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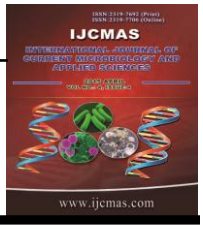

Review Article

An Environmental Cleanup Strategy - Microbial Transformation of Xenobiotic Compounds

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A B S T R A C T

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. Microorganism exhibit capability to degrade xenobiotics 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. Molecular-biology-based techniques including DNA fingerprinting, microarrays and metagenomics are used for monitoring and identification of novel bacteria involved in degradation of xenobiotics. These reviews provide an overview of microbial degradation process and catabolic genes, molecular techniques to study the microbial transformation of xenobiotic compounds in modern day technology.

Introduction

The progress in science, technology and industries a huge amount of anthropogenic compounds ranging from raw sewage to nuclear wastes is released into the environment. These anthropogenic compounds are xenobiotic compounds which are toxic to living organisms and cause a global concern. Xenobiotic compounds are relatively persisting in the environment because they are highly thermodynamically stable. Xenobiotic compounds can have various toxic effects on humans; they exhibit acute carcinogenic, mutagenic, and teratogenic effects. The overall damage in ecosystem caused by xenobiotic compounds has motivated researchers to develop new strategies for their removal from the contaminated environment. The application of microbial technology for the biodegradation of xenobiotics from biosphere has received much attention.

Xenobiotics are those chemical compounds that are foreign to a living organism. Human activity creates a lot of recalcitrant xenobiotic compounds. According to Sinha et al. (2009) principal xenobiotics include alkanes, polycyclic aromatic hydrocarbons

(PAHs), antibiotics, synthetic azo dyes, pesticides, fuels, solvents, pollutants (dioxins and polychlorinated biphenyls), polyaromatic, chlorinated and nitro-aromatic compounds. The xenobiotic creates a deleterious effect on the public health. Xenobiotic compounds e.g. biphenyl compounds, phenols and phthalates work as endocrine disruptors (Nagao, 1998; Borgeest *et al.,* 2002). Lindane (HCH) is a neurotoxin that interferes with the GABA neurotransmittor function affects the nervous system, liver and kidneys. The overall damage these contaminants have motivated scientists to develop strategies for their sequestration and removal from the bio-spheres (Saleem *et al.,* 2008).

Biodegradation is a microorganism mediated transformation of contaminants into non-hazardous or less-hazardous substances (Karigar and Rao, 2011). Microorganisms are nature's recyclers, converting toxic organic compounds to innocuous compounds, often carbon dioxide and water (Jain *et al.,* 2005). Vidali (2001) and Leung (2004) reported the appropriate use of various organisms like bacteria, fungi and algae for efficient bioremediation of pollutants. According to Tropel and Meer (2004) most organisms, particularly bacteria are known for detoxifying abilities. They mineralize, transform or immobilize the pollutants. Bacteria play a crucial role in biogeochemical cycles for sustainable development of the biosphere.

The enormous genetic diversity of microorganisms, their metabolic plasticity and high reproduction rates, the capacity for horizontal gene transfer, ensure the development and adaptation of microorganisms to rapidly changing conditions of the environment (Timmis and Pieper, 1999; Diaz and Prieto, 2000; Kim and Crowley, 2007; Khomenkov *et al.,* 2008). As reported by Ellis (2003) and Tropel and Meer (2004) recent researches are being updated in Biocatalysis/Biodegradation Database, these include metabolic pathways of many different microorganisms. Bioremediation can be effective only when environmental conditions permit microbial growth and activity. Bioremediation involves the manipulation of environmental parameters (pH, temperature, moisture and oxygen) to allow microbial growth and degradation procedure at a faster rate (Karigar and Rao, 2011). The development of recombinant Genetically Modified Organisms (GMOs) is very significant for the bioremediation of complex waste; through this we can identify the gene responsible for specific compound degradation.

The purpose of this review paper is to analysis a brief summary of the physiological, genetical and the molecular approaches for microbial biodegradation of certain xenobiotic compounds.

Role of microbes in biodegradation

According to Curtis and Reinhard (1994) microorganisms represent half of the biomass of our planet. Human activity disturbs the environment; they introduce xenobiotic chemicals in the biosphere. Microorganism exhibit capability to degrade xenobiotics by their metabolic pathways in consideration of exploiting as new carbon sources to detoxify toxic compounds (Copley, 2000). Microbes show ecofriendly behavior to overcome environmental pollution and to help in biodegradation of xenobiotic compounds. Microorganisms apply two modes of action for degradation of xenobiotics compound - 1. Aerobic biodegradation; 2. Anaerobic biodegradation. Aerobic biodegradation processes require excess O_2 delivery

systems, because it is necessary to supply continuous O_2 due to biofouling in subsurface remedial applications (Baker and Herson, 1994), when bioreactors are applied its energy costs and sludge production are high (McCarty and Smith, 1986; Jewell, 1987). Anaerobic habitats, including sludge digesters, groundwater, sediments, water-laden soils, gastrointestinal contents, feedlot wastes and landfill sites (Williams, 1977) and some xenobiotic compounds (e.g., tetrachloroethylene, polychlorinated biphenyls (PCBs), and nitro-substituted aromatics) can be effectively transformed or mineralized by anaerobic bacteria (Zhang and Bennett, 2005). According to Chowdhury *et al.* (2008) and Varsha *et al.* (2011) example of aerobic degradative bacteria of xenobiotics are *Pseudomonas, Gordonia, Bacillus, Moraxella, Micrococcus, Escherichia, Sphingobium, Pandoraea, Rhodococcus*,and anaerobic xenobiotics degradative bacteria are *Pelatomaculum, Desulphovibrio, Methanospirillum, Methanosaeta Desulfotomaculum, Syntrophobacter, Syntrophus*. Among them, *Pseudomonas* species have been the most widely studied due to their dominant performance in degrading a wide range of poly cyclic aromatic compounds from benzene to benzo (pyrene) (Cao *et al.,* 2009). Overney (1979) isolated a *Flavobacterium* that was able to grow aerobically with the simple model compound 4, 4-dicarboxyazobenzene. *Pseudomonas desmolyticum* NCIM 2112 exhibit a tremendous capability of biodegradation of xenobiotic compound (Rokde and Mali, 2013). Many other bacterial species which assist in degradation of recalcitrant xenobiotic compounds are listed in Table 1. Microbes apply xenobiotics as their substrates and grow on them, degrading or fragmenting them, which is highly beneficial in case of bioremediation (Iyovo *et al.*, 2010; Surani *et al.,* 2011; Varsha *et al.,* 2011). Effective Microorganism (EM) is the consortia of valuable microorganisms which secretes organic acids and enzymes for utilization and degradation of xenobiotic compounds (Monica *et al.,* 2011). Microbes are collected from the contaminated sites like waste water, residual sites and distillery sludges; they are excessively resistance to higher concentrations of xenobionts (Narasimhulu *et al.,* 2010). Some of toxic organic pollutants and Heavy metals which show resistance to some of the microbes can be degraded using tolerant microbes (Tripathi, 2011). For the removal of solid waste effluent activated sludges and aerated lagoons are used they are the richest source of microbial consortium (Priya *et al.,* 2011). *Pseudomonas* sp. is most efficiently useful in the degradation of xenobiotics such as aromatic and aliphatic hydrocarbon of oils. Wasi *et al.* (2010) reported *Pseudomonas fluorescens* SM1 strain is a good candidate for remediation of some heavy metals and phenolics in heavily polluted sites. According to Hadad *et al.* (2005) plastics are manufactured by polyethylenes are degraded by *Brevibaccillus borstelensis* and *Rhodococcus ruber*. The scientist has been made an attempt to characterize bacterial communities and their responses to xenobiotic pollutants, to isolate potential degraders and to identify the genes involved in biodegradation processes (Greene *et al.,* 2000; Watanabe *et al.,* 2002). The detailed analysis of microbial diversity, in an environment can be divided into two broad categories: culture-dependent studies and culture independent studies (Juck *et al.,* 2000). A wide range of unidentified pollutant-degrading microorganisms can identified by culture independent techniques that can be harbored in contaminated environments (Margesin *et al.,* 2003). Conventional characterization of microbial strains is dependent on the ability of the

strains to grow under specific environmental conditions (Bakonyi *et al.,* 2003). In the past two decades, molecular tools exemplified by 16S rRNA analyses have facilitated the study of natural microbial populations (Kubicek *et al.,* 2003). An advance in genetic engineering and applying new strategies like mutagenesis and screening is a great opportunity to develop potentially degradative xenobiotics. This guideline helps in the development of a new field of metabolic engineering, using recombinant DNA technology; cellular activities of microbes can be modified. We can also manipulate enzymatic, transport and regulatory functions of the cell. In the past decade metabolic engineering has emerged as an interdisciplinary field its aim to improve cellular properties by using modern genetic engineering tools to modify metabolic pathways (Nielsen *et al.,* 2001). Metabolic pathway and cellular function of microbes can be analyzed by a very powerful analytical techniques like gas chromatography, gas chromatography–mass spectrometry (GC–MS), nuclear magnetic resonance (NMR), two-dimensional gel electrophoresis, matrix-assisted laser desorption ionization-time of flight (MALDI-TOF), liquid chromatography-mass spectrometry (LC-MS) and DNA chips (Jain *et al.,* 2005).

Biodegradation pathway of xenobiotics compound

In biodegradation processes, depending on the oxidation state of the pollutant, compounds can be either electron donors or electron acceptors. In the bacterial respiration, oxygen is the most common electron acceptor. In aerobic biodegradation of aromatic compounds, oxygen plays an important dual role: (1) act as an electron acceptor for the aromatic pollutants and (2) with the help of oxygenation reactions activate the substrate. The aerobic degradation of aromatic compounds has been widely studied; some polluted environments are often anoxious such as aquifers, aquatic sediments, and submerged soils, requiring alternative electron acceptors such as nitrate, Fe (III), and sulfate (Chakraborty and Coates, 2004; Wilson and Bouwer, 1997; Bouwer and Zehnder, 1993; Cao *et al.,* 2009).

Aerobic biodegradation pathway

Some of the xenobiotics like petroleum hydrocarbons, chlorinated aliphatics, benzene, toluene, phenol, naphthalene, fluorine, pyrene, chloroanilines, pentachlorophenol and dichlorobenzenes are rapidly and potentially degraded by the aerobic degradation process. Many bacterial consortia capable to grow on these chemicals they are producing enzymes which degrade toxic compounds to non-toxic compounds. The degradation process can be divided into (1) aerobic and (2) anaerobic degradation

Aerobic biodegradation:

Xenobiotic compound + O_2 $\longrightarrow$ CO_2 + H_2O + biomass + residue(s) Shimao (2001)

Anaerobic biodegradation:

Xenobiotic compound $\longrightarrow$ CO_2 + CH_4 + H_2O + biomass + residue(s) Jayasekara *et al.* (2005)

In the process of aerobic degradation, carbon dioxide is produced. If there is no oxygen, an anaerobic degradation process occurs and methane is produced instead of carbon dioxide (Swift, 1998; Grima *et al.,* 2002; Kyrikou *et al.,* 2007). The conversion of biodegradable materials to gases like carbon dioxide, methane, and nitrogen

compounds, this process is called mineralization. Mineralization process is completed, when all the biodegradable biomass is consumed and all the carbon is converted into carbon dioxide (Kyrikou *et al.,* 2007). Alkanes consisting long carbon chains and straight structures considered to be more prone to aerobic biodegradation. Aerobic degradation pathway of alkane degradation is the oxidation of the terminal methyl group into a carboxylic acid through an alcohol intermediate, and after all completes mineralization through β-oxidation (Leahy, 1990; Cookson, 1995; Vander, 1997; Zhang and Bennet, 2005). The aerobic degradation process of aromatic compound involves their oxidation by molecular oxygen; after oxidation steps intermediates are outcome, then it enters into central metabolic pathways, including the Krebs cycle and β-oxidation (Dagley, 1975; Wilson and Bouwer, 1997; Sims and Overcash, 1983). During aerobic respiration microorganisms use oxygen to hydroxylate the benzene ring (Fig. 1), resulting in the subsequent fission of the ring. Enzymes are involved in these processes are mono- and di-oxygenase enzymes, incorporate one or two atoms of oxygen, respectively, into the ring (Gibson *et al.,* 1970). Hayaishi and Nozaki (1969) coined that major reactions catalyzed by di-oxygenases for aerobic biodegradation is the cleavages of

- The aromatic double bond located between two hydroxylated carbon atoms (ortho pathway),
- Adjacent to a hydroxylated carbon atom (meta pathway),
- An indole ring

In the benzene aerobic biodegradation process, three intermediates (Fig. 2) are catechol, protocatechuate, and gentisic acid, which are broken down by similar pathways of simple acids and aldehydes that are readily used for cell synthesis and energy Alexander (1977). Similarly Polycyclic aromatic compounds e.g. toluene, xylenes, naphthalene and ethylbenzene are degraded by similar mechanisms as that of benzene. *Rhodococcus* RHA1 and *Arthrobacter keyseri* 12B bacteria play major role in the degradation of 3, 4- dihydroxybenzoate, for example: (Eaton, 2001; Hara *et al.,* 2007).

Anaerobic biodegradation pathway

Some pollutants are not mineralized by an aerobic degradation process; they are highly recalcitrant due to increase in halogenations. Substitution of halogen, nitro and sulfo groups on the aromatic ring is increase the electrophilicity of the molecule. These xenobionts resist the electrophilic attack by oxygenases in aerobic degradation. Some recalcitrant that are persisting under aerobic condition are polychlorinated biphenyls (PCBs), chlorinated dioxins and some pesticides like DDT. It is necessary to overcome the high persistence of halogenated xenobiotics from the biosphere, for achieving these, reductive attacks by anaerobic bacteria is of great value. Anaerobic bacteria performed reductive dehalogenation either by a gratuitous reaction or a new type of anaerobic respiration, this process reduces the degree of chlorination and makes the product more accessible for mineralization by aerobic bacteria (Van Agteren *et al.,* 1998; Fritsche and Hofrichter). During anaerobic degradation reductive dehalogenation is the first step of degradation of PCBs (Poly chlorinated biphenyl), dehalogenation done under anaerobic conditions where organic substrates act as electron donors. PCBs accept electrons to allow the anaerobic bacteria to transfer electrons to these compounds. Anaerobic bacteria are capable to degrade xenobiotics that are present in various anaerobic habitats like water laden

soils, reticuloruminal contents, inter alia sediments, gastrointestinal contents, sludge digesters, feedlot wastes, groundwater, and landfill sites (Williams, 1977). The major groups of anaerobic bacteria that are capable of degrading xenobiotic compounds - *Acidovorax, Bordetella, Pseudomonas, Sphingomonas, Variovorax, Veillonella alkalescens, Desulfovibrio* spp., *Desulfuromonas michiganensis,* and *Desulfitobacterium halogenans, D. oleovorans, G. metallireducens, D. Acetonicum*. Anaerobic sulfate-reducing and methanogenic condition can be applied to isolate pure culture of anaerobic bacteria (Zhang and Bennet, 2005). Anaerobes can also utilize substituted and complex aromatic compounds in the way that do not perturb the benzene nucleus itself (Fig. 3). Aromatic compounds can also serve as electron shuttles; they serve as electron acceptors, with accompanying modifications of ring substituents (Gibson and Harwood, 2002).

The sulphate reducing bacteria (SRB) represent a large group of anaerobic organisms that play crucial role in many biogeochemical processes and also able to degrade crude oil (Barton and Hamilton, 2007). SRB is obligated anaerobic bacteria, utilize sulphate as final electron acceptor during anaerobic respiration and generate hydrogen sulphide (H_2S) from the reduction of sulphate (Boetius *et al.,* 2000; Sahrani *et al.,* 2008). The anaerobic degradation process is a renewable energy source, biogas generated from anaerobic digestion. It's mainly consist methane, that can be collected efficiently and used for eco-friendly power generation which has been demonstrated on a larger scale (Lier *et al.*, 2001; Angelidaki and Sanders, 2004; Holm-Nielsen *et al.,* 2009). Anaerobic digestion is a part of an integrated waste management system; it reduces the emission of landfill gas into the atmosphere (Dolfing and Bloemen, 1985; Angelidaki and Ahring, 1993; Soto *et al.,* 1993). Anaerobic organisms (Kazumi *et al.,* 1995, Song *et al.,* 2000) act on chlorinated aromatic (Vargas *et al.,* 2000) have been reported. Biochemical mechanisms (particularly enzymes) of the anaerobic biodegradation of chlorinated aromatic including PCP, PCBs, and dioxins. Anaerobic PCP degradation pathways have been illustrated a putative pathway is shown in Fig. 4. A bacterium takes several paths simultaneously for the removal of five chlorine atoms leading to the formation of phenol (the rate-limiting step) and finally mineralization to CH_4 and CO_2.

Microbial enzymes involved in biodegradation

Biodegradation is a microorganism depended enzymatically process which convert pollutants to innocuous products.

Microbial Oxidoreductases: These enzymes cleave chemical bonds and transfer the electrons from a reduced organic substrate (donor) to another chemical compound (acceptor). During these oxidation-reduction reactions, contaminants are oxidized to harmless compounds (ITRC 2002; Karigar and Rao, 2011). Oxidoreductases detoxify toxic xenobiotics like phenolic or anilinic compounds, either by polymerization, copolymerization with other substrates, or binding to humic substances (Park *et al.,* 2006). Microbial enzymes have been employed in the decolorization and degradation of azo dyes (Williams, 1977; Vidali, 2001; Husain, 2006).

Microbial Oxygenases- Oxygenases classified under the oxidoreductase group of enzymes (E.C. Class 1) (Karigar and Rao, 2011). Oxidation reaction is the major

enzymatic reaction of aerobic biodegradation is catalyzed by oxygenases. Oxygenases oxidize the substrates by transferring oxygen from molecular oxygen (O_2) and utilize FAD/NADH/NADPH as the co-substrate. Oxygenases metabolize organic compounds; they increase their reactivity, water solubility and cleave the aromatic ring (Arora *et al.*, 2009). On the basis of the number of oxygen atoms used for oxidation, oxygenases can be further categories into two grouped – 1. monooxygenases 2. Dioxygenases.

Monooxygenases Monoxygenases transfer one atom of molecular oxygento the organic compound (Arora *et al.*, 2009). Monooxygenases can be categorized into two subclasses based on the presence cofactor:

1. Flavin-dependent monooxygenases
2. P450 monooxygenases.

Flavin-dependent monooxygenases contain flavin as prosthetic group and NADP or NADPH as coenzyme. P450 monooxygenases are heme containing oxygenases that persist in both eukaryotes and prokaryotes. Monooxygenases act as biocatalysts in the bioremediation process and synthetic chemistry because they are highly regionselectivity and stereoselectivity on a wide range of substrates (Cirino and Arnold, 2002; Arora *et al.*, 2010; Karigar and Rao, 2011). Monooxygenases catalizes enormous reactions such as desulfurization, dehalogenation, denitrification, ammonification, hydroxylation, biotransformation, and biodegradation of various aromatic and aliphatic compounds (Arora *et al.*, 2010).

Dioxygenases: Dioxygenases are multicomponent enzyme systems that incorporate molecular oxygen to the substrate. On the basis of the complexity of the degradation pathways, the biodegradation phenomenon can be categorized into two types:

1. Convergent mode
2. Divergent modes of degradation

In the convergent mode, structurally varied aromatic compounds are converted to aromatic ring cleavage substrates catechol, gentsate, protocatechuate and their derivatives (Meer *et al.*, 1992). In divergent mode, a metal-dependent dioxygenase channels operate and dihydroxylated intermediates are formed by one of the two possible pathways: the *meta*-cleavage pathway or the ortho-cleavage pathway (Harayama and Rekik, 1989; Eltis and Bolin, 1996; Takami *et al.*, 1997).

The dioxygenases have been categorized into two classes 1. extradiol 2. intradiol dioxygenases (Harayama and Rekik, 1989). Extradiol dioxygenases contain nonheme iron (II) in their active site, catalyzes ring cleavage of the carbon-carbon (C-C) bond adjacent to the vicinal hydroxyl groups (meta-cleavage) whereas intradiol dioxygenases contain non-heme iron (III) in their active site, catalyzes ring cleavage at the C-C bond between the vicinal hydroxyl groups (ortho-cleavage).

Microbial Dehalogenases: Dehalogenase plays an important role in the degradation of chlorinated pollutant (Copley, 1998). Some anaerobic microorganisms exploit dehalorespiration; use halogenated compounds as terminal electron acceptors (Wohlfarth and Diekert, 1997). An example of this process is the conversion of PCE (Perchloroethylene) eitherdichloroethylene (DCE) (Scholz-Muramatsu *et al.*, 1995, Schumacher and Holliger, 1996), ethylene or ethane depends on the conditions.

Magnuson *et al.* (1998) reported the partial purification of two reductive dehalogenases from *Dehalococcoides ethenogenes* strain 195, both enzymes are membrane proteins. The first enzyme PCE-reductive dehalogenase reduces PCE to TCE and the second enzyme TCE-reductive dehalogenase reduces TCE, trans-DCE, cis-DCE, 1,1-dichloroethene and vinyl chloride.

Phosphotriesterases (PTEs): PTEs are microbial isolated enzyme whichhydrolyze and detoxify organophosphate pesticides (OPs). This reduces OP toxicity, it decrease the ability of OPs to inactivate AchE (Ghanem and Raushel, 2005; Singh and Walker, 2006; Porzio *et al.,* 2007; Shen *et al.,* 2010a; Theriot and Grunden, 2010). These enzymes mainly hydrolyze phosphoester bonds like P–O, P–F, P–NC, and P–S, and these hydrolysis mechanism include water molecule in the phosphorus center (Ortiz-Hernandez *et al.,* 2003).

Catabolic gene organigation involve in xenobiotic degradation

The genes reliably for the degradation of xenobiotics are generally present in a clustered organization that comprising catabolic genes encoding catabolic enzymes, transport genes encoding proteins perform active uptake of compounds and regulatory genes operate the regulation of the expression of catabolic and transport genes (Cao *et al.,* 2009). According to Widada *et al.* (2002) the diversity of catabolic genes in bacteria can be investigated by two different approaches from environmental samples: 1. Culture-dependent and 2. Culture-independent methods.

1. Culture-dependent methods - Nucleic acid is extracted from isolated bacterial culture from environmental samples. Over 300 catabolic genes have been cloned and identified from culturable bacteria which are involved in catabolism of aromatic compounds. Several approaches,such as shotgun cloning by using indigo formation (Ensley *et al.,* 1983; Goyal and Zylstra, 1996), clearing zone formation (Souza *et al.,* 1995), meta-cleavage activity (Sato *et al.,* 1997) use as screening methods for cloning; applying proteomics (two dimensional gel electrophoresis analysis) of xenobiotic-inducible proteins to achieve genetic information (Khan *et al.,* 2001), transposon mutagenesisto obtain a defective mutant (Foght and Westlake, 1996), transposon mutagenesis using a transposon-fused reporter gene (Bastiaens *et al.,* 2001), applying a degenerate primer to generate a probe (Saito *et al.,* 2000), and applying a short probe from a homologous gene (Moser and Stahl, 2001), have been used to find out catabolic genes from various bacteria.

2. Culture-independent methods -Nucleic acid is directly extracted from environmental samples (Okuta *et al.,* 1998; Watanabe *et al.,* 1998; Lloyd-Jones *et al.,* 1999). The charterization of catabolic gene diversity using culture-independent molecular biological methods involve the amplification of DNA or cDNA from RNA extracted from environmental samples by PCR amplification via a degenerate primer set that is prepared by consensus or unique DNA sequence. The resultant PCR products are separated by cloning or gel electrophoresis (Watanabe *et al.,* 1998; Hedlund *et al.,* 1999; Lloyd-Jones *et al.,* 1999; Wilson *et al.,* 1999). The PCR-amplified gene is proper or not, it is necessary to sequence the product, so that the resultant information can be used to reveal the diversity of the corresponding gene. According to Khomenkov *et al.* (2008) catabolic gene clusters encoded in both the chromosomes and the plasmids, chromosomes act as insertion elements and

plasmids as mobile genetic elements and they also facilitate horizontal gene transfer (Sinha *et al.,* 2009).The plasmid-encoded catabolic pathway has the special benefit of facilitating the horizontal transfer of the particular catabolic genes in the microbial population, these results a rapid adaptation of microbial population to the presence of new aromatic pollutants in an ecosystem (Cao *et al.,* 2009). Some catabolic plasmids and chromosomes for the biodegradation of xenobiotics compounds are summarized in Table 2.

Various factors for example the structure of the genes, enzymes, substrates, and the metabolites, influence the expression of catabolic genes (Mishra *et al.,* 2001). According to Mishra *et al.* (2001) TOL, OCT, CAM, NAH are typical catabolic plasmids. The mechanisms of gene action for degradation vary in different organism; genes are organized on one, two or more operon in phenol, polychlorinated biphenyls respectively. Genes are also organized on transposons, e.g. 2, 4, 5-trichlorophenoxyacetate (2, 4, 5-T is an herbicide) (Don and Pemberton, 1981; Khan *et al.,* 2001; Shimizu *et al.,* 2001). According to Chaudhry and Chapalamadugu (1991) *Pseudomonas* AC1100 contains two insertion elements, RS110 selected as IS931 and IS932; they participate a major role in degradation of 2, 4, 5-T.

Molecular approaches to study catabolic gene

The environment contains several recalcitrant degrading bacteria, to enumerate and monitoring of these degrading bacterial populations from contaminated environments via traditional microbiological methods have taken an excessive time and a lot of underestimate numbers of result of our incapability to cultivate the widely held of soil organisms (Lloyd-Jones *et al.,* 1999). Several molecular approaches are used to characterize the nucleic acids of different bacteria from environmental samples (Hurt *et al.,* 2001). The molecular techniques give us a more comprehensive interpretation in comparison with standard microbiological methods for in situ microbial community. Its response to both engineered bioremediation and natural attenuation processes (Brockman, 1995). PCR amplification, subsequent analysis of bacterial rRNA genes by sequencing, preparing metagenomic libraries, RFLP, dot-blot, southern blot, denaturing gradient gel electrophoresis (DGGE), microarrays are several techniques which are applied for degradation (Sinha *et al.,* 2009). Direct DNA hybridization techniques can be used to monitor TOL (for toluene degradation) and NAH (naphthalene degrading plasmid) (Sayler and Layton, 1990). In these study colonies were hybridized by entire plasmids as probes to compute the cells containing catabolic plasmids, then we observed positive relationship between plasmid concentrations and the rates of mineralization. These techniques were used to monitor the xylE and ndoB genes involved in creosote degradation in soil communities (Hosein *et al.,* 1997). Amplicon length heterogeneity PCR (LH-PCR) and terminal restriction fragment length polymorphisms (TRFLP) technique was used to monitor the effect of nutrient amendments on microbial community during bioremediation of petroleum-contaminated soils (Mills *et al.,* 2003).

Colony hybridization in combination with most-probable-number (MPN) technique was used to monitor the microbial community in flow through lake microcosm contain chlorobenzoate degrading *Alcaligenes* strain (Fulthorpe and Wyndham, 1989).

Table.1 List of xenobiotic compounds and their degrading bacterial species

TARGET COMPOUNDS	BACTERIA DEGRADING THE COMPOUNDS	ISOLATED SITES	REFERENCES	WORK PLACE
PAH compounds				
Naphthalene	*Streptomyces* spp. isolates AB1, AH4, and AM2	Bacterial strains were isolated from surface soils at Mitidja plain (North of Algeria).	Ferradji *et al.* (2014)	Algeria
	Streptomyces sp. strain QWE-35	Bacterial strain was isolated from acclimated activated sludge from a coal gasification wastewater plant.	Xu *et al.* (2014)	China
	Pseudomonas sp. CZ2 and CZ5	Bacterial strains CZ2 and CZ5, isolated from polycyclic aromatic hydrocarbons contaminated sludge in Wuhan, China.	Zhou *et al.* (2013)	China
	Pseudomonas stutzeri Strain B1SMN1	A strain isolated from a waste water sample taken at a lagooning treatment plant in Menorca (Balearic Islands, Spain).	Busquets *et al.* (2013)	Spain
	Achromobacter sp. BAB239, *Pseudomonas* sp. DV-AL2, *Enterobacter* sp. BAB240 and *Pseudomonas* sp. BAB241	Bacterial consortium (DV-AL) was developed by enrichment culture technique from sediment collected from the Alang-Sosiya ship breaking yard, Gujarat, India.	Patel *et al.* (2012)	India
	Geobacillus sp. SH-1	Bacterium SH-1 was isolated from a deep oil well.	Zhang *et al.* (2012a)	China
	Rhodococcus	Bacterial strain was isolated from soil samples and slime pit bottom sediment of the Verkhnekamsk salt mining region of Russia.	Ananina *et al.* (2011)	Russia
	Pseudomonas putida S2	Studied by Plakett-Burman (PB) design, and mineral medium with an additional carbon source of citric acid, ammonium sulfate and sodium chloride.	Zafar *et al.* (2010)	Washington, USA
	Bacillus fusiformis (BFN)	Bacterial strains were isolated from oil refining waste water sludge.	Lin *et al.* (2010)	Fuzhou, China
	Paenibacillus, Pseudomonas	Bacterial strains were isolated from Orbetello lagoon, Italy, which is highly contaminated with both organic compounds and metals.	Pepi *et al.* (2009)	Italy
	Novosphingobium naphthalenivorans sp. nov.	Bacteria isolated from polychlorinated-dioxin-contaminated soil.	(Suzuki and Hiraishi, 2007)	Toyohashi, Japan
	Polaromonas naphthalenivorans sp. nov.Strain CJ2^T	Bacterial strain was isolated from coal-tar-contaminated surface sediments from South Glens Falls, NY, USA.	Jeon *et al.* (2004)	USA
	Bacillus naphthovorans strain MN-003, *Staphylococcus* sp. strain MN-005 and *Micrococcus* sp. strain MN-006	Bacterial strains were isolated from oil-contaminated tropical marine sediments.	Zhuang *et al.* (2003)	Norman, USA
	Neptunomonas naphthovorans gen. nov., sp. nov.	Bacteria were isolated from creosote-contaminated Puget Sound sediment.	Hedlund *et al.* (1999)	Seattle, Washington
Phenanthrene	*Pseudomonas* sp. Ph6	Endophytic bacterium was isolated from clover (Trifolium pratense L.) grown in a PAH-contaminated site.	Sun *et al.* (2014)	China
	Massilia sp. Strain Pn2	Endophytic bacterium, Pn2, was isolated from Alopecurus aequalis Sobol grown	Liu *et al.* (2014a)	China

		in soils contaminated with polycyclic aromatic hydrocarbons (PAHs).		
	Sphingobium sp. Strain PNB	Strains were isolated from municipal waste-contaminated soil.	Roy *et al.* (2013)	India
	Sphingomonadaceae PHPY *and Rhodobacteraceae* SK	Bacteria were isolated from seawater using an enrichment method.	Pinyakong *et al.* (2012)	Bangkok, Thailand
	Mycobacterium sp. strain A1-PYR and *Sphingomonas* sp. strain PheB4	Studied by mixed culture.	Zhong *et al.* (2011)	China
	Brevibacillus sp. PDM-3	Bacterial strain was isolated by enrichment method from hydrocarbon contaminated sludge samples.	Reddy *et al.* (2010)	Hyderabad, India
	Sphingomonas sp. ZP1 and *Tistrella* sp. ZP5	Bacterial strain was isolated from soil samples contaminated with polycyclic aromatic hydrocarbon (PAH)-containing waste from oil refinery field in Shanghai, China.	Zhao *et al.* (2007)	China
	Sphingomonas sp. strain GY2B	Aerobic bacterial consortia GY2 isolated from three different sites in Guangzhou, Guangdong Province of China.	Tao *et al.* (2007)	China
	Vibrio parahaemolyticus	Phenanthrene-degrading bacteria were isolated from Chesapeake Bay.	West *et al.* (1984)	Maryland
Anthracene	*Microbacterium sp. strain SL10*	Bacteria were isolated from a hydrocarbon-contaminated soil at a mechanical engineering workshop in Lagos, Nigeria.	Salam *et al.* (2014)	Lagos, Nigeria
	Martelella sp. AD-3	bacterial strain was isolated from highly saline petroleum-contaminated soil.	Cui *et al.* (2012)	China
	Ochrobactrum sp. VA1	Studied by a halotolerant bacterial strain under saline conditions.	(Arulazhagan and Vasudevan, 2011)	India
	Rhodococcus opacus 412	Bacterial cell was adopted in solid mineral medium.	Leneva *et al.* (2009)	Russia
	Ps. aeruginosa and Ps. Citronellolis	*Pseudomonas*sp. isolated from a petrochemical sludge landfarming site.	Jacques *et al.* (2005)	Brazil
PCP (pentachlorophenol)	*Kocuria* sp. CL2	Bacteria isolated and characterized from the sludge of pulp and paper mill.	Karn *et al.* (2011)	Patiala, Yamunanagar India
	Comamonas testosteroni CCM 7530	Studied in soil bioaugmented and addition of organomineral complex (OMC) or lignite as possible sorbents for PCP immobilization.	Zuzana *et al.* (2009)	Bratislava, Slovakia
	Sphingobium sp. UG30	Studied by use of electrokinetics in unsaturated soil.	Harbottlea *et al.* (2009)	Oxford, UK
	Bacillus cereus (DQ002384), *Serratia marcescens* (AY927692) and *Serratia marcescens* (DQ002385)	Studied by Synergistic biodegradation.	Singh *et al.* (2009)	Lucknow, India
	Sphingomonas chlorophenolica	Bacteria was isolated from a PCP-degrading mixed culture.	Yang *et al.* (2006)	Taiwan
Chloroaniline	*Acinetobacter baylyi* strain GFJ2	Bacterial strain was isolated from soil, able to degrade4-chlroaniline (4CA) and 3, 4-dichloroaniline (34DCA), monohalogenated anilines (chloro-, bromo-, and fluoro-anilines).	(Hongsawat and Vangnai, 2011)	Bangkok, Thailand
	Delftia tsuruhatensis H1	Bacteria able to degrade 3, 4-dichloroaniline, 4-methylaniline, 2, 3-dichloroaniline and 2, 4-dichloroaniline by mineralization.	Zhang *et al.* (2010a)	Hangzhou, China,Singapore
	Acinetobacter baumannii CA2, *Pseudomonas putida* CA16and	Bacteria able to degrade 4-Chloroaniline and isolated from agricultural soil.	(Vangnai and Petchkroh, 2007)	Bangkok

	Klebsiella sp. CA17			
1,2,4-trichlorobenzene (1,2,4-TCB)	*Pseudomonas putida*	Studied by metabolic flux analysis.	Finley *et al.* (2010)	Switzerland
	Bordetella sp.	Bacteria isolated from soil which has been polluted with chlorinated benzenes for more than 25 years.	Wang *et al.* (2007)	Germany
2-chlorobenzoic acid	*Pseudomonas* sp., *Enterobacter* sp., *Acinetobacter* sp., and *Corynebacterium* sp.	Bacteria isolated from Landfill centers (landfills) in Shiraz city.	Kafilzadeh *et al.* (2012)	Iran
Fluoranthene	*Herbaspirillum chlorophenolicum*	Bacteria isolated from activated sludge.	Xu *et al.* (2011)	Nanjing, China
Pyrene	*Klebsiella oxytoca* PYR-1	Effect of nonionic surfactant Tween 80 on the biodegradation of pyrene.	(Zhang and Zhu, 2012)	China
	Bacillus vallismortis strain JY3A	Bacterial strain was isolated from the polluted soil in the Jinan Oil Refinery Factory, Shandong Province of China.	Ling *et al.* (2011)	China
	Diaphorobacter sp. And *Pseudoxanthomonas* sp.	Two new bacterial strains, KOTLB and RN402, were isolated from soil.	Klankeo *et al.* (2009)	Bangkok, Thailand
	Enterobacter sp. 12J1	Endophytic bacterium was isolated from plants grown in polycyclic aromatic hydrocarbon-contaminated soils.	Sheng *et al.* (2008)	China
	Mycobacterium sp.	Bacterial strain was isolated near a point source for petrogenic chemicals.	Heitkamp *et al.* (1988)	Arkansas
Phthalate compounds				
Phthalate	*Achromobacter denitrificans* strain SP1	Isolate from heavily plastics-contaminated sewage sludge.	Pradeep *et al.* (2015)	Kerela, India
	Arthrobacter sp.C21	A bacterial strain C21 isolated from constructed wetland soil.	Wen *et al.* (2014)	China
	Agrobacterium sp.JDC-49	Bacteria were isolated from river sludge.	Wu *et al.* (2011)	China
	Ochrobactrum sp.JDC-41	The strain was obtained from river sludge using mixtures of phthalate esters as the sole source and energy	Wu *et al.* (2010)	China, Taiwan
	Enterobacter sp. T5	Isolated from municipal solid waste in a landfill bioreactor.	Fang *et al.* (2010)	China
	Rhodococcus sp. L4	Isolated from activated sludge collected from a dyeing plant.	Lu *et al.* (2009)	Wuhan, china
	Pseudomonas fluorescens B-1	A pure culture isolated from mangrove sediment.	Xu *et al.* (2005)	China
	Sphigomonas sp. DK4 and *Corynebacterium* sp O18	Bacteria strains, DK4 and O18, were isolated from river sediment and petrochemical sludge, respectively.	Chang *et al.* (2004)	Taiwan
Pesticides				
Endosulfan compounds	*Paenibacillus sp. ISTP10*	Isolated from activated sludge.	Kumari *et al.* (2014)	New Delhi, India
	Achromobacter xylosoxidans strain C8B	Bacteria were isolated from soil through selective enrichment technique in sulfur free medium with endosulfan as a sole sulfur source.	(Singh and Singh, 2011)	Delhi, India
	Stenotrophomonas maltophilia and Rhodococcus erythropolis	A mixed culture isolated from a pesticide-contaminated soil was studied in batch experiments.	Kumar *et al.* (2007)	Nagpur, India
	Klebsiella oxytoca KE-8	Isolate an endosulfan sulfate degrader from endosulfan-polluted soils.	Kwon *et al.* (2005)	South Korea
	Klebsiella pneumonia	Bioremediation of toxic endosulfan, endosulfan degradation bacteria were isolated from various soil samples.	Kwon *et al.* (2002)	South Korea

HCH/ lindane (1,2,3,4,5,6-hexachlorocyclohexane)	*Sphingobium czechense* LL01^T	Bacterial strain was isolated from (HCH) contaminated soil at Spolana Neratovice, a former Czech producer of lindane.	Niharika *et al.* (2013)	India
	Sphingomonas sp. NM05	Studied by Surfactant (rhamnolipid, sophorolipid and trehalose) mediated enhanced biodegradation.	Manickam *et al.* (2012)	India
	Streptomyces sp. M7	Studied by the use of lindane as the only Carbon source.	Cuozzo *et al.* (2009)	Argentina
	Pseudomonas strains	Strains isolated from agricultural soil possess c-hexachlorocyclohexane degrading ability.	Nawab *et al.* (2003)	Aligarh, India
2,4-D (2,4-dichlorophenoxyacetic acid)	*Maribacter* sp AMSU	Bacerial strain was isolated from aquaculture effluent by enrichment culture technique.	Sankaralingam *et al.* (2013)	Tamilnadu, India
	Delftia sp.	Bacterial strain was isolated from a polluted river in Buenos Aires, Argentina.	Gonzalez *et al.* (2012)	Argentina
	Pseudomonas putida SM1443	Studied by fed-batch microcosm system and a lab-scale sequencing batch reactor (SBR) to enhance degradation capacity of 2, 4-D.	Quan *et al.* (2010)	China
	Comamonas koreensis strain CY01	Anaerobic reductive dechlorination of 2,4D and the role of humic substances in the degradation.	Wang *et al.* (2009)	China
DDT (Dichlorodiphenyltrichloroethane)	*Pseudoxanthobacter liyangensis* sp. nov.	Bacterial strain, DDT-3T, was isolated from DDT contaminated soil in Liyang, PR China.	Liu *et al.* (2014b)	China
	Novosphingobium arabidopsis sp. nov.	Bacterium, designated strain CC-ALB-2T, was isolated from the Arabidopsis thaliana rhizosphere.	Lin *et al.* (2014a)	Taiwan
	Alcaligenes sp. strain DG-5	Bacteria were isolated from DDTs contaminated sediment.	Gao *et al.* (2011)	China
	Serratia marcescens DT-1P	Bacteria were isolated by long term enrichment of soil samples collected from DDT-contaminated fields.	(Bidlan and Manonmani, 2002)	Karnataka, India
Diuron DCMU (3-(3,4-dichlorophenyl)-1,1-dimethylurea)	*Arthrobacter* sp. BS2 and *Achromobacter* sp. SP1	Bacterial strain was isolated from Enrichment cultures of buffer strip soil (BS) and in the sediments (SED) of the Morcille river in the Beaujolais vineyard where diuron found.	Devers-Lamrani *et al.* (2014)	France
	Micrococcus sp. strain PS-1	Bacterial strain was isolated from diuron storage site.	(Sharma and Suri, 2011)	India
	Pseudomonas sp. and *Stenotrophomonas* sp.	Diuron degrading bacteria were isolated from enrichment culture of lotic surface water.	Batisson *et al.* (2007)	France
	Streptomyces sp.	17 streptomycete strains, obtained from agricultural and non-agricultural soils, were determined in the laboratory.	Castillo *et al.* (2006)	Spain
	Arthrobacter sp.	A bacterial strain was isolated from a soil by enrichment procedures.	Widehem *et al.* (2002)	France

Halogenated organic compounds				
Vinyl chloride	*Micrococcus species*	Bacterial strain was isolated using enrichment culture technique.	(Patil and Bagde, 2012)	Mumbai, India
	Mycobacterium chubuense strain NBB4	Microorganism has grown under pure-culture and microcosms conditions.	(Le and Coleman, 2011)	Australia
	Sphingopyxis sp. PVA3	Bacteria was isolated a poly (vinyl alcohol) (PVA)-degrading bacterium from an activated sludge sample obtained from the drainage of a dyeing factory.	Yamatsu *et al.* (2006)	Japan
	Pseudomonas aeruginosa, designated strain MF1	Bacteria were isolated from aerobic enrichment culture.	Verce *et al.* (2000)	South Carolina
Herbicides				
Atrazine (2-chloro-4-ethylamino-6-isopropylamino-1, 3-5-triazine)	*Raoultella planticola*	Bacterial cells were isolated from the wastewater treatment plant of a herbicide factory.	Swissa *et al.* (2014)	Israel
	Bacillus subtilis Strain HB-6	Bacterial strain HB-6 was isolated from industrial wastewater.	Wang *et al.* (2014a)	China
	Rhodococcus sp.	A batch enrichment technique was used to isolate *Rhodococcus* sp. strain from an agricultural land.	Umar *et al.* (2012)	Nigeria
	Arthrobacter sp. HB-5	Bacteria were isolated from an industrial wastewater sample.	Wang *et al.* (2011b)	China
	Nocardioides sp. SP12	Bacteria isolated from atrazine-treated bulk- and maize rhizosphere soil.	Piutti *et al.* (2003)	France
	*Arthrobacter sp.*AD1	Bacteria were isolated from industrial wastewater.	Cai *et al.* (2003)	China
PCE(Tetrachloroethylene or Perchloroethylene)	*Dehalococcoides* spp.	The expression of DHC dehalogenase genes were demonstrated for Yangtze enrichment cultures.	Kranzioch *et al.* (2014)	Germany
	Propionibacterium sp. HK-1and *Propionibacterium* sp. HK-3	Bacteria were isolated from environmental sediments.	Chang *et al.* (2011)	Japan and korea
	Desulfitobacterium sp. strain KBC1	Bacterial strain was isolated from a contaminated site.	Tsukagoshi *et al.* (2006)	Japan
	Clostridium bifermentans DPH-1	Bacterial strain DPH-1, was isolated from a contaminated site.	Chang *et al.* (2000)	Japan
Propanil	*Xanthomonas* sp., *Acinetobactercalcoaceticus*, *Rhodococcus* sp. and *Pseudomonas* sp.	Studied by continuous small scale bioprocess.	Herrera-Gonzalez *et al.* (2013)	Mexico
	Catellibacterium nanjingense sp. nov.	Bacterial strain, designated Y12T, was isolated from activated sludge of a wastewater bio-treatment facility.	Zhang *et al.* (2012b)	China

Petroleum products				
	Acinetobacter sp. LS-1	Isolating novel crude-oil-degrading bacteria from oil-water mixture in Dagang oilfield, China. .	Liu *et al.* (2014b)	China
	Pseudomonas, Achromobacter, Bacillus and *Micromonospora*	Bacteria isolated from petroleum sludge and polluted sandy soil from an oil refinery.	Gojgic-Cvijovic *et al.* (2012)	Belgrade, Serbia
	Pseudomonas aeruginosa DQ8	Crude oil was obtained from Daqing oil field in china and bacterial strain was isolated.	Zhang *et al.* (2011a)	China
	Dietzia strain DQ12-45-1b	Bacterial strain was isolated from the production water of a deep subterranean oil-reservoir.	Wang *et al.* (2011a)	China
	Bacillus species	A collection of bacteria was obtained by enrichment cultivation from oil-contaminated soils of an oil field in Daqing, China.	Zhang *et al.* (2010b)	China
	Flavobacterium sp. *Acinetobacterium calcoaceticum* and *Pseudomonas aeruginosa*	Bacteria were isolated from contaminated soils using the enrichment technique.	(Mandri and Lin, 2007)	South Africa
	Bacillus spp, *Micrococcus* spp. *and Proteus* spp.	Isolated from two rivers and refinery effluent to degrade two Nigerian Crude oils.	(Okerentugba and Ezeronye, 2003)	Nigeria
Azo dyes				
	Morganella sp. HK-1	Bacteria were isolated from dye contaminated industrial landfill.	Pathak *et al.* (2014)	Gujarat, India
	Sphingomonas sp.	Isolated from Petroleum Sludge.	Ali *et al.* (2014)	UAE
	Sphingomonas paucimobilis	Bacteria were isolated from the effluent treatment plant of a textile and dyeing industry (SITEX) located in Ksar Hellal, Tunisia.	Ayed *et al.* (2011)	Tunisie
	Proteus hauseri ZMd44	Studied for dye-bearing wastewater treatment.	Chen *et al.* (2010)	Taiwan
	Staphylococcus arlettae VN-11	Bacteria were isolated from an activated sludge process in a textile industry under microaerophilic conditions.	Elisangela *et al.* (2009)	Brazil, Portugal
	Aeromonas caviae, *Proteus mirabilis* and*Rhodococcus globerulus*	A novel bacterial consortium (TJ-1) decolorize Acid Orange 7 (AO7) and manyother azo dyes, was developed.	Joshi *et al.* (2008)	Kanpur, India
Other compounds				
PCB(Poly chlorinated biphenyl)	*Rhodococcus biphenylivorans* sp. nov.	Bacteria .was isolated from a polychlorinated biphenyl (PCB)-contaminated sediment in Taizhou city, Zhejiang province, eastern China.	Su *et al.* (2015)	China
	Rhodococcus erythropolis U23A	Bacteria were isolated rhizosphere of plants grown on a PCB-contaminated soil.	Toussaint *et al.* (2012)	Canada

	Sinorhizobium meliloti	Studied by resting cell assay and soil microcosms.	Tu *et al.* (2011)	China, Uk
	Achromobacter sp.	A bacterial strain, BP3, capable of degrading biphenyl, was isolated from petroleum-contaminated soil.	Hong *et al.* (2009)	China
	Enterobacter sp. LY402	A Gram-negative bacterium, named LY402, was isolated from contaminated soil.	Jia *et al.* (2008)	China
	Paenibacillus sp. KBC101	Bacterial strain KBC101 has been newly isolated from soil.	Sakai *et al.* (2005)	Japan
PCP (pentachlorophenol)	*Streptomyces* sp.	PCP remeadiation studied by either free or immobilized cultures of bacteria strain.	Fuentes *et al.* (2013)	Argentina
	Kocuria sp. CL2	Bacterial strain was isolated from sludge of pulp and paper mill.	Karn *et al.* (2011)	India
	Acinetobacter sp. ISTPCP-3	Bacterial strains were isolated from sediment core of pulp and paper mill effluent discharge site.	Sharma *et al.* (2009)	New Delhi, India
	Serratia marcescens	Aerobic bacterial strains were isolated from pulp paper mill waste.	Singh *et al.* (2007)	Lucknow, India
	Sphingomonas chlorophenolica	Bacterial strains were isolated from a PCP-degrading mixed culture.	Yang *et al.* (2006)	Taiwan
Dioxins	*Pseudomonas mendocina* strain NSYSU	Bacterial strain NSYSU (NSYSU strain) has been isolated from dioxin-contaminated soil by selective enrichment techniques.	Lin *et al.* (2014b)	Taiwan
	Pseudomonas sp. strain ISTDF1	Bacterial strains were isolated from effuent of the pulp and paper industry and this strain utilize dibenzofuran as a sole source of energy and carbon.	Jaiswal *et al.* (2011)	New Delhi, India
RDX (Cyclotrimethylenetrinitramine)	*Rhodococcus rhodochrous* strain 11Y	Biodegradation of RDX by Cytochrome P450 XplA gene.	Halasz *et al.* (2012)	Canada
	Rhodococcus species T9N	Studied was done in Israel's coastal aquifer.	Bernstein *et al.* (2011)	Israel
	Shewanella *sediminis* sp. nov.	A psychrophilic rod-shaped marine bacterium (strain HAW-EB3T) isolated from Halifax Harbour sediment was noted for its ability to degrade (RDX).	Zhao *et al.* (2005)	Canada
	Clostridium acetobutylicum (ATCC 824)	Determine the biodegradation kinetics of RDX by crude cell extract of *Clostridium acetobutylicum.*	(Zhang and Hughes, 2003)	Houston, USA
Quinoline	*Brevundimonas* sp. K4	Bacteria was isolated from activated sludge of a coking wastewater treatment plant	Wang *et al.* (2014b)	China
	Bacillus sp. Q2	Strain was isolated from petroleum-contaminated soil.	Tuo *et al.* (2012)	China

	Pseudomonas sp. BC001	Bacterial strain was isolated from activated sludge in a coking wastewater treatment plant.	Bai *et al.* (2010)	Beijing, China
	Pseudomonas putida	Bacterial strain was isolated from activated sludge of the municipal wastewater treatment Plant.	(Lin and Jianlong, 2010)	Beijing, China
	Rhodococcus sp. QL2	A novel aerobic gram-positive bacterial strain was isolated from activated sludge of a coke plant wastewater treatment process.	Zhu *et al.* (2008)	China
	Burkholderia pickettii	Microorganism was isolated from activated sludge of coke-oven wastewater treatment plant.	Jianlog *et al.* (2002)	China
TNT (Trinitro-toluene)	Pseudomonas spp.	Bacterial strain was isolated from a TNT-contaminated environment.	Chien *et al.* (2014)	China
	Bacillus cereus	Bacterial strain was isolated from North Atlantic Treaty Organization (NATO) TNT contaminated soils.	Mercimek *et al.* (2013)	Adana, Turkey
	Clavibacter agropyi (Corynebacterium) (RL1) and *Sphingomonas sanguinis* (R.L2)	Bacterial strains were isolated from TNT contaminated soil.	(Rahal and Moussa, 2011)	Giza
	Bacillus sp. YRE1	Bacterial strains were isolated from red effluent in free state and also cells immobilized on charcoal and polystyrene.	Ullah *et al.* (2010)	*Pakistan*
	Raoultella terrigena strain HB	Bacterial strains were isolated from TNT contaminated site.	Claus *et al.* (2007)	Germany
	Klebsiella sp. strain C1	Bacterial strain C1 isolated from activated sludge.	Kim *et al.* (2002)	Korea
BTEX	*Janibacter* sp. SB2	An enrichment culture was established to isolate a BTEX-degrading bacterium from contaminated sea-tidal flat.	Jin *et al.* (2013)	Korea
	Bacillus Sphaericus	Studied by a biofilter reactor.	Rahul *et al.* (2011)	Agra, India
	Pseudoxanthomonas spadix BD-a59	Bacteria were isolated by plating gasoline-contaminated sediment from a gasoline station in Geoje, Republic of Korea.	Kim *et al.* (2008)	Korea
Ethyl tert-butyl ether (ETBE)	*Rhodococcus* sp. IFP 2042, *Bradyrhizobium* sp. IFP 2049	Bacterial strains were isolated from a polluted aquifer.	Digabel *et al.* (2013)	France
	Comamonas testosteroni	Two bacterial strains, E_1 and E_2, isolated from gasoline-polluted soil.	Kharoune *et al.* (2001)	France
Acrylamide	*Moraxella osloensis* MSU11	Bacterium was isolated from paper mill effluent at Charan mahadevi, Tamilnadu, India.	Jebasingh *et al.* (2013)	Tamil Nadu, India
	Burkholderia sp. strain DR.Y27	Strain DR.Y27 was purified to homogeneity by a combination of anion exchange and gel filtration	Syed *et al.* (2012)	Malaysia

		chromatography.		
	Geobacillus thermoglucosidasius AUT-01	Bacteria were isolated from soil collected from a hot spring area in Montana, USA.	(Cha and Chambliss, 2011)	USA
	Enterobacter aerogenes	Bacteria were isolated from domestic wastewater in Chonburi, Thailand.	(Buranasilp and Charoenpanich, 2011)	Thailand
	Pseudomonas aeruginosa	A bacterial isolate was isolated from AM-contaminated soil.	(Prabua and Thatheyusb, 2007)	Madurai, India
Phenol	*Rhodococcus ruber* SD3	Bacterial strain was isolated from rotting wood and polluted sludge.	Peng *et al.* (2013)	China
	Rhodococcus sp.	Bacterial strain CS1 isolated from tannery sediments.	Paisio *et al.* (2012)	Argentina
	Acinetobacter calcoaceticus P23	Bacteria were isolated from the rhizosphere of duckweed (Lemna aoukikusa) using an enrichment culture method.	Yamaga *et al.* (2010)	Japan
	Acinetobacter, *Alcaligenes*, and *Rhodococcus*	Bacteria capable of phenol degradation were isolated from the leaves of green ash trees grown at a site rich in airborne pollutants.	Sandhu *et al.* (2009)	USA
	Pseudomonas, Acinetobacter, Comamonas and *Cupriavidus*	Six phenol-degrading bacteria designated as PND-1–PND-6 were isolated from natural soil.	Dong *et al.* (2008)	China
	Pseudomonas aeruginosa	A novel indigenous strain (MTCC 4996) isolated from a pulp industrial effluent-contaminated site.	Kotresha and Vidyasagar, 2008)	Karnataka, India
	Pseudomonas cepacia and *Bacillus brevis*	Two bacterial strains were isolated from the phenol bearing industrial wastewater.	Arutchelvan *et al.* (2005)	Annamalai nagar, India
	Alcaligenes faecalis and *Candida tropicalis*	Two microorganisms were isolated from Amazonian rain forest soil samples after enrichment in the presence of phenol and a high salt concentration.	Bastos *et al.* (2000)	Brazil

Fig.1 Aerobic benzen biodegradation (Wilson and Bouwer, 1997)

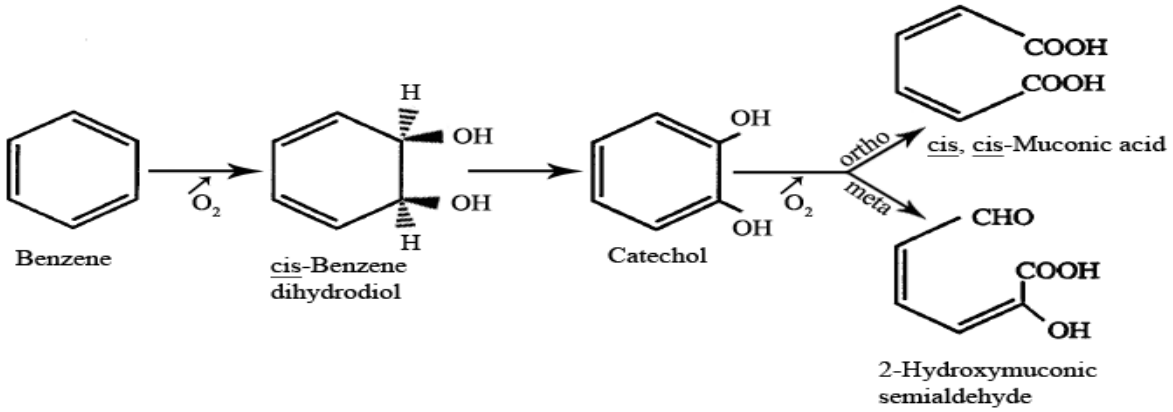

Fig.2 Degradation of aromatic, natural and xenobiotic compounds into two central intermediates, catechol and protocatechuate (after Fritsche and Hofrichter)

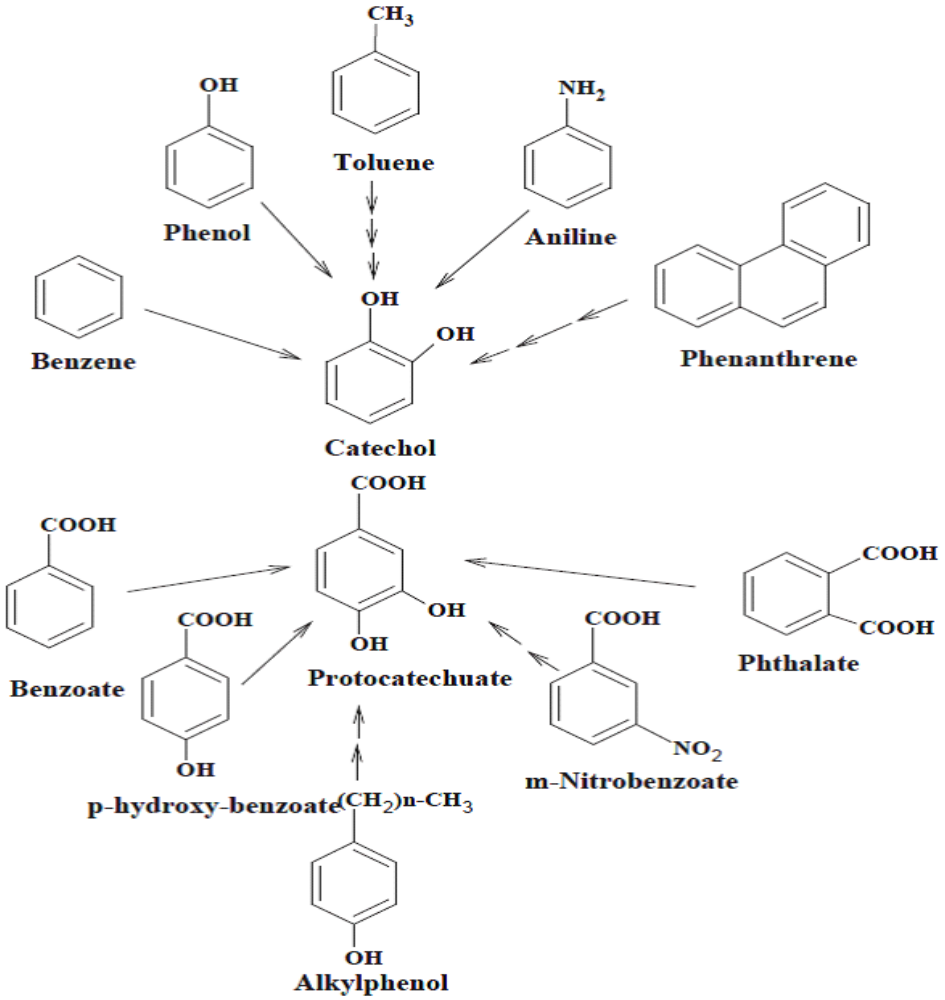

Fig.3 -Microbes mediated attacks on aromatic ring substituents (Gibson and Harwood, 2002)

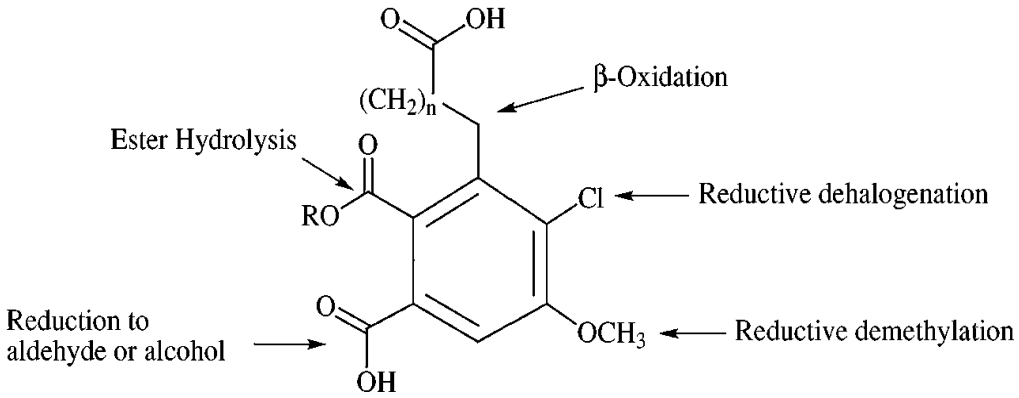

Fig.4 Anaerobic pathways of biodegradation of chlorinated aromatic pentachlorophenol (PCP) (Bryant *et al.*, 1991; Mikesell and Boyd, 1986). The letter o, m, p denotes dechlorination at the o, m, and p positions

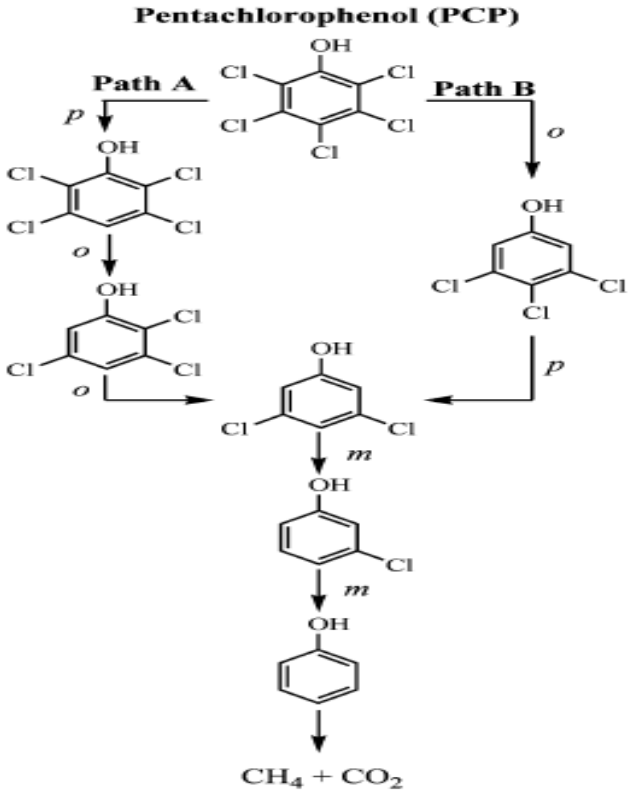

Fig.5 Monooxygenase and dioxygenase reactions: monooxygenase initially incorporates one O atom from O2 into the xenobiotic substrate while other is reduced to H2O and dioxygenase incorporates both O atoms into the substrate (after Fritsche and Hofrichter)

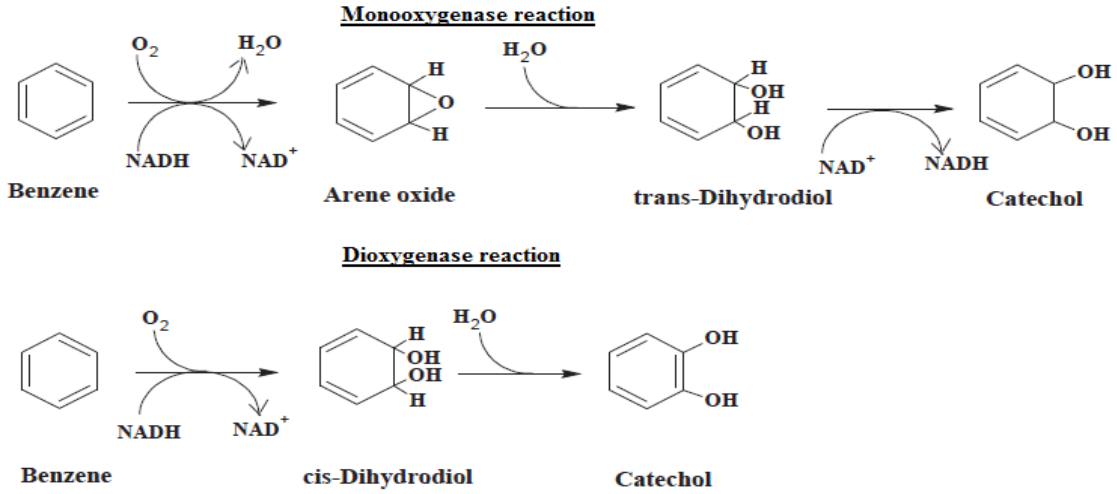

Fig.6 The role of aromatic dioxygenases in the bacterial degradation of aromatic compounds (Que and Ho, 1996, Arora *et al.*, 2009

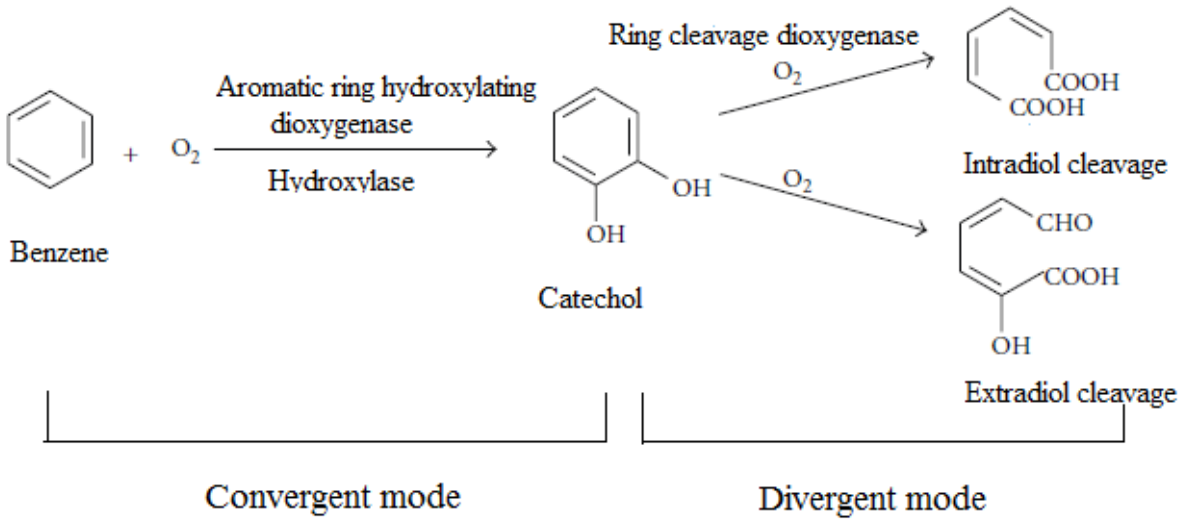

Table.2 List of catabolic genes which perform biotransformation of xenobiotic compounds

Compound	Location	Genes	Source organism	References
HCH	Plasmid	*linF* on pISP0; *linA*, *linC*, and truncated *linF* on pISP1; *linRED* on pISP3; and *linB*, *linC*, and truncated *linF* on pISP4	*Sphingomonas* sp. Strain MM-1	Tabata et al (2013)
PCB	Plasmid pSK4	bphA1,A2,A3,A4,B,C D, H,I,J,K	*Cupriavidus* sp. strain SK-4	Ilori et al (2013)
Pthalate	Plasmid	*phtBAaAbAcAdCR*	*Arthrobacter* sp. 68b	Stanislauskiene et al (2011)
Naphthalene	Chromosome	nar gene cluster (narAa, narAb)	*Rhodococcus opacus* R7	Gennaro et al (2010)
Phenanthrene	Chromosome	PhnZP, PhnZP2	*Sphingomonas*, sp. ZP1 , *Pseudomonas* sp. ZP2	Zhao et al (2011)
Pyrene	Chromosome and plasmid	nidA	*Mycobacterium* sp. strain KMS	(Zhang and Anderson, 2013)
Carbazole	Plasmid	carAcRAaCBaBb	*Kordiimonas Gwangyangensis* OC9	Maeda *et al.*, 2010
Chlorobenzene	Plasmid	*cbs* gene cluster, CbsA and CbsB	*Pandoraea* sp. strain MCB032	Jiang et al (2009)
Benzene, toluene, and xylene (BTX)	Chromosome	pheA, todC1, xylM,	Bacterial consortium used, Sps are *Ralstonia insidiosa, Cellulomonas hominis, Burkholderia kururiensis,* and *Serratia Marcescens*	Ortega-Gonzalez et al (2013)
p-nitrophenol	Plasmid	PnpA, PnpC1C2.	*Pseudomonas putida* DLL-E4	Shen et al (2010b)
2,4-D	Plasmid pKJS32	tfdA, tfdS	*Pseudomonas* and *Ralstonia*	Lipthay et al (1999)
Atrazine	Chromosome	trzN, atzB and atzC	*Arthrobacter* sp. DNS10	Zhang et al (2011b)

Reverse transcription-PCR (RT-PCR) gives us a picture of the metabolically active consortium in the system (Weller and Ward, 1989; Nogales *et al.*, 1999). RT-PCR also useful to study expression of individual structural genes (Widala *et al.*, 2002). The sequencing of cloned RT-PCR amplified product of 16S rRNA used to identify metabolically active bacterial community in soil highly polluted with PCB (Nogales *et al.*, 1999). Differential display (DD),

an RNA-based technique is used to study eukaryotic gene expression; can be optimized to estimate bacterial rRNA diversity (Yakimov *et al.,* 2001). The DD technique can be optimized and directly clone actively expressed genes isolated from soil-extracted RNA (Fleming *et al.,* 1998). Fleming *et al.,* (2001) using this approach successfully to clone a novel salicylate-inducible naphthalene dioxygenase from *Burkholderia cepacia* (Fleming *et al.,* 1998) and identified the bacterial members that are degrading 2, 4, 5- trinitrophenoxyacetic acid. The genetic fingerprinting technique gives us a profile of the genetic diversity in a microbial community. Matrix-assisted laser desorption/ionization time-of flight mass spectrophotometry (MALDI-TOF-MS) is an effective method for analyzing the restriction fragments of PCR-amplified products (Taranenko *et al.,* 2002). Terminal restriction fragment length polymorphism (T-RFLP) analysis helps measure the size polymorphism of terminal restriction fragments from a PCR-amplified marker. Denaturing gradient gel electrophoresis (DGGE) and TGGE (Thermal-GGE) is a potent method to analyze DNA fragments of the same length but different sequence can be resolved electrophoretically (Muyzer, 1999). Denaturing high performance liquid chromatography (DHPLC) can detect single base-pair mutations in a specific sequence (Taliani *et al.,* 2001).

Metagenomic libraries are another powerful approach for the identification of the desired catabolic genes. Mostly metagenomic is a culture dependent genomic analysis; it is either a function or sequence driven approach of total microbial communities, which provides access to find information about unknown sequences (Schloss and Handelsman, 2003). Metagenomic is a sequence-driven approach which is based on conserved regions in the bacterial genome, can also be studied. Certain hybridization probes which are screened out clone libraries for specific DNA sequences can also help to identify the required genes for recalcitrant degradation.

In the past few years, several new techniques have been employed in the study of the biodegradation of xenobiotic compounds. New potential microbes have been isolated with a great capacity to degrade xenobiotics. Novel genes are also identified which encodes catabolic genes responsible for bioremediation of many toxic compounds in a very short period of time. These microbes possess greater ability to overcome the environmental pollution problem.

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