene-utilizing, strictly anaerobic bacterium. Archives of Microbiology, 163, 48-56.

Shimao, M. (2001). Biodegradation of plastics. Current opinion in biotechnology, 12(3), 242-247.

Shweta, N., Samatha, S., &Keshavkant, S. (2021). An innovative approach to degrade xenobiotics through microbial system. In Microbial Ecology of Wastewater Treatment Plants (pp. 73-100). Elsevier.

Sinha, S., Chattopadhyay, P., Pan, I., Chatterjee, S., Chanda, P., Bandyopadhyay, D., ...& Sen, S. K. (2009). Microbial transformation of xenobiotics for environmental bioremediation. African Journal of Biotechnology, 8(22).

Sobti, R. C., Sharma, A., &Soni, S. K. (2022). Applications of Biotechnological Techniques in Mitigating Environmental Concerns. In Genomic, Proteomics, and Biotechnology (pp. 249-312). CRC Press.

Spain, J. C., & Van Veld, P. A. (1983). Adaptation of natural microbial communities to degradation of xenobiotic compounds: Effects of concentration, exposure time, inoculum, and chemical structure. Applied and Environmental Microbiology, 45(2), 428-435.

Steinberg, C. E. (2014). NOM as natural xenobiotics. In Advances in the Physicochemical Characterization of Dissolved Organic Matter: Impact on Natural and Engineered Systems (pp. 115-144). American Chemical Society.

Timmis, K. N., & Pieper, D. H. (1999). Bacteria designed for bioremediation. Trends in biotechnology, 17(5), 201-204.

Tourova, T., Sokolova, D., Nazina, T., Grouzdev, D., Kurshev, E., & Laptev, A. (2020). Biodiversity of microorganisms colonizing the surface of polystyrene samples exposed to different aqueous environments. Sustainability, 12(9), 3624.

Tripathi, B. D. (2011). A Short Term Study on Toxic Effects of Distillery Sludge Amendment on Microbiological and Enzymatic Properties of Agricultural Soil in a Tropical City. Journal of Earth Science & Climatic Change, 2(1).

Van der Meer JR, E. R. (1991). Sequence analysis of Pseudomonas sp. Strain P51 tcb gene cluster, which encodes metabolism of chlorinated catecols: evidence for specialization of catecol 1, 2-dioxygenases for chlorinated subst. J. Bacteriol., 173: 2425-2434.

Varsha, Y. M., Naga Deepthi, C. H., &Chenna, S. (2011). An emphasis on xenobiotic degradation in environmental cleanup. J BioremedBiodegrad S, 11(001).

Wasi, S., Tabrez, S., & Ahmad, M. (2011). Suitability of immobilized Pseudomonas fluorescens SM1 strain for remediation of phenols, heavy metals, and pesticides from water. Water, Air, & Soil Pollution, 220, 89-99.

Watanabe, K., Futamata, H., &Harayama, S. (2002). Understanding the diversity in catabolic potential of microorganisms for the development of bioremediation strategies. Antonie Van Leeuwenhoek, 81, 655-663.

Widada, J., Nojiri, H., & Omori, T. (2002). Recent developments in molecular techniques for identification and monitoring of xenobiotic-degrading bacteria and their catabolic genes in bioremediation. Applied Microbiology and Biotechnology, 60, 45-59.

Wohlfarth, G., &Diekert, G. (1997). Anaerobic dehalogenases. Current opinion in biotechnology, 8(3), 290-295.

Yadav, M., Lomash, A., Kapoor, S., Pandey, R., & Chauhan, N. S. (2021). Mapping of the benzoate metabolism by human gut microbiome indicates food-derived metagenome evolution. Scientific reports, 11(1), 5561.

Zhang, C., & Bennett, G. N. (2005). Biodegradation of xenobiotics by anaerobic bacteria. Applied Microbiology and Biotechnology, 67, 600-618.

Zhang, M., Lee, E., Vonghia, E., Hong, Y., & Liao, B. (2020). Introduction to aerobic membrane bioreactors: Current status and recent developments. Current Developments in Biotechnology and Bioengineering, 1-23.